Ecological assessment of the limestone habitat of Vietnam's Critically Endangered primates: *Trachypithecus poliocephalus, Rhinopithecus avunculus, Nomascus nasutus*, and implications for conservation

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Declaration

This thesis contains no material which has been accepted for the award of any other degree or diploma in any university. To the best of the author's knowledge, it contains no material previously published or written by another person, except where due reference is made in the text.

Kirrily Apthorp

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Left: Dr The Van Pham, botanist and researcher at Van Lang University during fieldwork on Cat Ba Island. Right: Dr Vu Anh Tai, botantist from the Department of Bio-Geography, Institute of Geography Vietnamese Academy of Science and Technology, during fieldwork in the CVGCA. Photos: K.Apthorp, 2016.

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Abstract

Non-human primates in Vietnam are facing increasing threats to their survival due to habitat destruction as a result of human expansion and development. As a biodiversity hotspot, Vietnam is home to a high density of non-human primate species, including some of the most Critically Endangered primates in the world. Three of these endangered primates – the cao vit gibbon (*Nomascus nasutus*), the Tonkin snub-nosed monkey (*Rhinopithecus avunculus*) and the Cat Ba langur (*Trachypithecus poliocephalus*) – are under serious threat due to habitat reduction and fragmentation. While occupying different ranges across northern Vietnam, these three species all inhabit limestone karst forest, an understudied and difficult to access habitat. Using a combination of in situ sampling and MaxEnt distribution analysis, this study compared the ecological profiles of each species and compared them to sites of potential habitat expansion to address the habitat fragmentation problem facing each species. Findings suggest that for the Cat Ba langur there may be viable corridor connections to increase connections between sub-populations, though suitability of this region for long-term settlement requires further investigation. Further work on overcoming corridor interruptions is also required. Results for the Tonkin snub-nosed monkey indicate that efforts to improve connections to the larger Du Gia is not recommended due to the high level of human activity is this region, including logging and mining. For the cao vit gibbon, results further support earlier recommendations by Fan et al. (2013) on the conservation prioritisation of an adjacent patch of forest as a potential habitat extension. Further recommendations for the cao vit gibbon include consideration of the introduction of an artificial corridor to supplement a discontinuous corridor between the two regions. Across all species, I recommend further long-term study of each area of potential expansion to further support conservation planning for these at-risk species. This research provides important information for conservation groups to plan for the future of these Critically Endangered species.

List of Abbreviations

BNNR	Bangliang National Nature Reserve
CBL	Cat Ba Langur
CBLCP	Cat Ba Langur Conservation Project
CR	Critically Endangered
CVG	Cao vit gibbon
CVGCA	Cao Vit Gibbon Conservation Area
DD	Data Deficient
DEM	Digital Elevation Model
EN	Endangered
EW	Extinct in the Wild
EX	Extinct
FFI	Fauna and Flora International
GIS	Geographic Information Systems
LC	Least Concern
MaxEnt	Maximum entropy modelling
NDMI	Normalized Difference Moisture Index
NDVI	Normalized Difference Vegetation Index
NMDS	Non-metric multidimensional scaling
NE	Not Evaluated
NT	Near Threatened
SDM	Species distribution modelling
TRI	Topographic Roughness Index
TSNM	Tonkin snub-nosed monkey
VU	Vulnerable

Table of Contents

Declaration iii

Acknowledgements iv

Abstract vii

List of Abbreviations ix

Table of Contents x

List of Tables xxi

List of Figures xxiv

Chapter 1 Introduction 1

1.1 Project introduction 1
1.2 Research aims 4
1.3 Research significance 5
1.3.1 *Trachypithecus poliocephalus* (Cat Ba langur) 6
1.3.2 *Rhinopithecus avunculus* (Tonkin Snub-nosed monkey) 6
1.3.3 *Nomascus nasutus* (cao vit gibbon) 7
1.4 Research limitations 7
1.5 Permissions obtained 9
1.6 Thesis overview 10

Chapter 2 Background 11

2.1 Primate conservation 11
2.1.1 Primate conservation in Vietnam 12
2.2 Vietnamese forests 16
2.2.1 Habitat Fragmentation 21
2.2.2 Corridors 27
2.3 Methods for studying primate habitats 30
2.4 Study habitat type and species 33
2.4.1 Limestone Karst 33
2.4.2 Asian Colobines 36
2.4.2.1 Limestone langurs (Trachypithecus) 37
2.4.2.1.1 *Trachypithecus poliocephalus* (the Cat Ba langur) 39
2.4.2.2 Rhinopithecus (snub-nosed monkeys) 58
2.4.2.2.1 *Rhinopithecus avunculus* (the Tonkin snub-nosed monkey) 60

2.4.3 Hylobatidae 75
2.4.3.1 Nomascus (crested gibbons) 80
2.4.3.1.1 Nomascus nasutus (cao vit gibbon) 84
Part one: *Trachypithecus poliocephalus* (Cat Ba langur) 98
Abstract 98
Chapter 3 A comparison of the two main home ranges of the Cat Ba langur (*Trachypithecus poliocephalus*) 99
3.1 Introduction 99
3.2 Methods 100
3.2.1 Study species and study sites 100
3.2.2 Interviews 103
3.3 Ecological sampling 103
3.4 Data analysis 108
3.4.1 Habitat characteristics 108
3.4.2 Plant species analysis 109
3.4.2.1 Plant species in the habitat of the CBL 109
3.4.2.2 Cat Ba langur food species 111
3.5 Results 111
3.5.1 Interviews 111
3.5.2 Cua Dong Habitat Characteristics 113
3.5.2.1 Generalised linear model, ANOVA and estimated marginal means analysis of Cua Dong 113
3.5.2.2 Cua Dong plant composition 113
3.5.2.2.1 Species abundances across Cua Dong plants 113
3.5.2.2.2 Non-metric multi-dimensional scaling analysis of Cua Dong plants 116
3.5.2.2.3 Cua Dong trees 118
3.5.2.2.4 Food species composition and NMDS in Cua Dong 119
3.5.3 Sanctuary Habitat Characteristics 121
3.5.3.1 Generalised linear model, ANOVA and estimated marginal means analysis of the Sanctuary 121
3.5.3.2 The Sanctuary plant composition 123
3.5.3.2.1 Species abundances across the Sanctuary plants 123
3.5.3.2.2 Non-metric multi-dimensional scaling analysis of Sanctuary plants 125
3.5.3.2.3 Sanctuary trees 126

3.5.3.2.4 Food species composition and NMDS in the Sanctuary 129
3.5.4 Cua Dong and Sanctuary comparison 130
3.5.4.1 Generalised linear model, ANOVA and estimated marginal means analysis of Cua Dong and the Sanctuary 130
3.5.4.2 Plant composition comparison for Cua Dong and the Sanctuary 132
3.5.4.2.1 Species abundances across both Cua Dong and the Sanctuary 132
3.5.4.2.2 Non-metric multi-dimensional scaling analysis (NMDS) of Cua Dong and Sanctuary plants 133
3.5.4.2.3 Trees in Sanctuary and Cua Dong 134
3.5.4.2.4 Food species composition and NMDS in the Sanctuary and Cua Dong 136
3.6 Discussion 138
3.6.1 Cat Ba Langur habitat 138
3.6.2 Food availability 141
3.6.3 Habitat compared to other limestone karst species' habitat 145
3.6.4 Conservation implications 147
3.7 Conclusion 149
Chapter 4 Analysis of the viability of a potential corridor between the two main populations of the Cat Ba langur (*Trachypithecus poliocephalus*) 151
4.1 Introduction 151
4.2 Methods 154
4.2.1 Study site and species 154
4.2.2 Ecological sampling 156
4.2.3 MaxEnt modelling 157
4.2.3.1 Occurrence data 157
4.2.3.1.1 Sampling Bias 158
4.2.3.2 Predictor variables 158
4.2.3.2.1 Pre-processing and datasets 159
4.3 Modelling technique 162
4.3.1 Predictor variable correlation 162
4.3.2 MaxEnt distribution analysis 162
4.4 Data Analysis 163
4.4.1 Habitat characteristics 163
4.4.2 Plant species analysis 164
4.4.2.1 All plant species 164
4.4.2.2 Food species of the CBL 164
4.5 Results 165

4.5.1 VHC ecological profile 165
4.5.1.1 Generalised Linear Model, ANOVA and estimated marginal means analysis of VHC 165
4.5.1.2 VHC Plant Species 166
4.5.1.2.1 Species composition across VHC plots 166
4.5.1.3 Non-metric multi-dimensional scaling analysis of VHC plant communities 168
4.5.1.4 Tree characteristics in VHC 169
4.5.1.5 Food species composition and NMDS in Viet Hai 171
4.5.2 Comparison between VHC and CBL habitats 174
4.5.2.1 Generalised Linear Model, ANOVA and estimated marginal means analysis of the VHC 174
4.5.2.2 VHC, Cua Dong and Sanctuary plant compositions 174
4.5.2.2.1 Species composition 174
4.5.2.2.2 Non-metric multi-dimensional scaling analysis comparison of plant communities in VHC, Cua Dong and the Sanctuary 175
4.5.2.3 Comparison of tree characteristics across VHC, Cua Dong and the Sanctuary 178
4.5.2.4 Food species composition and NMDS comparison across VHC, Cua Dong and the Sanctuary 178
4.5.3 Distribution analysis for Cat Ba langur 180
4.5.3.1 Pearson's correlation of predictor variable results 180
4.5.3.2 MaxEnt modelling results of feature class and regularization multiplier variations 180
4.5.3.3 Top performing model comparison 183
4.5.3.4 Cat Ba langur distribution 183
4.6 Discussion 187
4.6.1 VHC ecology 187
4.6.2 VHC use and wider CBL distribution 190
4.6.3 Other potential factors impacting corridor use 193
4.6.4 Corridor viability 196
4.7 Conclusion 199
Part two: *Rhinopithecus avunculus* (Tonkin snub-nosed monkey) 201
Abstract 201
Chapter 5 A comparison of the habitat of the Tonkin snub-nosed monkey in Khau Ca and Du Gia National Park, Ha Giang Province. 202
5.1 Introduction 202
5.2 Methods 205

5.2.1 Study species 205
5.2.2 Study site 206
5.2.3 Interviews 209
5.2.4 Ecological sampling 209
5.2.4.1 Study limitations 213
5.2.4.1.1 Differences to earlier studies 213
5.2.4.1.2 Corridor and buffer zone sampling 214
5.3 Data analysis 215
5.3.1 Habitat characteristics 215
5.3.2 Plant species analysis 216
5.3.2.1 All plant species 216
5.3.2.2 Food species 216
5.4 Results 217
5.4.1 Interviews 217
5.4.2 Khau Ca habitat characteristics 219
5.4.2.1 Generalised linear model, ANOVA and estimated marginal means analysis of Khau Ca 219
5.4.2.2 Khau Ca Plant species analysis 220
5.4.2.2.1 Plant species composition in Khau Ca 220
5.4.2.2.2 Non-metric multi-dimensional scaling analysis of Khau Ca plants 223
5.4.2.3 Khau Ca Trees and NMDS analysis 225
5.4.2.4 Food species and genera in Khau Ca and NMDS analysis 228
5.4.3 Du Gia habitat characteristics 231
5.4.3.1 Generalised linear model, ANOVA and estimated marginal means analysis of Du Gia 231
5.4.3.2 Du Gia Plant Species analysis 231
5.4.3.2.1 Plant species composition in Du Gia 231
5.4.3.2.2 Non-metric multi-dimensional scaling analysis of Du Gia plants 234
5.4.3.3 Du Gia Trees and NMDS analysis 237
5.4.3.4 Food species and genera in Du Gia and genera NMDS 239
5.4.4 Comparison of Du Gia to Khau Ca 242
5.4.4.1 General linear model, ANOVA and estimated marginal means analysis comparison of Du Gia and Khau Ca 242
5.4.4.2 Plant species comparison of Du Gia and Khau Ca 244
5.4.4.2.1 Species composition comparison 244
5.4.4.3 Food species composition and NMDS comparison between Khau Ca and Du Gia 246
5.5 Discussion 249

5.5.1 Khau Ca habitat 249
5.5.1.1 Composition 249
5.5.1.2 Sleeping sites 251
5.5.1.3 Feeding sites 253
5.5.1.4 Availability of food species 254
5.5.2 Du Gia habitat 256
5.5.2.1 Composition 256
5.5.2.2 Comparison to Khau Ca 257
5.5.2.3 Availability of food species 260
5.5.2.4 Habitat protection and human interaction 263
5.5.3 Corridor 266
5.6 Conclusion 267
Part three: *Nomascus nasutus* (cao vit gibbon) 269
Abstract 269
Chapter 6 Analysis of the Cao Vit Gibbon Conservation Area (CVGCA) habitat of the cao vit gibbon (*Nomascus nasutus*) and potential for expansion. 270
6.1 Introduction 270
6.2 Methods 273
6.2.1 Study site 273
6.2.1.1 Site one: Cao Vit Gibbon Conservation Area 273
6.2.1.2 Site two: Zone IV 276
6.2.2 Study species 278
6.2.3 Interviews 280
6.1.1 Ecological sampling 280
6.3 Data analysis 284
6.3.1 CVG habitat characteristics and potential habitat characteristics 284
6.3.2 Plant species analysis 285
6.3.2.1 Analysis of plant species 285
6.3.2.2 Food species analysis for the CVG 286
6.4 Results 287
6.4.1 Interviews 287
6.4.2 CVGCA habitat characteristics 288
6.4.2.1 Generalised Linear Model, ANOVA and estimated marginal means analysis of the CVGCA 288
6.4.2.2 CVGCA Plant Species 289
6.4.2.2.1 Species composition of plots in CVGCA 289

6.4.2.2.2 Non-metric multi-dimensional scaling analysis of CVGCA plants _ 292
6.4.2.3 Tree characteristics in CVGCA and NMDS analysis _____ 294
6.4.2.4 Food species composition and NMDS across CVGCA plots_____ 297
6.4.3 Zone IV Potential Habitat characteristics _____ 299
6.4.3.1 Generalised Linear Model, ANOVA and estimated marginal means analysis of Zone IV _____ 299
6.4.3.2 Zone IV Plant Species _____ 300
6.4.3.2.1 Species composition of plots in Zone IV _____ 300
6.4.3.2.2 Non-metric multi-dimensional scaling analysis of Zone IV plants 302
6.4.3.3 Tree characteristics in Zone IV and NMDS analysis_____ 303
6.4.3.4 Food species composition and NMDS analysis across Zone IV _____ 306
6.4.4 CVGCA habitat and Zone IV potential habitat comparison _____ 309
6.4.4.1 Generalised Linear Model, ANOVA and estimated marginal means analysis of CVGCA and Zone IV comparison _____ 309
6.4.4.2 Plant species comparisons _____ 310
6.4.4.2.1 Species composition comparison of CVGCA and Zone IV _____ 310
6.4.4.3 Non-metric multi-dimensional scaling analysis comparison of CVGCA and Zone IV _____ 310
6.4.4.4 Tree comparison between sites _____ 313
6.4.4.5 Food species composition and NMDS comparison between the CVGCA and Zone IV _____ 314
6.4.5 CVGCA, Corridor and Zone IV Potential habitat comparison _____ 317
6.4.5.1 Vegetation of Corridor area _____ 317
6.4.5.2 Comparison of tree characteristics in the Corridor, CVGCA and Zone IV ___ 319
6.4.5.3 Diet species in corridor _____ 320
6.5 Discussion_____ 320
6.5.1 CVGCA habitat _____ 320
6.5.1.1 Composition and historical use _____ 320
6.5.1.2 CVGCA sleeping trees and canopy _____ 322
6.5.1.3 Food species in CVGCA _____ 323
6.5.2 Zone IV potential habitat _____ 327
6.5.2.1 Composition and current use _____ 327
6.5.2.2 Tree characteristics within Zone IV _____ 329
6.5.2.3 Food species in Zone IV _____ 331
6.5.3 Corridor connection _____ 333
6.6 Conclusion _____ 336
Chapter 7 MaxEnt modelling of cao vit gibbon distribution _____ 339
7.1 Introduction _____ 339

7.2 Methods 342
7.2.1 Study site and species 342
7.2.2 Occurrence data 345
7.2.2.1 Sampling bias 346
7.2.2.2 Study limitations 347
7.2.3 Predictor variables 348
7.2.3.1 Pre-processing and datasets 348
7.2.3.2 Limitations 349
7.2.4 MaxEnt modelling technique 351
7.2.4.1 Predictor variable correlation for CVG variables 351
7.2.4.2 MaxEnt distribution analysis settings for the CVG 351
7.3 Results 352
7.3.1 Pearson's correlation of predictor variable results 352
7.3.2 MaxEnt modelling results 352
7.3.3 Top performing model comparison for the CVG 354
7.3.4 Distribution 355
7.4 Discussion 360
7.4.1 Model design for the CVG distribution 360
7.4.2 Potential distribution of the CVG 360
7.4.2.1 Contribution of predictor variables to the distribution of the CVG 363
7.5 Conclusion 366
Chapter 8 Conclusion 369
8.1 Key findings on current habitat fragments 369
8.1.1 Limestone karst as a refuge or preference? 373
8.2 Corridor connections and areas for potential habitat expansion 374
8.2.1 Cat Ba langur 376
8.2.2 Tonkin snub-nosed monkey 376
8.2.3 Cao vit gibbon 378
8.3 Conservation Engagement 379
8.4 Conservation recommendations 382
8.4.1 Cross-site recommendations 382
8.4.2 Cat Ba langur 384
8.4.3 Tonkin snub-nosed monkey 384
8.4.4 Cao vit gibbon 385
8.5 Significance 386
References 389

Appendix 445

Appendix 1 Methods 445

1.1 Interview script and questions 445

1.2 Vegetation layer definitions and visual representation 446

1.3 General vegetation density scale 448

1.4 Topographic density scale 450

Appendix 2 Cat Ba langur 452

2.1 ANOVA analysis and Estimated marginal means result tables for Cat Ba langur (CBL) habitat on Cat Ba Island 452

2.1.1 Summary data tables for Cua Dong, the Sanctuary and Viet Hai Corridor ANOVA analyses 452

2.1.2 ANOVA analysis results table for Cua Dong habitat 455

2.1.3 Estimated marginal means results table for Cua Dong habitat 456

2.1.4 ANOVA analysis results table for the Sanctuary habitat 457

2.1.5 Estimated marginal means results table for the Sanctuary 458

2.1.6 ANOVA analysis results table of comparison between Cua Dong and the Sanctuary 459

2.1.7 Estimated marginal means results table for the comparison between Cua Dong and the Sanctuary 460

2.1.8 ANOVA analysis results table of Viet Hai corridor 461

2.1.9 Estimated marginal means results table for the Viet Hai Corridor 462

2.1.10 ANOVA analysis results table of comparison between Cua Dong and the Sanctuary and Viet Hai corridor 463

2.1.11 Estimated marginal means results table for the comparison between the Viet Hai Corridor, Cua Dong and the Sanctuary 464

2.2 Plant species captured in Cat Ba langur analysis 465

2.2.1 All species captured in both Cua Dong and the Sanctuary 465

2.2.2 Tree species captured in Cua Dong and the Sanctuary 477

2.2.3 All species captured in the Viet Hai corridor 480

2.2.4 Tree species captured in the Viet Hai corridor 487

2.2.5 Food species identified in Cua Dong, the Sanctuary and Viet Hai 489

2.3 Results for MaxEnt analysis for the Cat Ba langur 491

2.3.1 Predictor variables for Cat Ba langur distribution 491

2.3.2 Pearson's correlation of variables for Cat Ba langur MaxEnt analysis 493

2.3.3 MaxEnt model results 494

2.3.3.1 Results of models with feature class and regularisation multiplier variations 494

2.3.3.2 Top performing model comparison for Cat Ba langur distribution modelling 496
2.3.3.3 Response curves of predictor variables for top performing model for Cat Ba langur distribution 497

Appendix 3 Tonkin snub-nosed monkey 500

3.1 ANOVA analysis tables for Tonkin snub-nosed monkey (TSNM) habitat 500
3.1.1 Summary data tables for Khau Ca and Du Gia ANOVA analyses 500
3.1.2 ANOVA analysis results table for Khau Ca habitat 503
3.1.3 Estimated marginal means results table for Khau Ca 504
3.1.4 ANOVA analysis results table for Du Gia forest 505
3.1.5 Estimated marginal means results table for Du Gia 506
3.1.6 ANOVA analysis results table of comparison between Khau Ca and Du Gia 507
3.1.7 Estimated marginal means results table for comparison of Khau Ca and Du Gia 508
3.2 Plant species captured in Tonkin snub-nosed monkey analysis 509
3.2.1 All species captured in Du Gia and Khau Ca 509
3.2.2 Tree species captured in Du Gia and Khau Ca 520
3.3 Food species for the Tonkin snub-nosed monkey 525
3.3.1 Food species identified in previous studies 525
3.3.2 Food genera identified in Khau Ca and Du Gia 529

Appendix 4 Cao vit gibbon 531

4.1 ANOVA Analysis tables for cao vit gibbon (CVG) habitat 531
4.1.1 Summary data tables for CVGCA and Zone IV ANOVA analyses 531
4.1.1.1 CVGCA and Zone IV analyses 531
4.1.1.2 CVGCA, Zone IV and the Corridor transects for tree analysis 533
4.1.2 ANOVA analysis results table for CVGCA area 534
4.1.3 Estimated marginal means results table for CVGCA 535
4.1.4 ANOVA analysis results table for Zone IV Potential Habitat 536
4.1.5 Estimated marginal means results table for Zone IV 537
4.1.6 ANOVA analysis results table for comparison between CVGCA and Zone IV Potential habitat 538
4.1.7 Estimated marginal means results table for comparison of CVGCA and Zone IV 539
4.1.8 ANOVA analysis results table for comparison between CVGCA, Zone IV and Corridor habitat 540
4.1.9 Estimated marginal means results table for comparison between CVGCA, Zone IV and the Corridor 541
4.2 Plant species captured in cao vit habitat 542
4.2.1 All species captured in both CVGCA and Zone IV potential habitat across both plots and transects 542

4.2.2 All species captured in the corridor area transects ____ 553
4.2.3 Tree species captured in both CVGCA and Zone IV potential habitat across both plots and transects ____ 557
4.2.4 Tree species captured in the Corridor, CVGCA and Zone IV transects only ____ 563
4.3 Food species for the cao vit gibbon ____ 566
4.3.1 Food species identified in previous studies ____ 566
4.3.2 Food species identified in CVGCA, Zone IV and the corridor ____ 569
4.4 Results for MaxEnt analysis for the cao vit gibbon ____ 570
4.4.1 Predictor variables for cao vit gibbon distribution ____ 570
4.4.2 Pearson's correlation of variables for cao vit gibbon MaxEnt analysis ____ 573
4.4.3 MaxEnt model results ____ 574
4.4.3.1 Results of models with feature class and regularisation multiplier variations ____ 574
4.4.3.2 Top performing model comparison for cao vit gibbon ____ 576
4.4.3.3 Response curves of predictor variables for top performing model for cao vit gibbon distribution ____ 577

List of Tables

Table 2.1 Primates found in Vietnam and their IUCN Red List status _____ 15
Table 2.2 Member species of the limestone langurs _____ 38
Table 2.3 Members of the snub-nosed family genus Rhinopithecus _____ 59
Table 2.4 Tonkin snub-nosed monkey sites _____ 62
Table 2.5 Primates inhabiting Khau Ca _____ 69
Table 2.6 Members of the crested gibbons _____ 82
Table 2.7 Primate species found within the CVG habitat in CVGCA and BNNR _____ 94
Table 3.1 Average temperature, rainfall and humidity on Cat Ba Island during data collection _____ 102
Table 3.2 Vegetation stratum types identified in the Cat Ba langur habitat _____ 106
Table 3.3 Demographics of interviewees from communes across Cat Ba Island _____ 111
Table 3.4 Top ten species across Cua Dong plots _____ 114
Table 3.5 Top ten species found in Cua Dong valley plots _____ 114
Table 3.6 Top ten species found in Cua Dong coast plots _____ 115
Table 3.7 Top ten species in Cua Dong found in slope plots _____ 115
Table 3.8 Top ten tree species in Cua Dong _____ 118
Table 3.9 Top ten food species found in Cua Dong _____ 120
Table 3.10 Top ten species found in the Sanctuary plots _____ 123
Table 3.11 Top ten species found in Sanctuary valley plots _____ 124
Table 3.12 Top ten species found in Sanctuary coastal plots _____ 124
Table 3.13 Top ten species found in Sanctuary slope plots _____ 125
Table 3.14 Top ten tree species across the Sanctuary plots _____ 126
Table 3.15 Top ten food species in Sanctuary plots _____ 129
Table 3.16 Top ten species shared in Cua Dong and the Sanctuary _____ 132
Table 3.17 Top ten tree species in the Sanctuary and Cua Dong _____ 134
Table 3.18 Top ten food species in Cua Dong and the Sanctuary _____ 136
Table 3.19 Number of food species consumed by Asian langurs _____ 145
Table 4.1 Top ten species found in Viet Hai corridor _____ 166
Table 4.2 Top ten species found in Viet Hai valley plots _____ 167
Table 4.3 Top ten species found in Viet Hai coastal plots _____ 167

Table 4.4 Top ten species found in Viet Hai slope plots 168
Table 4.5 Top ten food species in VHC plots 172
Table 4.6 Top ten species shared across Viet Hai, Cua Dong, and the Sanctuary 175
Table 4.7 Top ten tree species shared across all three sites 178
Table 4.8 Top ten food species shared across all three sites 179
Table 5.1 Average temperature, rainfall and humidity in Ha Giang during data collection 209
Table 5.2 Vegetation stratum types identified in the TSNM habitat 211
Table 5.3 Demographics of interviewees from communes surrounding Khau Ca 218
Table 5.4 Top ten species found in Khau Ca plots 221
Table 5.5 Top ten species identified within Khau Ca ridge plots 221
Table 5.6 Top ten species identified within Khau Ca slope plots 222
Table 5.7 Top ten species identified within Khau Ca valley plots 222
Table 5.8 Top ten tree species identified within Khau Ca plots 225
Table 5.9 TSNM food species captured in Khau Ca plots 228
Table 5.10 Top ten food genera for TSNM in Khau Ca plots 229
Table 5.13 Top ten species found in Du Gia plots 232
Table 5.14 Top ten species identified within Du Gia ridge plots 232
Table 5.15 Top ten species identified within Du Gia slope plots 233
Table 5.16 Top ten species identified within Du Gia valley plots 234
Table 5.17 Top ten species of tree identified within Du Gia plots 237
Table 5.18 Food species captured in Du Gia 239
Table 5.19 Top ten food genera identified in Du Gia plots 241
Table 5.20 Top ten shared species between Du Gia and Khau Ca 245
Table 5.21 Key food species captured in this study 255
Table 5.22 Food species found in Khau Ca and Du Gia 260
Table 5.23 Top ten food genera captured across Du Gia and Khau Ca 261
Table 6.1 Habitat types sampled for plots and transects 283
Table 6.2 Average temperature, rainfall and humidity in Cao Bang city during data collection 284
Table 6.3 Demographics of interviewees from communes surrounding CVGCA 287
Table 6.4 The top ten species across CVGCA 289

Table 6.5 Top 10 species identified within CVGCA valleys _____ 290
Table 6.6 Top 10 species identified within CVGCA slopes _____ 291
Table 6.7 Top 10 species identified within CVGCA ridges _____ 291
Table 6.8 The top ten species across Zone IV potential habitat _____ 300
Table 6.9 Top ten species found in valleys in Zone IV potential habitat _____ 301
Table 6.10 Top ten slope species in Zone IV potential habitat _____ 301
Table 6.11 Top ten ridge species in Zone IV potential habitat _____ 302
Table 6.12 Top ten shared species in CVGCA and Zone IV _____ 310
Table 6.13 Top ten tree species shared by CVGCA and Zone IV sites _____ 313
Table 6.14 Food species captured within CVGCA and Zone IV _____ 316
Table 6.15 Top ten species in Corridor transects _____ 319
Table 6.16 Food species captured in corridor transects _____ 320
Table 7.1 Input predictor variables for CVG MaxEnt modelling _____ 350

List of Figures

Figure 2.1 Examples of Limestone karst landscapes 34
Figure 2.2 Location of Cat Ba Island, Hai Phong, Vietnam 41
Figure 2.3 The Cat Ba langur (Trachypithecus poliocephalus) colouring 42
Figure 2.4 Cat Ba Island, Hai Phong 44
Figure 2.5 Goats on Cat Ba Island 47
Figure 2.6 Floating village adjacent to langur home range 51
Figure 2.7 Fisherman collecting fishing cages and bivalves below CBL sleeping sites 52
Figure 2.8 Rubbish from marine waterways along coast of the CBL habitat 53
Figure 2.9 Evidence of illegal activity in the CBL habitat 58
Figure 2.10 Locations of Tonkin snub-nosed monkey habitats 61
Figure 2.11 Tonkin snub-nosed monkey (Rhinopithecus avunculus) 63
Figure 2.12 Location of Khau Ca and Du Gia National Park in Vietnam 66
Figure 2.13 Surrounding landscape beyond Khau Ca limits 67
Figure 2.14 Location of the cao vit gibbon within the CVGCA and BNNR 85
Figure 2.15 Colouring of the cao vit gibbon 86
Figure 3.1 Map of main CBL populations 101
Figure 3.2 Location of plots placed in Cua Dong and the Sanctuary habitats 104
Figure 3.3 NMDS of species within Cua Dong plots 117
Figure 3.4 Tree metrics across plots in Cua Dong 119
Figure 3.5 NMDS of food species in Cua Dong plots 122
Figure 3.6 NMDS of plants within the Sanctuary 127
Figure 3.7 The DBH and canopy height distribution of trees across Sanctuary plots 128
Figure 3.8 NMDS of food species within Sanctuary plots 131
Figure 3.9 NMDS of species in Cua Dong and the Sanctuary 135
Figure 3.10 NMDS of food species in the Sanctuary and Cua Dong 137
Figure 3.11 Evidence of Human Activity in Cua Dong 142
Figure 4.1 Map of main CBL populations and potential corridor 155
Figure 4.2 Location of plots placed within the VHC 156
Figure 4.3 NMDS of plants within the VHC 170
Figure 4.4 Distribution of tree canopy heights and DBH in VHC plots 171

Figure 4.5 NMDS of food species in VHC plots 173
Figure 4.6 NMDS of all species across VHC, Cua Dong, and the Sanctuary 177
Figure 4.7 NMDS of food species across VHC, Cua Dong, and the Sanctuary 181
Figure 4.8 Median summary of CBL distribution across Cat Ba Island 185
Figure 4.9 Potential distribution of the CBL at 90 per cent and 60 per cent habitat suitability 186
Figure 5.1 Satellite image of the boundary of the Du Gia National Park (yellow) with Khau Ca (red) within 204
Figure 5.2 Map of Khau Ca as part of Du Gia National Park 206
Figure 5.3 Regeneration of Khau Ca and surrounding farmland 207
Figure 5.4 Location of plots within Khau Ca and Du Gia 210
Figure 5.5 Example of farmland within the corridor between Khau Ca and Du Gia 215
Figure 5.6 NMDS of plants in Khau Ca 224
Figure 5.7 Tree metrics across plots in Khau Ca plots 226
Figure 5.8 NMDS of trees in Khau Ca with 0.95 confidence ellipses 227
Figure 5.9 NMDS of diet genera within Khau Ca plots 230
Figure 5.10 NMDS of plants within Du Gia species 236
Figure 5.11 Du Gia tree DBH and height distributions 238
Figure 5.12 NMDS of trees in Du Gia plots 240
Figure 5.13 NMDS of food genera identified in Du Gia plots 243
Figure 5.14 NMDS of plant species identified across Du Gia and Khau Ca 247
Figure 5.15 NMDS of food genera identified in Du Gia and Khau Ca plots 248
Figure 5.16 Plot types in Du Gia 257
Figure 5.17 Evidence of logging in Minh Son 264
Figure 5.18 Land-use map showing high level of disturbance around Khau Ca and Du Gia 266
Figure 6.1 Boundaries of the CVGCA and BNNR protected zones 274
Figure 6.2 Terrain of the CVGCA 274
Figure 6.3 Boundaries of CVG protected zones 275
Figure 6.4 Base camp in CVGCA 276
Figure 6.5 Map of potential habitat expansion for the CVG in Zone IV 277
Figure 6.6 Limestone karst and topography of Zone IV and surrounding farmland 278

Figure 6.7 Corridor belt along Vietnamese and Chinese International border _____279
Figure 6.8 Location of plots across CVGCA, Zone IV and corridor _____281
Figure 6.9 NMDS of plants in CVGCA _____293
Figure 6.10 Tree metrics across plots and transects in CVGCA _____294
Figure 6.11 NMDS of trees in CVGCA _____296
Figure 6.12 NMDS of food species in CVGCA _____298
Figure 6.13 NMDS of all species in Zone IV _____304
Figure 6.14 Tree DBH and canopy height distribution in Zone IV _____305
Figure 6.15 NMDS of trees in Zone IV _____307
Figure 6.16 NMDS of food species in Zone IV _____308
Figure 6.17 NMDS of CVGCA and Zone IV sites _____312
Figure 6.18 NMDS of tree species in CVGCA and Zone IV _____315
Figure 6.19 NMDS of food species in CVGCA and Zone IV _____318
Figure 6.20 Evidence of tree cutting in two Zone IV valleys _____328
Figure 6.21 Small trap found in forest of Zone IV _____328
Figure 7.1 Map of the current extent of the CVG protected zones _____343
Figure 7.2 River bounding CVGCA and forest fragments on limestone karst slopes and peaks to the southwest of the CVGCA _____343
Figure 7.3 Border crossing separating the CVGCA and adjacent forest fragments _____344
Figure 7.4 Areas of conservation priority identified by Fan et al. 2013 _____345
Figure 7.5 Median model summary projected onto the study area _____356
Figure 7.6 Distribution of suitable habitat with a probability of 90% or greater _____358
Figure 7.7 Distribution of suitable habitat with a probability of 60% or greater _____359
Figure 7.8 Location of additional ecological sampling within Zone IV _____363

Chapter 1 Introduction

1.1 Project introduction

Around the world, non-human primates (from here on primates) are under increasing pressure from a growing human population (Estrada et al., 2017; Nadler, 2007). A majority of the world's primates inhabit tropical forest contained within countries undergoing major development, making anthropogenic pressure the number one threat to the health and future of primates around the world (Gouveia, Villalobos, Dobrovolski, Beltrao-Mendes, & Ferrari, 2014; Isabirye-Basuta & Lwanga, 2008; Marsh, 2003a; Xiao, Ding, Cui, Zhou, & Zhao, 2003). Increasing urban sprawl, land conversion for development, agricultural land or for industrial uses, a rise in the exploitation of natural resources and lagging conservation policies have all had serious impacts on primate populations (Blair, Sterling, & Hurley, 2011; Nadler, 2007). As a result, habitat loss as a result of human intervention, be it direct or through climate change, is now the most critical threat to primates (Ni et al., 2018; Russon & Wallis, 2014), the effects of which have the potential to cause mass extinctions and permanently alter landscapes and ecosystems

While African primates such as Great Apes attract large amounts of research and public attention, Asian primates are less well studied despite the high density of species found throughout Southeast Asia (Blair et al., 2011; Nadler & Streicher, 2004). This is particularly the case with Vietnamese primates, where detailed research only began in earnest from the 1990s as Vietnam became more accessible to researchers (Nadler, Thanh, & Streicher, 2007). Whilst our collective knowledge of Vietnamese primates is increasing, it has not occurred at a rate sufficient to offset the rapidly increasing threats to their survival (Blair et al., 2011; Nadler et al., 2007). Further impeding some of these efforts is that as our collective understanding grows, so does our knowledge of the taxonomic intricacies of Southeast Asian primates, often leading to the discovery of new species requiring their own detailed study. In the last decade, taxonomic revisions and new discoveries a have seen at least 10 new Southeast Asian species described (*Hoolock tianxing*: Fan et al., 2017; *Rhinopithecus strykeri*: Geissmann et al., 2011; *Macaca leucogenys*: C. Li, Zhao, & Fan, 2015; *Nycticebus kayan*: Munds, Nekaris, & Ford, 2013; *Pongo tapanuliensis*: Nater et al., 2017; *Trachypithecus phayrei*: Roos et al., 2020; *Tarsius*

spectrumgurskyae and Tarsius supriatnai: Shekelle, Groves, Maryanto, & Mittermeier, 2017; *Tarsius niemitzi*: Shekelle, Groves, Mittermeier, Salim, & Springer, 2019; *Nomascus annamensis*: Thinh, Mootnick, Thanh, Nadler, & Roos, 2010).

As part of the Indo-Burmese biodiversity hotspot, Vietnam has some of the highest levels of endemic primate taxa in the world and some of the most threatened (Blair et al., 2011; Catullo et al., 2008; Nadler & Streicher, 2004; B. T. Nguyen, 2004; Sodhi, Koh, Brook, & Ng, 2004). These high levels of primate diversity occur in one of the most densely populated regions in Southeast Asia and of any biodiversity hotspot (Eames & Robson, 1993; Nadler et al., 2007). It is unsurprising then that while Vietnam is home to 25 species of primates, 12 are considered critically endangered (Quyet, 2014; Nadler & Streicher, 2004). The high levels of biodiversity in Vietnam mean that each species has evolved to cover a huge variety of physical, social and ecological niches. This variation makes the study of Vietnamese primates difficult as we seek to understand and protect the diverse array of speciation that has occurred. For species endemic to Vietnam, any failure in conservation efforts due to poor knowledge of their ecological requirements has the potential to be catastrophic. These species, which are found nowhere else in the world, must be prioritised for conservation.

Encapsulating this niche specialisation and need for prioritisation are three of the most critically endangered primates in the world: *Trachypithecus poliocephalus* (Cat Ba langur), *Rhinopithecus avunculus* (Tonkin snub-nosed monkey) and *Nomascus nasutus* (cao vit gibbon). All three species are listed as Critically Endangered by the International Union for Conservation of Nature (IUCN, 2019) and are at threat of extinction in the wild. As none of these species have significant captive populations their disappearance in the wild would signal their global extinction.

While each species has evolved their own specific ecological niche, all three of these primates are experiencing similar pressures from anthropogenic threats particularly that of population fragmentation due to high rates of habitat fragmentation, degradation and destruction (Isabirye-Basuta & Lwanga, 2008; Nadler & Streicher, 2004). These threats exacerbate the effects of other threats including poaching and resource depletion, resulting in increasingly dire forecasts for their ongoing survival. For these species, the ongoing risk of extinction is

further compounded due to their highly restricted geographic ranges, thereby limiting their ability to escape additional threats as their habitats continue to shrink (Estrada et al., 2017; Quyet, 2014).

Despite the taxonomic, social, behavioural and physical differences of the Cat Ba langur (CBL), Tonkin snub-nosed monkey (TSNM) and cao vit gibbon (CVG), all three inhabit geographically distinct patches of limestone karst forest in Northern Vietnam. Limestone karst occurs in a large band across northern Vietnam and southern China and is characterised by steep sheer cliffs, rocky outcrops and collapsed valleys (P.-F. Fan, Fei, Scott, Zhang, & Ma, 2011; Li & Rogers, 2005a). It is also characterised by high levels of endemism, however due to the difficulty in accessing the harsh terrain, it is typically understudied and the species inhabiting it are poorly understood (Blair et al., 2011; Workman, 2010).

As limestone karst forest is topographically difficult to access, local ongoing human intervention is restricted to incursions into the forest valleys and parts of the valley slopes for hunting, resource collection, ad hoc logging and cattle grazing. These interventions have had serious local impacts on all three species to some degree, leaving their habitat fragmented and degraded (Sodhi et al., 2004). On a landscape scale, the habitat of each species represents an island of forest in predominately agricultural or urbanised landscapes, isolating them from larger forest stretches that might offer the opportunity for individual species' growth.

The CBL, TSNM and CVG each have their own history of study and conservation efforts; however, our collective understanding of their habitats is alarmingly limited considering the very real threat of extinction they currently face. Understanding their habitat and habitat preferences is critical to enable meaningful planning for their conservation and long-term survival (Pyritz, Buntge, Herzog, & Kessler, 2010).

In order to overcome this lack of information, this dissertation will investigate the habitat profile and usage of the CBL, TSNM and the CVG, and the implications that information may have for the ongoing conservation of each species. This research will also include a multidisciplinary approach to undertaking habitat studies of primates, employing both ecological sampling and where appropriate, maximum entropy distribution modelling.- This study will provide the first habitat datasets on the CBL, and expand upon older datasets for

the TSNM and CVG by considering new regions for potential habitat expansion. In doing so, this study will be critical to increasing our understanding of three critically endangered primates and assist in making well-informed conservation planning for their futures.

1.2 Research aims

This thesis aims to further the understanding and conservation of the limestone-karst dwelling species the CBL, the TSNM and the CVG, by undertaking ecological analyses of their distinct habitats. Using qualitative interview techniques to capture local knowledge of the distribution of the species, traditional in situ ecological sampling, linear generalised linear modelling of vegetation characteristics, non-metric multidimensional scaling (NMDS) ordination analyses of plant and food species communities, and maximum entropy modelling of their distribution, the outcomes of this research will assist in improving conservation planning for the future of each of these Critically Endangered species. Several questions were posed to address the aims of this study:

Qualitative: interviews, historical records.

1. What is the historical distribution of each species?
    a. How has this changed over time?
    b. Has the composition of the habitat changed over this time?
    c. How has the human-use of the forest changed over time?

Quantitative: ecological sampling and statistical modelling, distribution modelling.

1. What is the current habitat profile of each species?
    a. What are the topographic and vegetation characteristics of each habitat?
    b. What is the distribution of plant and diet species across their habitats?
2. Are there potential areas for range expansion, or habitat corridors to be identified?
    a. How do these areas compare to the current habitat of the species?
3. Are there areas that could be improved for future use?

   a. Are connections required to ensure access by the primates?

4. What are the main risks to the habitat at each site?

   a. How are these being currently addressed?

1.3 Research significance

Perhaps the greatest threat to primate species today is the loss of their natural habitat (Russon & Wallis, 2014). For many threatened species, the loss of their habitat will be catastrophic and result in their extinction - yet our knowledge of many species' habitats is limited. A majority of the world's primate species live within tropical forests, making these areas important for study and conservation, yet so far, the uptake of specific ecological research is lacking (Isabirye-Basuta & Lwanga, 2008; Wei Wang, Ren, He, & Zhu, 2008). Primates are believed to play an important role in the health of their habitats as seed dispersers (C.A. Chapman & C.A. Peres, 2001); and the loss of individual species could seriously impact both the survival of their local ecosystems and catalyse the collapse of tropical forest ecosystems around the world. With forests around the world experiencing degradation, fragmentation and in the worst cases, complete destruction, it is essential that we work to understand the relationship of these forests with the primates that rely on them (Chapman & Peres, 2001; Isabirye-Basuta & Lwanga, 2008).

The small, fragmented, and isolated populations of the CBL, TSNM and CVG, leave them at serious risk of going extinct in the wild. Despite targeted conservation efforts for each of these three species, we still have an alarmingly scarce understanding of t their habitats (Y. Zeng, Xu, Wang, & Zhou, 2013).

By understanding the habitat profiles of primates and the current state of their habitat, it may be possible to identify key areas for protection and halt the ongoing loss of important primate ecosystems. This dissertation aims to offer insights into the habitats and potential distribution of the CBL, TSNM and CVG, and start to fill some of the critical gaps in our understanding of these at-risk primates.

1.3.1 *Trachypithecus poliocephalus* (Cat Ba langur)

The CBL, the most at risk of the three species, has an estimated global wild population of 65 individuals. An additional six individuals are currently housed at the Endangered Primate Rescue Centre in Cuc Phuong National Park however these individuals are not fit for release or for breeding purposes within the centre.

Since dedicated conservation efforts began on Cat Ba Island in 2010, education programs have highlighted the importance of the species to the local community (Schrudde, Levelink, & Raffel, 2010). Our scientific knowledge of the species, however, is very limited. Only a small number of major studies of the langurs have focussed on their socio-ecology and behaviour (Hendershott, 2017; Hendershott, Behie, & Rawson, 2016; Lees, Rawson, Behie, Hendershott, & Leonard, 2014; Luan, 2013) and diet (K. Ruskin, unpublished, 2016); yet no extensive studies have been carried out on the ecology and habitat of these endangered primates. These studies have also only focussed on the main study population, situated close to a popular tourist area and a high-traffic waterway. Until the commencement of this study, no research has been carried out on the second larger population within an area protected from human access.

This dissertation provides insight into the habitat of both main breeding groups, offering a fuller picture of the habitat preferences of the CBL. It also provides an assessment of the potential suitability of a vegetation corridor to connect the two groups. This information when combined with our behavioural and dietary knowledge of the langurs, can assist with meaningful conservation planning to work towards securing the CBL population from extinction.

1.3.2 *Rhinopithecus avunculus* (Tonkin Snub-nosed monkey)

The TSNM, once thought to be extinct, now has a population of approximately 200 (C. Schwitzer et al., 2014; C. Schwitzer, Mittermeier, R.A., Rylands, A.B., Chiozza, F., Williamson, E.A., Byler, D., Wich, S., Humle, T., Johnson, C., Mynott, H., and McCabe, G., 2019) and is fragmented across several forest patches in northern Vietnam. The biggest population in Khau Ca, Ha Giang, currently inhabits an island of limestone karst forest surrounded by farms and urban areas. Several studies have been conducted on the TSNM focussing on the locomotion, diet, conservation, and including some ecology surveys. This dissertation offers a

multidisciplinary approach to the study of the TSNM's habitat and provides a more recent dataset by which to compare older studies, allowing us to track the status of their forest patch. In addition, this dissertation provides an analysis of the suitability of plans to connect the TSNM current pocket of forest to a larger, less secure forest region. The results of this dissertation may assist in future conservation decisions and National Park policies.

1.3.3 *Nomascus nasutus* (cao vit gibbon)

Like the TSNM, the CVG was thought to be extinct until its rediscovery in Vietnam in 2002 (Geissmann et al., 2003) across the border in China in 2006 (Chan, Tan, & Tan, 2008; Insua-Cao et al., 2012). Today, the population is estimated at 135 individuals, inhabiting a patch of limestone karst forest straddling the Vietnamese-Chinese border. The Vietnam CVG habitat is currently enclosed on three sides by farmland and rural areas, including some small farm patches within the CVG habitat. This dissertation will build on earlier work on the potential distribution of the CVG undertaken by Fan et al. (2011) and Fan et al. (2013) and further increase our understanding of the habitat of the CVG and identify areas for potential expansion.

By using both traditional in situ ecological sampling and geographic information systems (GIS) to support MaxEnt species distribution modelling, this study will also offer insights into the benefit of a multidisciplinary approach to studying primates in poorly accessible regions. By understanding the similar yet individual ways the CBL, TSNM and CVG are experiencing habitat fragmentation, this dissertation will contribute to our collective knowledge of these primates beyond the current behavioural data, allow a clearer understanding of their relationship to the poorly studied limestone karst, and contribute to meaningful conservation planning for their futures.

1.4 Research limitations

While every effort was made to collect as much detailed data as possible, there were some limitations that constrained the scope of this study.

A major limitation of this study was a lack of accurate, detailed maps of the conservation sites. This meant that a full understanding of the surrounding region was difficult to establish and

may have limited where in situ sampling occurred. This was a particular issue when sampling the habitat of the TSNM, where maps of the protected habitat and surrounding landscape were difficult to access, and those available were often inaccurate and out of date. This meant that preselected comparison sites in some cases were found to no longer exist, requiring changes to the approach at each site. In each case where changes were made, back up sites were chosen to create meaningful and useful comparisons.

None of the species covered in this study were habituated, which is preferable due to the impact that familiarisation with humans can have, particularly on species at risk of poaching (Workman, 2010). As a result, in some cases it was difficult to gain accurate GPS location data for each species. In the case of the CBL, observations are primarily obtained from a boat, thereby creating a superficial bias towards coastal observations within the MaxEnt modelling. While efforts were made to account for this bias, due to the small scale of their available habitat, such a bias will unavoidably impact the final distribution model.

In the case of the CVG, exact GPS coordinates can be difficult to obtain. Due to the steep terrain of their habitat, exact GPS locations of the gibbons are very rare and instead the method of location triangulation is generally used to extrapolate their approximate positions (Warren Y Brockelman & Ali, 1987; B. M. Rawson, 2010). Despite these limitations, I believe that any information as preliminary as presented here, is useful and informative for species with very little habitat information available in order to assist in conservation planning.

To overcome ecological sampling bias, stratified randomised ecological plotting within each species' habitat was employed. This was at times constrained however, with sampling feasibility needing to be weighed against terrain accessibility, associated safety, and the impact of sampling to the habitat. In instances where chosen plots were deemed too dangerous due to terrain, possibility of landmines, or that undertaking a plot would cause too much damage to the vegetation, plots were moved to the closest, safest point within the same habitat type. Due to this caution, it is possible that the ecological sampling across the three sites is at risk of a bias against dense vegetation (Garshelis, 2000). Due to the fragmented nature of the three habitat areas, I considered it preferable to preserve high density areas

rather than risk seriously damaging the vegetation (Garshelis, 2000; T. Haus, Vogt, Forster, Vu, & Ziegler, 2009).

Finally, budget and time constraints of available experts and support staff meant that access and time at each site was restricted. While this limitation was accounted for in the initial design of this study, it nevertheless constrained the scope of available data that could be collected.

The combination of these limitations resulted in less fine-scale data than I would have preferred, and it may have impacted the statistical power of the ecological analysis and the modelling power of the distribution analysis. Yet despite these limitations, I believe that the data presented here contributes to our better understanding of these critically endangered primates and identifies avenues for future further investigation.

1.5 Permissions obtained

As this study did not seek to directly engage or interact with the species under investigation, it did not require specific animal ethics approval. However, as the CBL component of this research was part of a larger longitudinal study being undertaken in the area, I was added as a co-investigator along with principal investigator Dr Alison Behie (Australian National University Animal Ethics, Researchers services, protocol number: 2013/8).

Additional approvals for in situ ecological sampling and research at each site were provided by the Hai Phong's People's Committee, the Cao Bang Province People's Committee and the Ha Giang People's Committee.

Ethics approval was granted by the Australian National University Human Ethics Committee (protocol number: 2015/761) for the period of 1 February, 2016 to 1 February, 2018 to undertake interviews with community members local to each of the national parks under investigation.

Research was also approved and supported by the Australian National University (ANU), Fauna and Flora International (FFI), the Cat Ba Langur Conservation Project (CBLCP), the Cat Ba National Park (CBNP), Trung Khanh National Park, Ha Giang National Park.

Funding for this study was provided through the Australian National University, the Margot Marsh Biodiversity Foundation, Primate Conservation Inc., and the Primate Action Fund.

1.6 Thesis overview

Due to the number of species under investigation, their specific relationships to their habitats and the methods used for each, this thesis is organised into a total of eight chapters. Initial chapters include an introductory chapter providing an overview of the thesis, and a background chapter (Chapter 2) with a discussion of primate conservation in Vietnam, Vietnamese forests and fragmentation, and limestone karst, followed by discussions of each individual species.

Two chapters (Chapters 3 and 4) are dedicated to the Cat Ba langur. Chapter 3 presents the methods, data and analysis of the existing CBL habitat in the two main CBL sub-populations. Chapter 4 presents an analysis of a potential corridor or habitat expansion region between the two sub-populations, including MaxEnt distribution modelling of the CBL across Cat Ba Island.

Chapter 5 is dedicated to the TSNM, which presents the methods, data and analysis of the TSNM habitat in Khau Ca, Ha Giang Province and a comparison to the habitat now officially linked as a result of the expansion of the boundaries of the adjacent Du Gia National Park. Based on the ecological sampling and status of the two areas under investigation, no distribution modelling was undertaken for this species.

Two chapters (Chapters 6 and 7) are dedicated to the CVG. Chapter 6 consists of an analysis of the existing CVG habitat, and an adjacent forest fragment previously identified as an area of potential habitat expansion (Fan et al., 2013). Chapter 7 continues the analysis of the viability of this potential habitat expansion by MaxEnt modelling.

A final conclusion chapter (Chapter 8) concludes the dissertation by synthesising the findings of each site, comparing the conservation efforts and offering insights into recommendations for future study and conservation opportunities based on my findings.

Chapter 2 Background

The CBL, TSNM and CVG are all listed as Critically Endangered on the International Union for Conservation of Nature's (IUCN) Red List (IUCN, 2022a) largely due to small population sizes, and ongoing threats to their habitats. All three are also found to exclusively inhabit their own fragments of limestone karst forest throughout northern Vietnam. This chapter will introduce the current status of primates and forests in Vietnam, and approaches to studying primate habitats. It will also introduce each of the three species and their shared habitat type: limestone karst.

2.1 Primate conservation

Sixty-five per cent of primate species are classified as threatened with extinction by the International Union for Conservation of Nature's (IUCN) Red List (Fernández et al., 2022). This reflects an increase from six years ago, when an assessment by Estrada et al. (2017) found that 60 per cent of primate species across all 16 families were threatened with extinction based on IUCN classifications (Estrada et al., 2017; Fernández et al., 2022).

The IUCN Red List of Threatened Species (Henceforth 'IUCN Red List') was established in 1964 as a tool to assess the conservation status of the world's species (IUCN, 2022a). Since its inception, it has become an important conservation tool that provides detailed information on target species from published and unpublished data to provide assessments on current conservation status (Rodrigues, Pilgrim, Lamoreux, Hoffmann, & Brooks, 2006). The IUCN Red List currently has 142,517 species assessments, 40,084 of which are listed as a risk of extinction (IUCN, 2022a). While all types of species are included, there is a bias towards terrestrial animal species, particularly those inhabiting forests (IUCN, 2022a). Each species is assessed and categorised into one of nine classifications based on their level of risk of extinction: Not Evaluated (NE), Data Deficient (DD), Least Concern (LC), Near Threatened (NT), Vulnerable (VU), Endangered (EN), Critically Endangered (CR), Extinct in the Wild (EW) and Extinct (EX). In addition to classifying extinction risks, the IUCN Red List also provides information on the taxonomy, range, ecology and threats facing each species. This information is used to inform global policy and conservation action, including several

international agreements such as the Convention on International Trade in Endangered Species (CITES) (Betts et al., 2020; IUCN, 2022a; Rodrigues et al., 2006). The breadth of the IUCN Red List means that the status of some species may be lagging and in need of reassessment, however, it remains an important tool in conservation planning and policy making.

The major drivers of the extinction risk for primates are hunting, and habitat loss as a result of logging and agriculture, particularly large-scale commodity-driven agriculture due to the long-term impact it has on primate habitats (Estrada et al., 2017; Fernández et al., 2022). Larger bodied primates have been identified as facing a greater range of threats, likely due to their longer life histories, greater diet input, and greater appeal for hunters compared to smaller primate species (C.A. Chapman & C.A. Peres, 2021; Fernández et al., 2022; McKinney, 1997; Purvis, Gittleman, Cowlishaw, & Mace, 2000; Rylands, Mittermeier, & Williamson, 2020).

Being able to prevent the disappearance of primates requires detailed knowledge of their biology, behaviour, socioecology, habitat and diet, and life history (Bezanson & McNamara, 2019; Rylands et al., 2020). It also requires greater preventative action on the behalf of humans through application of protective measures including anti-hunting policies and patrolling activities (Chapman & Peres, 2021; Fernández et al., 2022), all of which can only truly be effective with the support of local community groups that live alongside primate species (Bezanson & McNamara, 2019; Chapman & Peres, 2021).

As our study of primates continues, the number of identified species grows (Rylands & Mittermeier, 2014), and inevitably, so does the need for greater in-depth studies and conservation action, despite a finite pool of resources. As a result, it increasingly means that greater buy-in from local governments and communities is required to establish long-term species-specific conservation action that can hope to turn the tide against primate extinction (Chapman & Peres, 2021).

2.1.1 Primate conservation in Vietnam

Primates in Vietnam live in fragmented habitats as a result of habitat loss stemming from human intervention (Chapman & Peres, 2021; Estrada et al., 2017). As canopy specialists, it

could be expected that primates would respond negatively to a reduction in habitat quality as a result of fragmentation (Z. Huang et al., 2017). It appears however that their responses are species and often diet specific. Studies have suggested that different primate species respond to fragmentation in varying ways, and no patterns in the responses have been clearly identified (Bicca-Marques, 2003; Crockett, 1996; Norconk & Grafton, 2003; Onderdonk & Chapman, 2000). For instance, large groups of generalist species may survive in large fragments with no habitat niches, but the same fragment would support only a small group of ecological specialists (Boonratana, 2013). *Nasalis larvatus* (proboscis monkeys) are such ecological specialists, with specific sleeping site requirements such that the presence of large trees overhanging waterways is more important than untouched forest (Boonratana, 2013).

A history of upheaval and international conflicts stalled serious primate research in Vietnam following the identification of many species in the first half of the 20th century (Covert, Quyet, & Wright, 2008; T. M. Hoang, 2016). In depth research into Vietnam's primates only took off in the late 1990s, yet unfortunately by this time Vietnamese forests had already undergone significant changes and loss (T. M. Hoang, 2016; W. Li et al., 2017).

Today, the forests of Vietnam are home to 25 taxa of primates across three families: Loridae, Cercopithecidae and Hylobatidae (Figure 2.1), all of which are experiencing some degree of habitat disturbance (Blair et al., 2011; Quyet, 2014). Of these taxa, five are endemic to Vietnam: *Macaca fascicularis condorensis* (crab-eating macaque), *Pygathrix cinerea* (grey-shanked douc langur), *Rhinopithecus avunculus* (Tonkin snub-nosed monkey), *Trachypithecus delacouri* (Delacour's langur), and *Trachypithecus poliocephalus* (Cat Ba langur) (Nadler et al., 2007). Our knowledge of these varied taxa has increased since the beginning of the century, however, clarity over their taxonomy continues to be controversial and there remain relationships and species that are not well understood (Nadler et al., 2007; Roos, Thanh, Walter, & Nadler, 2007; Sha, Matsuda, Zhou, Ang, & Nadler, 2022).

The World-Wide Fund for nature was the first international conservation group to establish themselves in Vietnam in 1999 (T. M. Hoang, 2016). Since then, other conservation groups in Vietnam, including Fauna and Flora International (FFI) and the Cat Ba Langur Conservation Project (CBLCP) have established programs working to protect the primates of Vietnam since

the late 1990s. Programs and centres such as the Endangered Primate Rescue Centre (1993), the Cat Ba Conservation Project (2000), the Cao Vit Gibbon Conservation Project (2002) and the Tonkin Snub-nosed Monkey Conservation Project (2004) all work towards the protection and conservation of Critically Endangered primates ("Fauna and Flora International: About Us," 2020; Quyet, 2014; Nadler, 2007). Other conservation groups and zoos are also active in the region, including Denver Zoo and the Frankfurt Zoological Society. These groups work in partnership and on individual projects aimed at working towards a better future for Vietnam's primates.

While limestone karst forests were a focus for FFI at the beginning of their work in Vietnam, their projects now span the whole of the country and include the protection of plants and marine animals and environments ("Fauna and Flora International: About Us," 2020).

This shift in focus for FFI is an important reminder that the importance of studying primates lies not only in the opportunity to save the primates themselves, but their entire ecosystems. The study of large bodied species such as primates can often act as a generalised proxy to understand the condition and health of the forests and their wider ecosystem. As critical seed dispersers in the tropical forests they inhabit, the loss of primates can significantly impact the future health and survival of their forests (Chapman & Peres, 2001; Isabirye-Basuta & Lwanga, 2008). Thus, by conducting studies into the habitat preferences of the CBL, TSNM, and the CVG, we are not only adding to our knowledge of these threatened species, but also to our knowledge of the pockets of forest that support them.

Understanding the character and structure of primate habitats in their entirety is critical to not only gather information on how these forests are used but also in being able to track changes overtime. For highly specialised species, the delay between habitat loss and extinction (W. F. Laurance, 2007) will be brief, and only through collecting this habitat information to add to our knowledge of their behaviours and social structures can we hope to make meaningful conservation decisions to delay their extinction altogether (Gouveia et al., 2014; Pyritz et al., 2010; Y. Zeng et al., 2013).

Table 2.1 Primates found in Vietnam and their IUCN Red List status

Species	**Geographic range***	**IUCN Red List status**
Macaca arctoides (Stump-tailed macaque)	Vietnam, Cambodia, China, India, Laos, Malaysia, Myanmar, Thailand	VU
Macaca assamensis (Assamese macaque)	Vietnam, Bangladesh, Bhutan, China, India, Laos, Myanmar, Nepal, Thailand,	NT
Macaca fascicularis (Common long-tailed macaque)	Vietnam, Bangladesh, Brunei, Cambodia, India, Indonesia, Laos, Malaysia, Myanmar, Philippines, Singapore, Thailand, Timor-Leste	VU
Macaca leonina (Northern pig-tailed macaque)	Vietnam, Bangladesh, Cambodia, China, India, Laos, Myanmar, Thailand	VU
Macaca mulatta (Rhesus monkey)	Vietnam, Afghanistan, Bangladesh, Bhutan, China, India, Laos, Myanmar, Nepal, Pakistan, Thailand, United States	LC
Nomascus annamensis (Northern yellow-cheeked crested gibbon)	Vietnam, Cambodia, Laos	EN
Nomascus concolor (Black crested gibbon)	Vietnam, China, Laos	CR
Nomascus gabriellae (Red-cheeked crested gibbon)	Vietnam, Cambodia, Laos	EN
Nomascus leucogenys (Northern white-cheeked gibbon)	Vietnam, China, Laos	CR
Nomascus nasutus (Cao vit gibbon)	Vietnam, China	CR
Nomascus siki (Southern white-cheeked gibbon)	Vietnam, Laos	CR
Nycticebus bengalensis (Bengal slow loris)	Vietnam, Bangladesh, Bhutan, Cambodia, China, India, Laos, Myanmar, Thailand, Malaysia	EN
Nycticebus pygmaeus (Pygmy slow loris)	Vietnam, Cambodia, Laos	EN
Pygathrix cinerea (Grey-shanked douc langur)	Endemic to Vietnam	CR
Pygathrix nemaeus (Red-shanked douc langur)	Vietnam, Cambodia, Laos	CR
Pygathrix nigripes (Black-shanked douc langur)	Vietnam, Cambodia	CR
Rhinopithecus avunculus (Tonkin snub-nosed monkey)	Endemic to Vietnam	CR
Trachypithecus crepusculus (Indochinese grey langur)	Vietnam, China, Cambodia, Laos, Myanmar, Thailand	EN
Trachypithecus delacouri (Delacour's langur)	Endemic to Vietnam	CR
Trachypithecus francoisi (François' langur)	Vietnam, China	EN
Trachypithecus germaini (Indochinese silvered langur)	Vietnam, Laos, Myanmar, Thailand, Cambodia	EN
Trachypithecus hatinhensis (Hatinh langur)	Vietnam, Laos	EN
Trachypithecus margarita (Elliot's silver langur)	Vietnam, Cambodia, Thailand	EN
Trachypithecus poliocephalus (Cat Ba langur)	Endemic to Vietnam	CR

This will also ensure that conservation decisions are based on the greatest available data for each species and supported by scientific studies (Kirkpatrick, 1995). As human intervention in the habitats of primates continues at alarming rates (W. Li et al., 2017; Nadler et al., 2007), research into the ecology of primates will also help us understand how to best allow humans and primates to co-exist in the coming decades. The rate at which changes to the environment are currently occurring through climate change, means that we must look to see how immediate changes can be made to accommodate the futures of both the primates and humans who live alongside them. New techniques and methods in studying primates alongside traditional in situ approaches can help us collect large amounts of data quickly and easily to assist in the planning and protection of some of the most endangered species on the planet.

2.2 Vietnamese forests

The forests of Vietnam have undergone decades of anthropogenic disturbance. Over 8000 years ago, Vietnam and the larger Southeast Asian region were covered by extensive forest (Sodhi et al., 2004). A significant factor in the rapid decrease of forest cover in Vietnam during the 20th century was the extensive damage caused by the Vietnam War (Eames & Robson, 1993; Westing & Westing, 1981). Over the course of the war, approximately 13 million bombs were dropped contributing to a loss of over 22 000 km^2 of agricultural land and forests (Eames & Robson, 1993).

Following the war, deforestation continued until the 1990s, driven largely by the rapidly expanding Vietnamese population (Levine, 2016; Meyfroidt & Lambin, 2008b; Nadler et al., 2007). Since the 1990s, a program of regeneration, and reforestation through plantations has seen an increase in tree coverage (Meyfroidt & Lambin, 2008a). Vietnam's turnaround from net deforestation to reforestation, termed 'forest transition' (Cochard, Nguyen, Ngo, & Kull, 2020), was the first such transition to occur in Southeast Asia (Cochard et al., 2020; Mather, 2007; McElwee, 2009; Meyfroidt & Lambin, 2008a, 2008b, 2009). Despite this, reforestation was largely a result of plantations for future logging. From 2002 to 2021, primary forest decreased by 7,180 km^2 representing 11 per cent of the total area of primary forest in Vietnam (University of Maryland and World Resources Institute). Overall net tree cover also declined

during this period by 32,600 km^2, as a result of loss of natural forest and plantations, representing a 20 per cent decrease (Global Forest Watch). Key drivers of this loss were commercial, and medium-scale agricultural expansion, plantation and natural forest harvesting and expanding urban centres (Curtis, Slay, Harris et al., 2018).

At the time of this study in 2016, Vietnam was home to approximately 287 people per km^2 (Levine, 2016). By 2020, this had increased to 314 people per km^2 (FOA & World Bank, 2020), making it one of the most highly populated countries in the world. With approximately 64 per cent of Vietnam's population still living outside the cities, poverty is considered to be the main contributor to forest destruction by the Vietnamese government (FAO, 2018; Gomiero, Pettenella, Trieu, & Paoletti, 2000). As infrastructure development and urbanisation outside major cities continues, intense pressure is put on the remaining natural environment. As the population of Vietnam grows, so too will the pressure on the environment, with the United Nations estimating the population to reach over 104 million by 2030 (United Nations, 2019).

Beyond the impact of outright deforestation, the forests of Vietnam are critical resources for local communities. Fertile valleys, particularly within limestone karst forests, have long histories of use for farming, plantations and grazing for livestock (C. Huang, Li, et al., 2008). Forests have historically provided firewood, food, and plants and animals used in local remedies (Estrada et al., 2017; Nadler & Long, 2000). In more recent times, the unchecked collection of these resources including illegal logging and poaching, and the use of fires to extract honey has led to the degradation of many forest patches, particularly on limestone karst (Boissiere, Sheil, Basuki, & Le, 2009).

Between the 1950s and 1980s, logging occurred unregulated and unchecked across Vietnam (McElwee, 2004). By the 1980s, the Vietnamese government began to legislate for protected forest regions deemed significant as a natural settings, historical sites or special recreation, and restricted logging and hunting in these regions (Phuong & Dung, 2001). Since the 1990s, certain special use protected areas began to be reclassified as national parks. Certain parts of the country also saw local families awarded sections of their local forest to oversee its protection and reforestation efforts as part of an effort to reforest 50,000 km^2 of degraded

land (Boissiere et al., 2009; McElwee, 2009). By 1997, 334 000 households had been allocated roughly 10,000 km^2 of forest to oversee (Gomiero et al., 2000).

This approach both gave responsibility of the forests to the local community and provided them with limited financial benefit, particularly in the management of controlled logging and plantations. While this contributed to the reforestation of large portions of the country, the overall longer-term success of the program is not clear (Boissiere et al., 2009; Meyfroidt & Lambin, 2008b; Nadler et al., 2007). Due to the advantages gained by being awarded patches of land, it has been suggested that the program disadvantaged low-income families by privatising previously common land and encouraged the clearance of native vegetation for plantations of exotic species for legal logging (Gomiero et al., 2000; McElwee, 2009).

Officially, current estimates of forest coverage suggest that reforestation strategies have been succeeding, but these estimates can be difficult to independently substantiate (Matthews, 2001; Meyfroidt & Lambin, 2008b). While reforestation may increase the total forest cover, the new replanted forests tend to be plantations of exotic species such as Acacia and Eucalypt, while natural forests continue to be lost (Gomiero et al., 2000; Nadler et al., 2007; Watch, 2014).

The first protected forest was established by the Vietnamese government in 1962 (ICEM, 2003), and since then in an effort to improve forest coverage, over 30 national parks and 134 natural reserves have been established within Vietnam with limitations on their use and protection (An, Markowski, & Bartos, 2018; Quyet, 2014). Yet local politics and a lack of policing at some national parks, has led to suggestions of mismanagement and a lack of long-term planning for the preservation and future sustainment of these areas (Meyfroidt & Lambin, 2008b; D. Tan, Thu, & Dell, 2012). This assertion was found to be consistent with the results of this study, with sampled national parks demonstrating highly variable rates of success in protection and policing.

Differences in enforcement and protection of special-use forests and national parks can give the impression that some protected areas in Vietnam are little more than ‘paper parks’, defined by the IUCN as ‘a legally established protected area where experts believe current protection activities are insufficient to halt degradation’ (IUCN, 1999). Claims of paper parks

stem from challenges around administration responsibilities, differences in funding and infrastructure, land-use and resource-use conflicts with local communities, population growth, and a lack of conservation management or planning (An et al., 2018; ICEM, 2003; IUCN, 1999; Meyfroidt & Lambin, 2008b).

Only protected areas with special nature conservation status are managed by the Ministry of Agricultural and Rural Development (MARD), while other parks are managed by Provincial People's committees (PPC), leading to differences in administration and available funding as budgets for the latter are derived through state and provincial budget allocations, and international conversation funding (An et al., 2018).

This variation in the administration of the natural parks and reserves, puts the biodiversity of Vietnam's forests at risk. While legal definitions and administrative responsibilities for protected areas and national parks have been standardised (Decision 08/2001/QDTTg of January 11, 2001), a lack of suitable funding continues to impact available infrastructure and staffing to enforce the protected status of special-use forests and national parks (ICEM, 2003). Protected forests in Vietnam are often enclosed by agricultural land or villages, where local inhabitants may have a high reliance on forest resources (An et al., 2018; ICEM, 2003). This can cause conflict with the protected status of the area and enforcement efforts, leading to continued degradation of the area through the illegal collection of forest resources, logging, and hunting (An et al., 2018). Damage to the forest from logging, deforestation for urban development and degradation for forest resources, reduces biodiversity and can lead to the large-scale loss of native species (Tuyet 2001; Lu 2016; Westing and Westing 1981).

In some cases, even those responsible for patrolling and protecting the forests also contribute to their decline either through turning a blind eye to known logging practices or direct interventions. During the data collection for this study, both situations were observed. At one site, national park rangers removed several plants for personal use, one of which was noted to be an at-risk species. When asked about it, it was explained that this was regular practice in this forest, particularly for high value plant specimens. At another site, rangers were on high alert to any illegal activities. The contrast between sites and attitudes was often attributed to

the varying level of funding for local rangers, and level of involvement from conservation groups.

Vietnam currently has over 370 fauna and flora species classified by the IUCN (2022a) as Endangered or Critically Endangered. A further 721 species are classified as Vulnerable or Near-Threatened (IUCN 2022a). Despite government efforts, species will continue to face an uncertain future whilst illegal and unregulated interventions into Vietnamese forests are able to persist.

Beyond the species they support, forests are important for the wider ecosystem in reducing erosion, maintaining the health and flow of rivers and waterways and the capture of carbon dioxide that would otherwise that would otherwise partition into the atmosphere (Kauppi et al., 2006). Their health and abundance can directly impact the health of local and global human communities. Thus, efforts towards saving primates and their local habitats contributes to the health of the wider forest and can have positive flow on effects to the health and survival of other global ecosystems.

Yet not all forests are created equal. Primary and secondary forests vary in the levels of species richness and biodiversity they are capable of supporting (Kauppi et al., 2006; Meyfroidt & Lambin, 2008b). Primary forests allow for maximum biodiversity and carbon fixation compared to secondary forests that have been logged or degraded in some way (Kauppi et al., 2006). Today, primary forest in Vietnam makes up approximately seven per cent of the remaining forest cover (Dunn, 2004; Nadler et al., 2007), with secondary forests and plantations making up the majority of the residual forest coverage (Dunn, 2004).

The quality of the remaining secondary forests raises concerns and questions as to whether these forests can maintain the high biodiversity levels attributed to primary and less disturbed forests (Furey, Mackie, & Racey, 2010; Gardner, Barlow, Parry, & Peres, 2007; Nadler et al., 2007). While some suggest that secondary forests may offer viable alternatives to species facing habitat destruction or fragmentation (Gardner et al., 2007), others question the ability of secondary or reforested forests to sustain biodiversity and suggest that specialised species can struggle to adapt to rapid habitat alteration or reforested forests in time to avoid extinction (Furey et al., 2010; Gouveia et al., 2014; W. F. Laurance, 2007).

2.2.1 Habitat Fragmentation

Habitat loss is a major threat to the world's biodiversity, impacting the abundance, spread and survival of species (Hanski, 2015). Between 2002 and 2019, approximately 600,000 km^2 of primary forest was lost world-wide (Weisse & Gladman, 2020). Habitat fragmentation is a function of habitat loss, occurring when habitats become disconnected and form smaller, discontinuous patches across the landscape (Arroyo-Rodriguez & Mandujano, 2009). Fragments may be loosely connected by highly degraded vegetation, scrub, or highly altered forest, or exist as islands of vegetation amidst urban and agricultural landscapes. This process is occurring at a rapid rate globally and is thought to be one the major factors resulting in loss of primary and secondary forests (Arroyo-Rodriguez & Mandujano, 2009; Z. Huang et al., 2017; W. F. Laurance, 2007).

As habitat areas become fragmented, they become more isolated and exposed to edge effects – ecological changes associated with forest edges that become transition zones between the interior forest and external matrix (Haddad et al., 2015; Lindenmayer & Fischer, 2006). In particular, fragmentation poses a significant threat to biodiversity as the outer edges of forest fragments become more exposed to abiotic factors such as wind, increased sunlight, humidity, and human interference, reducing a forests capacity to maintain species numbers (Arroyo-Rodriguez & Mandujano, 2009; Damschen, Haddad, Orrock, Tewksbury, & Levey, 2006; Hanski, 2015; Z. Huang et al., 2017; Korotky et al., 1995; William F. Laurance, Goosem, & Laurance, 2009; Norconk & Grafton, 2003; Pohlman, Turton, & Goosem, 2009). These abiotic factors can impact the nutrients and health of the species along the edges of the fragment, which can then have flow-on impacts for species deeper within the fragment.

For instance, increased edges in small tropical forest fragments can lead to increased temperatures in the internal forest affecting the local microclimate, particularly within tropical ecosystems. Changes in the temperature of forest edges and interiors can be influenced by the forest/edge composition, contrast to surrounding landscape matrix, and even edge orientation and age (Arroyo-rodríguez, Saldaña-vázquez, Fahrig, & Santos, 2017; Didham & Lawton, 1999). Thus, the age of the fragment can also play a role in the extent to which edge effects impact the interior habitat. This is because young fragment edges may be largely composed of young, less dense vegetation, resulting in greater incursion of hotter

temperatures, particularly in areas where forest clearing for conversion to agricultural or urban use, logging or clear cutting reduces canopy cover and increases fragment/matrix contrast (Didham & Lawton, 1999). Older edges may exhibit older trees and greater canopy cover, resulting in a stronger buffer against temperature changes (Didham & Lawton, 1999). The size of the forest fragment can also influence how temperature and other abiotic factors at the edges may impact the interior forest (Soomers, Karssenberg, Verhoeven, Verweij, & Wassen, 2013), with smaller, open fragments experiencing greater influx of warmer temperatures than larger denser fragments, particularly in tropical areas (Arroyo-rodríguez et al., 2017; Didham & Lawton, 1999).

Even small disconnections between forest patches can have severe impacts on species (K. A. Gilbert, 2003). Fragmentation not only impacts the size of the available forest, but its internal configuration (M. J. Hansen, Franklin, Woudsma, & Peterson, 2001); the fragmentation of forests has been shown to reduce plant diversity and species richness (K. A. Gilbert, 2003; Norconk & Grafton, 2003; Westing & Westing, 1981). This is particularly evident at the forest edges which can become degraded as a result of reduced nutrient (carbon and nitrogen) retention (Haddad et al., 2015).

Vegetation composition and density can change as a result of fragmentation and poor nutrient retention in the soil, threatening established vegetation and providing entry points for exotic and invasive plant species to enter forest habitats (Arroyo-Rodriguez & Mandujano, 2009; Chiarello, 2003; Fletcher et al., 2018; Haddad et al., 2015; Hansen et al., 2001; Marsh, 2003a; Norconk & Grafton, 2003). The structure of vegetation and canopy within fragments can be impacted through the increased loss of old growth trees, reduced diameter at breast height (DBH) of trees, and reduced density of seedlings in fragments compared with larger contiguous forests (Arroyo-Rodriguez & Mandujano, 2009; Arroyo-rodríguez & Mandujano, 2006a, 2006b; Bolt et al., 2018; R. Wang et al., 2020). Reduced vegetation density at forest edges can also increase accessibility to invasive species, livestock such as goats and cattle, wildfire and human incursions (Fletcher et al., 2018; Goosem, 2000). Fragmented forest may also have fewer trees due to accessibility for logging or forest resource collection leading to further habitat loss (Arroyo-Rodriguez & Mandujano, 2009; William F. Laurance et al., 2009; Marsh, 2003b).

While overall habitat loss is accepted as having a negative consequence for species, the impact of the changes caused by habitat fragmentation are not as universally agreed upon (Fahrig, 2017; Fletcher et al., 2018). Based on the theory of island biogeography, smaller patches or fragments of habitat are assumed to result in negative effects on species, including reduced species richness and in the longer term, this results in changes to the overall composition and function of habitat fragments (de Lima Filho, Vieira, de Souza, Ferreira, & de Oliveira, 2021; Haddad et al., 2015). In contrast, more recent research by Fahrig (2017; 2003) suggests that habitat fragmentation can increase the amount of habitat available to a species compared to straight habitat loss, thereby positively affecting biodiversity. It is worth noting however, that in Fahrig's (2003) review of 17 studies of the effect of biodiversity, eight looked at bird species, three at insects or butterflies, two at vole species, two at ocean habitats, and one at a virus. Most, if not all, of which can move between habitats without the need to travel through specific matrices and may not be as restricted by fragmentation across a landscape. This is common occurrence, for many localised studies which have often focussed on the effect of fragmentation on smaller species such as birds and small mammals or reptiles (Harcourt & Doherty, 2005; Marsh, 2003a). Fahrig's (2017, 2003) assertions are still controversial (Fletcher et al., 2018) and may ignore the impact of habitat fragmentation on larger, habitat-specialised mammals that are limited by the physical constraints of their habitat to travel from one patch to another or survive in smaller habitat fragments.

Although habitat fragmentation occurs on a landscape scale, the effects can vary significantly at the local level and species within the same ecosystem may respond differently to habitat loss and fragmentation events (Lindenmayer & Fischer, 2006). Edge effects can have a positive impact on some species; however these are predominately generalist or invasive species while negatively affected species often inhabit the forest-core (Fletcher et al., 2018; Pfeifer et al., 2017). For instance, an analysis of the impact of edge effects on 1673 vertebrates species by Pfeifer et al. (2017) showed that species of conservation concern by the IUCN such as the Critically Endangered *Manis javanica* (Sunda pangolin), and the Endangered *Eleoscytalopus psychopompus* (Bahia tapaculo), *Cacatua tenuirostris* (long-billed cockatoo) and *Tapirus bairdii* (Baird's tapir) (IUCN, 2022a), were the most likely to inhabit the inner forest and respond negatively to edge effects caused by fragmentation.

Species with specialised habitat requirements are likely to have a negative response to reduced habitat through fragmentation, and changes to their habitat's composition as a result of edge effects (Bista, Baxter, Hudson, Lama, & Murray, 2022). Changes to the vegetation can alter the availability and quality of food species and increase feeding competition between species within fragments (Arroyo-Rodriguez & Mandujano, 2009; Arroyo-rodríguez & Mandujano, 2006a; de Lima Filho et al., 2021). Changes to fragment compositions can also change accessibility to important resting and refuge areas for species, leaving them at greater risk of predation (Bista et al., 2022; M. F. Schneider, 2001). These increased pressures can lead to species being at greater risk of extinction as a result of local fragmentation and can also be compounded at the landscape level where isolated pockets of species can restrict gene flow and leave species more at the mercy of stochastic events (de Lima Filho et al., 2021).

A study (Lenz, Jack, & Spironello, 2014) of the edge effects on six primate species in the Brazilian Amazon demonstrated varying responses. Three of the species, *Alouatta macconnelli* (Guyanan red howler), *Chiropotes chiropotes* (bearded saki), *Sapajus apella apella* (tufted capuchin), and *Saguinus midas* (golden-handed tamarin), displayed higher densities within the fragment edges, while *Ateles paniscus* (red-faced spider monkey) had lower densities and *Pithecia chrysocephala* (white-faced saki) showed no response to edge effects (Lenz et al., 2014). While the fruit intake of certain species may influence their response to edge effects, it is also possible that the edge contrast, i.e. whether the fragment borders other vegetative matrices, agricultural land, or urban settlements and the age of the edge vegetation can impact species responses (Bolt et al., 2018; Lenz et al., 2014).

An exploration of the different responses of several primate species: *Ateles geoffroyi* (black-handed spider monkey), *Cebus capucinus* (Colombian white-faced capuchin) and *Alouatta palliate* (mantled howler monkey) to varying forest edge contrasts found that while edge effects may impact vegetation composition and the quality of food resources, some primate species are able to withstand the changes (Arroyo-Rodriguez & Mandujano, 2009; Bolt et al., 2018). In fact, fragmented habitats may improve the availability of food for folivores as increased sunlight and lower tree density have been suggested to improve the quality and quantity of leaves and fruits by increasing protein levels (Chiarello, 2003; Gibson & Koenig, 2012; Korotky et al., 1995). These findings appear to be particularly true for howler monkeys

(genus *Alouatta*), which appear to be capable of adapting to environmental change and fragmentation based on the flexibility of their diet (Behie & Pavelka, 2012; Bicca-Marques, 2003; Norconk & Grafton, 2003). In contrast, larger and mainly frugivorous primates may be most affected by fragmentation as their size generally demands greater space and food species (Chiarello, 2003; K. A. Gilbert, 2003).

While some species' responses to fragmentation may be influenced by their dietary and ecological flexibility (Z. Huang et al., 2017; Onderdonk & Chapman, 2000; Pyritz et al., 2010), this is not true for all primates. For instance, a study of various folivore/frugivore lemur responses to edge effects in fragmented forests (Lehman, Rajaonson, & Day, 2006) have found that despite changes in densities of food trees, lemurs are fairly tolerant to edge effects regardless of their dietary requirements. The short-term responses of primates to fragmentation then, cannot be easily discerned without close study of the context of fragment edges.

Besides changes in found resource availability, fragmentation can also impact canopy continuity within a fragment, leaving arboreal primates at risk of hunting or terrestrial predators, as they must spend more time on the ground (Arroyo-Rodriguez & Mandujano, 2009; Umapathy & Kumar, 2003). It can also lead to increased competition both between conspecifics and sympatric primate species (Bista et al., 2022; Colin Austin Chapman, 1987; de Lima Filho et al., 2021; Erinjery, Kavana, & Singh, 2017; Westing & Westing, 1981). This can occur by reducing home ranges and increasing points of conflict within and between groups.

Fragmentation can also change the genetic composition of primate populations by isolating sub-groups from one another. Disconnected fragments can limit successful dispersal of primates to new groups following sexual maturity (de Lima Filho et al., 2021). This can be exacerbated in smaller fragmented populations where individuals are unable to move out of their natal groups to find unrelated mates. This in turn can lead to a disruption of group sex ratios and juvenile survival within groups, thereby slowing the normal growth rate of populations (Umapathy & Kumar, 2003). For instance, a study of *Alouatta pigra* (Yucatán black howler) found that females, preferring shorter dispersal distances, were found to be more abundant in larger fragments with higher connectivity, while males were more abundant in

more isolated, smaller fragments (Klass, Van Belle, Campos-Villanueva, Mercado Malabet, & Estrada, 2020). The costs of dispersal between fragments can have lasting implications on the composition of primate populations (Klass et al., 2020; Umapathy & Kumar, 2003). Thus, limiting growth factors and the reduction of primate home ranges and isolate sub-populations, also puts species at risk of low genetic diversity (C. Huang, Li, et al., 2008; Z. Huang et al., 2017; Lu, Wen, & Chen, 2016).

Studying fragmentation is made more complicated due to the fact that many primate species are studied in habitats that are not pristine and have been fragmented for a long time making it very difficult to understand the exact cause and effect of fragmentation on primate behaviour (Marsh, 2003b). Some Critically Endangered primates existing in fragments, such as those studied in this dissertation, have persisted in very small populations for decades - making it difficult to confidently ascertain patterns or trends (Boonratana, 2020). Despite this, we can still make some conclusions in an effort to help target species experiencing fragmentation (K. A. Gilbert, 2003). The ecological impact on species is still unclear in the short-term, but the long-term impact of fragmentation is better understood. Fragmented habitat is known to limit the population growth of species, however the upper limits of the number of individuals of a species that can be maintained by a habitat fragment varies depending on the species and fragment size (Chiarello, 2003; Z. Huang et al., 2017; Umapathy & Kumar, 2003). The minimum viable size of a population is unclear and may vary from species to species. I. R. Franklin and Frankham (1998) proposed a need for 500 to 1000 individuals for a species to hope to continue to have “evolutionary potential,” while Lynch and Lande (1998) put the minimum viable number at 1000 to 5000 individuals. Both studies, however, agreed that in practice in the wild, species would require a few thousand to have a hope of surviving with healthy populations (Lynch & Lande, 1998).

It is expected in these studies of minimum viable populations, however, that populations are not fragmented across a landscape. Even small distances between fragments can have the potential to limit dispersals depending on the surrounding matrices (W. Wang, Qiao, Li, Pan, & Yao, 2017). This makes it critical to avoid the creation of population islands as much as possible. This is particularly relevant for the CBL, TSNM and CVG, whose total global populations are alarmingly small. Over time, the impact of fragmentation and edge effects

may continue to increase and further negatively affect the endangered primates within (Haddad et al., 2015).

Opportunities to increase connectivity between fragments have the potential to offset the effects of island biogeography, edge effects, and genetic isolation by keeping populations and their habitats connected (Chapman & Peres, 2001; Haddad et al., 2015). This is particularly important for arboreal species such as primates to assist their dispersal (Arroyo-Rodriguez & Mandujano, 2009). At the current rate however, efforts to maintain connectivity between fragments are being vastly outpaced by the rate at which primate habitats are being lost (Boonratana, 2020; Boonratana & Canh, 2013; Estrada et al., 2017; C. Schwitzer, Mittermeier, R.A., Rylands, A.B., Chiozza, F., Williamson, E.A., Byler, D., Wich, S., Humle, T., Johnson, C., Mynott, H., and McCabe, G., 2019).

2.2.2 Corridors

Corridors are typically defined as portions of vegetation linking two or more habitat fragments, within a dissimilar surrounding matrix that potentially enables gene flow, seed dispersal, range expansion and physical movement of species between the fragments (Beier & Noss, 1998; Damschen et al., 2006; W. Li et al., 2017; McRae, Dickson, Keitt, & Shah, 2008). As fragmentation creates a disconnect between forest patches across the landscape, vegetation corridors may offer the opportunity to maintain connectivity and facilitate movement between forest fragments (Beier & Noss, 1998; Estrada & Coates-Estrada, 1996).

Corridors are popular ecological and conservation strategies to facilitate the movement of endangered or at-risk species experiencing habitat fragmentation, however, their effectiveness has not been clearly demonstrated on large scales (Damschen et al., 2006; McRae et al., 2008). Studies on small-scale artificially created corridors have been demonstrated to have some benefits for insects or small-bodied mammals (Estrada & Coates-Estrada, 1996; Knowlton & Graham, 2010).

Studies of the benefits of corridors for endangered large-bodied mammals are difficult due to the scale at which these types of studies must be undertaken. In order to properly test the success of corridors in linking habitat fragments and encouraging use by target species, the corridor must offer the only, or most convenient, link between the fragments (Bennett &

Davies, 1994; Ricketts, 2001). This means that corridor studies are best conducted at a landscape scale for large-bodied mammals (Arroyo-Rodriguez & Mandujano, 2009), making them expensive, time consuming and difficult to undertake successfully.

The differences between natural corridors and constructed or regenerated corridors must also be considered. Natural corridors connecting fragments are likely to be more successful as they should reflect some vegetation of the forests they link and offer a real-time passage for movement (Gilbert-Norton, Wilson, Stevens, & Beard, 2010). The use of remnant habitat as corridors, however, has also been shown to be somewhat effective, as in the case of some Howler monkey species in fragmented habitat (Estrada & Coates-Estrada, 1996).

Yet, for primates in situations where no remnant habitat remains, it is unclear whether corridors can be effectively rehabilitated or created. This is largely due to the difficulty in creating canopy connectivity for arboreal primates. Canopy connectivity between fragments and corridors may act as a critical factor in successful uptake of corridors by primates (Arroyo-Rodriguez & Mandujano, 2009; Bennett & Davies, 1994). Unfortunately, canopy connectivity is hard to artificially construct and the timescales upon which to naturally create these pathways may already be too far gone for many of the endangered primates it could potentially benefit.

The use of artificial arboreal corridors, however, has been used more widely as a mechanism to help at-risk species avoid habitat breaks such as roads, fences and fragment breaks (Birot, Campera, Imron, & Nekaris, 2020; Bliss-Ketchum, 2019; Das, Biswas, Bhattacherjee, & Rao, 2009; Linden, Foord, Horta-Lacueva, & Taylor, 2020; Nekaris et al., 2020; Weston, Goosem, Marsh, Cohen, & Wilson, 2011). Artificial bridges have also recently been demonstrated to have some success with *Nomascus hainanus* (Hainan gibbon) (Chan, Lo, Hong, Mak, & Ma, 2020). The use of ropes to replace a lost connection in a former gibbon pathway, covering distances of 15.8m and 17.2m and were eventually increasingly utilised by the gibbon study group as well as other smaller mammals (Chan et al., 2020). A similar experiment testing the uptake of a rope and PVC canopy bridge vs wooden pole bridges by *Leontopithecus chrysopygus* (black lion tamarin), found that the wooden artificial bridges were utilised by multiple arboreal mammal species, including tamarins (Garcia, Culot, de Carvalho, & Rocha,

2022). Not only do these successes suggest that some primate species may benefit from artificial corridor connections, but it also provides a cheaper and faster option to ensure connectivity is maintained compared to longer-term options involving corridor regeneration or replanting.

The success of corridors in linking habitat fragments can depend on understanding the way in which the target species use their habitat and view their surroundings (Knowlton & Graham, 2010). While fragments may contain sub-populations of primates in increasingly reduced areas, the primates may not view this entire fragment as habitat based on ecological, climatic, dietary or territorial factors (Arroyo-Rodriguez & Mandujano, 2009). The characteristics of a corridor, its location to existing primate ranging or habitat, and the connected fragment must be considered in order to understand how the method is best applied to the conservation problem. Whether or not the corridor area is actively sought out and used by the primate or entered passively is an important indicator of how the corridor might be used and the timeframe in which it might be considered effective (Lima & Zollner, 1996).

Despite this uncertainty, corridors are viewed by many as the best solution to maintaining connections between fragments and promoting gene flow between isolated populations (Beier & Noss, 1998; Estrada & Coates-Estrada, 1996; Z. Huang et al., 2017; McRae et al., 2008). With habitat destruction continuing at a rapid pace around the world, corridors may be our best hope to combat the effects of fragmentation and provide a buffer against extinction of species while conservation management strategies are fully realised.

The application of behavioural ecology can improve the identification and success of corridors in linking habitat fragments and their use by species (Knowlton & Graham, 2010; Li, Clements, Shan & Memmott, 2021). The quality of the corridor is a critical factor in whether it is utilised by a species (Henein & Merriam, 1990; Lees & Peres, 2008; Li et al., 2021), however, the definition of quality is likely to be species-specific (Li et al., 2021). A study by Lees & Peres (2008) found that in the case of riparian forest corridors, corridor width and canopy structure were key determinants for use by mammals, while understory density, bamboo abundance and forest quality also played an important role (Lees & Peres, 2008).

Factors impacting the quality of a corridor may include the size of the corridor, dispersal behaviours, vegetation composition, predation risk, presence of food species and the body size of the target species (Knowlton & Graham, 2010; Li et al., 2021). The use of ecological and behavioural data combined with landscape-scale analyses in corridor studies has the potential to improve outcomes for conservation planning (Li et al., 2021).

Studies exploring the use of corridors to address habitat fragmentation for primates should thus endeavour to use a combination of ecological, nutritional and behavioural data with landscape-level methods in an effort to improve outcomes (Li et al., 2021), particularly for endangered species. To enable this work, efforts should be made to increase the breadth of dietary and ecological studies to complement the in-depth behavioural knowledge of endangered primates. This trifecta of data will provide the best opportunity for conservationists, primatologists and policy-makers to implement targeted conservation activities.

2.3 Methods for studying primate habitats

As our understanding of primate habitats grows, we can better understand their ecological requirements to assist their conservation. Where traditional primatology typically focussed on primate behaviour and social ecology, a continued uptake of studies exploring the dietary and ecological constraints of primate populations allow us to understand the relationship between primates and their habitat within the context of the wider landscape (Bista et al., 2022; Boonratana, 2020; Chapman & Peres, 2001). The increasing threat of habitat fragmentation has made identifying and preserving connections between fragments increasingly important (McRae et al., 2008). A key difficulty in habitat studies is the high level of pre-existing disturbance many primate species have undergone due to anthropogenic interventions. For species that may have once been widespread, it can be difficult to determine if their current range represents a preference or refuge (Garshelis, 2000; Lovejoy et al., 1984; Workman, 2010a). This should not deter researchers from placing a stronger focus on primate habitat studies to establish baseline datasets, and to revisit sites to maintain monitoring. Without a baseline and ongoing data for at risk species, it will be difficult to implement meaningful conservation planning for their futures.

Traditional methods for habitat-focussed studies use in situ sampling via ecological plots or transects with phenological monitoring (Arroyo-Rodriguez & Mandujano, 2009). These methods are essential for understanding the structure and interaction of primates with their habitat, however they are often limited in considering the habitat on a local scale. To understand the context of primate habitats within their surrounding matrix, a landscape scale analysis can provide additional insights into ongoing habitat pressures and assist in future modelling (Chapman & Peres, 2001; Knowlton & Graham, 2010). Large scale identification of these connections can be difficult or even impossible through traditional in situ studies of primates. Localised studies offer important insights into primate-habitat relationships and the on the ground status of vegetation, however they can be further enhanced through the adoption of additional monitoring methods.

Technologies such as satellite imagery and geographic information systems (GIS) can allow us to contextualise primate habitats within the wider landscape. Planning for primates and their habitats is fundamentally a spatial problem (Robbyn, Scott, & Wilcove, 2000). This is particularly the case for species living adjacent to large human populations; understanding the boundaries, the quality, and future areas of conflict requires the ability to view the habitat in its entirety and its situation in the wider landscape (C. J. Johnson, Seip, & Boyce, 2004; Ricketts, 2001; Robbyn et al., 2000).

The use of satellite imagery provides a digital image of the target area using different wavelengths. A single image can be manipulated using GIS software to explore different layers of the habitat, from the elevation, slope, vegetation density and different vegetation profiles to provide an in-depth picture of the target area. This can then be analysed including by modelling the past, present and future distribution of target species using observational data (Buermann et al., 2008; Willems & Hill, 2009).

Limestone karst forests are difficult to monitor in situ due to the danger and difficulty of the terrain. In addition, accurate estimates of limestone karst vegetation through traditional methods such as ecological sampling can be restricted by accessibility to plots and sampling bias (Q. Huang & Yunlong, 2009; Workman, 2010; Yue, Wang, Liu, & Li, 2012). The use of satellite imagery and GIS analysis can overcome issues faced in the field such as difficult

terrain, large areas, shy target species and in some cases, the cost (Nadler & Streicher, 2004; Podobnikar, Schöner, Jansa, & Pfeifer, 2008; Stark, Vaughan, Evans, Kler, & Goossens, 2018). It can also permit long-term tracking of habitats to monitor changes, real-time monitoring, and model future outcomes for species (Buermann et al., 2008; Gould, 2000; Stark et al., 2018). While GIS has been used extensively in conservation and ecological studies (Gould, 2000; Hansen et al., 2001; C. J. Johnson et al., 2004; Kobbler & Adamic, 2000; N. Pettorelli et al., 2005; Robbyn et al., 2000; Simonson, Allen, & Coomes, 2014; Stark et al., 2018; Wei Wang et al., 2008), its use to assist with primate habitat studies has been comparatively limited, though it is becoming increasingly used to support distribution modelling and prediction (Fan et al., 2013; Freire Filho & Palmeirim, 2020; Q. Huang & Yunlong, 2009; Palminteri, Powell, Asner, & Peres, 2012; Tien Bui, Le, Nguyen, Le, & Revhaug, 2016; Van Phung et al., 2023; Willems & Hill, 2009).

A slower uptake of GIS for primatological studies may in part be due to some of the limitations of the use of satellite imagery in primate habitats. The tropics, where most primates are found, can be difficult or expensive to get high resolution satellite imagery due to humidity and cloud cover (Palminteri et al., 2012). This can increasingly be overcome through the use of composite images to remove cloud cover. Satellite imagery and GIS analysis have dramatically improved over the last few decades, and the quality of freely available imagery has also improved (Buermann et al., 2008). The increased number of private satellites and those used in national space programs, has also seen an increase in the availability of satellite imagery for purchase, though the cost becomes more prohibitive the higher the resolution and larger the area of investigation. As a result, GIS analysis can provide detailed maps and assessment of habitats without the need to trample through the delicate undergrowth of the habitats of endangered species.

As new technologies continue to provide higher quality, bigger picture ways in which to explore primate habitats, there is still value in our traditional in situ approaches to provide insights into the nuances of primate habitats. Combining the two approaches will continue to provide greater insights and opportunities to support conservation planning.

2.4 Study habitat type and species

2.4.1 Limestone Karst

Limestone karst results from the gradual weathering of sedimentary limestone (calcium carbonate), which over millions of years has eroded to form impressive landscapes across approximately 12-15 per cent of the world's surface (Clements, Sodhi, Schilthuizen, & Ng, 2006; Dai, Peng, Yang, & Zhao, 2017; Hamilton-Smith, 2001; Insua-Cao et al., 2012; Peng, Dai, Ding, Shi, & Li, 2020).

A series of tectonic uplifts throughout Southeast Asia roughly 300 Ma, exposed the limestone laid down by calcium-secreting marine organisms millions of years prior (Averyanov, Loc, Hiep, & Harder, 2003; Clements et al., 2006; Gillieson, 2005; Mark, 2009). Ongoing climate and sea level fluctuations during the Middle and Late Pleistocene subsequently revealed a patchwork of limestone karst and tropical rainforest pockets throughout Laos, Northern Vietnam and Southern China (Groves, 2007; Miller et al., 2005). Today, limestone karst is estimated to cover 900 000km^2 of Southeast Asia and southern China, 60 000 km^2 of which covers Vietnam (Abramov & Kruskop, 2012; Clements et al., 2006; M. Day & Urich, 2000; Furey et al., 2010; Gillieson, 2005; Peng et al., 2020).

While largely restricted to northern Vietnam, a large limestone karst band runs the breadth of the country and into the Bay of Tonkin to form the World Heritage area Ha Long Bay and Cat Ba archipelago, where it forms spectacular limestone karst towers (Abramov & Kruskop, 2012; Gillieson, 2005; Gunn, 2003; Van, Duc, & Van, 2010). Millions of years of mechanical and chemical weathering of the karst has resulted in an array of karst landscapes across Vietnam (Figure 2.1), from limestone karst towers and vertical cliffs reaching elevations of 2000m to closed valleys, caves and hidden underground tunnels and rivers (Averyanov et al., 2003; Clements et al., 2006; M. Day & Urich, 2000; Quinn & Woodward, 2015; Tuyet, 2001).

The complexity of the weathered limestone karst has created pockets of specialised ecological niches that foster rich speciation, particularly for plants (Clements et al., 2006; Hamilton-Smith, 2001). Soil accumulation on karst is slow; it can take over 2500 years for one centimetre of soil to form through weathering (D. Guan & Su, 2014), leading to shallow layers of soil exposed to climatic effects (Song et al., 2022). As a result, it typically has poor soil and water

retention, particularly on the cliffs and steep slopes where soil is easily lost by rain and wind. However, the shallower slopes and valleys can sustain dense vegetation as result of soil accumulation (Fan et al., 2011; Quinn & Woodward, 2015). The low soil accumulation means that karst is vulnerable to erosion, loss of vegetation and desertification (Song et al., 2022). Once soil becomes degraded on karst, natural restoration of vegetation is almost impossible and requires targeted intervention to restore plant diversity and improve biodiversity (Peng et al., 2020; Song et al., 2022).

Limestone karst supports tropical evergreen and semi-deciduous broad-leafed and mixed forest (Averyanov et al., 2003). Due to the severity of karst landscapes, the vegetation density and quality vary depending specific levels within the karst formations (C. Huang & Li, 2005; Workman & Schmitt, 2011). Summits and cliff vegetation is scraggy and lower in quality than in comparison to vegetation in valleys and shallower slopes where soil accumulates (Li & Rogers, 2005b; Yue et al., 2012).

Figure 2.1 Examples of Limestone karst landscapes Top: Cat Ba Island, Hai Phong. Bottom left: Trung Khanh district, Cao Bang Province. Bottom right: Khau Ca, Ha Giang Province. Photos: K. Apthorp, 2016.

Limestone forest canopies also differ from more traditional forests, with trees being typically smaller and distributed in a more vertical orientation due to the steepness of slopes resulting in disconnected canopy pathways (Xiong, Gong, Qiu, & Li, 2009). Large patches of karst are often devoid of any trees or vegetation, instead displaying bare rock (C. Huang & Li, 2005; Xiong et al., 2009). Valleys and shallow slopes, where soil has been able to accumulate, offer the highest density of limestone karst forest, with evergreen leaves, vines and woody climbers and often, the most established trees (Tuyet, 2001). Despite the patchy distribution of vegetation across limestone karst, it is thought to have higher flora and fauna endemism levels compared to other forest types, particularly in Southeast Asia (Bystriakova, Alves De Melo, Moat, Lughadha, & Monro, 2019; Clements et al., 2006; C. Huang & Li, 2005; Tuyet, 2001). This high endemism occurs due the many ecological niches created by the complex topography, including sunken caves, high cliff faces, and crevices formed from layered limestone, and varied microclimates (Clements et al., 2006).

Despite the high level of endemism, research into the ecology of limestone karst is not well developed (M. Day & Urich, 2000; Furey et al., 2010; Sodhi et al., 2004). This is, at least in part, due to the limited accessibility of the harsh and dangerous terrain (Clements et al., 2006). This, however, has not stopped the local exploitation of the accessible parts of limestone karst and its forest for agricultural purposes, water and forest resources and tourism, around the world (Bystriakova et al., 2019; M. Day & Urich, 2000; Gillieson, 2005). This has put limestone karst environments at risk of permanent degradation (Hamilton-Smith, 2001; Parise, Waele, & Gutierrez, 2008; Yue et al., 2012). Ongoing resource collection by local communities including hunting and firewood and plant collection damage the vegetation, resulting in poorer vegetation and the introduction of pollution and invasive species to the area (Zhaoyuan Li & Rogers, 2006). As the amount of vegetation decreases on slopes and summits, erosion and weathering can increase soil loss, further impacting the health of the karst forests (C. Huang & Li, 2005; Insua-Cao et al., 2012; Yue et al., 2012). Poor soil and water retention as a result of this degradation makes chances of natural recovery of karst vegetation slow and highly unlikely in practice (Fan et al., 2011; Insua-Cao et al., 2012; Tuyet, 2001). Limestone karst is also at risk from climate change-driven drought, which will further amplify the effects

of desertification as a result of deforestation from resource collection (Bystriakova et al., 2019).

Limestone karst is highly sought after in the mining sector due to the demand for limestone and other minerals, particularly for concrete (Clements et al., 2006; Simoes & Hidalgo., 2022). Limestone mining can occur via open pits at the surface level, or through underground mining (Pambudi et al., 2020). Both methods pose risks for the biodiversity of their surrounding environments. Open pit mining can devastate surrounding vegetation through pollution and soil erosion, resulting in high biodiversity loss, while underground mining can risk karst collapses and impact groundwater systems (Pambudi et al., 2020).

This ongoing exploitation contributes to the degradation of limestone karst forest and puts the biodiversity of limestone karst at risk (Lu et al., 2016; Parise et al., 2008). While programs to protect and conserve limestone karst throughout Vietnam and the wider Southeast Asia region exist, both through local government policies and external conservation efforts, efforts are restricted to small patches, leaving vast tracts of limestone karst and its high levels of speciation at risk of continued destruction (Clements et al., 2006; M. Day & Urich, 2000). Further study and greater conservation of these regions are critical to identify and protect the highly diverse flora and fauna that have adapted to this severe environment (Clements et al., 2006; M. Day & Urich, 2000; Furey et al., 2010; Workman & Schmitt, 2011).

2.4.2 Asian Colobines

Colobines are part of the subfamily Colobinae within the family Cercopithecidae. It includes over 50 species, which inhabit a diverse range of forest habitats from tropical Africa to Southeast Asia (Oates & Davies, 1994; Roos et al., 2011; Sterner, Raaum, Zhang, Stewart, & Disotell, 2006). Members of the subfamily Colobinae are characterised in part by their enlarged salivary glands and a three-chambered stomach to help them digest a diet predominately made up by fibrous plants and leaves (Chivers, 1994; Groves, 2001; Oates & Davies, 1994; Roos et al., 2011; Sterner et al., 2006).

Colobines are believed to have spread from Africa to Asia in the late Miocene, approximately 10.8 MA (Sterner et al., 2006). The Hengduan Mountains in southwest China may be the area from which modern Asian colobines originated (Liedigk et al., 2012). This region gives rise to

the Mekong, Salween and Yangtze rivers, which may have acted as dispersal barriers for early colobines (Liedigk et al., 2012). Since then, they have adapted to range of habitats, from temperate forests, harsh limestone karst forests to the temperate climates of southern China (Workman & Schmitt, 2011).

The Asian colobines can be divided into two groups: the langurs, and the odd-nosed group (Sterner et al., 2006), represented in this research by *Trachypithecus poliocephalus* (Cat Ba langur) and *Rhinopithecus avunculus* (Tonkin snub-nosed monkey), respectively. Perhaps due to a history of hunting throughout Asia, colobines are generally shy and unhabituated groups can be difficult to locate, as exemplified by several species reappearing after years of assumed extinction (Covert et al., 2008; Oates & Davies, 1994). As the study of colobines grows, new species continue to be identified (Trachypithecus popa: Roos et al., 2020), however there are still gaps in our knowledge of the ecological requirements for many endangered species, making species-specific conservation planning difficult to implement in many instances (Fashing, 2007).

2.4.2.1 Limestone langurs (Trachypithecus)

The majority of langurs found in Southeast Asia are members of the taxonomically complex limestone langur group (Table 2.2), so called due to their adaptation to limestone karst habitats throughout the region (Groves, 2004; Liedigk, Thinh, Nadler, Walter, & Roos, 2009). As one of the most diversely distributed genera, the relationships of this group remain unclear (Liedigk et al., 2009; Liu et al., 2013; Osterholz, Walter, & Roos, 2008; Roos, Liedigk, Thinh, Nadler, & Zinner, 2017; Roos et al., 2007; Roos et al., 2011). The severe impact of habitat loss, degradation and fragmentation, hunting, and increasing human influences on their natural geographic ranges have also made it difficult to identify clear patterns that unite all of the limestone langurs including density, overall ranging, and social behaviours.

It is also unclear for several of these species such as *Trachypithecus leucocephalus* (white-headed black langur) as to whether or not their use of limestone karst forest can be considered an adaptation or refuge (Li & Rogers, 2005a; Workman, 2010). For species such as the CBL, limestone karst must be considered a preferred habitat due to their arrival on the entirely limestone karst island between 0.5 and 0.25 MA based on divergence estimates from

Trachypithecus francoisi (François' langur) (Liu et al., 2013). At this time, sea levels between Cat Ba Island and the mainland of Vietnam were estimated to have been less than 20 metres deep (Liu et al., 2013), potentially allowing for island hopping from the mainland.

Table 2.2 Member species of the limestone langurs

Species	Country	Home range size estimates (ha)	Total population	IUCN Red List status	Source
Trachypithecus francoisi (Francois' langur)	South-western China, Northern Vietnam, Central Lao PDR*	19 69.3 44 - 110	2000-2,100	EN	Burton, Snarr, & Harrison (1995); Grueter & Ding (2006); C. Huang, Wu, Zhou, Li, & Cai (2008); IUCN (2022a); D. Li, Zhou, Tang, et al. (2011); Li & Rogers, (2005a, 2005b); Tsuji, Hanya, & Grueter (2013)
Trachypithecus leucocephalus (White-headed langur)	Southern China	28 - 48 23.8 - 33.8 52	1,183	CR	Grueter & Ding (2006); C. Huang, Li, et al. (2008); C. Huang, Wei, Li, & Li (2003); C. Huang, Wei, Li, Quan, & Li (2002); Z. Huang et al. (2017); Li & Rogers, (2005a, 2005b); Li & Rogers (2006); H.X. Tang et al. (2024)
Trachypithecus poliocephalus (Cat Ba langur)	Cat Ba Island, Vietnam	22 - 50	65	CR	Hendershott (2017); Hendershott et al. (2016); Hendershott, Rawson, & Behie, (2018); Nadler & Long (2000); Schrudde et al. (2010); Stenke & Canh (2004)
Trachypithecus delacouri (Delacour's langur)	Northern Vietnam	36 - 46	240-250	CR	Agmen, (2014); Duckworth, Boonratana, Robichaud, & Timmins (2010); IUCN (2022a); Workman (2010b); Workman & Schmitt, (2011)
Trachypithecus hatinhensis (Hatinh langur)	Central Vietnam, Lao PDR	1 - 10	No reliable data	EN	Duckworth et al. (2010); T. Haus et al. (2009); Nadler, Momberg, Nguyen et al. (2003); Manh Ha Nguyen (2006); B. V. Tran et al. (2017)
Trachypithecus laotum (Laotian langur)	Central and North Lao PDR	Unknown	No reliable data	EN	Duckworth et al. (2010); Steinmetz, Timmins, & Duckworth (2011)
Trachypithecus ebenus (Indochinese black langur)	Central Lao PDR, Vietnam*	unknown	No reliable data	EN	Duckworth et al. (2010)
Trachypithecus phayrei	North-east Thailand,	27.5 73.7 - 93	Est. 1500*	EN	Adimallaiah, Thiyagesan, & Gupta (2014); Borries,

(Phayre's leaf monkey)	Bangladesh, Myanmar, North-eastern India, Vietnam, China				Primeau, Ossi-Lup, et al. (2014); Carl (2009); Gibson & Koenig (2012); Groves (2001); Li & Rogers (2005a); Stanford (1991)
Trachypithecus barbei (Tenasserim lutung)	Myanmar-Thailand border	Unknown	No reliable data	EN	Geissmann, Groves, & Roos (2004); Nadler, (2021)
Trachypithecus crepusculus (Indochinese grey langur)	East Myanmar, North Thailand, Lao PDR, North Vietnam, South-east China	400 400 - 450 446	2,400-2,500	EN	Groves (2001); Nadler et al. (2003); Roos et al. (2017)
Trachypithecus pileatus (capped langur)	North-central Bangladesh, Assam India, Northern Myanmar*	14 - 64	No reliable data	VU	Bennett & Davies, (1994); Das, Chetry, Choudhury, & Bleisch, (2020); Mazumder, (2014); Mukherjee & Saha (1974); Stanford (1991)
Trachypithecus geei (Gee's golden langur)	Assam India and Bhutan	64 120, 430 150 - 600	6,000-6,500	EN	Chetry, Chetry, Ghosh, & Bhattacharjee (2010); IUCN, (2022a); Mazumder (2014); Mukherjee & Saha, (1974); Srivastava, Biswas, Das, & Bujarbarua (2001)
Trachypithecus shortridgei (Shortridge's capped langur)	South-western China, North-eastern Myanmar	Unknown	No reliable data	EN	L.-w. Cui et al. (2016); Y.-C. Li et al. (2015)
Trachypithecus germaini (Germain's langur)	South Vietnam, South Myanmar, South Thailand, South Lao PDR, Cambodia	Unknown	Est. 1800*	EN	Fiore (2015); Timmins et al. (2013); B. V. Tran et al. (2017)
Trachypithecus margarita (Annamese langur)	Cambodia, Lao PDR, Vietnam	256	No reliable data	EN	Duc et al., (2022); Monge (2016)

*Estimate totals from country surveys (IUCN, 2022a)

2.4.2.1.1 *Trachypithecus poliocephalus* (the Cat Ba langur)

The CBL first described in 1911 (Trouessart, 1911), is endemic to Cat Ba Island, Vietnam (Figure 2.2). It is one of the world's most Critically Endangered primates and has consistently been

included on the IUCN's 25 most endangered primates list since 2000 (IUCN, 2019; R.A. Mittermeier et al., 2022).

There is no evidence that the CBL ever inhabited the mainland of Vietnam or China, where its closest relative, the white-headed black langur is found (Nadler & Long, 2000). There is some dispute as to the taxonomic relationship of the CBL to the white-headed black langur (Brandon-Jones, 1995; Groves, 2004), but for the purposes of this study, the two langurs are treated as distinct full species.

Prior to 1960 when the human population of Cat Ba Island increased dramatically, the CBL population is estimated to have numbered between 1500 and 2700 individuals. (I. Schneider, Tielen, Rode, Levelink, & Schrudde, 2010; Thuc, Bosch, Nguyen, & Tuyen, 2014). The number of CBL on Cat Ba Island has steadily declined since the 1970s, with only an estimated 50-100 individuals remaining in 2000 when the conservation group the Cat Ba Langur Conservation Project was established on the island (Schneider et al., 2010; Stenke, 2001). Today, CBL has a global population of approximately 66 individuals (pers. comm.Leonard, 2018), with 60 residing in three fragmented wild populations on Cat Ba Island, and six in a small captive group at the Endangered Primate Rescue Centre in Cuc Phuong National Park (Hendershott et al., 2016; Nadler & Long, 2000).

Appearance of the CBL

The colouring of the CBL changes over the course of their lifetime, with infant langurs born bright orange, before their coat gradually changes to a dark brown/black with a bright yellow-white head and shoulders and a grey band that runs from their thighs to their tail (Figure 2.3) (Groves, 2001; Hendershott, 2017; Nadler & Long, 2000). Brightly coloured infants are common amongst colobines, however the reason for the dramatic changes in colour are still uncertain; theories generally suggest that it has evolved as signalling or protection against predation or infanticide (Liu et al., 2013).

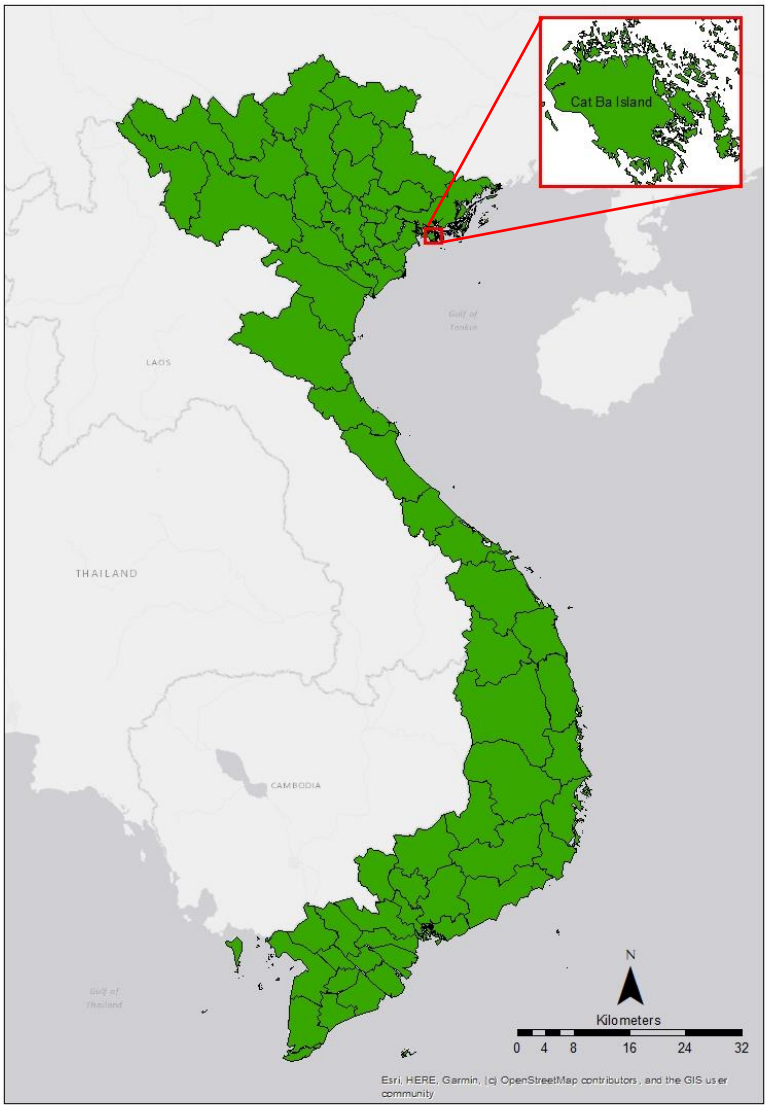


Figure 2.2 Location of Cat Ba Island, Hai Phong, Vietnam. Basemap source: (ESRI 10.8, Michael Bauer Research GmbH, & General Statistics Office, 2022; H. Esri, Garmin, OpenStreetMap contributors, 2022)

Adult langurs exhibit very little sexual dimorphism beyond a slight coloured pubic patch visible on females but not found on males (Brandon-Jones, 1995; Hendershott, 2017; Nadler & Long, 2000). In terms of size, there is little difference between the two sexes: the CBL have an average weight of 9-11kg (Schrudde et al., 2010); male langurs measure around 53.7cm from head to the base of the tail, with an additional 85.4cm for their long tails, while females have an average length of 53.0cm and tails at 85.3cm long (Nadler & Long, 2000).

Figure 2.3 The Cat Ba langur (*Trachypithecus poliocephalus*) colouring. Left: juvenile and adult. Infants are born with bright orange fur, which gradually darkens as they become sub adults. Right: adult langur. Adults have black fur with white heads and shoulders and a grey band covering their thighs. Photos: K. Apthorp, 2016.

Social grouping of the CBL

As folivores, CBL mainly consume leaves and fruits (Hendershott, 2017; Hendershott et al., 2016). As a result, they experience reduced intra-group competition between individuals and spend large periods of the day sleeping or inactive (Hendershott, 2017; Richard W. Wrangham, 1980). They appear to have a wide range of food preferences, however detailed study on the diet of CBL has only been undertaken in the last few years (Ruskin, unpublished, 2016).

Langur groups are generally single male, multi-female and made up of 25 to 30 individuals (Brandon-Jones, 1995; Burton et al., 1995; Hendershott, 2017; Steinmetz et al., 2011). Males disperse from their birth group and can form bachelor groups with other males until they find their own group. Groups are female-bonded and exhibit high levels of allo-mothering, with females sharing the care of infants and juveniles. As single male groups, there is low intra-sexual competition between males, however ad hoc observations during data collection did show aggressive behaviour toward and perhaps between females of one group. At least one female was observed partially scalped during the study period, however she went on to make a full recovery. This wound also appeared amongst other female langurs in the group, however the cause or culprit of the attack was never witnessed (pers. comm K. Ruskin).

There is limited territoriality exhibited by the CBL – observations during data collection showed that the ranges of groups within Cua Dong frequently overlapped, including sharing some sleeping site locations. During data collection, some confrontations were observed between males of neighbouring groups upon encountering one another. This generally involved calling and aggressive charging; however, instances of short bursts of fighting were

also seen. In 2020, the first recorded observation of infanticide as a result of a group takeover by a bachelor male was made (pers. comm, Cam). It is possible that the increased pressure on males to access females due to the small population numbers in the Cua Dong region, and the small size of the forest fragment available to them, is triggering aggressive behaviour.

Geography and climate of Cat Ba Island

CBL are exclusively found on Cat Ba Island, situated within the Cat Hai district, Hai Phong city, and located east of Hai Phong, Vietnam in the Gulf of Tonkin (20°42'-20°54', 106°54'-107°09') (Figure 2.4). The island sits at the western end of Ha Long Bay, a world-famous UNESCO world heritage site established in 1994 (Nadler & Long, 2000). Cat Ba Island comprises a main karst island approximately 140km^2, surrounded by approximately 366 smaller islands which form the Cat Ba Archipelago, an area covering approximately 240km (Mark, 2009; Nadler & Streicher, 2004; Van et al., 2010; Viet & Lin, 2001).

Cat Ba Island and the surrounding islands are part of a Carboniferous and Permian limestone formation that stretches across Northern Vietnam (Viet & Lin, 2001). The islands, which are the remains of karst mountains submerged over 7000 years ago, are the third largest cluster of coastal islands in Vietnam, with Cat Ba Island the largest limestone island in Southeast Asia (Van et al., 2010). The topography of Cat Ba Island is characterised by large vertical cliffs of limestone with elevations up to 200m, rocky slopes and long depressions forming valleys (Nadler & Long, 2000; Quinn & Woodward, 2015). The limestone is sharp and grooved from rainfall (Quinn & Woodward, 2015) and cuts through material and skin easily.

The main forest type on Cat Ba Island is tropical monsoon humid forest, with wetlands and mangroves to the north-west of the island (I. Schneider et al., 2010; Tien Bui et al., 2016). Due to the nature of the limestone karst, surface water is not retained in the rock, instead draining off to underground rivers or lost to the surface environment completely (Fan et al., 2011). Soil is also difficult to retain, resulting in scrub-like shrubs on the summits and ridges tropical monsoon humid limestone-karst rainforest on the lower slopes and valleys (J.-W. Kim & Thin, 1998; Quinn & Woodward, 2015; Stenke & Canh, 2004; D. Tan et al., 2012).

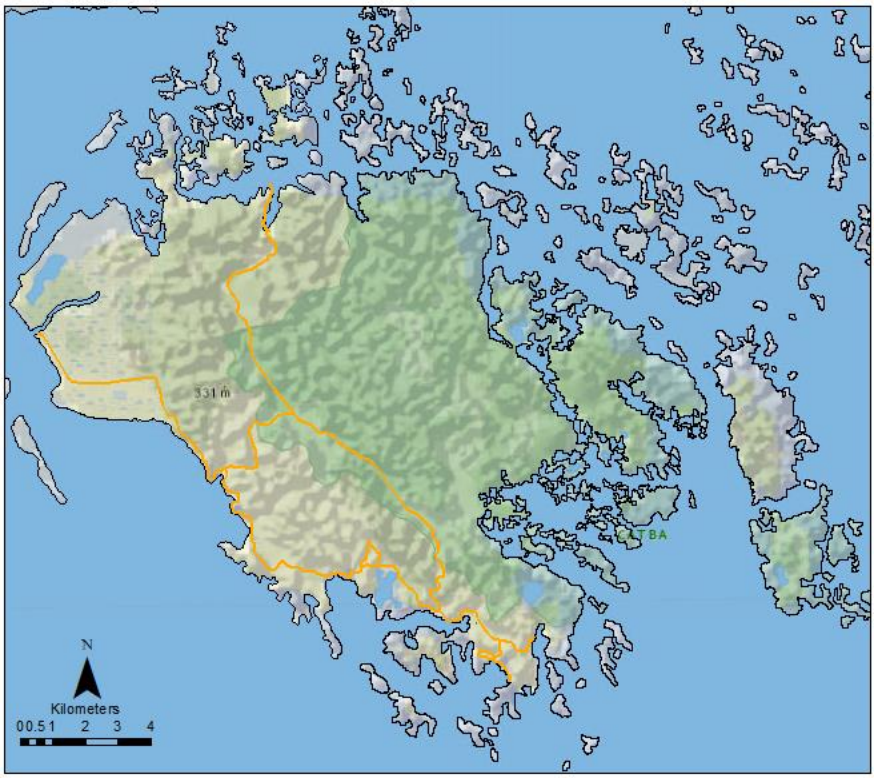


Figure 2.4 Cat Ba Island, Hai Phong. Orange lines indicate major roads on Cat Ba Island. Basemap source: ESRI et al. (2021); National Geographic et al. (2011)

Very little primary forest remains on Cat Ba Island, due to extensive exploitation, leaving most forest highly disturbed or secondary forest (Nadler & Long, 2000; D. Tan et al., 2012). The remaining primary forest found on the island is within the centre of the Cat Ba National Park, however there are no records of CBL being found within this area in the recent past (Nadler & Long, 2000).

While limestone forest is the main habitat of the CBL, much of this has undergone disturbance, with areas replaced by degraded forest, shrubs, or exposed rock as a result of human development and over-use of forest resources (Thuc et al., 2014; Van et al., 2010). Historical logging and collection of forest resources such as firewood and honey collection, hunting and clearing of forest for agriculture as well as a history of fires on the island, has resulted in the loss of most of Cat Ba's primary forest (Nadler & Long, 2000; Tien Bui et al., 2016). This has resulted in current vegetation being largely secondary forest, with large patches of shrubs or bare rock on limestone slopes (D. Tan et al., 2012; Van et al., 2010). Some primary forest remains, largely around the centre of the Cat Ba National Park (est. 1986) (Stenke & Canh, 2004). Mangroves, which once found extensively along the north-west coastline, have also

undergone destruction and degradation as a result of large-scale aquafarming (Nga & Tung, 2018). Despite the degradation of the forests, Cat Ba Island and its associated islands are believed to have some of the highest levels of biodiversity in Vietnam (Clements et al., 2006; Van et al., 2010).

The climate is a typical tropical hot-cool cycle, with a humid, monsoon season lasting from May to October and a cooler, dry season from November to April (Hendershott, 2017; Hendershott et al., 2016; Van et al., 2010). The average annual rainfall is 1800-2000mm, and the average temperature is 23.8°C (V. Hoang & Lin, 2001; Merkel, 2019; Van et al., 2010). Typhoons are common during the wet season, with 28 per cent of all typhoons affecting the Vietnamese coastline, also falling at Cat Ba Island (UNESCO, August 2015).

Fauna of Cat Ba Island

During the Late Pleistocene to early Holocene, Cat Ba Island is believed to be connected to the mainland, allowing for the dispersal of fauna to the island (Abramov & Kruskop, 2012). A wide array of microhabitats is created by the complexity of the limestone karst landscape, creating high levels of animal and plant biodiversity (Abramov & Kruskop, 2012; Goldscheider, 2019; Tuyet, 2001). The number of species endemic to Cat Ba Island is difficult to estimate and vary across sources due to the difficulty of undertaking species surveys in the region (Abramov & Kruskop, 2012; Clements et al., 2006; V. Hoang & Lin, 2001; UNESCO, August 2015). Estimates suggest there are up to 142 terrestrial animal species on the island, including at least 58 mammal species, 70 species of amphibians and reptiles, and 205 bird species (V. Hoang & Lin, 2001; Nga & Tung, 2018; UNESCO, August 2015).

Larger mammal species include *Macaca mulatta* (the rhesus macaque), the only other primate found on the island, which lives sympatrically with one of the CBL breeding groups. While rangers suggest that the CBL flee from the macaques, very little is known regarding their interactions. Observations have been made of other langur species such as François's langur and *Semnopithecus entellus* (Hanuman langur) living sympatrically with macaques and their interactions, including instances of interspecies grooming and play in different areas (Burton et al., 1995; J. M. Johnson, 1982; Manohar & Mathur, 1992; Nerlekar, 2012). In other

instances, habitat fragmentation has been suggested to increase aggression and competition over food resources both within and between species (Erinjery et al., 2017).

Macaca fascicularis (the crab-eating macaque) from southern Vietnam have been introduced to Cat Dua, a small island off Cat Ba Island, popularly termed 'Monkey Island.' The macaques are billed as a tourist attraction, and there is extensive and unregulated contact between guests to the island and the primates. During a visit to the island, high levels of aggression were observed between individual macaques, and between macaques and humans. Tourists often try to feed the monkeys and touch infants, resulting in reports of attacks by macaques, which can cause serious injury to humans. As the island experiences low levels of return visits by tourists, there is little incentive to regulate interactions between humans and the macaques.

Other larger species inhabiting the island potentially include *Viverricula indica* (small Indian civet), *Paradoxurus hermaphrodius* (palm civet), *Melogale moschata* (ferret badgers), *Capricornis maritimus* (serow), *Sus scrofa* (wild pigs), and even *Prionailurus bengalensis* (leopard cat) (Abramov & Kruskop, 2012; Hendershott, 2017; Nadler & Long, 2000). It is uncertain how many of these species actually remain on the island (Hendershott, 2017; Nga & Tung, 2018). Sightings of the leopard cats are particularly vague in nature, reported by local farmers as second-hand stories they had heard with no distinct details. While the presence of larger predators has the potential to threaten or even hunt the CBL (Borries et al., 2014), no reports have been found to suggest that their habitats overlap with the CBL, or that they are still extant on the island. The island is also home to *Ratufa bicolor* (giant black squirrel) (Nadler & Long, 2000), which can be mistaken for the CBL due to its size and colouring.

Other vertebrates include up to 29 species of bats (Abramov & Kruskop, 2012), and 205 bird species (Clements et al., 2006; Nadler & Long, 2000; Nga & Tung, 2018). While raptors have been reported to prey on langurs at other sites (Hrdy, 1977), occurrences appear to be rare on langurs in Vietnam in general. Hendershott (2017) reported that she observed several occasions where kites and crows swooped CBL groups, however their threat as predators is unclear. In fact, Nadler and Long (2000) suggest that there is an absence of natural predators for the CBL remaining on the island, however, during this study, two rangers recounted

occasions in the past when they had witnessed langurs being killed and eaten by large pythons.

The limestone karst of Cat Ba Island also appears to be home to a diverse array of amphibians and reptiles though exact numbers are difficult to determine due to the complexity of the terrain (Clements et al., 2006; Nadler & Long, 2000). During the study period, rangers reported catching a foreign researcher who had come to study geckos on the island, illegally capturing samples to smuggle off the island. Cat Ba Island offers diverse terrestrial taxa that are yet to be fully discovered and as a result must be carefully managed to prevent exploitation.

Beyond native fauna, Cat Ba Island is also home to diverse array of introduced species, including goats, domestic dogs and cats. Introduced species can represent a serious threat to biodiversity, particularly in closed ecosystems such as that found on Cat Ba Island (Carrete et al., 2009; Chetry et al., 2010; D. Tan et al., 2012). Goats and dogs are found in large numbers around Cat Ba town, but there are also an alarming number of free roaming goats in the Viet Hai corridor region – an area within the CBNP (Figure 2.5). Goats can have serious implications for the environment by destroying vegetation and impacting native animals if left unchecked (Carrete et al., 2009)**.** There seemed to be very little concern regarding their presence within the coastal region of the CBNP amongst authorities, despite the presence of CBL in the area.

Figure 2.5 Goats on Cat Ba Island. Left: Goats on the road from Viet Hai village to the Viet Hai harbour. Right: Goats free roaming along the coast to Viet Hai, within the national park boundary. Photos: K. Apthorp, 2016.

Flora of Cat Ba Island

The vegetation of Cat Ba Island has not been widely researched, and our knowledge of the forests is still limited (Nga & Tung, 2018). Yet even with the limited work undertaken to date, it appears that the limestone karst of Cat Ba Island is home to at least 1561 species of plant. Within the Cat Ba National Park, 245 species have been identified as agricultural plants and 69 have been classified as rare (V. Hoang & Lin, 2001; Nga & Tung, 2018; D. Tan et al., 2012).

A survey conducted by J.-W. Kim and Thin (1998) identified seven main vegetation types: tropical monsoon humid forests found on the limestone are comprised of both limited primary and the more widely distributed secondary forests; wind dry scrubs on summits; mangroves along the northwest region of the island; scramble vegetation, predominately found alongside roads and in areas cleared of forests; weed vegetation commonly found along highly trafficked paths; limestone cave vegetation; and anthropogenic trampling vegetation found within pasture and agricultural areas (J.-W. Kim & Thin, 1998).

Within the Cat Ba National Park, at least 38 invasive plant species have been identified (D. Tan et al., 2012). These species have mainly been found within areas that have experienced high levels of disturbance and alongside roads (D. Tan et al., 2012). The two most invasive species, both originating from Central America, *Chromolaena odorata* and *Mimosa diplotricha* are widely spread across Cat Ba Island and threaten the health of adjacent native species (D. Tan et al., 2012). The presence of these species along roads and walking tracks indicate that their spread is occurring due to the movement of humans as well as via natural means (D. Tan et al., 2012). Invasive species can cause significant damage to ecosystems and alter environments irrevocably, yet there appears to be little coordinated effort by the Cat Ba National Park or conservation groups to manage this threat (Dawkins, 2007; D. Tan et al., 2012). Despite this, the CBL appear to have adapted to eating at least two invasive species, *Ageratum sp.* and *Lantana camara* (West Indian lantana), suggesting that the CBL may be somewhat flexible in responding to changes to their environment, which could have positive implications for their future conservation (Nadler & Long, 2000).

Human Impact

Archaeological evidence suggests that first human occupation of Cat Ba Island dates to 25 000 BP (Van et al., 2010). The island has been used as a military base since French colonisation of Vietnam. Limestone caves were used as hospitals and shelters for the local communities during periods of fighting. The island was also used as a military base during the Vietnam War; prior to the outbreak of the war, the local inhabitants, who were largely fisherman of Chinese ancestry, were removed from the island by the Vietnamese government (Dawkins, 2007; V. Hoang & Lin, 2001; Nadler & Long, 2000). Following the war, the government promoted a 'Return to the Village' program of resettlement, predominately from the highly populated regions around the Red and Mekong River Deltas to less populated areas, including Cat Ba Island (A. Dang, Goldstein, & McNally, 1997; Dawkins, 2007; Robinson, 2003). Vietnamese families were offered land and encouraged to migrate from the crowded areas of the Vietnamese mainland to designated 'New Economic Zones' (A. Dang et al., 1997). The presence of soldiers on Cat Ba Island during the war and the subsequent migration to Cat Ba Island appears to have been a turning point in the human-langur relationship. Those whose families were brought to the island via the Return to Village program recollected memories of langurs being regularly close to the villages and lacking any great fear of humans.

This lack of fear may be the reason langurs were hunted so easily in the period following the 1970s. Soldiers stationed on the island between 1970 and 1986 are generally blamed for the rise in CBL hunting, with the loss of 500-800 langurs estimated (Van et al., 2010). Interviews with ex-poachers also suggest that some hunting of the langurs was due to a lack of food following the migration to the island. An ex-poacher, now a community leader in one of the communes, described the ease with which the langurs could be shot in large numbers due to their lack of fear of people and historical presence near many villages. Langurs are often curious about people and groups and rarely run, making them easy targets for poachers (N. Mai, 2004). While other reports suggest that the langurs were not particularly appetizing to eat, there is evidence that suggests those encouraged to migrate to New Economic Zones such as Cat Ba Island, lacked resources and food following their move (Robinson, 2003), perhaps leading them to hunt easy sources of food regardless of the taste.

Beyond bushmeat, langurs are predominately hunted for use in traditional remedies; an estimated 2000 langurs have been killed due to demand for such remedies since the 1960s (N. Mai, 2004; Nadler & Long, 2000; Thuc et al., 2014). In addition to direct hunting, langurs are threatened by ongoing resource depletion and illegal logging within their home ranges (Nadler & Long, 2000; Schrudde et al., 2010; Stenke & Canh, 2004).

In 1986, as part of the Vietnamese Government's commitment to reforming forest management, the Cat Ba National Park was established designating a large proportion of forest on Cat Ba Island as 'Prohibited Forest', later re-termed 'Special-use Forest' (Decision No. 79-CT, 31 March 1986) (Boissiere et al., 2009; Meyfroidt & Lambin, 2008b; Phuong & Dung, 2001). Originally under control of the People's Committee of the City of Hai Phong, responsibility of the park was transferred to the Ministry of Forestry - now the Ministry of Agriculture and Rural Development (Phuong & Dung, 2001). This original area of protection included 98 km^2 of Cat Ba Island, and 54 km^2 of the surrounding ocean and smaller islands (V. Hoang & Lin, 2001). In 2006 the national park was increased to cover 85km^2, more than 50 per cent of island and established 14 ranger stations, requiring the removal of several small villages within what is now the centre of the Cat Ba National Park (I. Schneider et al., 2010; Stenke & Canh, 2004).

The population of Cat Ba Island is predominately of Kinh and Chinese ancestry and has steadily grown from 5,850 people in 1986, to 10,673 individuals living on the island in 1999, and 20,000 in 2017 (V. Hoang & Lin, 2001; Nga & Tung, 2018; Son, Pigram, & Rugendyke, 1999; Van et al., 2010). Permanent residents on Cat Ba Island live within seven communes in addition to the fluctuating tourist numbers in Cat Ba town, the main town and tourist destination on the island. Almost half of Cat Ba's population lives in rural areas, relying on agriculture and associated industries, with an average estimated net annual income of US$325 (AU$468) per capita (T. Mai & Smith, 2015). As a result, most of those living in rural areas of Cat Ba Island are living in poverty. As the human population have continued to grow, the numbers of langurs have rapidly dropped in response to ongoing human intervention via logging, forest degradation, poaching and the encroachment of human residential, tourist and urban areas (Nadler & Long, 2000).

The communes border the National Park boundaries, with the exception of Viet Hai, home to roughly 77 households (Dawkins, 2007; Van et al., 2010). Viet Hai is the only village remaining within the national park core zone, and a popular stop for tourist boats. Despite the popularity, very little income from the tourism makes it to the wider Viet Hai community (T. Mai & Smith, 2015). Viet Hai residents are largely farmers, with all of the valleys within the Viet Hai region converted to farms (Dawkins, 2007). As a low-income region, the residents of Viet Hai may be expected to rely on forest resources despite their position within the national park, a protected zone; on one occasion, I observed several individuals from the Viet Hai region hunting within the protected forest. Due to its location within the boundaries of the National Park, and between the two main breeding groups of CBL, the future development and impact of Viet Hai should be monitored closely.

A floating village to the east of the island, also appears to put pressure on the protected nature of the Cat Ba National Park (Son et al., 1999 275). Located to the east of Cat Ba Island, the village is made up of dozens of floating fish farms, attached to family homes (Figure 2.6). In some cases, this village sits against the home range of the Cua Dong CBL, the main study group researched to date (Hendershott, 2017; Hendershott et al., 2016; Hendershott et al., 2018; Lees et al., 2014).

Figure 2.6 Floating village adjacent to langur home range. Photos: K. Apthorp, 2016.

The inhabitants of these floating homes are predominately employed in marine aquaculture, including collecting bivalves on the shore of Cat Ba Island, particularly around the protected area that is home to the Cua Dong CBL group (Figure 2.7). While Hendershott et al. (2016) suggests that the presence of humans is not causing behavioural stress on the Cua Dong langurs, the fisherman themselves have reported witnessing langur groups changing their

sleeping location in the early hours of the morning as a result of being disturbed by the activities of the fisherman.

Figure 2.7 Fisherman collecting fishing cages and bivalves below CBL sleeping sites. Fisherman would start prior to sunrise. Photos: K. Apthorp, 2016.

Tourism and the associated industry have also had a significant impact on Cat Ba Island and the CBL. Cat Ba Island became a tourist hotspot for Vietnamese and Chinese holiday-goers during the 1990s with numbers rapidly climbing from 45 000 visitors in 1995 to 720 000 by 2009 (Thuc et al., 2014; Van et al., 2010). As a result, tourism has become a major economic driver for Cat Ba, with the National Park drawing a large number of tourists each year, mainly between the months of June and August (V. Hoang & Lin, 2001; Son et al., 1999; Stenke & Canh, 2004; Sundqvist, 2013).

Today, over 1 000 000 tourists visit the island each year, with over 100 hotels built between 1995 and 2009 – the last few years from 2015-2017 have also seen a flurry of hotels renovated and built as owners attempted to beat the restrictions that a successful World Heritage site bid would bring (Van et al., 2010). Plans for several large-scale resorts on the island also have potential to significantly impact the small langur population remaining on the island (Sundqvist, 2013; Vinaconex, 2011). Currently, tourist activities include rock climbing, kayaking and swimming day trips to areas close to the two remaining langur home ranges. While tourists are warned not to approach the langurs and to stay out of protected and prohibited areas, they are not closely monitored during their activities, and it is common for individuals and groups to seek out the langurs through these activities.

Studies by T. Mai and Smith (2015, 2018), have modelled the current rate of tourism and its social, economic and environmental impacts and have found it to be unsustainable for the island. In particular, they identify the impact that continued hotel and resort development will have by encroaching upon protected forest, the freshwater limitations of the island, and the dramatic increase in pollution as a result of massive tourism to the island (T. Mai & Smith, 2015, 2018). Pollution around Cat Ba Island, particularly within the marine environment is already at alarming levels, with meters of rubbish washed up onto the beaches and coastline within the CBL habitat (Figure 2.8). At the rates observed during their study, T. Mai and Smith (2018) predicted that tourism on Cat Ba Island would likely reach capacity by 2022 unless serious planning around the sustainability of development and tourism and the floating village was undertaken (T. Mai & Smith, 2015, 2018; Son et al., 1999).

This is particularly concerning due to plans for a mega resort to be built on the island covering 17227.48km^2 from Cat Ba Town to the Tran Chan Commune (Sundqvist, 2013; Vinaconex, 2011). The Cat Ba Amatina project proposes to encompass a marina, casino, several five-star resorts, golf course, theme park and shopping centre (Vinaconex, 2011). Initial infrastructure for this had been built, including roads and basic utilities (Vinaconex, 2011), however as of 2022, it appears that investors are still being sought. While not directly impacting the current National Park, the increase in tourists and pollution would have a serious impact on the local community and natural forest and marine ecosystems. In light of the assessments undertaken by T. Mai and Smith (2015, 2018), the completion of such a massive resort is likely to push tourism on Cat Ba Island to unsustainable levels.

Figure 2.8 Rubbish from marine waterways along coast of the CBL habitat. Left: rubbish extended within the tree line and measured 0.5m deep. Photos: K. Apthorp 2016.

Tourism is also having a more direct impact on the CBL; as tourism increased during the 1990s, demand for the CBL for use in local herbal remedies led to an increase in poaching (Nadler et al., 2007; Stenke, 2001; Thuc et al., 2014; Van et al., 2010). While hunting of the langurs is illegal and rangers are employed to monitor and protect the langurs, poaching has not been wiped out and is still a threat to the survival of the CBL.

Conservation of the CBL

In 1983, the Cat Ba Protected Area was established before becoming the Cat Ba National Park in 1986 (Nga & Tung, 2018). In 2006, the area of the national park was expanded to cover 85 km^2 of Cat Ba Island and surrounding waters (I. Schneider et al., 2010; Stenke & Canh, 2004). The two main home ranges of the CBL are currently contained within the boundaries of the national park, with a third smaller group of langurs outside the park.

In 2000 the Cat Ba Conservation Project was established by the Munster Zoo and the Zoological Society for the Conservation of Species and Populations (ZGAP) to assist in the conservation and protection of the CBL and to assist in advising the CBNP in relation to CBL policies (I. Schneider et al., 2010; Stenke, 2001; Stenke & Canh, 2004). As the primary conservation group in situ on the island, the CBLCP has had great success in promoting education-based programs amongst the local communities and businesses. Local knowledge of the langur is widespread, particularly amongst the businesses in Cat Ba town. Local restaurants promote CBL conservation, however amongst tourists, promotion of the CBL may serve to drive interest in locating the species. During the data collection phase of this study, many tourists and local rock climbers expressed interest in finding the CBL, lacking an understanding of why this may have a negative impact on the species. The potential of ecotourism, particularly unregulated ecotourism, may be a major threat for the CBL going forward as local awareness grows beyond the permanent Vietnamese population and tourism continues to increase (Nadler et al., 2007; Son et al., 1999).

In 2004, UNESCO designated the Cat Ba Biosphere Reserve encompassing 262.41 km^2 of limestone karst forest, wetlands, mangroves and coral reef (UNESCO, August 2015). Despite this, the impact from fish farming and sea floor farming is having a detrimental effect on the

ecosystems intended to be protected by the reserve (Abramov & Kruskop, 2012; Van et al., 2010).

As part of the efforts of CBL conservation, the CBLCP, in association with Fauna and Flora International (FFI) has established a ranger and community-based protection network of almost 200 people including national park rangers, ranger stations and local community members (Schrudde et al., 2010). This also includes a protected 'Sanctuary' area within the boundaries of the national park, established in 2001 and covering 28 km^2 (I. Schneider et al., 2010; Stenke, 2001; Stenke & Canh, 2004). The area is home to one of the main breeding populations of CBL, though they are highly under studied and little is known about their behaviour in comparison to the Cua Dong group.

In 2012, two female langurs that had become isolated from the main breeding groups were successfully translocated to the Sanctuary group (Leonard, Raffel, Zsalakó, Adler, & Passaro, 2014). The two females were fitted with GPS collars and monitored following their release. Tracking their locations revealed that following some movement around the sanctuary region, the two females finally settled with Sanctuary groups (Leonard et al., 2014; Mai Sy, 2013). The successful assimilation of the females with the larger langur groups is a positive outcome and suggests that future translocation of isolated individuals and even groups, such as the third non-breeding group of langurs to the north of Cat Ba Island may be possible.

Tourists and locals are prohibited from entering the Sanctuary, however just outside the entrance to the sanctuary is a popular stopping point for tourist boats for kayaking and swimming. The area is patrolled by National Park rangers, yet the langurs groups within the sanctuary are not well monitored. Poaching events still occur in the area, possibly as a result of poor monitoring and the difficulty of the terrain – it is impossible to patrol all parts of the sanctuary, and the isolated nature of some boundaries leave it open to access from poachers.

In contrast, the Cua Dong population is constantly monitored and sits in a popular tourism and marine thoroughfare. The Cua Dong population neighbours the floating village, parts of which sit immediately against parts of the CBL home range. Due to their proximity to the langurs, locals often assist the national park ranger who monitors the groups in the area, in locating individual groups of CBL. Fishermen or oyster farmers were often able to provide information

about the location of the langurs, and in some cases, were responsible for alerting the ranger to the presence of strangers in the area who asked questions about the location of the langurs or had been seen in the protected areas. This provides an extra layer of monitoring in the form of an informal community watch, emphasising the importance of local involvement in conservation.

While local informants may be important in monitoring and protecting the CBL, the increased informal surveillance of the Cua Dong group does not lead to increased prosecution of potential poachers. Penalties for encroaching upon the CBL habitat or poaching are not well enforced, as is the case for other highly endangered primates in Vietnam (Burton et al., 1995). Social relationships are critical to Vietnamese society, which can have both negative and positive impacts on the langurs.

Due to the importance of maintaining positive social connections, rangers can be reluctant to formally punish suspected or actual poachers in the area (Burton et al., 1995; Hendershott, 2017). While poachers are generally thought to be non-locals, the risk of offending a potential social connection makes punishment rare. This results in little in the way of deterrents. In contrast however, some rangers have found that developing a social bond with suspected poachers reduces their likelihood of offending. One ranger explained that by developing a friendship with suspects and making it clear that any poaching will cause negative consequences for the ranger, the suspects were then reluctant to continue. Whether or not reluctance extended to the whole island, or just the region around the ranger, is uncertain, and may just ensure that in the future, poachers will target areas they know are not closely monitored – as is the case of seven langurs poached from the Sanctuary in 2015.

While guns and hunting are tightly restricted on the island and wider Vietnam, on one occasion, I observed several individuals from the Viet Hai region hunting within the protected forest. On a separate occasion on the west side of the island, I also came upon an individual with a gun, firing into the forest. During data collection, I came across the occasional poaching trap for marine lizards or reptiles (Figure 2.9), however the presence of these traps suggests that current monitoring of the Cat Ba langur habitat is inadequate to prevent hunters whether they are locals or strangers to the island, from accessing the areas.

The ongoing collection of forest resources is also a serious threat to the future of the CBL and its habitat. Due to widespread poverty on Cat Ba Island, some residents continue to rely on the forest to provide food, fuel and income (T. Mai & Smith, 2015; Nadler & Long, 2000; Tien Bui et al., 2016). During data collection, it was evident that there was some ongoing firewood collection taking place in some parts of the Cua Dong region (Figure 2.9). Honey collection has also become a serious issue in Cat Ba as locals use fire to clear bees, putting the habitat of the langurs at risk (N. Mai, 2003; Nadler & Long, 2000). To combat this threat, FFI developed a bee-keeping program to educate locals and teach domestic beekeeping to protect the natural resources of the CBNP and CBL habitat (N. Mai, 2003). Locals are now able to keep their own hives and use and sell their honey products, including a potent honey rice wine. While this has been successful for some of Cat Ba's residents, there is still demand for illegal honey collection. During the study period, strangers were found within the Cat Ba langur Cua Dong home range suspected of searching for local honey. The collection of forest resources threatens to degrade the langurs' habitat further and puts increased pressure on the fragmented population.

Extensive wildfires have also damaged the forests of Cat Ba Island, particularly between 2004 and 2011 (O'Brien, Kinnaird, Nurcahyo, Prasetyaningrum, & Iqbal, 2003; Thuc et al., 2014; Tien Bui et al., 2016). Most fires are started either directly or indirectly by residents of Cat Ba Island, and have occurred across the island, including within the CBL habitat; though most appear to have been focussed on the centre and west of the island (Tien Bui et al., 2016). Fires such these threaten the already fragile and fragmented habitat of the langurs and the wider Cat Ba ecosystem. The small size and highly fragmented nature of the remaining population of the CBL, leaves them at high risk from genetic issues, habitat loss and degradation, environmental disasters such as typhoons, fires, climate change, and the continued impact from human activity (Nadler & Long, 2000; Stenke & Canh, 2004; Van et al., 2010).

The CBL component of this thesis will undertake the first detailed analysis of the habitats of the two main breeding populations, and an analysis of a region that may represent a corridor or area for habitat expansion.

Figure 2.9 Evidence of illegal activity in the CBL habitat. Left: Poacher's trap for water monitors found within the CBL home range. Right: Evidence of tree cutting. Photos: K. Apthorp, 2016.

2.4.2.2 Rhinopithecus (snub-nosed monkeys*)*

The snub-nosed monkeys are members of the odd-nosed group within the sub family Colobinae, characterised by their flat noses. The earliest snub-nosed monkey fossils dated to 1.2 MA, suggesting that they once inhabited a large part of central and southern China (Kirkpatrick, 1995). Modern snub-nosed monkeys were first described in the 19th century by Milne Edwards (Groves, 2001; Jablonski & Peng, 1993; Kirkpatrick, 1995). Originally considered a single species, *Semnopithecus roxellana,* with a wide geographical range and variation in habitat, they have since been recognised as five separate species (Table 2.3) of the genus *Rhinopithecus* (Jablonski & Peng, 1993; Kirkpatrick, 1995; B. Li, Pan, & Oxnard, 2002; Liedigk et al., 2012; Napier & Napier, 1967).

Today, three of these species are still endemic to China, while *Rhinopithecus strykeri* is endemic to Myanmar, on the border with China (Geissmann et al., 2011; Yang et al., 2019) and *Rhinopithecus avunculus* (TSNM); is the only snub-nosed monkey endemic to Vietnam. The TSNM is also the only member of the snub-nosed monkey family found in sub-tropical forest; the other members of the snub-nosed monkey group are found predominately in temperate forests (Grueter et al., 2017).

Table 2.3 Members of the snub-nosed family genus *Rhinopithecus*

Species	**Location**	**Est. Population**	**IUCN Red List status**	**References**
Rhinopithecus avunculus (Tonkin snub-nosed monkey)	Vietnam	200	CR	FFI (2020)
Rhinopithecus bieti (black and white snub-nosed monkey)	China	2500	EN	Grueter, Li, Ren et al. (2017); Z.-F. Xiang, Huo, & Xiao (2011)
Rhinopithecus strykeri (Myanmar snub-nosed monkey)	Myanmar	260-330	CR	Geissmann et al. (2011)
Rhinopithecus brelichi (grey snub-nosed monkey)	China	750	EN	Z.-F. Xiang et al. (2009)
Rhinopithecus roxellana (golden snub-nosed monkey)	China	15 000	EN	Liedigk et al. (2012)

The phylogeny of *Rhinopithecus* suggests they are monophyletic, with hybridisation occurring between the different species as they became differentiated likely due to habitat specialisation during the Pleistocene (B. Li et al., 2002; Liedigk et al., 2012). *Rhinopithecus avunculus* diverged first, however, it appears it later came into additional contact with early members of *Rhinopithecus bieti* and *Rhinopithecus strykeri* (Groves, 2001; Liedigk et al., 2012).

Snub-nosed monkeys live in large bands – in some cases of up to 400 individuals for some of the Chinese species, with flexible social structures (Quyet, 2004). These bands are comprised of multiple one male, multi-female units (OMU), which flexibly congregate together, along with multi-male groups for periods of time before separating (Boonratana & Le, 1998; Kirkpatrick, 1995; Kirkpatrick & Grueter, 2010). Fission-fusion between OMU can occur for a short number of days or for longer periods of weeks (Kirkpatrick & Grueter, 2010). The cause of the fission-fusion of these bands is unclear but has been attributed as a seasonal occurrence or food related, however the variation in frequency of these events, and composition of the different species' diets, makes the effect of food availability on group cohesion unclear (Boonratana & Canh, 2013; Boonratana & Le, 1998; Kirkpatrick & Grueter, 2010; Le & Boonratana, 2006).

The home ranges of bands appear to overlap, and food competition between groups is low (Boonratana & Le, 1998; Kirkpatrick & Grueter, 2010). Despite high levels of sexual dimorphism, there appears to be very low rates of aggression between OMU, and grouping

between OMU and multi-male groups is common as they come together to feed, sleep, and even travel together (Boonratana & Le, 1998; Kirkpatrick & Grueter, 2010; Quyet, 2014). Due to difficulty in locating and following groups, finer details of social behaviour such as allomothering, has yet to be determined as individuals are not easily distinguishable for observation purposes (Hai, 2008; Kirkpatrick & Grueter, 2010).

As a result of human expansion into their forests over hundreds of years, ongoing hunting and habitat destruction, all members of the snub-nosed genus are endangered or critically endangered (Quyet, 2014; B. Li et al., 2002). As folivores, snub-nosed monkeys are described to be distasteful to eat, however, like many colobines, they have historically been hunted for use in traditional remedies (Le & Boonratana, 2006; Levine, 2016; Thach, 2009). All species are experiencing some form of habitat fragmentation, however the TSNM is experiencing this threat at an alarming rate, making it the most threatened of the snub-nosed monkeys.

2.4.2.2.1 *Rhinopithecus avunculus* (the Tonkin snub-nosed monkey)

First described by Dollman (1912) from a site by the Song Koi River in Yên Bái Province, the historical distribution of the TSNM included populations in Yen Bai, Ha Giang, Tuyen Quang, Cao Bang, Bac Kan, Thai Nguyen and Quang Ninh provinces (Dollman, 1912; Groves, 2001; Quyet & Covert, 2010; Thach, 2009). Yet by 1986, a lack of observations of the species led Russell A. Mittermeier and Cheney (1987) to announce its likely extinction.

A small group rediscovered by Ratajszczak in the 1990s in Bac Kan Province, led to a series of rediscoveries of the monkey in Tuyen Quang Province, and eventually the discovery of a population near Khau Ca, Ha Giang Province, within the buffer zone of the former Du Gia National Reserve by Quyet in 2002 (Covert et al., 2008; Ratajszczak, Ngoc, & Pham, 1992; Thach, 2009). The discovery of another population in Tung Vai, Ha Giang Province near the border with China, raised questions around the possibility of TSNM also inhabiting limestone karst forests in China (Quyet & Covert, 2010). Until the discovery of any evidence supporting this however, the TSNM is still considered endemic to Vietnam.

Historically, the total population of the TSNM has been highly fragmented across several provinces (Figure 2.10), including Ha Giang, Yen Bai, Tuyen Quang, Cao Bang, Bac Kan, Quanh Ninh (Le & Boonratana, 2006; Thach, 2009). Today, due to ongoing hunting, habitat

destruction and human development, significant populations are only believed to still exist in Tung Vai, with 42-53 individuals and Khau Ca, with approximately 150 individuals (Table 2.4), making for a total global population of approximately 200 (Dine, 2012; Fauna & Flora International, 2020; Quyet & Covert, 2010). Due to the location of Khau Ca within the buffer zone of the former Du Gia National Reserve, there has been speculation that there may be additional populations within the Du Gia Forest region (X. C. Le & Boonratana, 2006).

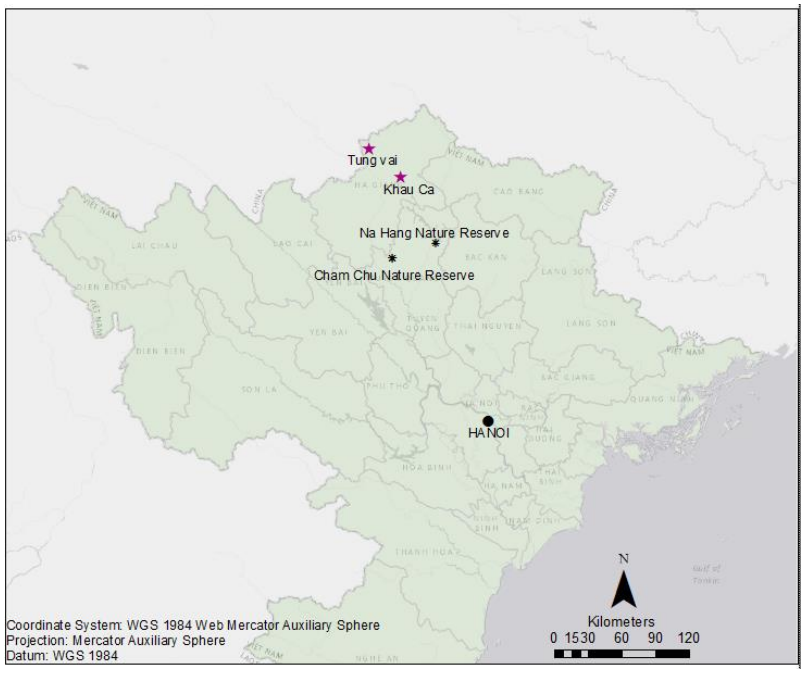


Figure 2.10 Locations of Tonkin snub-nosed monkey habitats. Stars indicate habitats with known populations as of 2022. Asterisks indicate habitats where populations previously existed but have not been confirmed for several years. Basemap source: H. Esri, Garmin, OpenStreetMap contributors, (2022).

The current population of TSNM in Khau Ca represents at least 80 per cent of the total population of TSMN (Fauna & Flora International, 2020). Based on a 2017 survey, this could indicate 25 per cent growth in the local population over two years (Fauna & Flora International, 2020). The viability of the second major population of TSNM in Tung Vai is uncertain as recent surveys have not always been able to locate the group (pers. comm. B. Rawson).

The species was listed as Endangered by the IUCN between 1988 and 1994, before its elevation to Critically Endangered in 1996 (Quyet, Rawson, Duc, Nadler, & Covert, 2020). The Vietnam Red Data Book also lists the TSNM as critically endangered, and the species is listed in the CITES Appendix I (CITES, 2019; IUCN, 2022a). It was consistently listed as one of the 25

most endangered primates in the world since its rediscovery from 2000 to 2018 (R.A. Mittermeier et al., 2022; C. Schwitzer, Mittermeier, R.A., Rylands, A.B., Chiozza, F., Williamson, E.A., Byler, D., Wich, S., Humle, T., Johnson, C., Mynott, H., and McCabe, G., 2019). Its removal from the 2022-23 list is not a reflection of the improvement if its status, but to highlight the at-risk status of other primates (R.A. Mittermeier et al., 2022).

Table 2.4 Tonkin snub-nosed monkey sites

Site	Estimated number of individuals (n)	Source
Khau Ca, Ha Giang	144-150	Fauna & Flora International (2020)
Tung Vai, Ha Giang	42-53	Dine (2012)
Na Hang Nature Reserve, Tuyen Quang	0-26*^	T. M. Hoang (2011)
Cham Chu Nature Reserve, Tuyen Quang	0-20^	Hai (2008)

*****A survey carried out in 2006 found no evidence of TSNM at the site (Thach, 2009), while a survey by Thach Mai Hoang (2011) recorded 26 individuals.
^It is unclear whether these groups remain (Fauna & Flora International, 2020).

Appearance

The colouring of TSNM includes black shoulders (Figure 2.11), back and tail, with white underside (Groves, 2001). They have unusual faces with white fur, large pink lips, blue-black cheeks and flat, upturned nostrils (Groves, 2001). The TNSM is the largest primate in Vietnam, with males weighing up to 14kg and measuring 65cm from head to rump, and 83cm tail, and females weighing 8.5kg and measuring 54cm, with 68cm tails (Dine, 2012; Ratajszczak et al., 1992)**.** In addition to the difference in size, male TSNM have significantly larger upper and lower canines compared to females (Boonratana & Le, 1998; Khac, 2014). The high levels of sexual dimorphism between the sexes indicates that males compete for access to females within their groups (Kirkpatrick & Grueter, 2010)**.**

Figure 2.11 Tonkin snub-nosed monkey (*Rhinopithecus avunculus*). Male, right and female, left with juvenile. Photos: Le Khac Quyet (FFI) & Herbert Covert (University of Colorado, Boulder) taken from Knight (2022).

Social grouping and behaviour

TSNM are reported to live in one male, multi-female groups (OMU), with unattached males forming one male units (AMU), a common group dynamic found in colobines (Boonratana & Le, 1998; L.-W. Cui et al., 2008; Kirkpatrick & Grueter, 2010). Multiple OMUs and a small number of AMUs group together to form a large band (Kirkpatrick & Grueter, 2010). Bands have been recorded up to 30 individuals in Khau Ca, however it is believed that historically groups numbered in the hundreds, similar to the Chinese *Rhinopithecus* groups (Quyet, 2014; Thach, 2009). Large bands are typical of snub-nosed monkeys, with groupings of over 400 individuals recorded for *Rhinopithecus brelichi* (gray snub-nosed monkey) (Bleisch, Ao-Song, Xiao-Dong, & Jia-Hua, 1993; Z.-F. Xiang et al., 2009), *Rhinopithecus roxellana* (golden snub-nosed monkey) (Kirkpatrick, Gu, & Zhou, 1999) and *Rhinopithecus bieti* (black-and-white snub nosed monkey) (Grueter & Li, 2008; Grueter et al., 2017). There does not appear to be any hierarchy across OMUs. Communication across bands to coordinate movement is still unclear, however is likely linked to increased calling prior to band movement or fission among black-and-white snub-nosed monkey (Grueter et al., 2017).

The dynamics between OMU and AMU groups is not well understood; Grueter and van Schaik (2009) propose that the threat of bachelor males or AMUs has led to the evolution of OMU grouping into large bands, either due to the option of collaboration between males from OMUs to combat a bachelor male threat, or through the sheer size of grouping acting as deterrents (Grueter et al., 2017; Grueter & van Schaik, 2009). Collaboration between males

from OMUs to attack a recently deposed adult male, has been observed by D. Zhao and Li (2009) among golden snub-nosed monkeys. The presence of high sexual dimorphism and high levels of aggression found in males of some species of snub-nosed monkey may further support this theory (Kirkpatrick & Grueter, 2010; Y. Li et al., 2015).

While the threat of bachelor takeovers may account for the evolutionary development of OMU banding in snub nosed monkeys (Grueter et al., 2017; Grueter & van Schaik, 2009), the current population fragmentation in modern snub-nosed monkey populations such as TSNM, means that is may also function to avoid heterospecific threats (L.-W. Cui et al., 2008). There have been regular observations of multiple groups of OMU and AMU travelling and feeding together with little to no aggression between males across snub-nosed monkey species (Boonratana & Le, 1998; L.-W. Cui et al., 2008; Grueter et al., 2017; Kirkpatrick & Grueter, 2010; Quyet, 2014; Qihai Zhou, Cai, Huang, Li, & Luo, 2007). It is also possible however, that males of OMU are more tolerant of males they are familiar with or that kinship between males of OMU facilitates a network approach to band formations – though genetic testing is required to determine familial connections across bands (Grueter & van Schaik, 2009). While the underlying cause for banding is still not clear, it appears that banding between multiple OMU is sustained by strong male-female social interactions (Grueter et al., 2017).

Bands have been found to undergo varied fission-fusion behaviour across *Rhinopithecus* species; in TSNM, fission-fusion between OMU groups appears to occur over short periods of a few days at a time (Kirkpatrick, 1995; Kirkpatrick & Grueter, 2010). In other snub-nosed monkey species, such as the black-and-white snub-nosed monkey, super groupings of OMU and AMU can occur over weeks (Grueter et al., 2009; Kirkpatrick & Grueter, 2010). Variation seen between Chinese snub-nosed monkey species and the TSNM may be accounted for by their differing diets. The availability of lichens, a widely available fall-back food, in golden snub-nosed monkey diets may explain why groupings stay together for longer periods due to the absence of competition for resources (Grueter, Li, Ren, Wei, & Schaik, 2009; Grueter et al., 2009; Grueter, Li, Ren, Xiang, & Li, 2012; Kirkpatrick, 1996). In contrast, the inclusion of clumped, uncommon species within the diet of black-and-white snub-nosed monkey in Baima Xueshan National Nature Reserve in Yunnan, China, suggests that the presence and degree of scramble or contest competition over resources may influence variations seen in band

formation and behaviour across the snub-nosed monkeys (L.-W. Cui et al., 2008; Grueter et al., 2009; K. Huang et al., 2021).

Due to flexibility in the social banding of groups, there is also some uncertainty about TSNM home ranges as they appear to overlap between groups and do not appear to exhibit strong territoriality (Boonratana & Le, 1998; Le & Boonratana, 2006). If home ranges do exist, they appear to vary from site to site, likely depending on the habitat fragmentation and degradation experienced within each populations' habitat (Boonratana & Le, 1998). Home range estimates vary from 1.5-2 km to 10 km^2 (Boonratana & Le, 1998; Thach, 2009), which are comparatively tiny compared to the 26-35km^2 home ranges of the Chinese snub-nosed monkeys (Quyet, 2014).

The sleeping behaviour of the TSNM is also not well understood. TSNM are noted to rarely leave the trees, including to sleep (N. X. Dang, Nghia, & Duy, 2014; Kirkpatrick, 1995; Thach, 2009). While the TSNM are known to sleep in trees rather than on cliff faces as seen by the CBL (Hendershott et al., 2016; Hendershott et al., 2018), it appears that they do not have set sleeping sites as seen in the CBL, and exhibit flexibility in their choice of nightly sleeping sites (Hai, 2008; Thach, 2009). Observations have recorded groups preferring to sleep in high trees or bamboo bushes, while others report that the TSNM prefer lower branches of trees 5-10m above the ground in valleys or close to limestone cliffs (Boonratana & Le, 1998; Hai, 2008; Thach, 2009). Groups of four or five are reported to settle on a single branch for the night, and groups have been recorded sleeping apart as part of the semi-regular fission-fusion that appears to occur (Grueter et al., 2017; Kirkpatrick, 1995; Thach, 2009).

Geography and climate of Khau Ca

The TSNM component of this thesis was conducted within the Tonkin Snub-nosed Monkey Species and Habitat Conservation Area at Khau Ca (Khau Ca), a small patch of forest situated on a limestone block within Ha Giang Province (220°49”-220°52”N and 105°05”-105°09”E), approximately 15 km from Ha Giang town (Hai, 2008; Kirkpatrick, 1995; Quyet, 2014). Khau Ca forest is a protected zone once positioned within the buffer zone of Du Gia Nature Reserve in North Vietnam (Figure 2.12). In 2016, Khau Ca National Park was administratively merged with Du Gia Nature Reserve, to form the Du Gia National Park (An et al., 2018).

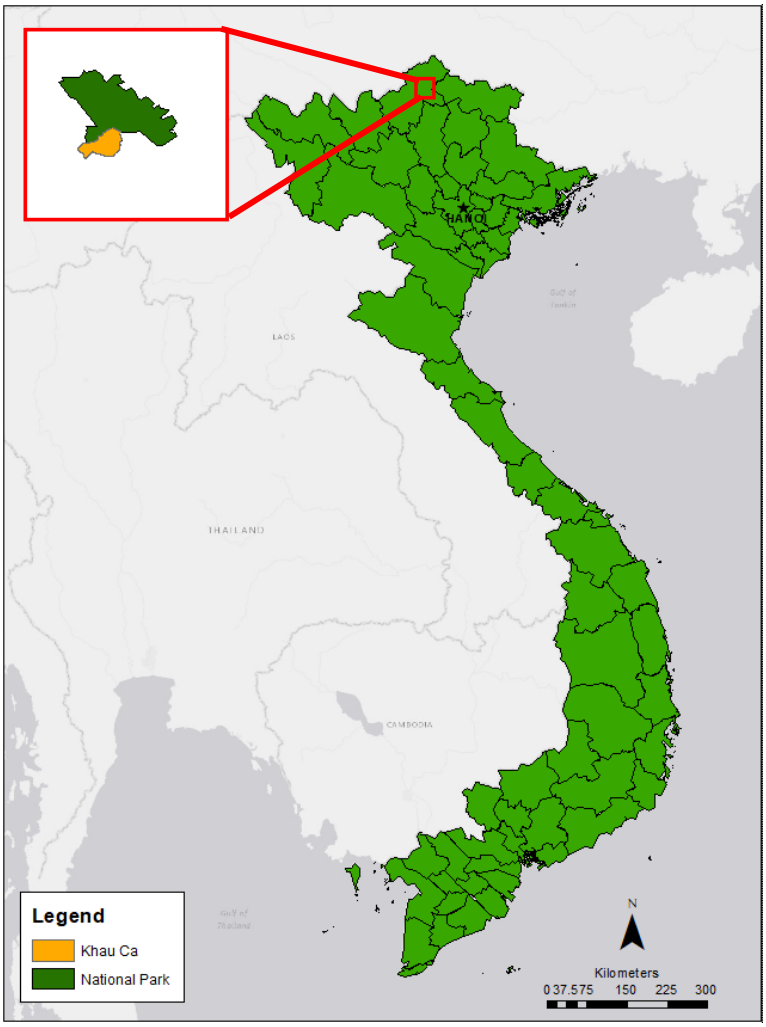


Figure 2.12 Location of Khau Ca and Du Gia National Park in Vietnam. Basemap source: ESRI 10.8 et al. (2022); H. Esri, Garmin, OpenStreetMap contributors (2022).

Khau Ca covers approximately 20.4 km^2, bordering three communes: Minh Son, Yen Dinh (Bac Me District) and Tung Ba (Vi Xuyen District) (Anh, Dang, Huan, & Duc, 2014; N. X. Dang et al., 2014; Hai, 2008; Quyet, Nguyen Anh Duc, Vu Anh Tai, Wright, & Covert, 2007). Within the larger Khau Ca area, a smaller, protected core patch of forest covering approximately 10 km^2 is home to the largest population of TSNM in the world (Fauna & Flora International, 2020). This core region resembles a bowl-like island of forest within the surrounding landscape of plantations, agricultural land, villages and roads (Figure 2.13).

Figure 2.13 Surrounding landscape beyond Khau Ca limits. Left, primary forest has been replaced by scramble vegetation. Right, farm located at campsite outside Khau Ca limits. Photos: K. Apthorp, 2016.

TSNM are now only found on steep limestone hills, however the terrain of Khau Ca is steeper, sharper and more difficult to access than other TSNM habitats (Hai, 2008). The elevation of Khau Ca varies from 400m to over 1300m (Hai, 2008; Thach, 2009). The southeast side of Khau Ca comprises steep, rocky limestone hills and peaks covered in primary evergreen limestone karst forest, with the northwest area shallower, and comprised predominantly of valleys characterised by disturbed forest and scrub (Anh et al., 2014; Boonratana & Le, 1998; Hai, 2008; Quyet, 2014; Thach, 2009). While the forest composition of other TSNM habitats may include bamboo forests, they are predominately found in tropical evergreen forests on limestone (Kirkpatrick, 1995; Le & Boonratana, 2006; B. Li et al., 2002). In Khau Ca, the forest is described as less dense than that of Na Hang, a former habitat of the TSNM, however, they are believed to prefer primary forest and may struggle to survive in degraded forests (N. Nguyen, 2000).

Due to the nature of the porous limestone, water is not preserved within Khau Ca and there is no water source within the forest, however, the main campsite located outside the core region accesses water runoff to provide water for washing and can be consumed after boiling.

The sharp and unstable nature of the limestone, steep hills, lack of water and high humidity levels within the forest make fieldwork within Khau Ca difficult and dangerous for researchers lacking the skills of the local guides (Hai, 2008; Thach, 2009). A series of trails established by previous researchers for use as transects, and maintained by the local guides and research assistants, make accessing parts of the TSNM habitat slightly easier and reduces impact to the

vegetation (Covert et al., 2008; Quyet, 2014; Quyet et al., 2007). However, these trails are not smooth or always easy to traverse, particularly when the limestone is damp or mossy.

The weather of Khau Ca is typical of Northern Vietnam, with two main seasons: a cold, dry season from October to April and a hot, rainy season from May to September (Quyet, 2014; Thach, 2009). The average rainfall is approximately 2300mm per year and the average temperature is 23.3˚C (Covert et al., 2008; Kirkpatrick & Grueter, 2010; Levine, 2016).

Fauna of Khau Ca

While studies of TSNM in Khau Ca took off in early 2000's following its rediscovery (Covert et al., 2008; Hai, 2008; Quyet, 2014; Quyet, 2004; Quyet et al., 2007; Levine, 2016; Thach, 2009; B. V. Tran et al., 2017), there has been very little targeted research into other fauna living alongside the TSNM in the area (N. X. Dang et al., 2014; "New Nature Foundation," 2016).

The few surveys that have taken place within Khau Ca using both observation and interview with local communities have identified 37 mammal species 153 bird species and 2 amphibian species inhabiting the limestone karst forest alongside the TSNM (N. X. Dang et al., 2014; "New Nature Foundation," 2016). In addition to the Critically Endangered TSNM, several species are listed as Vulnerable or above, including three primate species, and the Critically Endangered *Manis pentadactyla* (yellow pangolin), Vulnerable *Neofelis nebulosa* (clouded leopard), and Vulnerable *Arctictis binturong* (Binturong) (IUCN, 2019). As the data collection of additional fauna in Khau Ca undertaken by N. X. Dang et al. (2014) included interviews, hunted specimens and animal traces including faeces, not all of the species were observed and it is possible that some species, particularly larger mammals, no longer occur within Khau Ca.

In particular, larger predators such as leopards, forest cats and bears, may no longer occur in the area (N. X. Dang et al., 2014; Kirkpatrick, 1995). It is possible that larger mammals and predators are scarce in Khau Ca due to anthropological pressures including hunting and logging. Other species, including gibbons (although mentioned as possibly occurring in the area) were excluded from the list compiled by N. X. Dang et al. (2014), as there had been no reported sightings in five to 20 years.

During the data collection phase of this project, I observed and heard groups of macaques on several occasions, however the line of sight was never clear enough to make a species-level identification. In contrast, N. X. Dang et al. (2014) identified five other primate species (Table 2.5), including three species of macaques. N. X. Dang et al. (2014) also identified the François' langur as occurring in the nearby Du Gia National Park, suggesting that there may have been a historical overlap between the langur and TSNM.

The presence of macaques in Khau Ca raises similar concerns to those faced on Cat Ba Island. These overlapping primate species are not monitored due to the conservation focus on the Critically Endangered TSNM and as a result, we have very little knowledge regarding their interactions and impact on the TSNM. While reports suggest that TSNM do not tolerate macaques and will attack to drive them off (Thach, 2009), other studies suggest that aggression in TSNM is rare (Boonratana & Le, 1998; Kirkpatrick & Grueter, 2010). Certainly, the small size of Khau Ca suggests that overlap between the TSNM and macaques are likely to occur frequently, and there is a lack of reports of regular conflict between the two groups despite the many TSNM surveys, suggesting that aggression between the two groups may be rare.

Table 2.5 Primates inhabiting Khau Ca

Family	**Taxonomic name**	**Common name**	**IUCN Category 2022-1**
Cercopithecidae	*Rhinopithecus avunculus*	Tonkin snub-nosed monkey	CR
	Macaca arctoides	Stump-tailed macaque	VU
	Macaca assamensis	Assam macaque	NT
	Macaca mulatta	Rhesus monkey	LC
Lorisidae	*Nycticebus bengalensis*	Bengal slow loris	EN
	Nycticebus pygmaeus	Pygmy slow loris	EN

Flora of Khau Ca

Past ecological studies of the wider Khau Ca area identified 730 plant species from 136 families (Quyet et al., 2007; Thach, 2009). At least 29 of these species have been recognised as rare and endangered ("New Nature Foundation," 2016).

There are at least five distinct vegetation types that have been identified within Khau Ca: primary, secondary forest on limestone, shrub savanna, grassland, and ex-cultivated regions

(FFI 2006). The surrounding landscape consists of agricultural land, plantations, and small communities. While some research has been done to determine the diet of the TSNM (Quyet et al., 2007; Le & Boonratana, 2006; Thach, 2009), and the ecology of the TSNM (Quyet, 2014) there is still work to be done regarding their wider ecology and habitat composition (Nüchel, Bøcher, Xiao et al., 2018).

Human Impact

Historically, the area of Khau Ca was once connected to the larger Du Gia Forest to the north (pers. comm. Mr Tue). Following the end of the war, the region between Khau Ca and Du Gia experienced expansion of the rural population, in particular the Hmong, an ethnic group native to Southeast Asia, whose use of the land for rice farms, cattle husbandry and plantations of cardamom, led to the eventual disconnection of Khau Ca and Du Gia Nature Reserve (pers comm. Anon) – however officially, Khau Ca remained within the buffer zone of Du Gia Nature Reserve (Covert et al., 2008).

Over two thirds of Vietnamese citizens live outside metropolitan areas (Gomiero et al., 2000; Levine, 2016). The northern mountains of Vietnam are home to a significant proportion of Vietnam's ethnic minorities; Ha Giang province in particular, is home to some of the highest rates of poverty amongst ethnic minorities in Vietnam (C. V. Nguyen, Tran, & Vu, 2016). The increasing density of local populations continues to put pressure on isolated forest fragments due to the potential for resources these areas offer (B. Li et al., 2002).

Khau Ca sits across two districts within Ha Giang Province and is bordered by three communes: Minh Son and Yen Dinh Communes (Bac Me district) and Tung Ba Commune (Vi Xuyen district) (Hai, 2008; Levine, 2016; Thach, 2009). These are entirely rural communes, with a total population of 17,852 at the last census in 2019 (Vietnam, 2019, 2020).

Forested areas continue to be central to the livelihoods of local communities for kindling, food and other resources, while the expansion of agricultural land, urban development and the exploration and exploitation of land for mining in the region also threatens TSNM habitats (Boonratana & Canh, 2013; Hai, 2011; Le & Boonratana, 2006). Over 80 per cent of households within the Bac Me district still rely on firewood for cooking, with only 17 per cent using biogas and two per cent relying on electricity (Vietnam, 2019). Households within the Vi Xuyen

District have a lower reliance on firewood (52 per cent) and a greater use of biogas (45 per cent) and electricity (almost 3 per cent), compared to those in Bac Me (Vietnam, 2019).

While Khau Ca is protected and prohibits collection of forest resources, the surrounding forest has been significantly degraded, including within the surrounding buffer zone. The destruction of forests for sub canopy plantations including potatoes, bananas, *Lysimachia,* and cardamom has become an increasing issue (Trinh Dinh Hoang, Dung, & Linh, 2015; James, 2016). In 2016, a population and habitat survey of Tung Vai identified the ongoing illegal hunting and habitat loss as a result of plantations such as *Amomum tsao* (cardamom) and *Lysimachia sp.* was continuing to impact TSNM numbers in the area (James, 2016, 2017; Knight, 2019).

The cultivation of crops such as cardamom for its spicy seeds and *Lysimachia* for medicinal uses, have increasingly become a source of cash income for ethnic minority households across north-western Vietnam since the 1990s (Trinh Dinh Hoang et al., 2015; Tugault-Lafleur & Turner, 2009). In some areas, reliance on cash crops and forest resources can account for up to 70 per cent of household income (N. Quang,& N. Sato, 2008). Around the TSNM habitat in Tung Vai, up to 80 per cent of households were found to be involved in planting cardamom (Trinh Dinh Hoang et al., 2015).

Cardamom and *Lysimachia* plantations typically occur in montane forest in valleys and slopes, however *Lysimachia* can also be grown on thinner soil higher on limestone karst (Buckingham & Petheram, 2004; Trinh Dinh Hoang et al., 2015). Due to the requirement of partial shade, forest used for cardamom plantations is often thinned to reduce closed canopy cover, often despite official protections in place (Buckingham & Petheram, 2004). Thinning of the forest, particularly on limestone karst, can lead to increased erosion and is difficult to reverse (James, 2017). Increased light transmission to the forest floor can also lead to increased growth of a mat layer of herbs, seedlings and invasive grasses (Dhakal, 2017).

Cardamom takes four years before first harvest, after which seeds can be harvested yearly for up to ten years, while *Lysimachia* can be harvested after six months and two to four times a year afterwards (Trinh Dinh Hoang et al., 2015). The in situ drying of cardamom seed using fire also poses risks to the forest, first by the collection of firewood and then the risk of fire spreading within the forest (Dhakal, 2017). Additional disturbance can come from the

presence of cultivators who often stay in the forest to manage crops and harvests (Trinh Dinh Hoang et al., 2015). As a result of these disturbances and forest canopy thinning, there is a risk that TSNM will not be able to persist due to limitation to their use of canopy for locomotion, possible loss of food or sleeping trees (Trinh Dinh Hoang et al., 2015). While officially there are plans to provide the forests around Tung Vai greater protections and limit the creation of new cardamom and *Lysimachia* plantations, the response of local households has been mixed, with a majority disagreeing with plans for households to surrender land within the forests historically allocated to their care (Trinh Dinh Hoang et al., 2015).

The presence of livestock in protected TSNM areas also poses a concern due to the impact that livestock such as goats and cattle can have on the ecology of an area (Boonratana & Canh, 2013; Carrete et al., 2009). Farms adjacent to the protected Khau Ca, graze goats on the side of the mountain, allowing some goats to access the inner protected zones via the established pathways in and out. Freely roaming livestock such as goats can contribute to habitat degradation (Boonratana & Canh, 2013) via trampling vegetation and stripping areas for food. In addition to damage caused by grazing and incursions of introduced invasive species, the presence of domestic livestock can also introduce transmission of zoonotic diseases (Afonso et al., 2021).

Whilst the Khau Ca population is the largest known breeding population of TSNM, the genetic viability of the group is uncertain. A study of the genomic diversity of the *Rhinopithecus* genus also found that snub nosed monkeys had lower diversity than other primates, likely as a result of genetic bottleneck events in the Pleistocene (X. Zhou et al., 2016). More recent habitat fragmentation events have likely compounded these historical impacts, with analysis of Mitochondrial DNA (mtDNA) sampling showing no genetic variability – the lowest reported for any wild primate population ever recorded (Ang et al., 2016). While the nuclear genetic variation in TSNM within Khau Ca is still unclear, the mtDNA results are concerning as they could indicate high vulnerability to future environmental change or susceptibility to disease that could lead to the extinction of the largest breeding population of TSNM in the world (Ang et al., 2016; W. Miller et al., 2011).

Habitat fragmentation has been shown to negatively impact genetic diversity in more agile species such as birds (Perrin et al., 2021; Wan, Cushman, & Ganey, 2018). Reduced gene flow as a result of habitat fragmentation has been found to affect not just the animals but also the plants, particularly those tropical and temperate forest fragments (Schlaepfer, Braschler, Rusterholz, & Baur, 2018). This means that a lack of genetic diversity could impact the TSNM through disruptions to their food sources and habitat as well as within their own genetic susceptibility to stochastic events. Furthermore, as the Khau Ca fragment increases in age, it is expected that the negative effects of a lack of genetic diversity will increase with time (Schlaepfer et al., 2018).

While the TSNM are legally protected (Boonratana & Canh, 2013; Covert et al., 2008; Dine, 2012; Kirkpatrick, 1995), they continue to face some of the highest rates of hunting of all snub-nosed monkey species (N. X. Dang et al., 2014; X. C. Le & Boonratana, 2006). Domestic and international demand for bushmeat continues to drive illegal hunting of protected species, with a large proportion ending up on the menu of restaurants (Songtao Guo, Ji, Li, & Li, 2008; Levine, 2016). TSNM are historically used in soups or as balms as a remedy or protection against dietary illnesses such as rickets (Levine, 2016; Thach, 2009). Poor monitoring of some protected areas containing TSNM outside the Khau Ca area and the lucrative potential of bushmeat (Levine, 2016) means that this practice is likely to continue unless there are significant economic and social shifts.

Conservation of the TSNM

The TSNM have been protected by Vietnamese law several times in 1964, 1992 and again in 1994 (Dine, 2012; Kirkpatrick, 1995; Thach, 2009). TSNM conservation efforts have been undertaken on a site-by-site basis since 1997. TSNM in Na Hang began in 1997 due to the efforts of Bettina Martin supported by Allwetterzoo Münster, the Zoological Society for the Conservation of Species and Populations (ZSCSP) and Primate Conservation Inc (PCI) (Covert et al., 2008; Martin, 2004). Following the discovery of the Khau Ca population in 2002, FFI also established a conservation monitoring programme (Covert et al., 2008).

The Tonkin Snub-nosed Monkey Species and Habitat Conservation Area at Khau Ca was established by the Ha Giang Provincial People's Committee (Decision no. 3115/QDUBND) in

2009 (Quyet, 2014). The local community, which once actively collected resources including timber and food, are now employed as community rangers by the Ha Giang Provincial Forestry Protection Department in partnership with FFI (Covert et al., 2008).

In other TSNM habitats, conservation efforts have not been as successful. Illegal hunting of wildlife is an ongoing concern across Vietnam; at least half of all hunted animals end up in domestic restaurants and local markets for consumption (Levine, 2016; Nga & Tung, 2018). The ongoing status of smaller populations in Bac Kan, Yen Bai, Tuyen Quang and Cao Bang is unclear as a result of suspected hunting and habitat degradation and loss in these regions (Boonratana & Canh, 2013; Thach, 2009). In some cases, populations are believed to have been lost by large-scale intervention, as is the case of the protected population in Na Hang Nature Reserve in Tuyen Quang province, following the development of a hydropower plant in 2003 (Martin, 2004; Thach, 2009). A survey carried out in the area in 2006 no longer found evidence of the TSNM (Thach, 2009).

Conservation efforts in the Khau Ca region have been more successful. Through support from FFI and other contributing groups, a small team of community rangers from the Tung Ba have been trained and employed through the Ha Giang Provincial Forestry Protection Department as rangers for the TSNM (Covert et al., 2008; N. X. Dang et al., 2014). These rangers are experts on the Khau Ca area and have a great success rate for locating the shy TSNM. Their jobs as rangers are somewhat coveted by other residents of their village and their expertise continues to make them highly sought after as guides and research assistants for TSNM studies, including this project.

Other active conservation programs, including those run by Denver Zoo, have worked to reduce the reliance of local communities on the fragmented forests inhabited by TSNM. A community outreach program funded by Denver Zoo and the New Nature Foundation, support local households to convert to fuel efficient stoves to reduce their reliance on firewood collected from TSNM habitats (Denver Zoo, 2020), These programs offer solutions that can benefit both local communities and TSNM populations.

In 2015, the Vietnamese Government announced that the 20.4km^2 Khau Ca Species and Habitat Conservation Area was to be merged with the 150km^2 Du Gia Nature Reserve to the

north and northeast to form the new Du Gia National Park (Decision No. 1377/2015/QD-TTg) (An et al., 2018). The motivation for this decision included efforts to afford the region greater protection but also thought to be an effort to promote ecological tourism of the area (pers. comm. Anonymous). While the two areas were likely linked in the past, the two forests are now separated apart from a purported barrier region around Khau Ca and a corridor of linking forest (pers. comm. Mr Tue). The Du Gia Nature Reserve was a popular area for nature tourism such as hiking and homestays in the surrounding villages. The accessibility of the Du Gia Nature Reserve poses risks to the TSNM, as it may make it more accessible to poachers and the public once fully united. During fieldwork, it became apparent that there was significant unmonitored human use of the Du Gia region causing degradation to the forest. In addition, it was determined that there may no longer be a corridor linking the two regions. The TSNM component of this study will undertake a comparison of the Khau Ca and Du Gia forests to determine suitability for any efforts to reunite these regions.

2.4.3 Hylobatidae

As members of the family Hylobatidae, gibbons are the smallest apes being small bodied (5-9kg) with a large brain size, long life span, and largely frugivorous diet; they are arboreal, territorial apes found in the tropical forests across southeast Asia (Penglai Fan et al., 2021; J. J. Feng, Cui, Ma, Fei, & Fan, 2014; Mootnick & Fan, 2011). Unlike the monkeys they share their distribution with throughout Asia, gibbons have a longer life-history similar to the Great Apes – and as such, are more vulnerable to stochastic events (Penglai Fan et al., 2021). Compared to their Great Ape relatives, there is a high level of diversity found across gibbon taxa (Fabre, Rodrigues, & Douzery, 2009; Thinh, Mootnick, Geissmann, et al., 2010).

Despite an expected divergence date from other primates in the early to mid-Miocene, the arrival of early hylobatids into mainland Asia from Africa is poorly documented in the fossil record (Alba et al., 2015; Chatterjee, 2009; Fabre et al., 2009; Thomas Geissmann, 2002; Gilbert, Ortiz, et al., 2020; Harrison, 2016). A relatively recent split between Hylobatidae and Hominidae of between 16 to 20 million years ago, (Carbone et al., 2014; Groves, 2001; Harrison, 2016; Thinh, Mootnick, Geissmann, et al., 2010) was followed by the divergence of Hylobatidae into four genera over only 1.65–2 Ma (Y.-C. Chan et al., 2013; Israfil, Zehr, Mootnick, Ruvolo, & Steiper, 2011; Thinh, Mootnick, Geissmann, et al., 2010). This rapid

divergence is in stark contrast to the divergence time of extant *Homo, Gorilla, Pan* and *Pongo* genera, which took over six million years (Almécija et al., 2021; Y.-C. Chan et al., 2013; Hobolth, Dutheil, Hawks, Schierup, & Mailund, 2011; Steiper & Young, 2006; Wilkinson et al., 2011).

The discovery of the *Kapi ramnagarensis* fossil, a lower third molar, represents the earliest presence of a stem hylobatid approximately 12.5-13.8 Ma in northern India (Gilbert, Ortiz, et al., 2020). Prior to this, the earliest potential hylobatid fossils included primarily *Yuanmoupithecus,* and less conclusively the *Laccopithecus*, and *Lufengpithecus* fossils all dated to 7-9 Ma from sites within China (Chatterjee, 2006; Harding, 2012; Jablonski & Chaplin, 2009; Meldrum & Pan, 1988; Wu & Pan, 1984; Wu & Pan, 1985; Yuerong, Waddle, & Fleagle, 1989). While the affinities of these latter fossils to early Hylobatidae or Hominoidea has been the subject of debate (Harrison, 2010; Ji et al., 2013; Takai, Lu, Kunimatsu, & Shigehara, 1998; Yuerong et al., 1989), it appears that the earliest primitive crown hylobatids appeared approximately 13.8 to 9 Ma (Carbone et al., 2014; Fabre et al., 2009; Gilbert, Ortiz, et al., 2020; Harrison, 2016; Matsudaira & Ishida, 2010; Y.-Q. Zhang et al., 2018). Despite this scarcity, a small number of Pleistocene-aged fossils identified throughout China and Southeast Asia, suggest that hylobatids were historically spread widely throughout the region (Gilbert, Pugh, & Fleagle, 2020; Harrison, 2016; Ingicco, de Vos, & Huffman, 2014; Jablonski & Chaplin, 2009; Mootnick & Groves, 2005; Ortiz et al., 2015; Turvey et al., 2018; Turvey, Crees, & Di Fonzo, 2015; Yumin, 1989; Y.-Q. Zhang et al., 2018).

Yunnan Province in China, is considered the most likely ancestral range for the hylobatids, possibly extending into Vietnam and Laos, with the Hengduan mountain ranges and major rivers (Mekong, Salween, Yangtze) found in this region key geographic barriers driving divergence events among both hylobatids and colobines (Chatterjee, 2006; Hallet & Molnar, 2001; Jablonski, 1998; Jablonski & Chaplin, 2009; Pei Li et al., 2020; Meijaard & Groves, 2006; Thinh, Mootnick, Geissmann, et al., 2010).

The timing of the hylobatid dispersal into the wider Southeast Asia region is thought to reflect geographical and climatic changes across Southeast Asia around also occurring at the time (Pei Li et al., 2020; Meijaard & Groves, 2006; Thinh, Mootnick, Geissmann, et al., 2010). Climate fluctuations towards cooler temperatures, changing sea levels and the uplift of the

Yunnan plateau in the late Miocene and early Pliocene, saw fluctuations in forest coverage across southeast Asia, resulting in rapid divergence across the hylobatids (Carbone et al., 2014; Pei Li et al., 2020; Woodruff & Turner, 2009; Xu, Ferguson, Li, & Wang, 2008). In particular, the fluctuation of sea levels and appearance of land bridges would have encouraged the dispersal of arboreal hylobatids south (Jablonski & Chaplin, 2009; Thinh, Mootnick, Geissmann, et al., 2010) to the Malay Peninsula and the islands of Borneo and Sumatra.

In 1771, *Homo lar* was the first formally published gibbon species (Chatterjee, 2009). While initially divided into two groupings of *Symphalangus* (Siamangs) and *Hylobates* (representing all gibbons) (Napier & Napier, 1967; Schultz, 1933), following a series of reviews and discovery of new species, four genera of hylobatids encompassing 20 recognised species (IUCN, 2022a) are now recognised, each with their own diploid number: *Symphalangus* (2n=50), *Hoolock* (2n=38), *Hylobates* (2n=44) and *Nomascus* (2n=52) (Brandon-Jones et al., 2004; Carbone et al., 2014; Y.-C. Chan et al., 2013; Chatterjee, 2009; Groves, 2001; Müller, Hollatz, & Wienberg, 2003; Wall et al., 2013).

The taxonomy, phylogeny and timing of divergence of the hylobatids have undergone multiple revisions based on morphology and vocalisations (J. Feng, Ma, Fei, Cui, & Fan, 2013; Geissmann, 2002; Geissmann, 2002; Groves, 2001; Groves, 1972; Haimoff, Chivers, Gittins, & Whitten, 1982; Mootnick, 2006; Thinh, Hallam, Roos, & Hammerschmidt, 2011; Trung & Hoang, 2004), chromosomal (Carbone et al., 2014; Chatterjee, 2006; Müller et al., 2003), mtDNA (Israfil et al., 2011; Matsudaira & Ishida, 2010; Monda, Simmons, Kressirer, Su, & Woodruff, 2007; Roos, 2004; Takacs, Morales, Geissmann, & Melnick, 2005; Thinh, Mootnick, Geissmann, et al., 2010; Whittaker, Morales, & Melnick, 2007), and nDNA analyses (Hall, Jones, & Wood, 1996; S. K. Kim et al., 2011; Roos & Geissmann, 2001), and are still not fully resolved (Blair et al., 2011; Carbone et al., 2014; Geissmann et al., 2011; Geissmann & Thanh, 2001; Groves, 2001; Wall et al., 2013). This is likely due to the rapid differentiation of the hylobatids underwent within 4-6 Ma and the possibility of multiple radiations into their current geographic ranges (Carbone et al., 2014; Israfil et al., 2011; Thinh, Mootnick, Geissmann, et al., 2010).

As a result of this rapid divergence, each of *Symphalangus, Hoolock* and *Nomascus* have variously been suggested as the most basal taxon without clear agreement (Chatterjee, 2006; Groves, 1972; Israfil et al., 2011; Müller et al., 2003; Roos & Geissmann, 2001; Takacs et al., 2005; Thinh, Mootnick, Geissmann, et al., 2010). The resolution of relationships within the genera are also similarly unclear, attributed to small sample sizes, recent divergence dates, or the possibility of ongoing gene flow between some species (S. K. Kim et al., 2011; Matsudaira & Ishida, 2010, 2021; Monda et al., 2007; Roos, 2016; Whittaker et al., 2007). Hybridisation zones between species of gibbons have been identified between *Hylobates lar* and *Hylobates pileatus* in wild populations in central Thailand (W. Y. Brockelman & Schilling, 1984) and *Hylobates albibarbis* and *Hylobates muelleri* in central Borneo (Marshall and Sugardjito 1986), however, hybrid groups are theorised to be unstable with poor reproductive success (Asensio, José-Domínguez, Kongrit, & Brockelman, 2017; W. Y. Brockelman & Schilling, 1984; Geissmann, 1995).

Today, the hylobatids have the widest geographic range of the non-human Great Apes. Siamangs are found in Sumatra and the Malay Peninsula, while the gibbons have a wider geographic range; *Hoolock* are found within China, India and Myanmar, *Hylobates* in northern Sumatra, Malay Peninsula, Borneo, Malaysia, Myanmar, Thailand, China, and *Nomascus* located in China, Vietnam, Laos, and Cambodia (D. Brandon-Jones et al., 2004; Chatterjee, 2009; Groves, 2001).

Despite the geographical range of gibbon species, they share several similar characteristics (Bryant, Olson, Chatterjee, & Turvey, 2015). They exhibit no sexual dimorphism, with both males and females being small with long arms specialised for brachiation and canopy living, and long canines (J. Marshall & Sugardjito, 1986; Michilsens, Vereecke, D'Août, & Aerts, 2009). The colouring of gibbons varies across species, and many species also exhibit changes in natal and adult pelage colouring as they mature (A. R. Mootnick, 2006).

Gibbons most commonly monogamous, living in small family units typically of a bonded pair with 2-3 offspring, in home ranges of 0.15 to 4 km^2 (Cunningham & Mootnick, 2009; J. J. Feng et al., 2014; Roos, 2016; D. Zhang et al., 2013). Some species have been observed to buck this trend; both *Sympalangus syndactylus* (the siamang) (Lappan, 2007) and *Hylobates lar* (lar

gibbon) (Barelli, Heistermann, Boesch, & Reichard, 2008) have been found in multimale-single female groupings, with mating occurring between all adult males and the adult female. Similarly, multifemale-single male groupings have been observed across many *Nomascus* species (P.-F. Fan, Xiao, Huo, & Jiang, 2009; A. R. Mootnick, Chan, Moisson, & Nadler, 2012; Zhenhe, Yongzu, Haisheng, & Southwick, 1989). It appears that gibbon grouping patterns are not as constrained to uni-male and uni-female as researchers expect and that further study into other gibbon species may reveal additional variations.

Gibbon species are highly territorial, using visual and species-distinct vocal displays to attract mates, reinforce bonds within groups and establish spacing and boundaries to external individuals (Cowlishaw, 1992; Cunningham & Mootnick, 2009; Mitani, 1985; A. R. Mootnick, 2006; Thinh et al., 2011). Gibbon vocalisations are highly diagnosable, with species- and sex-specific calls, thought to have several functions such as reaffirming intra-group relationships, and inter-group and inter-specific territoriality across vast distances (Asensio et al., 2017; Cowlishaw, 1992; J. J. Feng et al., 2014; Geissmann, 1995; Koda et al., 2013; J. T. Marshall & Marshall, 1976). Typically, males and females sing together with sex-specific contributions forming a duet, however some species also exhibit solo singing (Cowlishaw, 1992; Thinh et al., 2011). In most gibbon species, females contribute the most prominent segment of the duet known as the great call, which in addition to contributing to territorial defence and communication, may also act as an 'honest signal' reflecting the age and physical fitness of the singer (Terleph, Malaivijitnond, & Reichard, 2016).

There is likely a parental-teaching element to learning calls for young gibbons who learn from adult duets, however, it has also been found that great-calls in females may be under strong genetic control (W. Y. Brockelman & Schilling, 1984; Geissmann, 1995). Despite an underlying genetic element, it appears that there is still a capacity for flexibility or personalisation of individual vocalisations, with individual identification possible in some instances, particularly within the introduction and climax components of calls (Dallmann & Geissmann, 2001; Hradec, Bolechová, & Svobodová, 2016; Koda et al., 2013; J. T. Marshall & Marshall, 1976; Oyakawa, Koda, & Sugiura, 2007). The same has been found in male gibbon singing for *Nomascus concolor*, with neighbouring males emphasising individuality in their calls, likely in

an attempt to differentiate themselves from one another (Sun, Huang, Guan, Geissmann, & Jiang, 2011).

All gibbons also share an ongoing threat of extinction. Gibbons have been subjected to anthropomorphic-led habitat destruction since at least 1600s in mainland China, with pressure increasing throughout the twentieth century as a result of population increases and poor conservation practices across their ranges (Turvey et al., 2015). Of the 20 gibbon species recognised by the IUCN Red List, five are listed as Critically Endangered, 14 are Endangered, and one species is considered Vulnerable (IUCN, 2022a). All species have populations in decline, with the exception of the Hainan Gibbon (*Nomascus hainanus*) which is considered stable at only 10 individuals (IUCN, 2022a). As brachiators, gibbons are reliant on the connected canopies of mature forests (Chatterjee, 2006; Harding, 2012), making them highly vulnerable to habitat destruction or decline.

2.4.3.1 Nomascus (crested gibbons*)*

While still not fully resolved, the *Nomascus* genera have been identified as the most basal taxa of gibbons (Chatterjee, 2006; Israfil et al., 2011; Roos & Geissmann, 2001; Takacs et al., 2005; Thinh, Mootnick, Geissmann, et al., 2010), with Thinh, Mootnick, Geissmann, et al. (2010) suggesting an extended divergence period from 4.2 to 0.4 Ma, unlike the rapid divergence episodes of other gibbon genera. Perhaps due to this prolonged differentiation process, the *Nomascus* group was originally considered a single species; today, seven individual species are now recognised, with six listed as Critically Endangered and one as Endangered (table X) (IUCN, 2022a; Thinh et al., 2010).

Nomascus species are among the rarest of all apes. In particular, the two most basal species *Nomascus hainanus* (Hainan gibbon) and *Nomascus nasutus* (cao vit gibbon), which form a sister clade to the other species (Monda et al., 2007; Roos, 2004; Takacs et al., 2005; Thinh et al., 2011; Thinh, Mootnick, Geissmann, et al., 2010; Thinh, Mootnick, Thanh, et al., 2010) are two of the rarest primates in the world (Mootnick et al., 2012). The Hainan gibbon population currently sits at approximately 35 mature individuals inhabiting Hainan Island, China, having grown from 10 mature individuals in the 1980s making it the most endangered gibbon (IUCN, 2022b; W. Wei et al., 2004). The CVG has a larger population but is still Critically Endangered,

located in a range that crosses the Vietnamese and Chinese border, with an estimated 135 in 2020, an increase from 102-110 in 2007 (Chang-yong et al., 2020; Fauna & Flora International, 2021).

Divergence analysis suggests that *Nomascus* species diverged as a result of continuous waves of migration North to South, originally arising in the Vietnamese/Chinese border region (Thinh, Mootnick, Geissmann, et al., 2010). Of the remaining crested gibbons, *Nomascus concolor* (black crested gibbon) was the first species to branch, followed by two groupings: *Nomascus annamensis* (Northern buffed-cheeked gibbon) and *Nomascus gabriellae,*(yellow-cheeked gibbon) and *Nomascus leucogenys* (Northern white-cheeked gibbon) and *Nomascus siki* (Southern white-cheeked gibbon), although the final resolution between these last four species is still somewhat unclear, possibly due to some continued gene flow between them until recently (Chatterjee, 2006; Harding, 2012; S. K. Kim et al., 2011; Matsudaira & Ishida, 2010; Monda et al., 2007; Roos et al., 2007; Takacs et al., 2005).

The current range of the crested gibbons encompasses parts of Southern China, Myanmar, Vietnam, Laos and Cambodia, likely as a result of historical waves of migration north to south from their origin within Vietnam and China (Harding, 2012; Thinh, Mootnick, Geissmann, et al., 2010). At individual species levels, populations are predominately small or fragmented, providing little opportunity for ongoing hybridisation. Population fragmentation is a direct result of anthropomorphic pressures across their range, including habitat destruction, hunting, poaching, and industrial and urban development.

Nomascus has shorter and denser hair than that of other gibbon genera, however, like other species, they exhibit sexual dichromatism and conspicuous natal coat colouring (Cunningham & Mootnick, 2009; Mootnick & Fan, 2011). Most *Nomascus* species are born buff coloured, with changes to black for males or tawny/buff for females (Mootnick & Fan, 2011). The CVG diverges from this pattern, with infants of both sexes born black, and females transitioning to a buffy colour as they mature (Fan et al., 2010).

Unlike other gibbon species, the duets of *Nomascus* duets are highly specialised between the sexes (Hradec et al., 2016; Hradec, Linhart, Bartoš, & Bolechová, 2017). They are male dominated with no overlap in the duets between males and females (T. Geissmann, 2002;

Hradec et al., 2017; Sun et al., 2011). Also, unusually for gibbons, unpaired individuals of *Nomascus* are the only individuals to perform solo songs (Thomas Geissmann, 2002).

The *Nomascus* group also appear to deviate from the traditional monogamous groupings of other gibbon genera, with several species exhibiting groupings of one adult male and two breeding females (Table 2.6) (Mootnick et al., 2012; Zhenhe et al., 1989). This unusual grouping has been found in CVG (Chan et al., 2008) yellow-cheeked gibbon, and Southern white-cheeked gibbons (Dat et al., 2008b), Hainan gibbon, (Bryant et al., 2015; Fan et al., 2010; Zhenhe et al., 1989; J. Zhou, Wei, Li, Lok, & Wang, 2008), and black crested gibbons (W. V. Bleisch & Chen, 1991; P.-f. Fan, Jiang, Liu, & Luo, 2006; E. H. Haimoff, Yang, He, & Chen, 1986). It is unclear whether this is habitual *Nomascus*-specific behaviour or due to the small populations and uneven sex ratios as a result of habitat limitations and population fragmentation limiting the options of females to locate unbonded males and vice versa (Ping Li et al., 2022; Mootnick et al., 2012; W. Wei et al., 2004; Zhenhe et al., 1989; J. Zhou et al., 2008). Species of other gibbon genera have also been reported to exhibit multi-male and multi-female social organisations such as the lar gibbon (Barelli et al., 2008), *Hoolock hoolock* (hoolock gibbon) (Ahsan, 1995) and siamang (Lappan, 2007), the stability of these groupings over multiple years is uncertain (Fan et al., 2010).

Table 2.6 Members of the crested gibbons

Species	Est. Population	Grouping style	Elevation (m)	Home range	Density	IUCN Red List status	References
Nomascus concolor	1500	Polygynous	200-2900	0.7 km^2	0.5 groups/ km^2	CR	Bleisch & Chen (1991); Fan et al. (2006); IUCN (2022a); Fan et al. (2020); Zhenhe et al. (1989)
Nomascus nasutus	135	Polygynous (1M:2F)	50-930m	1.28-1.33 km^2	1.6 groups/ km^2	CR	Dat et al. (2008a); Fan et al. (2006); Fan et al. (2010)

Nomascus annamensis	Unknown	Monogamous	100-1200m	0.5 km^2	0.6-0.21 groups/km^2 Laos; 0.32 groups/km^2 Cambodia	EN	Frechette, Hon, Behie, et al. (2017); Hoang, Hoang Minh, Bui, et al. (2018); Kidney et al. (2016); Thịnh & Hai (2016); Williams & Behie (2020)
Nomascus hainanus	35	Monogamous Polygynous (1M:2F, 2M:2F, 3M:2F)	650-1200m	1.48 km^2	-	CR	Bryant et al. (2015); IUCN (2022a); Ping Li et al. (2022); W. Wei et al. (2004); J. Zhou (2018); J. Zhou et al. (2008)
Nomascus leucogenys	>455	Monogamous	200-1400m	0.29-0.44 km^2	-	CR	Bolechová, Chaloupková, Hradec, et al. (2019); P.-F. Fan, Fei, & Luo (2014); Penglai Fan et al. (2021); Harding (2012); Margulis & Hálfdanardóttir (2021); Rawson et al. (2011); Ruppell (2013)
Nomascus gabriellae	500 (Vietnam) 646-974 (Cambodia)	Polygynous (1M:2F)	100-1,650m	-	Av 1.47 groups/ km^2	EN	Bach, Chen, Hoang et al. (2017); Dat et al. (2008a); Eames & Robson (1993); C. Hoang et al. (2018); Hradec et al. (2017); Rawson et al. (2011)
Nomascus siki	600	Polygynous (1M:2F)	30-1800m	0.38 km^2	Av 1.47 groups/ km^2 (D. Tan et al., 2012)	CR	Dat et al. (2008a); IUCN (2022a); Ngoprasert, Coudrat, Nanthavong, et al. (2015); Nguyen, Coudrat, Roos et al. (2020); Rawson et al. (2011); Traeholt et al. (2005)

2.4.3.1.1 Nomascus nasutus (cao vit gibbon)

The CVG was initially described as a subspecies of *Hylobates (Nomascus) concolor* (Delacour, 1951; Groves, 1972) with a range stretching from the left bank of the Red River to the east coast of Vietnam (Dao Van, 1983), until it was recognised as a distinct species with two subspecies: *Nomascus nasutus nasutus* and *Nomascus nasutus hainanus* (D. Brandon-Jones et al., 2004). The two were further separated and raised to species-level *Nomascus nasutus* and *Nomascus hainanus* based on differences in coloration (A. R. Mootnick, 2006; Roos & Geissmann, 2001), call (J. Feng et al., 2013; Trung & Hoang, 2004),and Genetic analysis (Roos et al., 2007).

The historical distribution of the CVG lies east of the Red River in southern Yunnan and Guangxi in China, and northern Vietnam (Dat et al., 2008b; Fan et al., 2010; Geissmann & Thanh, 2001), however, they were considered extinct throughout this region from the 1950s and 1960s (Chan et al., 2008; Fan et al., 2010; Insua-Cao et al., 2012; B. Tan, 1985). In 2002, a small population of 26 individuals was discovered by FFI undertaking a survey in Vietnam on the border of China (Geissmann et al., 2003). In 2006 another population was found across the border in China, bringing the total global population of CVG to 110 individuals (Chan 2008; Chan et al., 2008; Fan 2010; Insua-Coa 2013). In 2012, 129 individuals were estimated to live in the region across 24 groups (Cuong, Luan, & Truong, 2014; Insua-Cao et al., 2012). Despite rumours that additional groups might be found in other border areas within China, no evidence of the CVG have been found there (Mootnick et al., 2012).

Today, an estimated 135 individuals a transboundary patch of limestone karst forest situated on the international border of Vietnam in Trung Khanh District, Cao Bang Province, and Jingxi County, Guangxi, China (Figure 2.14) (P.-F. Fan, Bartlett, Fei, Ma, & Zhang, 2015; Fan , Fei, & Ma, 2012; Fauna & Flora International, 2021; IUCN, 2022a). The CVG is classified as Critically Endangered and featured as one of the World's 25 Most Endangered primates from 2008 to 2012 (C. Schwitzer et al., 2014). Its removal from subsequent lists is not due to improvement in the CVG situation but instead due to an effort to highlight the status of other equally at-risk primates (C. Schwitzer, Mittermeier, R.A., Rylands, A.B., Chiozza, F., Williamson, E.A., Byler, D., Wich, S., Humle, T., Johnson, C., Mynott, H., and McCabe, G., 2019).

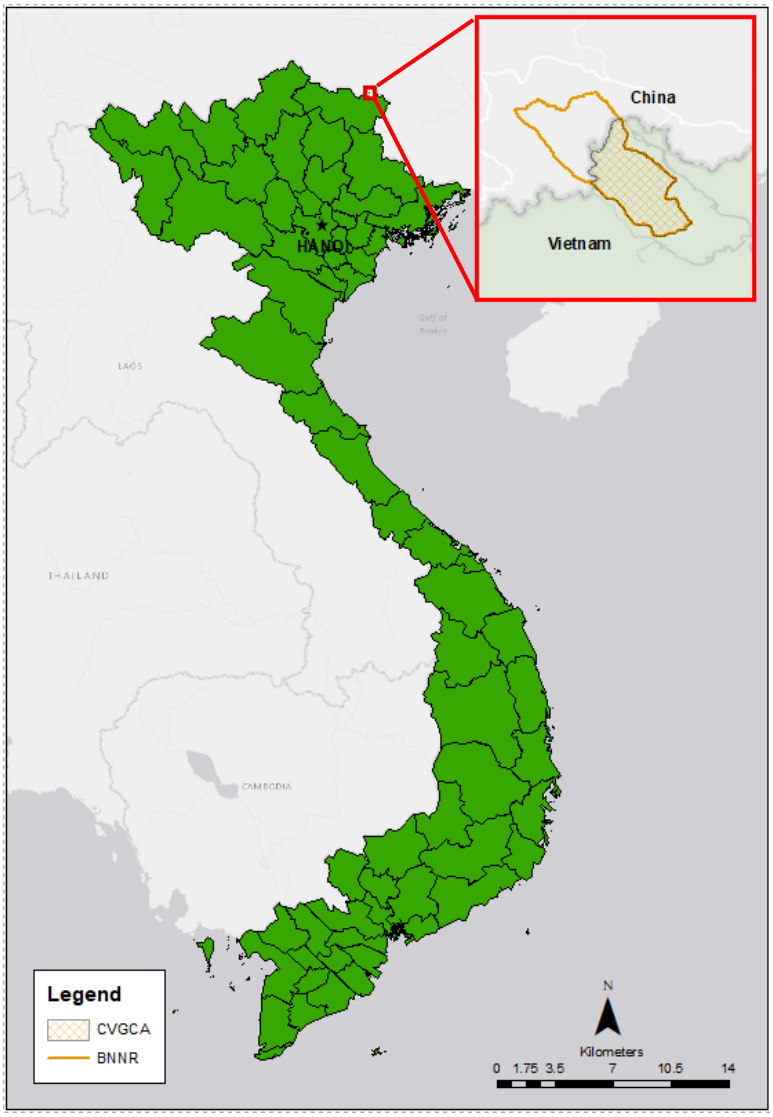


Figure 2.14 Location of the cao vit gibbon within the CVGCA and BNNR Basemap source: ESRI 10.8 et al. (2022); H. Esri, Garmin, OpenStreetMap contributors (2022)

The majority of CVG inhabit the Vietnamese forest, with only three groups found to reside in the Chinese forest, with some movement of these groups back and forth across the border (Chang-yong et al., 2020). The presence of an international border makes studies encompassing the extent of the CVG habitat difficult to undertake however, progress is being made in this regard, particularly through the increased use of remote imaging and geospatial information systems (Fan et al., 2013; C.-Y. Ma et al., 2020).

Potential expansion of the population on the Vietnamese side of the border is limited. The limestone karst forest is surrounded by valleys encompassing natural and human-made barriers including a river on two sides, a road, farmland, and villages - though there is an

uninhabited region within the forest that is undergoing regeneration. Successful breeding within the CVG groups has been observed, however, geographic limitations of their karst limestone habitat may limit the dispersal opportunities for sub adults.

Appearance of the CVG

Unlike other *Nomascus* infants, which are born light in colour, those of the CVG are born black, with males retaining this colouring into adulthood (Figure 2.15) (Fan et al., 2010; Harding, 2012; Mootnick & Fan, 2011). Males also exhibit a brown-black patch on the chest and a round crested face (Insua-Cao et al., 2012; Mootnick & Fan, 2011). The colouring of females changes as they mature, with adult female colouring becoming buff or gold and retaining a black streak from the forehead down across the shoulders to the mid back (Bolechová et al., 2019; Harding, 2012; Mootnick & Fan, 2011). Females also exhibit a dark chest patch and dark black hair on the fingers and in a faint ring around the face.

In other *Nomascus* species, infants are born with blonde colouring, and females change to all-black at around one year of age, and then again at five to nine years of age, back to blonde (Margulis & Hálfdanardóttir, 2021; Mootnick & Fan, 2011). Captive studies have suggested that the colour change of female *Nomascus* occurring at the onset of sexual maturity may act as a signal to potential mates of her reproductive health (Bolechová et al., 2019; Margulis & Hálfdanardóttir, 2021; Mootnick & Fan, 2011).

Figure 2.15 Colouring of the cao vit gibbon. Left: Adult female CVG with newborn. Photo: Zhao Chao (Fauna & Flora, 2013). Right: Black CVG brachiating; due to distance age class of individual unknown. Photo: K. Apthorp, 2016.

Captive females provided hormonal contraceptives have been observed reverting to juvenile colouring following a loss of reproductive ability, further indicating a link between reproductive ability and colour (Bolechová et al., 2019; Margulis & Hálfdanardóttir, 2021; Mootnick & Fan, 2011). Coloration changes may also be under the influence of social factors, with Bolechová et al. (2019) finding a link between colour changes, the age of the female and the presence or absence of their mothers. This further suggests that the final colour change in *Nomascus* is linked to the timing of sexual maturity when female gibbons disperse from their family units to find their own pairing.

The dark colouring of CVG infants has been hypothesised by Mootnick and Fan (2011) to allow better absorption of heat in cold climates, particularly when away from their mothers (Mootnick & Fan, 2011). However, it seems unlikely that the climate would dictate colouring as infants begin to change colour as they leave the constant care of their mothers, a time when they are more likely to need to stay warm on their own.

Social grouping of the CVG

CVG have long life histories and females typically give birth to a single infant from the age of six to nine years, with a gestation period of seven months and an average interbirth period of 34 months (Fan et al., 2015; Fan et al., 2013; Insua-Cao et al., 2012). In gibbons both sexes disperse from the natal group, however in some species such as the lar gibbon, dispersal can be delayed for a few years beyond initial sexual maturity due to high levels of population saturation within limited habitats (Warren Y. Brockelman, Ulrich, Treesucon, & Jeremy, 1998; Matsudaira, Ishida, Malaivijitnond, & Reichard, 2018). Dispersal patterns appear to differ across species: the lar gibbon exhibits sex-specific behaviours where males disperse short distances into adjacent groups and females into more distant groups (Matsudaira et al., 2018), while the black crested gibbon of both sexes appear to disperse opportunistically based on reproductive prospects (N. Hu et al., 2018). Some instances of co-dispersal have been observed in CVG gibbons in China, though these included adults and juveniles dispersing together potentially to establish new territories and groups (Fan et al., 2010).

Understanding of species-specific dispersal patterns for gibbons can be difficult due to the lengthy life history of gibbons. Gibbons reach maturity at approximately five to eight years of

age and typically leave the natal group to find a mating group or territory (Cunningham & Mootnick, 2009; Ping Li et al., 2022). Groups are family based, with one male and typically one female, plus two or three offspring, and defend a dedicated territory from external groups (Fan , Xiao, Feng, & Scott, 2011; Insua-Cao et al., 2012).

In the case of CVG, family groups can contain a single male and two adult breeding females in polygynous groupings (Fan et al., 2010). Similar groupings have been observed in several crested gibbon species (W. V. Bleisch & Chen, 1991: *N. concolor*; Bryant et al., 2015: *N. hainanus*; Dat et al., 2008b: *N. gabriellae, N. siki*), with both females breeding with the male with no aggressive behaviour towards one another. Resident females in CVG groupings were observed to chase floating females and exhibited increased numbers of great calls when floating females encroached on groups (Fan et al., 2010). In *Nomascus concolor jingdongensis* (black crested gibbon subspecies), a third female was interrupted in her duet with the resident male by both resident females and chased out of the area (Fan et al., 2006). Analysis of feeding competition within CVG groups suggests that while bi-female groupings do not exhibit obvious feeding competition, within-group feeding competition may constrain the number of breeding females to two (Fan et al., 2015).

These bi-female, uni-male groupings may be a consequence of limited mating opportunities for dispersing females in restricted habitat, however they appear to be stable polygynous mating groups, including the CVG (Fan et al., 2015; Fan et al., 2010). The fact that polygynous mating is found predominately within the crested gibbons, also some of the most endangered gibbon species, could indicate that the smaller population sizes are influencing mating patterns that may differ from their historical grouping behaviours. For instance, while 1M:2F groupings are found in the Hainan gibbon, they have also been observed to group in various other compositions, e.g. with 1M:1F, 2M:2F and 3M:2F (Ping Li et al., 2022; J. Zhou et al., 2008). Limitations in available habitat for the creation of new territories and groups, or differences in sex ratios may also impact the composition of groups within these small populations (Ping Li et al., 2022).

It has also been found that more flexible mating groupings, the less risk of extinction they face compared to species that rely on even sex ratios for groupings, such as socially monogamous

pairings found in many gibbon species (Leach, Shaw, & Weiss-Lehman, 2020; Lootvoet, 2015). Other factors including environmental and social changes may also impact the mating-behaviours of species (B. Huang et al., 2013; U. H. Reichard, 2009). Even among those gibbon species assumed to exclusively exhibit monogamous mating, extra-pairing copulations can occur, suggesting that the mating strategies of all gibbons including the CVG, are much more flexible than historically assumed (Fan et al., 2015; Ping Li et al., 2022; U. H. Reichard, 2009).

CVG vocalisations are sexually specific, with male and female components of duets individualised with no overlap (Hradec et al., 2016; Hradec et al., 2017). CVG duets generally occur in the early morning around sunrise, with male adults initiating and dominating the duet with modulated phrases (J. Feng et al., 2013; H. Ma, Ma, & Fan, 2022; Yat-Sen, Fan, Xiang, & Ma, 2010). Males select the highest tree at high elevations on ridges or slopes to initiate the singing bout maximizing the range of his calls throughout the karst forest, with calls recorded as far as 1.5km away (Fan et al., 2009; C.-Y. Ma et al., 2020).

Male sub-adult males develop their vocal repertoires over several years before they are able to produce complex vocalisations (J. J. Feng et al., 2014). Once they have reached maturity, males produce individualised vocalisations that remain stable throughout their lives, allowing for individual identification and tracking of male replacements and dispersals (Fan et al., 2011; J. J. Feng et al., 2014; Sun et al., 2011). The female mate – or mates in the case of CVG polygynous groupings (1M:2F) – respond with great calls to create a duet or trio bout (J. Feng et al., 2013; H. Ma et al., 2022). In groupings with two adult females, female responses are simultaneous, making individual recognition based on vocalisation more difficult (M. Huang, Ma, Ma, Garber, & Fan, 2020). In the absence of female responses, males continue to vocalise in a solo bout adjusted to compensate for a lack of female contribution (M. Huang et al., 2020; H. Ma et al., 2022).

The use of coordinated vocalisations between paired individuals has been observed across many species, particularly in bird species, and hypothesised to strengthen social bonds, reinforce territory boundaries, and even signal the health or fitness of the singers (Cowlishaw, 1992; J. J. Feng et al., 2014; M. L. Hall, 2004; H. Ma et al., 2022). The underlying function of singing can vary across species and can serve many different functions for a species where the

vocalisations can transmit multiple messages at any one time and vary seasonally (J. Feng et al., 2013; M. L. Hall, 2004; H. Ma et al., 2022; Marshall-Ball, Mann, & Slater, 2006). While singing may enforce territorial boundaries, low levels of antagonism have been observed between groups of CVG interacting with one another and have even been observed grooming across groupings (Geissmann et al., 2002).

Due to the dense habitat of gibbons and the size of homes ranges, gibbon duets are predominately vocal communication with visibility between the singers not required. As a result of this, vocalisations are compressed to make communication more efficient to relay multiple messages (M. Huang et al., 2020). To reduce the loss of meaning due to compression, males can manipulate their vocal tracts to maintain loud melodious calls to improve the carry of their call over vast distances (M. Huang et al., 2020; Koda et al., 2012). The timing of gibbon duets in the early morning when background noise is reduced and the use of repeated sequences in the male call may also increase clarity of the communications (Mitani, 1985; Yat-Sen et al., 2010).

In the case of CVG, in situ observations from the Chinese habitat range indicate that duets are at times used to signal the location of the singers to external groups (Chan et al., 2008). The use of lengthy duet bouts averaging 22.4 minutes and up to 30 minutes, provide groups time to travel relative to the calls of other groups, with observations of confrontations between simultaneously singing groups (Chan et al., 2008). Similar behaviours have been observed between groups of black crested gibbon subspecies (Fan, Liu, Luo, & Jiang, 2007).

Duets have also been found to advertise, rather than actively strengthen, CVG male and female social bonds through the intensity of their singing bouts (H. Ma et al., 2022). Such advertisements could act as a signal to any interloping males of the commitment between paired male and female(s) (H. Ma et al., 2022). Duets are not necessarily static events; during data collection a female and two juveniles were observed brachiating and calling. H. Ma et al. (2022) also found that in CVG duets between adults of the opposite sex advertised proximity, potentially as a method of mate guarding.

The choice of tree used for gibbon morning duets is closely tied to that of their sleeping tree (J. T. Marshall & Marshall, 1976), as this is often the location of their daily vocalisations. CVG

inhabiting the Chinese BNNR site, have been observed to prefer trees taller than their neighbours, with no lianas (H. L. Fei et al., 2012). These groups had a high number of sleeping sites (57-87) that were used irregularly and rarely repeated (H. L. Fei et al., 2012). A total of 29 species of sleeping trees were identified, five species of which were used most frequently by the CVG: *Broussonetia papyrifera, Ficus macrocarpa, Platycarpa longipes, Sapium rotundifolium, Spondias lakonensis* (H. L. Fei et al., 2012).

The choice of sleeping sites in primates can be linked to reinforcing evolutionary behaviours such as predation avoidance (Cunningham & Mootnick, 2009; R. T. Day & Elwood, 1999; D. Li et al., 2011; U. Reichard, 1998) , foraging and food access (R. T. Day & Elwood, 1999; D. Li et al., 2011; Mekonnen et al., 2021; Mills, Nekaris, Campera, & Patel, 2021; Teichroeb, Holmes, & Sicotte, 2012), range protection (R. T. Day & Elwood, 1999), and thermoregulation and hygiene (Fan & Jiang, 2008; H. L. Fei et al., 2012; Mekonnen et al., 2021; Mills et al., 2021; Z.-F. Xiang, Nie, Chang, Wei, & Li, 2010).

In the case of the CVG, sleeping tree selection by groups within the BNNR, China has been linked to predator avoidance (H. L. Fei et al., 2012). Groups of CVG enter their sleeping sites on average, over an hour before sunset when their historical predators (clouded leopards and golden cats) become active (H. L. Fei et al., 2012). While the continued presence of these predators within the BNNR is uncertain (H. L. Fei et al., 2012), the anti-predator behaviours of the CVG may persist. Encounters with serpent eagles, possible juvenile-predators, have also been observed to result in CVG relocating to new sleeping sites (H. L. Fei et al., 2012). Their preference for trees without lianas, and their positions on small branches at the top of trees may also act as a safeguard against predator access (Fan & Jiang, 2008; Phoonjampa, Koenig, Borries, Gale, & Savini, 2010). Irregular use of sleeping trees and low levels of repetition may also function as a predator avoidance behaviour (Fan & Jiang, 2008; U. Reichard, 1998).

Unlike some other *Nomascus* species (H.-L. Fei, Thompson, & Fan, 2019; H. Zhang et al., 2020), the CVG does not appear to preference sites based on seasonal temperatures, instead preferring trees on slopes near ridges rather than valley floors throughout the year, between elevations of 700m and 910m (H. L. Fei et al., 2012). Access to food resources is also not thought to impact sleeping site selection in CVG, as they were observed to rarely sleep in food

trees and generally slept over 100m away from the last feeding tree of the day and the first feeding tree of the next day (H. L. Fei et al., 2012). It is possible however, that a lack of feeding competition between the three groups that reside within the BNNR allow these groups to make other considerations in their sleeping sites. Further research is required to determine the preferences of the CVG groups within the CVGCA.

Geography and climate of the CVGCA in Trung Khanh

The CVG inhabits the Cao Vit Gibbon Conservation Area (CVGCA) in Trung Khanh District, Cao Bang Province, Vietnam and the Bangliang National Nature Reserve (BNNR) in Jingxi County, Guangxi, China. They inhabit a patch of tropical monsoon forest on karst limestone covering an area of 16.56 km^2 in Vietnam, and 65.30 km^2 in China (J. J. Feng et al., 2014; Insua-Cao et al., 2012; C.-Y. Ma et al., 2020). The karst limestone is characterised by sharp limestone peaks, with an elevation of 400-950m, steep slopes, vertical ridges, and lowland valleys and depressions (Dat et al., 2008b; Insua-Cao et al., 2012; C.-Y. Ma et al., 2020).

The CVGCA is bounded by the forks of the Quay Son River in Vietnam (Dat et al., 2008b), as well as agricultural land and roads, limiting the movement of the gibbons beyond the bounds of their forest habitat. Three communes surround the CVGCA, and five villages surround the Chinese BNNR side (Insua-Cao et al., 2012). The close human habitation is responsible for the degradation of much of the region due to logging, agricultural use and collection of forest resources (Dat et al., 2008b; Insua-Cao et al., 2012). As a result, most of the valleys have been historically used for farming and now exhibit degraded vegetation, with remaining limited to slopes and mountains (Insua-Cao et al., 2012; Trung & Hoang, 2004). Today, no livestock farming or grazing within the CVGCA is permitted, however this still occurs in parts of the BNNR (C.-Y. Ma et al., 2020).

While the BNNR covers a greater area than that of the CVGCA, the majority of CVG are found to inhabit and remain within the CVGCA – only two to three groups live within the BNNR and only one group exclusively remains in this area (Fan et al., 2013). The limestone composition of Trung Khanh makes it difficult and dangerous for researchers to follow the CVG closely (Fan et al., 2015; J. J. Feng et al., 2014), instead, observations of the CVG are generally made from outposts on karst peaks. This is compounded by the international border, which limits the

ability of many researchers to undertake studies encompassing the entire distribution of the CVG.

Trung Khanh District has a monsoonal climate with two main seasons: a warm rainy season May to October, and a dry, cold season November to April (H. L. Fei et al., 2012; C.-Y. Ma et al., 2020). Temperatures reach their peak in July at an average of 29˚C and their lowest in January, with an average low of 8˚C (Spark, 2018). Annual mean rainfall for the region is between 1188mm to 2870.6mm.

Fauna of the CVGCA

Surveys of the CVG habitat across both the BNNR and CVGCA have also recorded the presence of 100 vertebrate species, comprising 56 bird species, 31 mammal species, 10 reptile species, and 3 amphibian species (B. P. L. Chan & Ng, 2006; Dat et al., 2008b). This includes several larger carnivore species and potential predators of the CVG, including *Ursus thibetanus* (Asiatic black bear), *Prionailurus bengalensis* (leopard cat), *Catopuma temmincki* (golden cat) and *Spilornis cheela* (crested serpent eagle). To date, no observations of predation of the CVG have been made. The disappearance of infants and juveniles in groups under observation have largely been attributed to male takeovers (C.-Y. Ma, Brockelman, Light, Bartlett, & Fan, 2019)

Alongside the CVG, four other primate species were also recorded as living within the limestone karst forest (Table 2.7). In addition to these species, local villages recalled seeing and hearing ‘black and white monkeys’ within the now CVGCA area as children, thought to be François’s langurs. B. P. L. Chan and Ng (2006) also reported that a single François langur had been observed travelling from China to a nearby forest patch in Ngoc Khe Commune to the east of CVGCA. While the historical distribution of the François’s langur may have included this region (Insua-Cao et al., 2012; IUCN, 2022a), no observations of their presence within this region have been reported since the rediscovery of the CVG.

The presence of an unmonitored macaque groups within the distribution of a Critically Endangered species is concerning. Vulnerable populations within constrained habitats such as the CVG, may face competition for resources and territory from sympatric larger primate populations (Dat et al., 2008b). Interactions, negative or otherwise, between the CVG and other primates have not been well-documented. One incident between a young adult male

lar gibbon and a group of 22-28 *Macaca nemestrina* (pig-tailed macaque) was recorded at Khao Yai National Park in Thailand (Whitington, 1992). In this case, the male gibbon attacked a group of female and young macaques who had entered a feeding patch that included a rare fruit tree (*Sandoricum koetjape)* (Whitington, 1992). In general, however, observations of negative interactions between gibbons and macaques at other sites are limited.

Table 2.7 Primate species found within the CVG habitat in CVGCA and BNNR

Family	Taxonomic name	Common name	IUCN Red List Status
Hylobatidae	Nomascus nasutus	Cao vit gibbon	CR
Cercopithecidae	Macaca assamensis	Assamese macaque	NT
	Macaca arctoides	Stump-tailed macaque	VU
	Macaca mulatta	Rhesus monkey	LC
Lorisidae	Nycticebus pygmaeus	Pygmy slow loris	EN

Flora of the CVGCA

The core habitat of the CVG is monsoon rainforest, surrounded by degraded secondary forest on karst limestone (Fan et al., 2011; J. J. Feng et al., 2014; C.-Y. Ma et al., 2019). Limestone is an uncommon habitat for gibbons (Fan et al., 2011). The Hainan gibbon is the only other gibbon species to also inhabit limestone karst in Hainan, China. Based on interviews conducted by Fan et al. (2011), the historical distribution of the CVG likely included the wider region, including lower montane forests surrounding the limestone karst forest in which they are currently restricted.

The porous nature of the limestone means that groundwater is limited, resulting in adaptations allowing plants to survive in an arid and high calcium environment (Insua-Cao et al., 2012; Chunni Liu et al., 2021). This includes extensive root systems to anchor plants and allow them to access underground water (Insua-Cao et al., 2012; Chunni Liu et al., 2021). Alternative strategies include plants with raised root structures to allow them to absorb moisture from the air (Insua-Cao et al., 2012).

Heavy logging and resource overutilization in the 1980s and 1990s has degraded much of the remaining forest (B. P. L. Chan & Ng, 2006; Fauna & Flora International, 2016), resulting in

distinct vegetation types across both Chinese and Vietnamese regions. Despite the contiguous forest joining the two protected areas of the CVG distribution, the forest within the CVGCA is reported to be of higher quality than that of the BNNR (H. L. Fei et al., 2012; Insua-Cao et al., 2012). Within the CVGCA, primary evergreen forest is limited to the more inaccessible limestone areas, such as the slopes and ridges, while the valleys exhibit degraded scrub or regenerating vegetation as a result of past agricultural use (B. P. L. Chan & Ng, 2006; Fauna & Flora International, 2016; Insua-Cao et al., 2012).

Human Impact

As of 2019, the population of Trung Khanh district was 48,955 people, with 88 per cent living in rural areas (Vietnam, 2020). Trung Khanh consists of 19 communes, three of which surround the CVGCA; Ngoc Khe commune to the north, and Ngoc Khe and Phong Nam to the south (B. P. L. Chan & Ng, 2006; Insua-Cao et al., 2012).

The forest and distribution of the CVG once covered the surrounding landscape and wider Trung Khanh district but both have since retreated to the confines of the CVGCA and BNNR due to extensive logging, agricultural expansion and collection of forest resources (Insua-Cao et al., 2012). In 1986, the Trung Khanh Nature Reserve was created, covering a region of 30km^2, however an administrative board and definition of the reserve were never established (B. P. L. Chan & Ng, 2006). Upon the rediscovery of the CVG in 2007 in Vietnam and in 2009 in China, the CVGCA and BNNR areas were established to protect the gibbons (Insua-Cao et al., 2012).

Following their rediscovery, FFI established patrols consisting of both local villagers and local government park authorities to raise awareness and education on the status of the CVG (Insua-Cao et al., 2012). Through this community-led approach, by 2010 reports of gibbon hunting had ceased (Insua-Cao, Lu, Cuong, & Tao, 2010).

The overexploitation of the forest by local communes had resulted in the forest in much of the CVGCA being heavily degraded, particularly throughout the 1980-1990s when logging was unregulated (Dat et al., 2008a; Trung & Hoang, 2004). FFI and local government have supported the uptake of biogas, more fuel-efficient stoves, and the establishment of fuelwood plantations to reduce the need for incursions into the protected forest (Fauna & Flora

International, 2016; Insua-Cao et al., 2012). The farming of goats was also prohibited in many villages around the CVGCA due to the damage known to be caused by the ranging animals, though may still occur in some areas (Carrete et al., 2009; Fan et al., 2013; Insua-Cao et al., 2012). In Vietnam, larger livestock grazing is also prohibited, however it still occurs within the BNNR in China (C.-Y. Ma et al., 2020).

Conservation of the CVG

Following the rediscovery of the cao vit gibbon, the CVGCA covering approximately 16.56 km^2, was established in Vietnam in 2007, and the BNNR covering 65.30 km^2 was established on the Chinese side of the border in 2009, the latter of which was upgraded to national protection level in 2013 (Insua-Cao et al., 2012). Despite the protection afforded the region, historical use of the Trung Khanh area as a site for resource collection by members of local villages and farming, has left a long-lasting impact of degraded areas, particularly in the valleys and hillsides (Insua-Cao et al., 2012).

The protected area is surrounded by three communes in Vietnam, and five villages in China (Insua-Cao et al., 2012). Farming and resource collection is illegal within the protected areas on both sides of the border, and initiatives run by international conservation groups such as FFI have reduced the need for locals to enter the protected zone. The introduction of an initiative by FFI to support the adoption of fuel-efficient stoves in local communities has significantly reduced the need for firewood, while another program trains farmers in the use of elephant grass, a hardy alternative to normal grass, as livestock feed (Tatarski, 2017). Both initiatives have significantly reduced the reliance of communities on the protected forest.

While both countries allow international NGOs to undertake conservation efforts for the cao vit gibbon, the presence of an international border can impede a cohesive approach to conservation methods (J. J. Feng et al., 2014). For instance, while livestock grazing is banned in Vietnam, it continues within the protected area in China (C.-Y. Ma et al., 2020). In an effort to reduce such conflicts, a memorandum of understanding between Vietnam and China was established in 2011 for cooperative conservation efforts (C.-Y. Ma et al., 2020). Regular formal and informal meetings also allow for a transmission of information and collaboration to unify approaches to cao vit gibbon conservation. This includes efforts to reverse habitat

degradation, with habitat rehabilitation pilots undertaken in China, and food tree restoration efforts undertaken in Vietnam (Chang-yong et al., 2020).

While collaboration at an administrative level can maintain consistency, the international border still makes conservation difficult for researchers in the field. During fieldwork for this study, 'illegal' campsites were identified, left behind by researchers who has crossed the border from China. Access to the region can also be restricted by limited approval processes, requiring renewal in Cao Bang city every four weeks.

There have been no reported incidents of cao vit gibbon poaching or direct deaths as a result of human interactions with the gibbons, a history of habitat degradation and the fragmentation of their habitat limits the ability for significant population growth at least in Vietnam (Fan et al., 2013). Drawing on earlier studies, the CVG component of this thesis will conduct an analysis of the current CVG habitat and a potential area for expansion. Continued research to expand habitat through vegetation rejuvenation will be critical to the future of the cao vit gibbon.

The CVG component of this study will undertake present the outcomes of ecological and maximum entropy distribution modelling undertaken to assess the suitability of a region previously identified as a habitat expansion for the CVG (Fan et al. 2013). This includes an evaluation of a connecting corridor between the two sites.

Part one: *Trachypithecus poliocephalus* (Cat Ba langur)

Abstract

The *Trachypithecus poliocephalus* (Cat Ba langur) is one of the world's most Critically Endangered primates. It has consistently been included on the IUCN's 25 Most Endangered Primates list since 2000 (IUCN, 2019), and is also included in CITES Appendix III (CITES, 2019; UNEP-WCMC, 2022). It is a member of the taxonomically complex limestone langur group, a group which is significantly understudied, in part due to the difficulty of the terrain they inhabit (Blair et al., 2011; Groves, 2001; Sodhi et al., 2004).

Major threats to the CBL have included hunting, for consumption and use in local herbal remedies, habitat destruction as a result of wildfires, logging, stripping of the forest for natural resources, and urban development and tourism (Nadler et al., 2007; O'Brien et al., 2003; Thuc et al., 2014; Van et al., 2010). While these threats are being managed today through the efforts of conservation groups and the Cat Ba National Park, they have yet to be eliminated across the remaining habitat of the langurs.

The Cat Ba Langur Conservation Project (CBLCP) was set up on the island in 2000 to monitor and protect the langurs, yet prolonged study of the species only began in 2014, focussing on the behaviour, home range and socioecology of the main breeding group located in Cua Dong (Hendershott, 2017; Hendershott et al., 2016; Stenke, 2001). As a result, there is an alarming lack of knowledge regarding the ecology of the CBL, which is crucial to assist with conservation planning.

The following chapters will provide the first ecological analysis of the two main CBL home ranges, a comparison analysis of a potential corridor to connect the two isolated breeding populations, and a species distribution analysis to identify areas for potential habitat expansion. This will provide a starting point for future habitat analyses and provide data for planning the next steps for the CBL conservation.

Chapter 3 A comparison of the two main home ranges of the Cat Ba langur (*Trachypithecus poliocephalus*)

3.1 Introduction

Preserving the habitats of the world's endangered primates is inextricably linked with our ability to save the primates themselves. As ecosystems around the world face continuing and growing threats from human influences, understanding the ecological preferences of endangered primate species is becoming increasingly critical to arrest the global decline in diversity and the ongoing survival of primates (Z. Huang et al., 2017; Pyritz et al., 2010; Schwarzkopf & Rylands, 1989).

While primate species around the world such as the CBL face the ongoing threat of habitat loss and fragmentation, hotspot areas such as Vietnam are of increasing concern due to rapid human development and population growth (Eames & Robson, 1993; Sodhi et al., 2004). Vietnam has some of the highest numbers of endemic primate species globally, and the rise in human induced threats, high rates of deforestation, and a lack of knowledge about the habitats its threatened species are putting endangered primates at a greater risk of extinction (Blair et al., 2011; Catullo et al., 2008; B. T. Nguyen, 2004; Y. Zeng et al., 2013).

Understanding the habitat and ecological needs of primates is critical to enabling species-specific conservation in the face of fragmentation and habitat destruction (Damschen et al., 2006; Y. Zeng et al., 2013). Yet despite its importance, determining the ecological needs of endangered primates in Vietnam proves difficult due to a lack of a baseline habitat profiles against which to compare current ones (Blair et al., 2011; Isabirye-Basuta & Lwanga, 2008). This is due to an extensive history of forest loss in the country with up to 80 per cent of original forest cover lost due to logging, climate change and deforestation for agriculture and development (Eames & Robson, 1993; Isabirye-Basuta & Lwanga, 2008; Y. Zeng et al., 2013). As a result, as primary forest is lost and replaced by increasing areas of secondary or highly disturbed primary forest, understanding the true relationship between primates and their habitats may no longer be possible (Dunn, 2004). This ongoing disruption has left primate species in Vietnam living in fragmented populations which are largely facing ongoing impacts from human development in some way (Blair et al., 2011). This means that habitat studies

undertaken now, are most likely measuring the way in which species are managing their altered habitats and not how we would expect them to behave in pristine habitat. Despite this, these studies are essential to promote effective ongoing management of these species and their diminishing habitats (Y. Zeng et al., 2013).

The CBL is a clear example of this due to a history of habitat loss and population decline directly resulting from human expansion on Cat Ba Island (Nadler & Long, 2000; Stenke & Canh, 2004; Tien Bui et al., 2016). Despite once encompassing the entire island, today the global wild CBL population is highly fragmented into two major breeding groups geographically isolated from one another. The two sub-populations inhabit two protected areas: Cua Dong, and the Sanctuary, both forested peninsulas on the southeast of Cat Ba Island.

The aim of this chapter is to determine the habitat profile of the home ranges of the two main wild breeding populations of CBL. An improved understanding of the composition of the CBL habitat is essential to support lasting conservation outcomes for this Critically Endangered species.

I hypothesise that Cua Dong and the Sanctuary, the two main habitats of the CBL, are highly similar in their topographic and vegetation characteristics, and that the plant communities, based on plant species and distributions, between the two areas will also be very similar. Based on the high population concentration in the two areas and success in breeding, I expect that the two sites have similar profiles and reflect their original habitat prior to human intervention. While the two areas are known to have undergone heavy use by humans in the past, the preference for these areas are likely to be due to ecological requirements and/or refuges.

3.2 Methods

3.2.1 Study species and study sites

The CBL is listed as Critically Endangered (IUCN, 2019) and has a global wild population of approximately 50-60 (Fauna & Flora International, 2022) and a captive population of six

langurs at the Endangered Primate Rescue Centre in Cuc Phuong National Park (Hendershott et al., 2016; Nadler & Long, 2000).

The CBL is endemic to Cat Ba Island, and their distribution, once covering a majority of the island, is now restricted to two separate peninsulas within the national park boundary, on the eastern coast of the island (Figure 3.1). Two main breeding groups are separated by roughly 23km of coastline and have not been observed to move between the two habitats, though there is a forested coastline that could potentially act as a corridor between the two groups.

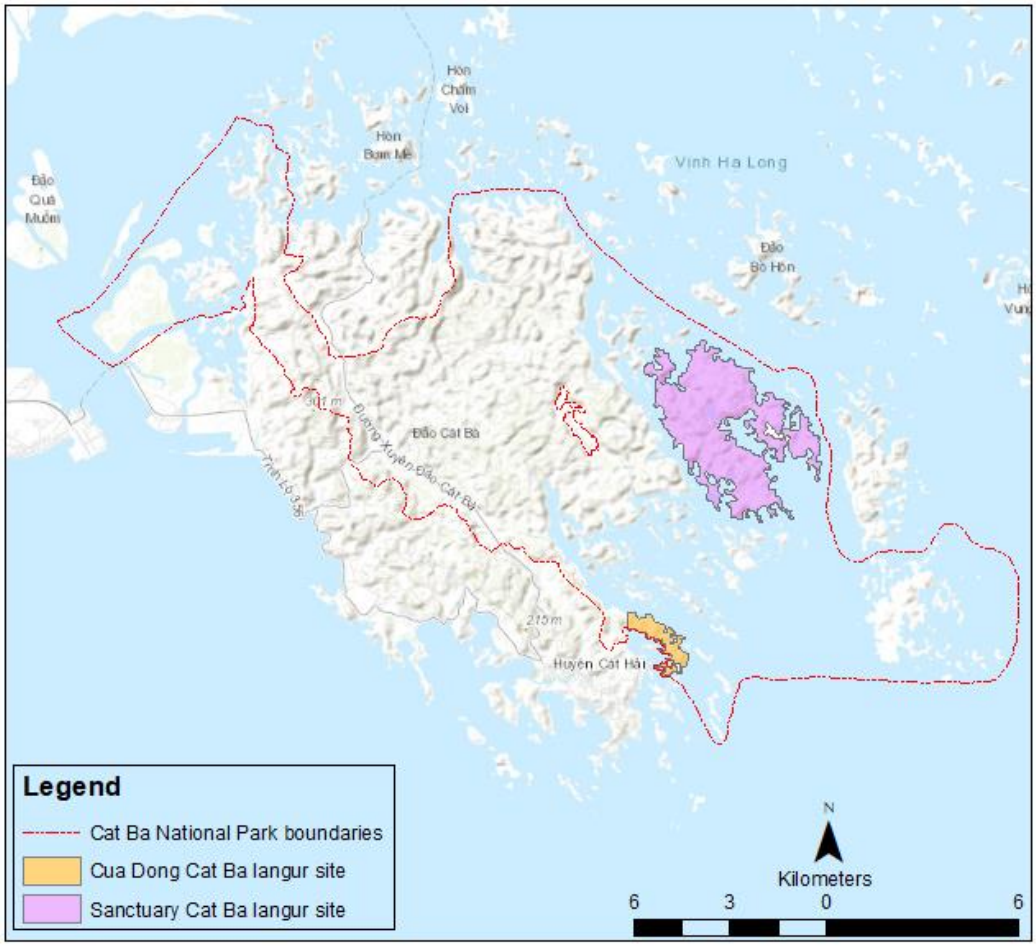


Figure 3.1 Map of main CBL populations. Basemap source: ESRI, Maxar, Geographics, and Community (2009).

The Cua Dong region covers approximately 1.1 km^2 to the south-east of the island and is home to the breeding population used primarily in behavioural research (Hendershott, 2017; Hendershott et al., 2016; I. Schneider et al., 2010). This region supports approximately 27 langurs (pers comm. Ruskin), who are monitored five days a week by a national park ranger funded by Fauna and Flora International (FFI). The waterways around the area are heavily

used by tourist boats, fishermen, and populated by a floating village, with some houses positioned against the limestone cliffs used by the langurs. As a result, this population appears to be somewhat habituated to the presence of boats and people moving around the cliffs on ground level (Hendershott, 2017; Hendershott et al., 2016).

The second site known as the Sanctuary is a protected peninsula (13.9km²) on the south of the island guarded by local rangers from the national park, supported by the Cat Ba Langur Conservation Project (CBLCP) (Stenke, 2001). While public access to the Sanctuary is prohibited, tourist boats stop just outside the boundary for kayaking. The number of floating houses in the area is very low, and inhabitants sometimes assist rangers by notifying them of any people entering the area. Approximately 20 langurs are thought to reside there, though very little tracking of groups is conducted.

Langurs in the Sanctuary live sympatrically with *Macaca mulatta* (rhesus macaques). Rangers report that they have observed aggressive interactions between the two species, generally resulting in the langur groups fleeing, yet as of 2016 there is no regular monitoring of the macaques or their relationship with the langurs.

A third smaller, non-breeding group of langurs, which includes up to five individuals is located on a small island to the north of the main island. This group is intermittently monitored and did not feature in the study due to difficulty in accessing the area.

Data collection for this study was undertaken February to May 2016 to avoid interruption from typhoons that regularly occur in the Gulf of Tonkin during the wet season (Table 3.1).

Table 3.1 Average temperature, rainfall and humidity on Cat Ba Island during data collection

Month (2016)	Average temperature (˚C)	Average rainfall (mm)	Average humidity (%)
February	15	4.3	68
March	20	16.88	80
April	24	37.03	89
May	27	127.38	83

All weather information is collected from 'World Weather Online' https://www.worldweatheronline.com/cat-ba-weather-averages/vn.aspx

3.2.2 Interviews

Seventeen interviews were undertaken across Cat Ba Island with locals from surrounding communes and villages, including individuals from the floating village around Cua Dong and the Sanctuary between February and May 2016. Interviewees were identified by the lead contact from the Cat Ba Langur Conservation Project in an effort to meet the following criteria that those interviewed should be adults, long-term residents of Cat Ba Island and represent a cross-section from the Communes across the island.

Information collected during interviews included the recent historical distribution of the CBL, forest health and changes, local use of the forest, and awareness of the CBL conservation efforts. All participants were adults and represented a mix of employments to capture a wide range of viewpoints. To establish reliability of the information collected, only information that was common across multiple interviews was reported unless otherwise noted, as per Fan et al. (2011). However, unlike Fan et al., (2011), information was not confirmed across interviews to avoid influencing responses (for interview questions see Appendix 1.1).

Ethics approval was granted by the Australian National University Human Ethics Committee (protocol number: 2013/8 and 2015/761) for the period of 1 February 2016 to 1 February 2018 to undertake interviews with community members local to each of the national parks under investigation.

3.3 Ecological sampling

The ecological characteristics of the langur home ranges were collected using 24 square ecological plots measuring 10x10m spread across the two sites: Cua Dong, and the Sanctuary (Figure 3.2). At each of the sites 12 plots were established using stratified random sampling across three key habitat strata used by the langurs: coastal habitat, slope habitat and valley habitat. This was achieved by placing a grid over the CBL habitats and numbering coastal, slope and valley grids separately, before using a random number generator to select four grids in each habitat type. If a plot was chosen in an area known to be inaccessible by National Park rangers, the grid was excluded, and a new number was generated. Due to the difficulty of the terrain, in cases where the identified area was unsafe once located, I placed plots as close as possible to the identified location while remaining in the vegetation of the same habitat type

to be sampled. These plots were located within the known ranges of the two langur populations as determined by local rangers and Hendershott (2017). Two other key habitat strata (cliff faces and summits) used by the CBL were also identified but not sampled due to difficulty in safely accessing these regions.

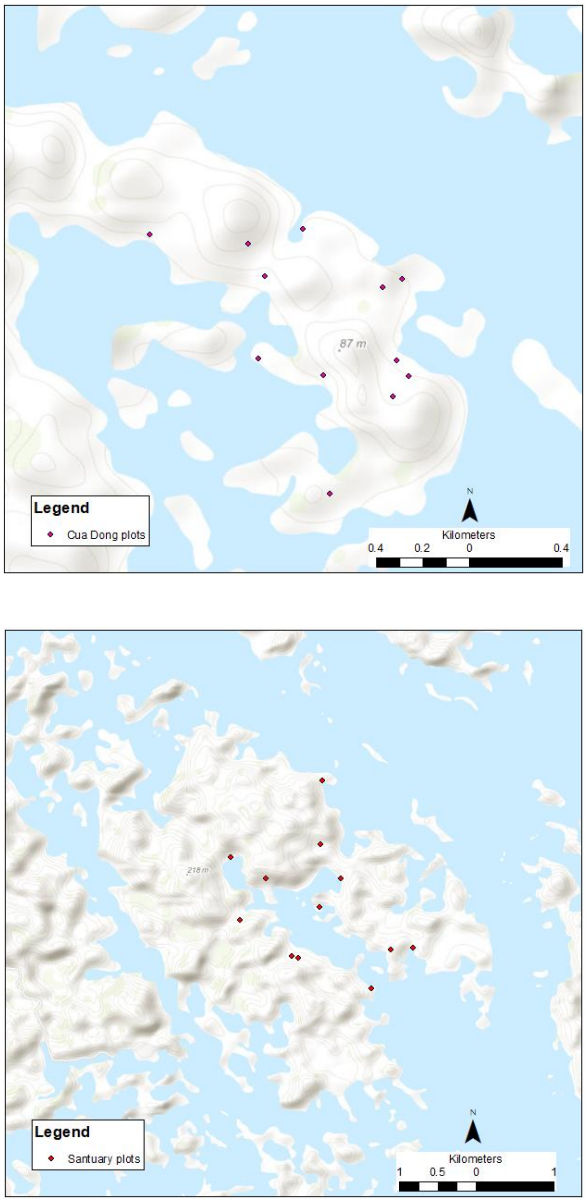


Figure 3.2 Location of plots placed in Cua Dong and the Sanctuary habitats. Twelve ecological plots 10x10m were placed at each site evenly spread across coasts, valleys and slopes. Basemap source: ESRI et al. (2021).

As limestone karst is at times extremely narrow and dangerous to navigate and because vegetation strata are often poorly defined, 10x10m grid plots were used as done in Dayong et al. (2016) and Estrada and Coates-Estrada (1996). Previous studies of limestone langurs have divided their habitats into three main zones: top, middle and bottom (or flat) (C. Huang, Xue,

Wei, & Li, 2000; Qihai Zhou et al., 2007), but recent studies of the CBL tend to identify four to five main activity zones, including summits/top, middle/slope, lowest/coastal, valleys and cliff faces (Hendershott, 2017; I. Schneider et al., 2010). While Hendershott (2017) classifies a valley as including the sloped sides of the valley as well as the valley floor, I restricted valleys to include only the valley floor due to an observed difference between the vegetation on the sides of the valley (slopes) compared to the valley floor. This is largely because most valley floors on Cat Ba Island have been previously, or are currently, used for agriculture.

J.-W. Kim and Thin (1998) undertook a vegetation analysis of CBNP where they identified seven vegetation types across the island. Based on this analysis and observations of the langurs carried out in a pilot study prior to the commencement of this study, I identified five main strata utilised by the CBL (Table 3.2). These strata represent five distinct vegetation/landscape combinations within the CBL habitat.

The GPS for each plot was taken in the SE corner, with two bearings also recorded. At the SE corner of each plot, I recorded the elevation, aspect, slope, and vegetation type. GPS coordinates were collected for each plot for use in future studies, however some coordinates were adjusted post-fieldwork with Google Earth Pro to match known locations and to correct for GPS error, which is a common issue in limestone environments (K. A. Phillips, Elvey, & Abercrombie, 1998).

Within each plot, an experienced botanist, Dr The Van Pham, botanist and researcher at Van Lang University, identified and categorised all stems to species level. All trees and shrubs with a diameter at breast height (DBH) of greater than 2cm were measured with a DBH measuring tape or callipers. This level of detail was undertaken in the survey with an aim to be able to characterise the vegetation profiles of the habitat zones. The diameter of all lianas over 2cm was also recorded. Due to the terrain, the use of a clinometer was not always possible to determine canopy height. Instead, Dr The and I independently estimated canopy heights visually (D. Li et al., 2006), to the nearest 50cm and then compared results. If estimates differed by over 50cm, they were triple checked. Visual estimation of tree heights and canopy using height categories has been employed in other studies (S. Cheyne, Thompson, & Chivers, 2013).

Table 3.2 Vegetation stratum types identified in the Cat Ba langur habitat

	Characteristics	Number sampled	Example
Coastal*	No more than 5m from the water or beach. Largely secondary forest.	*8*	
Valley	Valley floor not open to the water. Generally ex-agriculture or previously inhabited.	*8*	
Slopes	Between 15-100m in elevation, facing water or valley. Some vegetation structure.	*8*	
Summits*	Rocky summits with stunted trees and vegetation (J.-W. Kim & Thin, 1998).	*n/a*	
Cliff faces*	Vertical (or near vertical) cliffs, with small shrub and mat vegetation.	*n/a*	

*Strata marked n/a (summits and cliff faces), were not sampled as they were too dangerous to access due to the nature of the limestone.
Photos: K. Apthorp, 2016.

Canopy coverage within a plot was determined using an assessment of the percentage of the total coverage within each plot by tree crowns. This is necessarily a qualitative estimate as tree crowns are not uniform in the density of their leaves or coverage within the circumference of their crowns (Bonham, 2013). The size of each crown was measured based on maximum and minimum diameters and recorded on graph paper. The amount of coverage depended on the amount of the plot covered by the canopy of the trees and the density of the canopy, with zero per cent indicating no canopy present in the plot and 100 per cent indicating full coverage with high density allowing little light to reach the plot floor.

As CBL have been noted to prefer the under canopy and shrub of forest layers (Nadler & Long, 2000), a full assessment and measurement of vegetation layers below the canopy layer was also carried out. The understory was divided into three parts (Appendix 1.2): a mat layer, comprising of small herbs, plants and seedlings measuring ≤20cm; a shrub layer comprising small plants, ferns and seedlings measuring between 20cm and 1.5m; a large shrub layer comprising larger plants, shrubs and saplings measuring between 1.5m and 2m, or above where DBH<2cm (Smith, Bull, & Driscoll, 2012). The general percentage of liana coverage was also estimated.

Using these layers, I first estimated the coverage of each layer across the plot and then estimated a general vegetation density of each plot based on a scale of one to five (Stickler & Southworth, 2008). A score of one represented the vegetation within the plot was easily passable and absent and a score of five indicating that the plot vegetation was largely impenetrable (Appendix 1.3). As plots may have patches of impenetrable vegetation due to dense shrubs and lianas, as well as empty patches, an average of vegetation density based on ease of access around the plot was taken.

A similar scale was used to determine topographic complexity, where one indicated no visible limestone within the plot and five indicated non-uniform and layered limestone sheets (Appendix 1.4), making the plot difficult to move around, and requiring some climbing within the plot.

Food species were taken from Ruskin (unpublished data, 2016).

3.4 Data analysis

3.4.1 Habitat characteristics

To determine the characteristics of the vegetation of the three sites, I calculated species richness, species diversity, tree area, basal area, average DBH and density of all vegetation types (stems/m^2), and exclusively tree density (stems/m^2) for each plot (Appendix 2.1.1).

Species richness was calculated to determine the total number of plant species within each plot by the total number of different species within the 10x10m plots.

Species diversity was calculated using the Shannon-Weiner index was calculated using:

$$H = -\sum_{i=1}^{s} p_i \ln p_i$$

Where:

p = proportion ($\frac{n}{N}$) of individuals of one species found (*n*) divided by the total number of individuals (*N*) found.

s = number of species

The density of total plant communities and then only tree species was determined by:

$$\text{Total Plant Density} = \frac{Total\ number\ of\ all\ stems}{Area\ sampled\ (m^2)}$$

$$\text{Tree Density} = \frac{Total\ number\ of tree\ stems}{Area\ sampled\ (m^2)}$$

Total basal area for each plot was also calculated by:

$$\text{Total basal area } (m^2) = \text{sum of the total area (A) of all tree species}$$

Where

$(A) = \pi r^2$

$r = \frac{Diameter}{2}$

I used a general linear model to explore the relationship between my ecological plots and variables measured within the plots. To understand differences between plots at each site, I used a one-way analysis of variance (ANOVA) from the linear model to assess significance of effects. To understand differences between sites, I used a two-way ANOVA. Estimated marginal means based on the linear models were then calculated and compared in a post hoc analysis employing a Tukey adjustment to the p-values. I undertook a visual inspection of residuals and determined that no transformation was required of variables as residual plots sufficiently satisfied normality constraints, noting a small sample size. Results were reported where $p<0.05$.

I carried out habitat characteristic calculations manually. All general linear models, ANOVAs and estimated marginal means calculations were carried out using the VEGAN package in R (4.2.1).

3.4.2 Plant species analysis

All models and calculations were carried out using the VEGAN package and visualisations using GGPLOT2 package in RStudio (2022.07.2) with R (4.2.1).

3.4.2.1 Plant species in the habitat of the CBL

Using the VEGAN package and METAMDS function in R, I undertook non-metric multidimensional scaling (NMDS) ordination analyses to assess the similarity or dissimilarity between: (1) the plant communities within Cua Dong; (2) the plant communities within the Sanctuary; (3) the plant communities across both Cua Dong and the Sanctuary.

A NMDS is a rank-based approach to scaling variables in a two-dimensional space, where distances between points on the plots will approximate their multivariate dissimilarity. Points more closely located to each other share more similar species composition than those points further away (Biostats, 2022). Being non-metric, it also allows for the use of ordinal data that is not in a normal distribution. NMDS is an iterative algorithm, which runs the same steps repeatedly until the best solution is found when convergence is achieved. In this case, the automatic 20 runs (unless otherwise noted) were used to determine best solution and identify stress. A stress less than 0.2 was considered to produce a good representation of the two-dimensional relationships, anything below 0.1 was considered very good.

To account for data values larger than common abundance class scales, the METAMDS function applies a Wisconsin double standardisation transformation to data (Oksanen, 2022). This transformation standardises each value by the column maximum and then by the row (plot) total, typically enhancing patterns in data (Logan, 2011). In cases where values remained large, a square root transformation is subsequently applied to reduce the impact of very large counts in the abundance data over unique counts.

An NMDS requires a distance matrix based on count data. As the vegetation counts collected within the ecological plots represented abundances rather than simply presence/absence data, I applied the Bray-Curtis Dissimilarity index. The Bray-Curtis dissimilarity index (Bray & Curtis, 1957) allows comparison of differences in plant species populations between plot types and between sites based on abundances. The Bray-Curtis dissimilarity index is bounded between 0 and 1, where 0 indicates plots have the same composition and 1 indicates no shared composition (Ricotta & Bacaro, 2010; Ricotta & Podani, 2017). To further investigate relationships between sites and plant species, I applied confidence ellipses (0.95) to determine overlap between the plot types and sites.

To test whether there were significant differences between the plot type and site groupings based on plant abundances, I applied a permutational multivariate analysis of variance (PERMANOVA) using distance matrices (McArdle & Anderson, 2001) and the function ADONIS2 in the VEGAN package. The model was run using the same community data matrix used in the NMDS analysis and a Bray Curtis dissimilarity method was used (Stevens & Oksanen., 2022).

I then applied the ENVFIT function to investigate which species most significantly contribute to the distribution pattern of plot types both within and between sites. The ENVFIT function calculates a multiple regression of the intrinsic species variables, and fits vectors onto an ordination (Oksanen, 2022). ENVFIT provides the p-value of correlation between the intrinsic species variables and the NMDS ordination. To improve visibility on the NMDS plots, only significant vectors where $p<0.05$ were plotted unless otherwise noted. The direction of each vector shows the maximum correlation between the NMDS arrangement and each variable.

Vector lengths represent their correlation to the plot, with shorter arrows being weaker predictors and longer arrows, stronger predictors (Oksanen, 2022).

3.4.2.2 Cat Ba langur food species

I repeated the NDMS ordination analyses, PERMANOVA and multiple regression of intrinsic variables analysis on food species reported for the CBL to determine how dissimilar food abundances are within sites, and then between the two sites.

As collection of food species consumed by the CBL was out of scope for this study, these data were taken from a list of 56 food species complied by Ruskin (unpublished data, 2016). This list represents the only known compilation of food species for the CBL. Food species were collected by Ruskin (unpublished, 2016), using scans and focals from a distance of over 50m.

3.5 Results

3.5.1 Interviews

Most interviewees had lived on Cat Ba Island for their entire lives, or since early childhood, with participants having lived on the island for an average of 43 years (Table 3.3). All participants knew of the CBL and all but one had seen them in the wild.

Table 3.3 Demographics of interviewees from communes across Cat Ba Island

Demographics		% Response (N=17)
Sex	Male	70.6
	Female	29.4
Years living in local area	0-15	5.9
	16-30	5.9
	31-45	47.1
	46-60	41.2
Occupation	Linked to National Park or CVG Conservation	29.4
	Teacher	5.9
	Fisherman	5.9
	Local governance	35.3
	Private business	23.5

Based on interviews, the CBL was once widely distributed across Cat Ba Island, and several responses indicated that langur groups were also once found living alongside villages. It is also possible that the CBL distribution had already retreated from the west of the island by the

time the families of many interviews moved into the region, up to 40 years prior. Participants local to this region did not recall seeing the CBL around their villages.

The CBL population was identified to have started to rapidly decline from the late 1970s following the government-led migration of Vietnamese from the mainland to Cat Ba to displace the Chinese populace. Poverty and increased presence of guns is reported to have increased hunting and trapping of both langurs and macaques on the island. This was exacerbated in the 1990s when tourism increased and the local population expanded to the detriment of the forests, reducing the available habitat for the CBL. The CBL was reported to have disappeared from the wider island except for their Cua Dong and Sanctuary ranges, and a small population in Hang Cai. Unlike the CBL, macaques have maintained a presence across large parts of the island. A small number of participants also reported either witnessing or hearing about historical predation of the CBL by pythons and young CBL by birds of prey such as kites.

The work of conservation groups and the national park to protect the CBL was universally known, with many either currently or previously involved in monitoring efforts. Education of younger generations as to the importance of CBL conservation was widely accepted as well delivered, however there were suggestions that continued targeted education of older generations should be implemented.

Use of the forest by local people was unanimously acknowledged to have decreased, with no logging or major hunting continuing. A majority of interviewees noted that trapping still continues for smaller animals such as snakes in some areas of the forest. Overall, the diversity of wildlife was thought to have declined, however the quality of forest was noted to have improved since greater protection was enforced from the early 2000s. The weather was also unanimously considered to have become more ‘abnormal’ with more extreme changes in weather patterns. For instance, many noted that there had been an increase in rain and summers were becoming hotter.

3.5.2 Cua Dong Habitat Characteristics

3.5.2.1 Generalised linear model, ANOVA and estimated marginal means analysis of Cua Dong

When I compared the topographical and vegetation measurements collected in my ecological plots using a one-way ANOVA based on a generalised linear model, I found that that elevation, species diversity, and general diversity significantly differ ($p<0.05$) across coast, valley and slope plots in Cua Dong (Appendix 2.1.2).

Based on the estimated marginal means (Appendix 2.1.3), the topography of the different plots within Cua Dong is generally uniform, with only the elevation of coast plots (7.75 ±5.22) significantly differing from slope plots (37.75 ±5.22, $p<0.007$). Slope plots on average, are more topographically complex and have greater slopes than both coast and valley plots, though the difference is not significant.

Coastal plots have a significantly greater general vegetation density (3.75 ±0.354) than slope plots (2.25 ±0.354, $p<0.036$), and only generally valley plots (2.50 ±0.354). In general, the vegetation across the plot types is uniform, however coast plots on average, have greater species richness and species diversity, as well as greater percentage of mat coverage and percentage of canopy coverage. In comparison, slope plots have less small and large shrub coverage, less canopy cover, fewer trees, with smaller diameters and heights in favour of greater liana coverage.

Valley plots in Cua Dong have on average, greater species density, shrub and large shrub coverage, and less liana coverage. They also have taller trees, with on average, large diameters and areas and a higher basal area than coastal and slope plots.

3.5.2.2 Cua Dong plant composition

3.5.2.2.1 Species abundances across Cua Dong plants

A total of 2094 stems were identified in the Cua Dong habitat, representing 186 species from 70 families (Appendix 2.2.1.), however only 36 species are shared across the three plot types indicating a 19 per cent overlap in species.

The top ten most frequently identified species across Cua Dong plots accounted for 41 per cent of the total stems identified (Table 3.4). The most frequently occurring species is *Streblus*

ilicifolius (n=193), a flowering shrub or tree with spines along the trunk native to hillsides and rocky ridges across Southeast Asia (NParks Flora & Fauna Web, 2022), found predominately on slope plots (n=142).

Table 3.4 Top ten species across Cua Dong plots

Species	Slope occurrence (n)	Valley occurrence (n)	Coast occurrence (n)	Total (n)	IUCN Red List Status
Streblus ilicifolius	142	42	9	193	LC
Chimonocalamus griffithianus	67	1	40	108	NE
Pilea peploides	77	11	10	98	NE
Taxotrophis macrophylla	84	0	0	84	NE
Pilea peltata	40	31	10	81	NE
Alchornea tiliifolia	0	81	0	81	LC
Alchornea scandens	6	55	5	66	NE
Cleistanthus tonkinensis	34	17	1	52	NE
Clausena indica	1	4	47	52	NE
Sterculia lanceolata	1	42	6	49	LC
Total	**452**	**284**	**128**	**864**	

*Descriptions from Flora of China Project (2020); POWO (2022)

Valley plots

Cua Dong valley plots have the largest number of individual stems (n=828) representing 119 species from 49 families, compared to coast and slope plots in Cua Dong. The most common species identified within the valley plots is *Alchornea tiliifolia*, an evergreen shrub or small tree native to Vietnam (Flora of China Project, 2020). The most frequently found species are typically shrubs and small trees, with several vines or climbing shrubs (Table 3.5).

Table 3.5 Top ten species found in Cua Dong valley plots

Species	Valley occurrence (n)	Description*	IUCN Red list Status
Alchornea tiliifolia	81	Shrub/tree	LC
Alchornea scandens	55	Vine	NE
Bleekrodea tonkinensis	44	Flowering tree	NE
Sterculia lanceolata	42	Evergreen tree	NE
Streblus ilicifolius	42	Flowering shrub	LC
Baccaurea ramiflora	32	Evergreen tree	LC
Pilea peltata	31	Herb	NE
Microtropis osmanthoides	26	Tree	NE
Celtis philippensis	26	Evergreen shrub/tree	LC
Sauropus racemosus	23	Flowering shrub	NE
Total	**402**		

*Descriptions from Flora of China Project (2020); POWO (2022)

Coastal plots

Coastal plots have the least number of stems (n=529) of all plot types, representing 100 species from 49 families. The most common species being *Clausena indica* (n=47), an evergreen shrub native to Southeast Asia, which may be collected and eaten by local human communities (Fern, 2014). The most frequently found species in coastal plots are scrub-species such as bamboo grass, grasses, small trees, small flowering plants and epiphytic ferns (Table 3.6).

Table 3.6 Top ten species found in Cua Dong coast plots

Species	Coast occurrence (n)	Description*	IUCN Red List Status
Clausena indica	47	Shrub/tree	NE
Chimonocalamus griffithianus	40	Bamboo grass	NE
Miliusa sinensis	23	Scrub tree	LE
Memecylon edule	16	Evergreen tree	NE
Dracaena cambodiana	15	Tree	NE
Ophiopogon latifolius	15	Grass-like shrub	NE
Derris trifoliata	13	Evergreen shrub	NE
Ichnanthus pallens var. major	13	Grass	NE
Drynaria bonii	12	Epiphytic fern	NE
Paraboea halongensis	11	Flowering shrub	NE
Total	**205**		

*Descriptions from Flora of China Project (2020); POWO (2022)

Slope plots

Slope plots within Cua Dong are dominated by the flowering shrub or tree *Streblus ilicifolius* (n=142). There were 510 stems identified within slope plots (Table 3.7) from 87 species and 46 families, characterised by bamboo grass, flowering herbs, ferns and trees, including *Diospyros mollis*, valued for its ebony wood (Flora of China Project, 2020).

Table 3.7 Top ten species in Cua Dong found in slope plots

Species	Slope occurrence (n)	Description*	IUCN Red List Status
Streblus ilicifolius	142	Tree	LC
Taxotrophis macrophylla	84	Tree	NE
Pilea peploides	77	Herb	NE
Chimonocalamus griffithianus	67	Bamboo grass	NE
Pilea peltata	40	Herb	NE
Cleistanthus tonkinensis	34	Shrub/Tree	NE
Diospyros mollis	18	Tree	NE
Derris trifoliata	17	Evergreen shrub	NE
Adiantum caudatum	16	Fern	NE
Primulina drakei	15	Flowering herb	LC
Total	**510**		

*Descriptions from Flora of China Project (2020); POWO (2022)

3.5.2.2.2 Non-metric multi-dimensional scaling analysis of Cua Dong plants

The NMDS ordination of all plant species across plots within Cua Dong, applied a Wisconsin double standardisation and square root transformation on the raw data before applying the Bray Curtis Dissimilarity distance. A solution was found within 20 tries and returned a stress value of 0.14, which is considered a good representation of the distances between abundances in two-dimensions.

The NMDS ordination shows that there is clear overlap across all three plot types (Figure 3.3), with minimal clustering between plots of the same 'type'. Coast plots have the closest clustering of plots, with the smallest variation, followed by slope plots. Valleys, however, have a higher variance, with the second valley plot (CDV2) grouping more closely to the third slope plots (CDS3) and first coastal plot (CDV1) based on the species abundances. This suggests that all three plots are similar based on the species abundances within their plant communities. A PERMANOVA shows that there is no significant difference between the three groups (R^2=0.17, F=0.88, P=0.56).

Fitting the species as intrinsic vectors (Figure 3.3) shows that twelve species significantly (p<0.0.5) contribute to the distribution of the plots in the NMDS ordination. A grouping of six species; *Bauhinia cardinalis* (p=0.021), *Microtropis osmanthoides* (p=0.010), Alchornea tiliifolia (p=0.023), *Bleekrodea tonkinensis* (p=0.038), *Pterospermum truncatolobatum* (p=0.019), *Uvaria tonkinensis* (p=0.009), all have positive gradients and are largely contributing to the plant communities in valley plots.

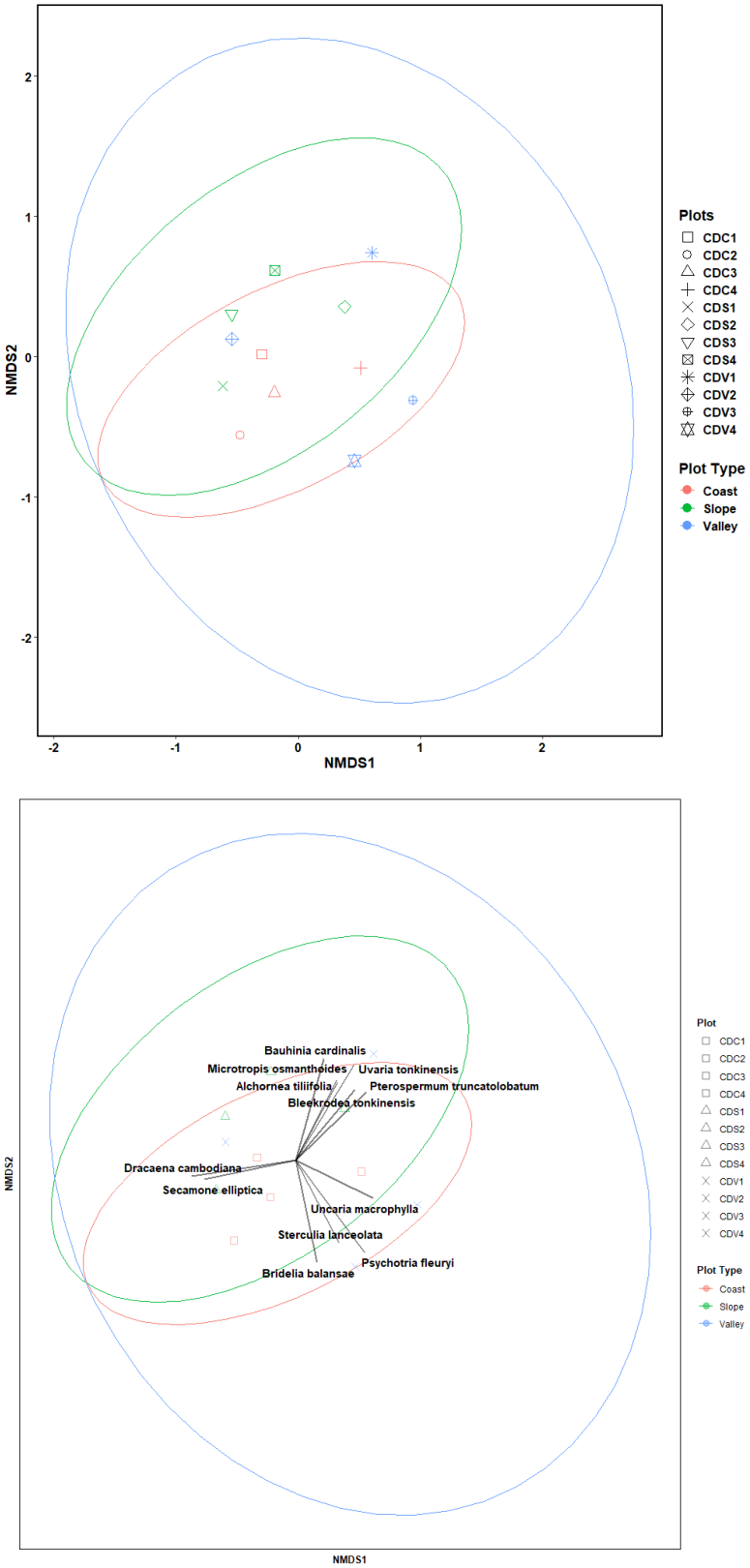


Figure 3.3 NMDS of species within Cua Dong plots. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors

Valley plot distribution is also significantly influenced by three species *Uncaria macrophylla* (0.035), *Sterculis lanceolata* (0.023)*, Psychotria fleuryi* (p=0.002) with a negative gradient.

Bridelia balansae (p=0.028) has a negative gradient and contributes to the distribution of coast and valley plant communities. *Dracaena cambodiana* (p=0.013) *Secamone elliptica* (p=0.049) have negative gradients and contribute to the distribution of coastal and slope plots.Cua Dong trees

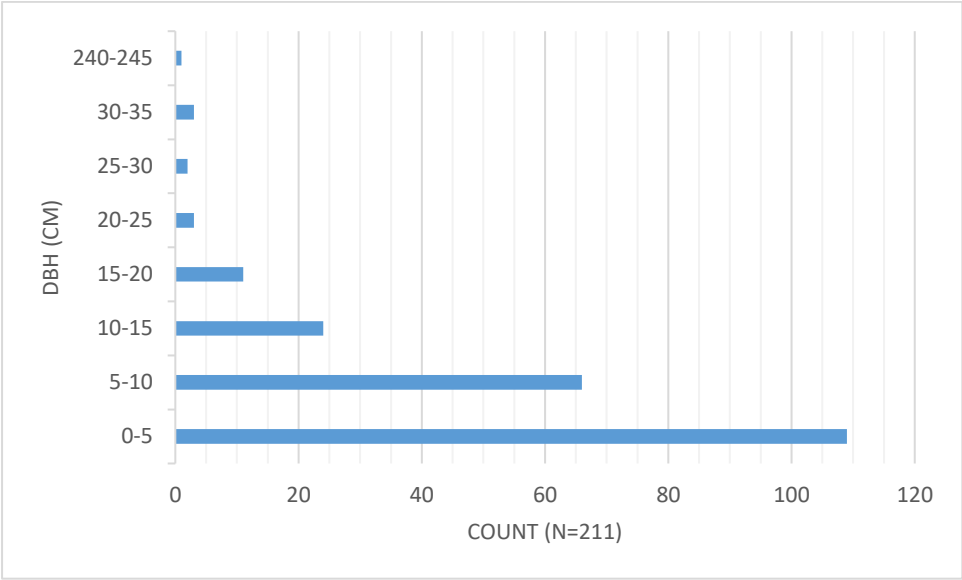
3.5.2.2.3 Cua Dong trees

Two hundred and twelve tree specimens were identified from 55 species across Cua Dong plots (Appendix 2.2.2). The most frequently occurring tree is *Streblus ilicifolius* (n=32), predominately across slope plots (n=22). Trees are most frequently found in valley plots (n=94), followed by coastal plots (n=64) and slope plots (n=54).

Table 3.8 Top ten tree species in Cua Dong

Species	**Slope occurrence (n)**	**Valley occurrence (n)**	**Coast occurrence (n)**	**Total (n)**	**IUCN Red List Status**
Streblus ilicifolius	22	8	2	32	NE
Bleekrodea tonkinensis	0	20	0	20	NE
Cleistanthus tonkinensis	2	10	0	12	NE
Sterculia lanceolata	0	8	3	11	NE
Bridelia balansae	2	5	4	11	LC
Dracaena cambodiana	1	4	6	11	NE
Firmiana simplex	1	0	9	10	LC
Aglaia elaeagnoidea	0	7	0	7	LC
Taxotrophis macrophylla	7	0	0	7	NE
Cerbera odollam	0	0	5	5	LC
Total	**35**	**62**	**29**	**126**	

Fifty-one per cent of tree within the Cua Dong have a small DBH of 2 to 5cm (Figure 3.4). The largest DBH recorded is a *Cleistanthus tonkinensis* (244.3cm) sampled within a slope plot. This species of tree is typically found on forested slopes in Vietnam (Flora of China Project, 2020)Tree canopies are generally within the 0-10m range, and the tallest is a specimen of *Microcos tomentose* (19.65m), identified in a valley plot.



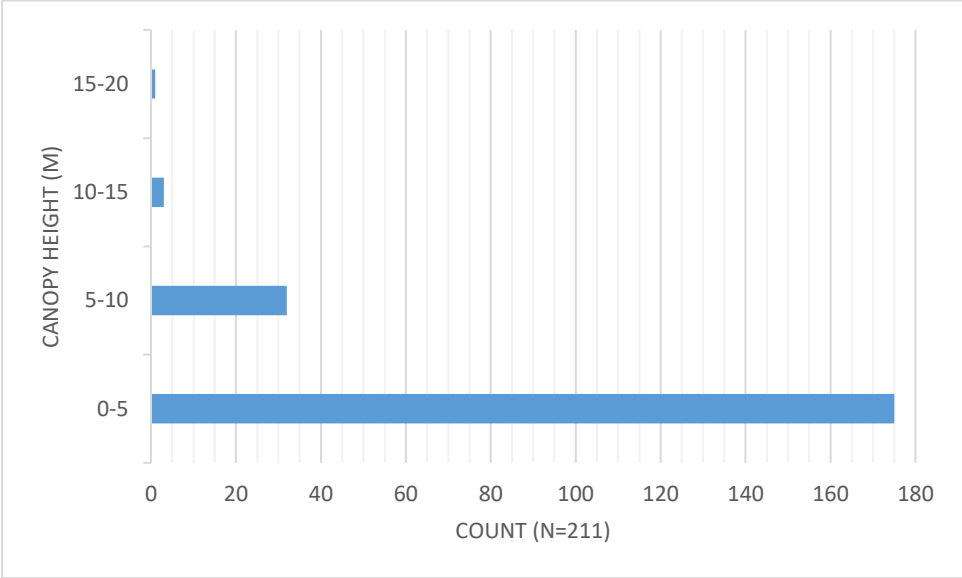


Figure 3.4 Tree metrics across plots in Cua Dong. Top: Frequency of DBH across Cua Dong plots. Bottom: Frequency of tree canopy heights across Cua Dong plots.

3.5.2.2.4 Food species composition and NMDS in Cua Dong

Thirty-four food species consumed by the CBL (Ruskin, 2016) from 384 individual stems were identified across the Cua Dong region and 29 families. The top ten food species (Table 3.9) represent 62 per cent of food stems found across the three plot types. The most commonly occurring food species is *Sterculia lanceolata*, a tree species found across Indochina (Flora of China Project, 2020), predominately found in valley and coastal plots. On slopes, *Derris trifoliata* a climbing-type shrub, is the most abundant species. Slope plots have the greatest

number of food species (n=26) and individual stems (n=133), followed by coastal plots (species=23, stems=123) and then valleys (species=20, stems=128).

Table 3.9 Top ten food species found in Cua Dong

Species	Coast occurrences (n)	Slope occurrences (n)	Valley occurrences (n)	Total
Sterculia lanceolata	6	1	42	49
Derris trifoliata	13	17	6	36
Dracaena cambodiana	15	10	6	31
Tetrastigma rupestre	4	12	7	23
Pilea hookeriana	0	2	16	18
Primulina drakei	0	15	3	18
Severinia monophylla	11	6	1	18
Litsea glutinosa	7	1	8	16
Secamone elliptica	9	6	1	16
Breynia fruticosa	7	0	7	14
Total	**72**	**70**	**97**	**239**

The NMDS ordination of food species found in Cua Dong, applied a Wisconsin double standardisation to standardise the abundance values, followed by a square root transformation to reduce the effect of high counts over unique counts when applying the Bray-Curtis dissimilarity distance. A solution was reached in 20 tries, for a stress value of 0.09 in three dimensions, making it a very good representation of the plot abundances.

There is a high level of overlap in the plot types, particularly slope and coast plots (Figure 3.5). Coastal plots have a loose grouping and very low variation, suggesting that food species abundances are similar to each other. Slope plots group closely to both coastal and some valley plots (CDV2 and CDV4) and the variation described by the slope plot confidence ellipses encompasses all of the Cua Dong plots, suggesting high similarity between slope and coastal plots, and a similarity between slope plots and valley plots. Valley plots show the greatest variation in abundances of their food species compositions. Valley plots group loosely together. The variation seen in valley plots may be a result of the historical use of many valleys within Cua Dong for agricultural use.

A PERMANOVA shows that there is no significant difference between the plot types (R^2=0.16, F=0.88, P=0.66), despite the wide variation of valley plots.

Applying the species as intrinsic vectors to highlight the species most significantly contributing ($p<0.05$) to the plot distributions shows that only four species are responsible (Figure 3.5). *Glochidion zeylanicum* (p=0.007) has a steep positive gradient and contributes significantly to the composition of the plot distribution, particularly valley plots. *Cissus annamicus* (p=0.04) has a negative gradient and contributes to the composition of slope and valley plots. *Homalium cochinchinensis* (p=0.02) has a negative gradient and contributes to coastal and slope plot compositions.

3.5.3 Sanctuary Habitat Characteristics

3.5.3.1 Generalised linear model, ANOVA and estimated marginal means analysis of the Sanctuary

A one-way ANOVA using a generalised linear model shows that elevation, slope, general density, species density, average canopy height, percentage of mat cover, and percentage of canopy cover have significant differences based on plot types (Appendix 2.1.4).

The estimated marginal means results (Appendix 2.1.5) show that the Sanctuary is topographically variable across its plot types; the difference in slopes varies significantly between the valley plots (6.00 deg ±3.59) and both the coastal plots (40.50 deg ±3.59, p=0.0002) and the slope plots (36.00 deg ±3.59, p=0.0006). While not significant, coast plots have a lower elevation mean (10.75m ±7.88) than that of slope plots (36.50m ±7.88, p=0.11), and valley plots (22.5m ±7.88, p=0.1). The variation in means of the topographic complexity of the plots was similarly not significant, however coast plots had a greater topographic complexity (3.75 ±0.52) than both slope plots (3.50 ±0.52, p=0.45) and valley plots (2.00 ±0.52, p=0.10).

Vegetation in the Sanctuary appears more heterogeneous than in Cua Dong. Coast plots in the Sanctuary have a significantly higher general density (3.50 ±0.28) than that of valley plots (2.25 ±0.28, p=0.03) but not slope plots (2.50 ±0.28, p=0.072). However, valley plots have significantly higher species densities (8.27 ±0.85) than both coast plots (3.52 ±0.85, p=0.008) and slope plots (2.83 ±0.85, p=0.003).

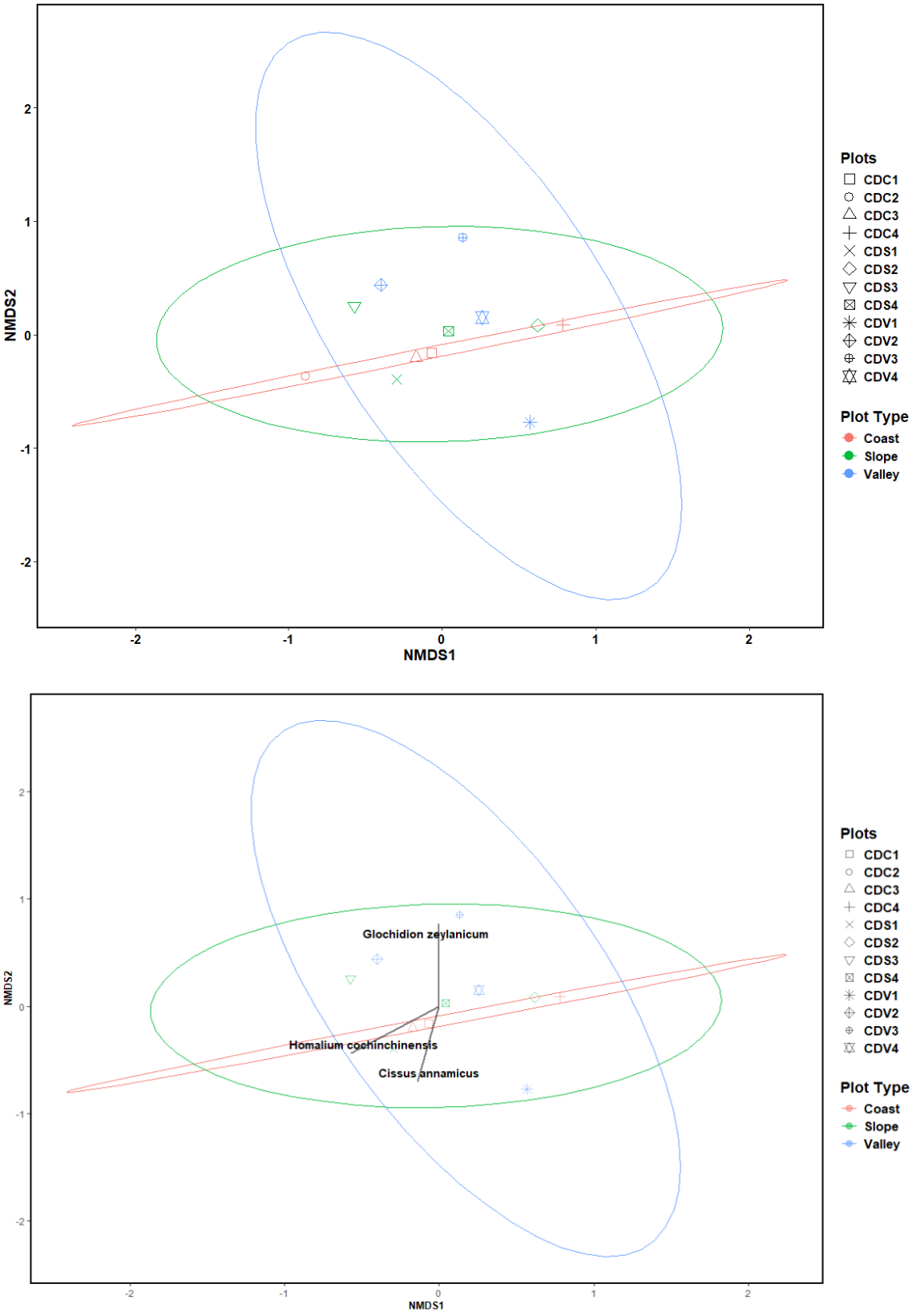


Figure 3.5 NMDS of food species in Cua Dong plots. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors.

Valley plots also have higher percentages of mat coverage (57.50 ±10.207) than coast plots (17.50 ±13.20, p=0.219), though not significantly. While not differing significantly, valley plots in the Sanctuary also have higher percentages of shrub cover, higher canopy heights, higher average tree diameters and larger average diameters of trees. In terms of canopy cover, however, coast plots have greater (87.50 ±15.6) canopy coverage than slope plots (30.50 ±15.6, p=0.069), and valleys (61.25 ±15.6, p=0.488).

3.5.3.2 The Sanctuary plant composition

3.5.3.2.1 Species abundances across the Sanctuary plants

Approximately 236 species from 78 families were identified across the Sanctuary plots, with a total of 5844 stems identified (Appendix 2.2.1). Across the three plot types, only 30 species are shared, accounting for 13 per cent overlap in species.

The most commonly found species (Table 3.10) is *Leptostachya wallichii*, a herb found across the forests of Vietnam and Southeast Asia (The Plant List, 2013) The most frequently found plants in the Sanctuary consist of epiphytic ferns, small flowering herbs and shrubs. None of the species are recorded on the IUCN Red List.

Table 3.10 Top ten species found in the Sanctuary plots

Species	Slope occurrence (n)	Valley occurrence (n)	Coast occurrence (n)	Total (n)	IUCN Red List Status
Leptostachya wallichii	3	712	0	715	NE
Claoxylon hainanense	0	490	0	490	NE
Ophiopogon latifolius	3	249	36	288	NE
Adiantum caudatum	44	133	42	219	NE
Drynaria bonii	0	0	216	216	NE
Pteris grevilleana	0	178	0	178	NE
Pilea peltata	130	0	43	173	NE
Pilea peploides	36	0	128	164	NE
Impatiens halongensis	1	25	137	163	NE
Carex cruciata	30	107	0	137	NE
Total	**247**	**1894**	**602**	**2743**	

Valley plots

Valley plots have almost 2.5 times the number of stems than both coast and slope plots with 3307 stems identified from 146 species. The most common species is *Leptostachya wallichii*

(n=712). The top ten species found in the Sanctuary valley plots (Table 3.11) comprise ferns, flowering herbs and shrubs, and small trees. None of the species are recorded on the IUCN Red List.

Table 3.11 Top ten species found in Sanctuary valley plots

Species	**Valley occurrence (n)**	**Description***	**IUCN Red List Status**
Leptostachya wallichii	712	Herb	NE
Claoxylon hainanense	490	Shrub	NE
Ophiopogon latifolius	249	Grass	NE
Pteris grevilleana	178	Fern	NE
Adiantum caudatum	133	Fern	NE
Xanthophytum balansae	109	Shrub/tree	NE
Carex cruciata	107	Herb	NE
Allantodia megaphylla	86	Shrub	NE
Machilus bonii	74	Tree	NE
Psychotria fleuryi	67	Flowering shrub	NE
Total	**2205**		

*Descriptions from Flora of China Project (2020); POWO (2022)

Coastal plots

Coast plots in the Sanctuary have 113 species from 1405 stems identified. The most common species found in the coastal plots is *Drynaria bonii* (n=216), an epiphyte commonly found on limestone rocks. The top ten species (Table 3.13) characterising these plots consist of epiphytic ferns on rocks, small herbs, grasses and shrubs and bamboo. None of the species are recorded on the IUCN Red List.

Table 3.12 Top ten species found in Sanctuary coastal plots

Species	**Coast occurrence (n)**	**Description***	**IUCN Red List Status**
Drynaria bonii	216	Epiphytic fern	NE
Impatiens halongensis	137	Flowering herb/shrub	NE
Pilea peploides	128	Herb	NE
Pyrrosia lanceolata	108	Epiphytic fern	NE
Cleistanthus tonkinensis	73	Shrub/tree	NE
Chimonocalamus griffithianus	52	Bamboo	NE
Pilea peltata	43	Herb	NE
Adiantum caudatum	42	Fern	NE
Begonia boisiana	36	Flowering shrub	NE
Ophiopogon latifolius	36	Grass	NE
Total	**871**		

*Descriptions from Flora of China Project (2020); POWO (2022)

Slope plots

Within the Sanctuary slope plot, 1132 stems from 118 species were sampled. The most frequently found species within these plots is *Pilea peltata* (n=130), a perennial herb typically found in shaded, moist forests (2013). The top ten species (Table 3.13) identified in these plots are comprised of flowering herbs, bamboo and the tree species, *Dracaena cambodiana* (n=38).

Table 3.13 Top ten species found in Sanctuary slope plots

Species	**Slope occurrence(n)**	**Description***	**IUCN Red List Status**
Pilea peltata	130	Herb	NE
Achyranthes aspera	91	Herb	NE
Impatiens verrucifer	91	Flowering herb/shrub	NE
Atalantia stenocarpa	62	Flowering shrub	NE
Adiantum caudatum	44	Fern	NE
Primulina drakei	40	Flowering herb	LC
Dracaena cambodiana	38	Tree	NE
Pilea peploides	36	Herb	NE
Chimonocalamus griffithianus	36	Bamboo	NE
Carex cruciata	30	Grass-like herb	NE
Total	**598**		

*Descriptions from Flora of China Project (2020); POWO (2022)

3.5.3.2.2 Non-metric multi-dimensional scaling analysis of Sanctuary plants

The NMDS ordination of al plant species across the Sanctuary plots applied a Wisconsin double standardisation and a square root transformation. A solution was reached within 20 tries and stress value of 0.09 was returned, which is considered a very good representation of distribution across two dimensions.

There is a high level of overlap across the three plot types (Figure 3.6), largely driven by the slope plot variation encompassing both valley and coastal plots. Coast plots had the lowest variation, and three plots grouped closely, however the first coast plot (SNC1) groups more closely to the third slope (SNS3). The valley plots group along the NMDS2 axis, however the second slope plot (SNS2) groups more closely to the second (SNV2) and third (SNV3) valley plots. The slope plots do not group closely together, suggesting differing abundances and compositions across the individual slope plots. Valley and coastal plots appear to differ from one another more than to slope plots.

A PERMANOVA shows that there is a significant difference between the plot types based on variation; there is 33 per cent difference between the plots (R^2=0.34, F=2.31, P=0.002). It appears that the difference is predominately in the variation and separation observed between coast and valley plots.

Applying the intrinsic vectors to show which species are most significantly contributing to the distribution and composition of the plots, shows eleven significant species (p<0.05) (Figure 3.6). *Primulina drakei* (p=0.05) and *Onychium siliculosum* (p=0.03) both have positive gradients and contribute to the distribution of the slope plots. *Alpinia chinensis* (p=0.02), *Ichnanthus pallens* (p=0.04) and *Allophylus livescens* (p=0.03) all have negative gradients and contribute to the composition and distribution of slope and valley plots. *Ardisia lecomtei* (p=0.03), *Beilschmiedia tsangii* (p=0.05), *Campylotropis bonii* (p=0.03), *Leptostachya wallichii* (p=0.022), *Piper saxicola* (p=0.03) and *Tropidia angulosa* (p=0.02) all have positive and steep gradients. They all significantly contribute to the distribution and composition of valley plots.

3.5.3.2.3 Sanctuary trees

Two hundred and thirty-seven individual tree specimens were identified across the Sanctuary plots, from 46 species and 24 families (Appendix 2.2.2). The top ten tree species accounts for 70 per cent of all stems in the Sanctuary plots (Table 3.14). The most frequently occurring species is *Cleistanthus tonkinensis* (n=44) a small tree (Flora of China Project, 2020) predominately found in coastal plots (n=43).

Table 3.14 Top ten tree species across the Sanctuary plots

Species	Slope occurrence (n)	Valley occurrence (n)	Coast occurrence (n)	Total (n)	IUCN Red List Status
Cleistanthus tonkinensis	0	1	43	44	NE
Machilus bonii	10	30	0	40	NE
Dracaena cambodiana	3	0	12	15	NE
Beilschmiedia tsangii	0	13	0	13	LC
Ardisia lecomtei	0	13	0	13	DD
Ficus hispida	0	11	0	11	LC
Diospyros mollis	3	6	1	10	NE
Pterospermum truncatolobatum	0	1	8	9	NE
Bridelia balansae	0	0	6	6	LC
Streblus ilicifolius	0	0	6	6	LC
Total	**16**	**75**	**76**	**167**	

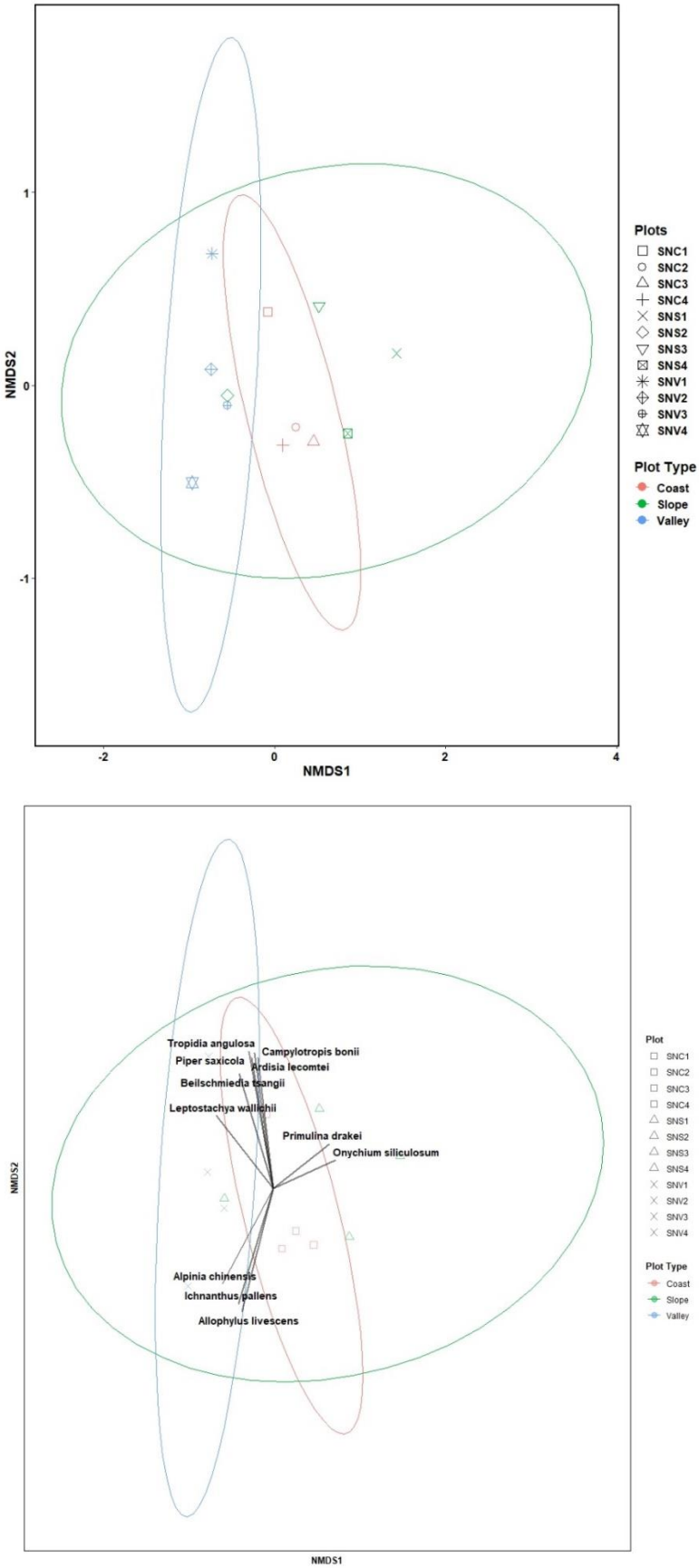


Figure 3.6 NMDS of plants within the Sanctuary. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors.

The trees within the Sanctuary are predominately small to medium, with 47 per cent with a DBH of 5cm or less and 72 per cent with a 5 metre canopy or less (Figure 3.7). Coastal plots had the greatest number of trees captured (n=107) and slopes the least (n=32). Within the coastal plots, tree canopies are predominately five metres or less in height (90 per cent). Slope canopies are also generally low, with 59 per cent falling within the five metre or less category. Valley plots also have a high proportion of trees with canopies five metres or less in height (59 per cent), however they also have a greater variation of heights present. The trees with the eight highest canopies are found in valleys, the highest, a species of *Castanopsis indica* (h=23m, DBH=88cm), is found in Southeast Asia from Taiwan to Nepal, and considered Least Concern by the IUCN Red List (Yu & Botanic Gardens Conservation International (BGCI) & IUCN SSC Global Tree Specialist Group, 2019).

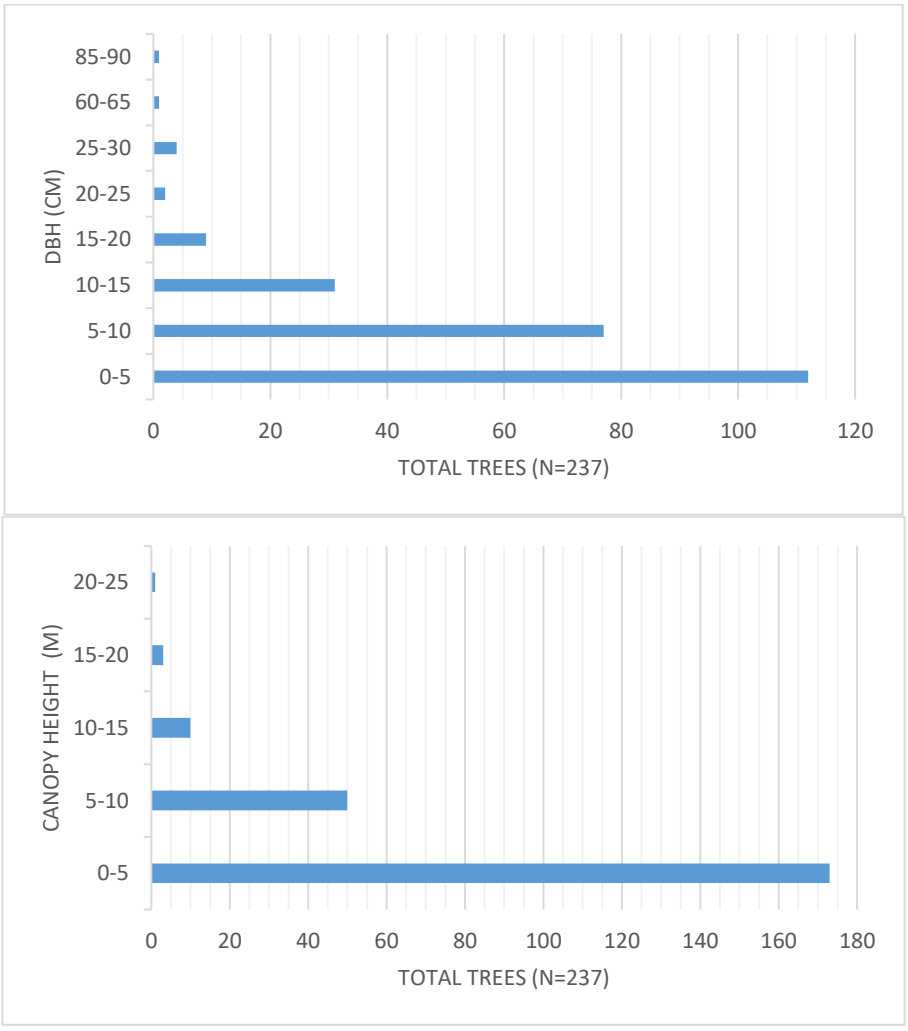


Figure 3.7 The DBH and canopy height distribution of trees across Sanctuary plots. Top: DBH distribution of trees. Bottom: the canopy height distribution of trees.

3.5.3.2.4 Food species composition and NMDS in the Sanctuary

Thirty food species from 406 stems were found across the plots in the Sanctuary (Appendix 2.2.5), representing 24 families. The most common diet species found across all plots is *Dracaena cambodiana* (n=59), found on slope and coastal plots. The top ten species identified account for 81 per cent of all food stems identified across the Sanctuary (Table 3.15). Food stems are most frequently found in slope plots (species=21, stems=203), followed by coast plots (species=17, stems=154) and valley plots (species=15, stems=49).

Table 3.15 Top ten food species in Sanctuary plots

Species	Coast occurrence (n)	Slope occurrence (n)	Valley occurrence (n)	Total (n)
Dracaena cambodiana	20	38	1	59
Pilea hookeriana	33	16	8	57
Derris trifoliata	15	27	1	43
Primulina drakei	1	40	0	41
Vitex trifolia	12	6	17	35
Tetrastigma rupestre	13	11	1	25
Breynia fruticosa	21	0	0	21
Glochidion zeylanicum	0	17	0	17
Aristolochia indica	0	16	0	16
Alpinia calcicola	12	2	0	14
Total	**127**	**173**	**28**	**328**

The NMDS ordination of food species across the Sanctuary plots applied a Wisconsin double standardisation to standardise the abundance values. A solution was reached in 20 tries, for a stress value of 0.07 making it a good representation of the plot abundances in three dimensions.

There is a high level of overlap between the plots (Figure 3.8), however coast plots have a tight grouping along the NMDS2 axis and low variation based on its 95 per cent confidence ellipsis. The coast plots cluster within the slope plot variation. Slope plots have a wider grouping, and the confidence ellipses encompasses all plots. Valley plots have the greatest variation along the NDMS2 axis and grouping between valley plots, is split, with SNV2 and SNV1 clustering closely, and SNV3 and SNV4 clustering generally together.

A PERMANOVA shows that there is no significant difference between the three plot types (R^2=0.21, F=1.23, P=0.19).

Applying the intrinsic vectors shows that three species significantly (p<0.05) contribute to the composition of food species across the plots (Figure 3.8). *Primulina drakei* (p=0.006) has a steep gradient and contributes to the composition of the slope plots. *Vitex trifolia* (p=0. 008) has a negative gradient and contributes to the composition of mainly valley and coast plots. *Pilea hookeriana* (p=0.03) also has a negative gradient and contributes mainly to the coast and slope plots.

3.5.4 Cua Dong and Sanctuary comparison

3.5.4.1 Generalised linear model, ANOVA and estimated marginal means analysis of Cua Dong and the Sanctuary

A two-way ANOVA shows that only slope, species density and mat cover percentage significantly differ between Cua Dong and the Sanctuary (Appendix 2.1.6).

When comparing the means of the two habitats based on their estimated marginal means (Appendix 2.1.7), the topography across the two sites of Cua Dong and the Sanctuary are relatively uniform, with no significant differences across elevation or topographic complexity measures. There is a significant difference in slope, with the Sanctuary being significantly steeper (27.50 ±0.183) than Cua Dong plots (18.67 ±2.60, p=0.027).

In terms of vegetation characteristics, there is very little in the way of significant differences between the two sites. The Sanctuary has a significantly greater species density (4.87 ±0.38) than Cua Dong (1.75 ±0.38, p<0.0001), as well as a significantly higher percentage of mat cover (33.08 ±5.89) than Cua Dong (9.42 ±5.89, p<0.011).

In general, the two sites are quite similar in terms of their vegetation characteristics, however, the Sanctuary has a greater species richness, and a higher percentage of canopy cover, and greater total basal area than Cua Dong. In contrast, Cua Dong has in general, greater elevation across its plots, a higher general density of vegetation and species diversity, and a greater percentage of shrub cover and liana cover than the Sanctuary plots.

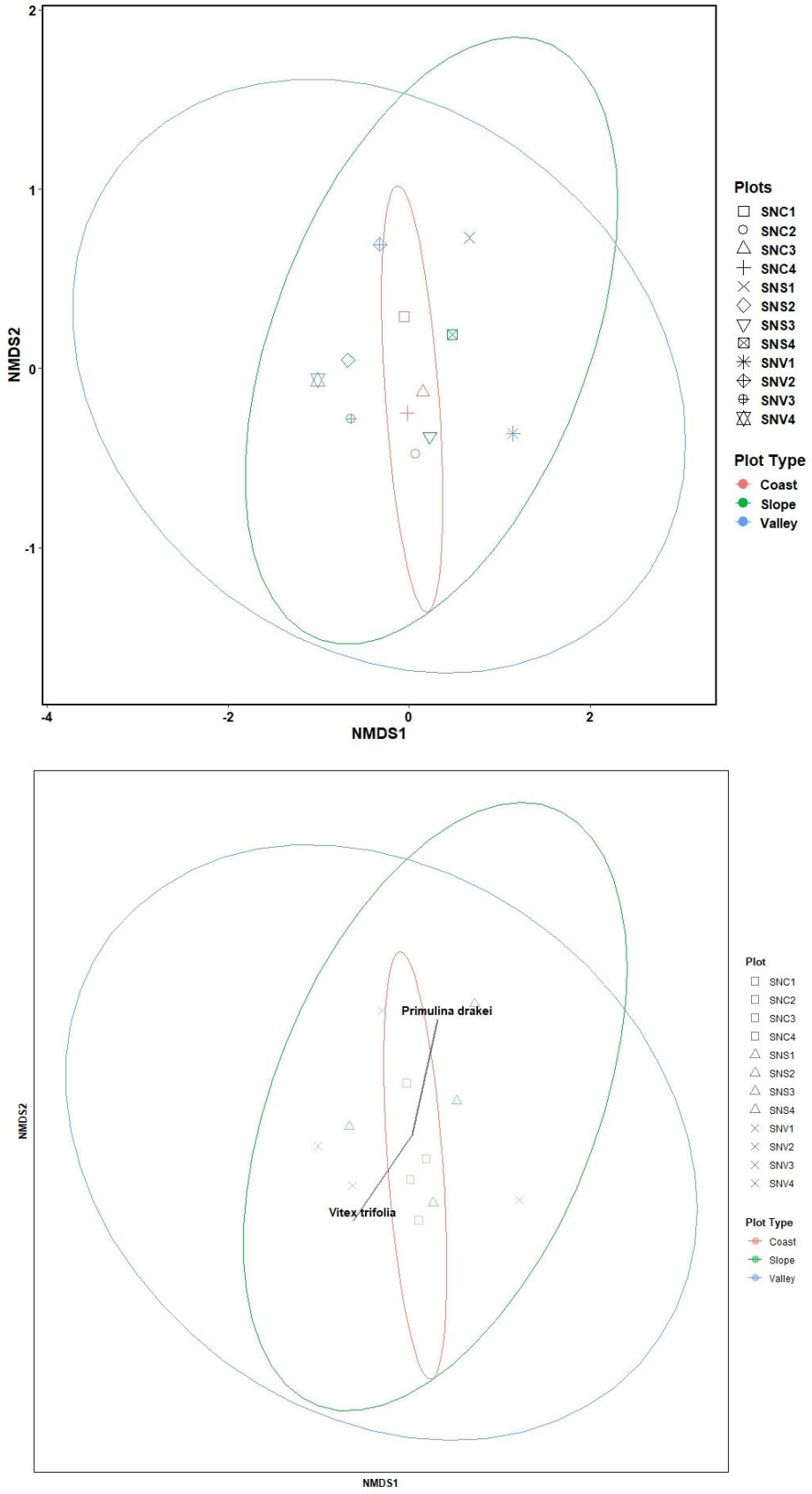


Figure 3.8 NMDS of food species within Sanctuary plots. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors.

3.5.4.2 Plant composition comparison for Cua Dong and the Sanctuary

3.5.4.2.1 Species abundances across both Cua Dong and the Sanctuary

The two CBL habitats share 111 species (38 families) from a combined total of 313 species, indicating only a 35 per cent overlap in shared species across the two sites. The most commonly occurring shared species is *Leptostachya wallichii* (n=716), however it is not an even distribution (Table 3.16). The Sanctuary has almost three times the number of individual stems (n=5844) compared to Cua Dong (n=2094).

Table 3.16 Top ten species shared in Cua Dong and the Sanctuary

Species	Cua Dong occurrence (n)	Sanctuary occurrence (n)	Total (n)	IUCN Red List Status
Leptostachya wallichii	1	715	716	NE
Ophiopogon latifolius	45	288	333	NE
Pilea peploides	98	164	262	NE
Pilea peltata	81	173	254	NE
Adiantum caudatum	24	219	243	NE
Drynaria bonii	22	216	238	NE
Streblus ilicifolius	193	11	204	NE
Chimonocalamus griffithianus	123	88	211	NE
Impatiens halongensis	17	163	180	NE
Cleistanthus tonkinensis	52	76	128	NE
Total	**569**	**2068**	**2754**	

Valley plots

Sanctuary valleys had 146 species identified and Cua Dong valleys had 119 species, for a total number of species found across valley plots within the two sites of 214 species, from a total of 4120 stems. Only 51 species are shared across valley plots at both sites, representing only 35 per cent of species shared between the two sites. The valley plots in the Sanctuary have almost four times the number of individual stems (n=3,307) than valley plots in Cua Dong (n=813).

Slope plots

A total of 164 species occurred in slope plots across both sites: 118 species and 1132 stems in the Sanctuary, and 87 species and 752 stems in Cua Dong. The two sites share 41 species, representing 25 per cent overlap in species.

Coast plots

The coasts within the Sanctuary and Cua Dong have a total of 169 species. The Sanctuary has 113 coastal species and 1405 stems, while Cua Dong has 100 coastal species and 529 stems. The number of stems in the Sanctuary outnumbered those identified in Cua Dong by more than double. The two sites share 44 species, representing only 26 per cent similarity in species between the coastal plots of the two sites.

3.5.4.2.2 Non-metric multi-dimensional scaling analysis (NMDS) of Cua Dong and Sanctuary plants

The NMDS ordination of all plant species across Cua Dong and the Sanctuary applied a Wisconsin double standardisation and a square root transformation. A solution was reached within 20 tries and stress value of 0.17 was returned, which is considered a reasonable representation of distribution across two dimensions.

There is overlap between the two sites (Figure 3.9). Cua Dong variation is spread more across NMDS2 axis, while the Sanctuary is spread more along NMDS1 axis. There is clear overlap in the sites based on their coast and slope plots. The Sanctuary valley plots, and the second Sanctuary slope plot (SNS2) group away from the rest of the Cua Dong plots. Similarly, there is some separation of Cua Dong valley plots one (CDV1) and three (CDV3) from the Sanctuary overlap.

A PERMANOVA shows that there is a difference between the two sites (R^2=0.07, F=1.71, P=0.02), however, the difference (7 per cent) is very low and is likely due to the variation seen in each site across the two axes, and as such does not reflect a major difference between the plant species compositions.

Applying the intrinsic vectors shows that 15 species contribute significantly (p<0.01) to the composition and distribution of the sites (Figure 3.9). The species *Alpinia chinensis* (p=0.001), *Amischotolype hispida* (p=0.005), *Bauhinia ornate* (p=0.006), *Leptostachya wallichii* (p=0.001), *Machilus bonii* (p=0.001), *Porella sp.* (p=0.006), *Syzygium bullockii* (p=0.002), *Vitis balansaeana* (p=0.006) all have steep positive gradients and are associated with the composition of the Sanctuary plots, particularly valley plots. Although not as steep, the species *Beilschmiedia tsangii* (p=0.008), *Lygodium japonicum* (p=0.007) also have positive gradients and contribute to the composition of Sanctuary plots. Three species: *Alchornea tiliifolia*

(p=0.003), *Bleekrodea tonkinensis* (p=0.003), *Vitex trifolia* (p=0.006) have steep negative gradients and are associated with the composition of Cua Dong plots, particularly some valley and coast plots.

Secamone elliptica (p=0.006) has shallow positive gradient and contributes to both the Cua Dong and Sanctuary plots. *Pilea peltata* (p=0.005) has a steep positive gradient and contributes to the composition of both sites.

3.5.4.2.3 Trees in Sanctuary and Cua Dong

A total of eighty-one species of trees are found across both sites (Appendix 2.2.2) but only 20 are shared across both Cua Dong and the Sanctuary. Cua Dong has the highest number of tree species (n=55), while the Sanctuary had 46 species but the greatest number of individual tree stems (n=238) compared to Cua Dong (n=212). The top ten species (Table 3.17) occur more frequently in the Sanctuary than in Cua Dong.

Table 3.17 Top ten tree species in the Sanctuary and Cua Dong

Species	Cua Dong occurrence (n)	Sanctuary occurrence (n)	Total (n)
Cleistanthus tonkinensis	12	44	**56**
Machilus bonii	0	40	**40**
Streblus ilicifolius	32	6	**38**
Dracaena cambodiana	11	15	**26**
Bleekrodea tonkinensis	20	0	**20**
Bridelia balansae	11	6	**17**
Pterospermum truncatolobatum	5	9	**14**
Ardisia lecomtei	0	13	**13**
Beilschmiedia tsangii	0	13	**13**
Diospyros mollis	1	10	**11**
Ficus hispida	0	11	**11**
Sterculia lanceolata	11	0	**11**
Total	**103**	**167**	**270**

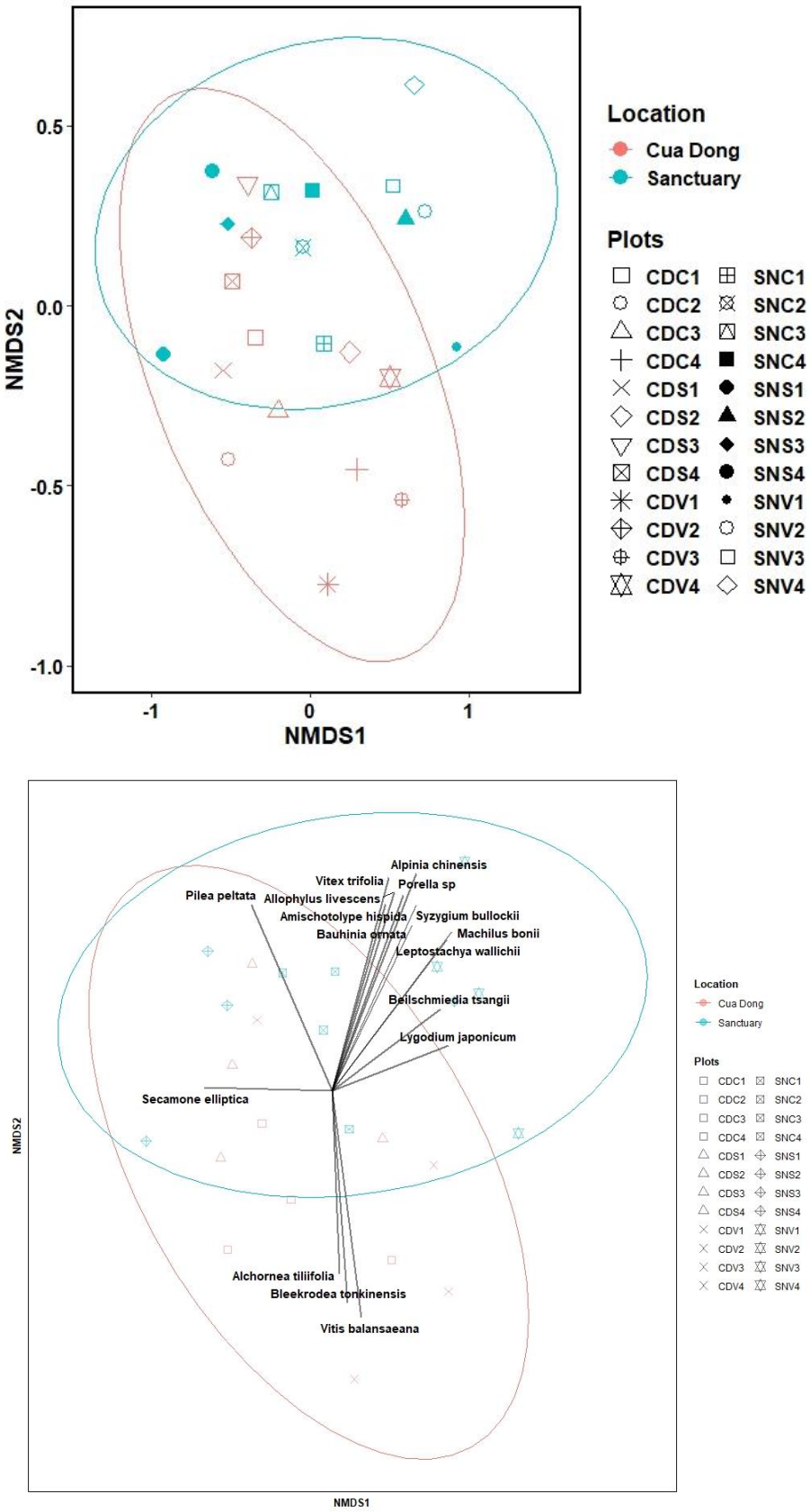


Figure 3.9 NMDS of species in Cua Dong and the Sanctuary. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors

3.5.4.2.4 Food species composition and NMDS in the Sanctuary and Cua Dong

Thirty-nine CBL food species from 25 families are captured across the two sites (Appendix 2.2.5), 25 species (20 families) of which are shared between the two sites. The top ten species identified (Table 3.18) account for 66 per cent of all food stems. *Dracaena cambodiana* is the most common species found at both sites. While more individual stems were found in the Sanctuary, more diet species are found in Cua Dong (n=34) compared to the Sanctuary (n=30).

Table 3.18 Top ten food species in Cua Dong and the Sanctuary

Species	Cua Dong occurrences (n)	Sanctuary occurrences (n)	Total (n)
Dracaena cambodiana	31	59	90
Derris trifoliata	36	43	79
Pilea hookeriana	18	57	75
Primulina drakei	18	41	59
Sterculia lanceolata.	49	2	51
Tetrastigma rupestre	23	25	48
Vitex trifolia	1	35	36
Breynia fruticosa	14	21	35
Secamone elliptica	16	10	26
Alpinia calcicola	11	14	25
Total	**217**	**307**	**524**

An NMDS ordination of the food species abundances across the two sites applied a Wisconsin double standardisation and a square root transformation. A solution was found in 20 runs, with a stress value of 0.13, forming a fair representation of the plot compositions in three dimensions.

The two sites overlap, with the Sanctuary variation shown by the 95 per cent confidence ellipsis spread across both axes, while the Cua Dong variation spreads predominately along NMDS2 axis (Figure 3.10). There is a clear mix between the plot types; there is no clear grouping by plot types, however, the sanctuary coast plots cluster centrally. The first Sanctuary slope plot (SNS1) appears as an outlier, sitting on the border of the Cua Dong ellipsis. The two sites appear to be quite similar based on their compositions, however, Cua Dong display less variation based on the confidence ellipses compared to the Sanctuary.

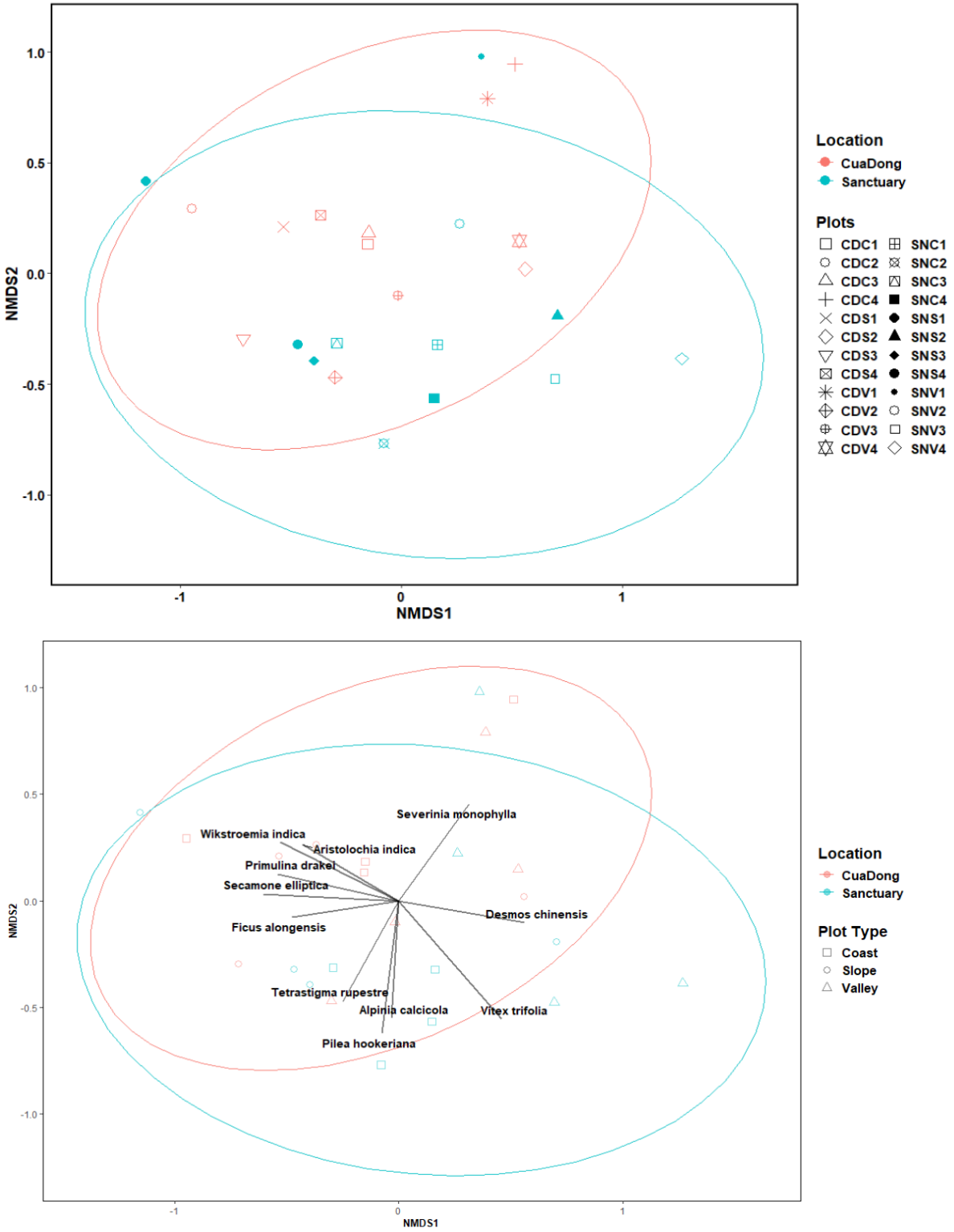


Figure 3.10 NMDS of food species in the Sanctuary and Cua Dong. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors.

A PERMANOVA shows that there is a significant difference between the two sites based on food species composition (R^2=0.07, F=1.70, P=0.031).

Applying the intrinsic vectors (Figure 3.10) shows that eleven species have significant (p<0.05) contributions to the composition of the food species in Sanctuary and Cua Dong plots. *Vitex trifolia* (p=0.001) has a negative gradient and significantly contributes to the Sanctuary food species composition.

Ficus alongensis (p=0.05) has a shallow negative gradient, while *Severinia monophylla* (p=0.02) has a steep positive gradient yet both contribute to the composition to the composition of food species at the Cua Dong site.

Pilea hookeriana (p=0.005), *Alpinia calcicola* (p=0.02) and *Tetrastigma rupestre* (p=0.03) have steep negative gradients and contribute to food species composition at both sites. *Desmos chinensis* (p=0.02) has a shallow negative gradient and contributes to the composition of both sites; *Secamone elliptica* (p=0.007) and *Primulina drakei* (p=0.02) have shallow gradients and contributes to both sites. *Aristolochia indica* (p=0.05) and *Wikstroemia indica* (p=0.01) have positive gradients and contributes to the composition of food species found at both sites.

3.6 Discussion

3.6.1 Cat Ba Langur habitat

This study provides the first analysis of the ecology of the current habitat of the CBL for both the Cua Dong and Sanctuary populations. It provides a comparison between the two sites to support customised conservation planning and monitoring of the two populations, providing insights to the ecological profile of each site and the distribution of food species. The outcomes of this study provide further insights into the ecology of a Critically Endangered species to support ongoing conservation planning and identifying key avenues for further research.

The vegetation appears generally homogenous across the two main CBL habitat sites as is expected due to the past linkages between the two sites. Further investigation into the specific points of difference between the two sites, however, may indicate differences in

activity budgets and dietary preferences between the two CBL populations that should be considered in future studies.

Based on the habitat characteristics analyses by the linear general model, the two main habitats of the CBL topographically differ based on significantly greater mean steepness of the Sanctuary topography (25.5 degrees) compared to Cua Dong (18.67 degrees). In terms of vegetation characteristics, the Sanctuary has significantly greater species density (4.87) compared to Cua Dong (1.75) and significantly greater percentage of mat cover. The vegetation differences are thus minimal, but obvious to general observational differences between the two sites. The Sanctuary vegetation is much denser, with stems identified outnumbering those identified in Cua Dong three to one.

The vegetation of Cua Dong does not significantly differ across the plot types, despite only 19 species in common across the coast, valley and slope vegetation. Based on the top ten species found in Cua Dong, the vegetation is characterised by herbs including *Pilea peploides* and *Pilea peltata*, and shrubs such as *Streblus ilicifolius, Alchornea tiliifolia, Alchornea scandens,* and *Clausena indica.* The bamboo species *Chimonocalamus griffithianus* is also typical of Cua Dong, as are small trees including *Taxotrophis macrophylla, Cleistanthus tonkinensis,* and *Sterculia lanceolate*.

In contrast, the vegetation in the Sanctuary varies based on the topographic strata. While in general, the Sanctuary vegetation is characterised by herbs such as *Pilea peltata, Pilea peploides,* and *Impatiens halongensis*. Other top species include shrubs such as *Leptostachya wallichii*, small trees including *Claoxylon hainanense* and grasses and ferns including *Ophiopogon latifolius, Carex cruciata Adiantum caudatum, Drynaria bonii,* and *Pteris grevilleana*. Unlike Cua Dong however, the Sanctuary has a significant difference in the plant communities present on coasts, valleys and slopes. The coasts in the Sanctuary are home to more bamboos and grasses compared to the valleys or slopes. Vegetation within the valleys and slopes of the Sanctuary also have less variation in plant communities between them compared to that of the coasts.

Both sites exhibit overlap based on their NMDS ordinations, however within the Sanctuary plots, coast and valley plots differed based on their species abundances. This indicates that

the vegetation in the Sanctuary separates according to topographic levels. In both Cua Dong and the Sanctuary, valleys have the highest number of sampled individual stems, often as a result of dense mat or shrub cover. For both sites it is possible that the regeneration of valleys and their relative inaccessibility since becoming protected has seen an increase in regrowth compared to coastal areas that are more exposed to the elements and accessible to humans.

The plant communities between the Cua Dong and the Sanctuary, despite sharing only 34 per cent of the same total species, do not significantly differ. The two sites overlap based on abundances; however, any difference that does occur is driven by greater variation in Sanctuary-specific species due to the higher capture of species and stems compared to Cua Dong.

It is possible that the differences found in species density between the two sites are a result of historical human interactions with the two areas. The Cua Dong region is closer to major human populations and is more accessible to the local community than the Sanctuary region. The Sanctuary is closed to public use and is located away from both main human town centres of Cat Ba Town, Viet Hai Town, and the floating community. This may explain why the vegetation of Cua Dong exhibits less diversity and species richness compared to the more isolated Sanctuary region. As the plant communities in the Sanctuary are much more diverse and dense - possessing three times the number of plant stems - than those in Cua Dong, the two regions may require different conservation planning to monitor and to support the health of their forests.

Compared to Cua Dong, the Sanctuary appears to have a generally higher quality vegetation. Based on vegetation characteristics, the Sanctuary has a greater species richness, greater species density, higher average canopies and greater percentage shrub cover. The Sanctuary also has more established trees, with greater diameters, higher canopy heights and greater canopy cover than Cua Dong. This is likely a result of the ongoing human activity occurring in Cua Dong compared to the Sanctuary, which is more isolated from humans and is closed to public access.

The consensus of interview participants is that the quality of the forest on Cat Ba Island has improved since greater protections were implemented in the 2000s, and the subsequent

decline in hunting and disturbance of the forest by local communities. Despite this, evidence of firewood collection and traps for water monitors were encountered in coastal plots around Cua Dong, as was a build-up of rubbish washed up from the surrounding waterways (Figure 3.11). Due to the vicinity of Cua Dong to the floating village, and the presence of tourists in the area, there is ongoing human access to the region despite its protected status. The Sanctuary, however, is closed to the public and is monitored by CBNP rangers.

In addition to less disturbed vegetation, the Sanctuary is also home to a population of rhesus macaques (*Macaca mulatta*), which lives sympatrically with the Sanctuary CBL (Hendershott, 2017; Nadler & Long, 2000). Very little is known about the impact of macaques on the CBL. Other sites with limestone langur and macaque overlap have reported interspecies cooperation or at least cohabitation between langurs and macaques at other sites (Burton et al., 1995; Mukherjee & Saha, 1974; Nerlekar, 2012), however incidental observations by the CBNP rangers suggest that groups of CBL have stopped using certain areas due to the growth of the macaque population. Rangers also suggested that langur and macaque interactions in the Sanctuary often result in the langur groups fleeing. Recent observations suggest that the macaque groups are starting to appear in the region between the Sanctuary and Cua Dong, with some smaller groups seen entering the edge of the Cua Dong CBL habitat (pers comm**,** Ruskin 2017). This has the potential have a significant effect on the Cua Dong langurs, particularly due to debate as to whether or not the area may be reaching carrying capacity (Lees et al., 2014; Tien Bui et al., 2016). As langur groups in the Sanctuary appear to be larger than those in the Cua Dong area, it is possible then that the smaller group sizes of langurs from Cua Dong may not be able to compete with larger groups of macaques.

3.6.2 Food availability

Thirty-nine of the 56 food species identified by Ruskin (unpublished, 2016) were captured by the sampling undertaken in Cua Dong and the Sanctuary. This discrepancy may be due to the differences in how sites were sampled; Ruskin (unpublished, 2016) was predominately restricted to sampling coasts and coast-facing slopes due to langur observation limitations, while this study sampled sites across the Cua Dong habitat.

Figure 3.11 Evidence of Human Activity in Cua Dong **a.** Evidence of tree cutting and wood collection. **b.** A poacher's trap, likely for water monitors. **c.** Rubbish washed up beyond the beach and into vegetation; rubbish at the site was at least 30cm deep. **d.** Styrofoam from floating village and passing boats washed up on the sand in Cua Dong. Photos: K. Apthorp, 2016.

There is a significant difference between the availability of food species between the two sites. While the Sanctuary contains a smaller number of individual food species compared to Cua Dong, they occur in greater abundances. This is particularly true of the top ten food species found in the Sanctuary; the top ten species represent 81 per cent of total food species stems. In contrast, the top ten food species in Cua Dong represent 62 per cent of total food species stems. Differences between the food species communities of the two sites are predominately driven by the presence of specific species *Vitex trifolia* a shrub, which occurs 35 times in the Sanctuary but only once in Cua Dong and the fig tree *Ficus alongensis* and shrub *Severinia monophylla* both which occur more frequently in Cua Dong.

The most common food species identified across both sites was *Dracaena cambodiana*, a small tree native to Cambodia and Vietnam (Flora of China Project, 2020). This plant is also the most commonly found food species in the Sanctuary, however in Cua Dong, it is only the third most frequently identified. The tree species *Sterculia lanceolata* and climbing plant

Derris trifoliata were both found at higher frequencies than *Dracaena cambodiana*. While all three species are found at both sites, *Sterculia lanceolata* was only found to occur twice in the ecological sampling of the Sancutary, compared to 49 times in Cua Dong.

The number of food species overall, however, indicate a very low availability of food species compared to the general species profile of the two sites. Of the 315 species found across the two sites, only 56 have been identified as part of the CBL diet, indicating that of their habitat, the CBL eat only 17 per cent of available species. This reflects a smaller percentage of selected food species compared to other langur species. A study of *Trachypithecus germaini* in Kein Giang Province Cambodia, showed the langurs consume 31 per cent of the total species identified (H. T. Le, Hoang, & Covert, 2019). Similarly, *Trachypithecus delacouri* in Van Long Nature Reserve, Vietnam consumes 29 per cent of the total species found at the site (Workman, 2010a). Only *Trachypithecus margarita* has been reported to consume a smaller percentage (8 per cent) of the overall available species (V. B. Tran, Hoang, Luu, Covert, & Workman, 2019).

The absolute number of species consumed by the CBL (n=56) is similar compared to other Asian langurs (Table 3.19) (V. B. Tran et al., 2019). Other *Trachypithecus* species range from 31-97 food species (Harding, 2010; Kool, 1993; H. T. Le et al., 2019; Zhaoyuan Li & Rogers, 2006; Roy, Ashokkumar, & Desa, 2012; Solanki, Kumar, & Sharma, 2008; V. B. Tran et al., 2019; Workman, 2010a). It is difficult to determine whether the low number of food species relative to the number of species available is reflective of a low variety of suitable species, or due to methodological issues. The list of food species consumed by the CBL is the first dedicated study of the diet to be compiled for the species, however it also only focussed on one sub-population and observations may suffer from location bias. Most observations are from coast and slope plots, making valleys underrepresented. There is also likely to be variation in diets across the two main habitats of the CBL based on vegetation differences (Behie, Apthorp, Hendershott, & Ruskin, 2022; Kool, 1993).

Only 30 food species were captured in my sampling of the Sanctuary, which could indicate that the other food species were not captured in the sampling or that the CBL in the Sanctuary may consume other available species. Considering the greater number of overall species

available in the Sanctuary (n=235 species) compared to Cua Dong (n=186 species), it is possible the langurs there have a greater variety of foods and that there is some variation in the food preferences between the two groups. These results suggest that further analysis of the feeding habits of the CBL within the Sanctuary should be prioritised to support conservation efforts in this area.

Table 3.19 Number of food species consumed by Asian langurs

Species	Number of food species	Reference
Trachypithecus margarita	31	V. B. Tran et al. (2019)
Trachypithecus delacouri	42	Workman (2010a)
Trachypithecus leucocephalus	50	Li & Rogers (2006)
Trachypithecus pileatus	52	Solanki et al. (2008)
Trachypithecus germaini	53	H. T. Le et al. (2019)
Trachypithecus poliocephalus	56	Ruskin (unpublished 2016)
Trachypithecus cristatus	94	Harding (2010)
Trachypithecus auratus	88	Kool (1993)
Trachypithecus johnii	97	Roy et al. (2012)

Food is considered a leading influence on primate distribution (Carl, 2009). The low number of food species relative to available overall species could suggest that the CBL are specialists, having adapted to a specific range of species within their available habitat, or that the number of available food species is lower due to poorer vegetation as a result of habitat loss (Bennett & Davies, 1994; V. B. Tran et al., 2019). Compared to the Sanctuary, Cua Dong, where the food sampling was undertaken (Ruskin, unpublished 2016), has a much lower species richness and lower diversity and density of species.

In contrast to a previous study by Hendershott et al. (2018), my results suggest that slope plots may be of more nutritional importance to the CBL than valleys. Slope plots at both sites offer the greatest number of individual food species stems and food species, whereas valleys offer the least. It appears that the slope plots and coastal plots may offer more options for the CBL,

due to the higher numbers of food species and the higher abundancies of these species within these areas. However, is possible that the results may be impacted by sampling bias (Moua, Roux, Seyler, & Briolant, 2020). Food species are taken from Ruskin (unpublished, 2016), which collected based on observations taken from a boat. As a result, observations of foraging in valleys may be under-represented compared to observations of slopes and coastal areas. Further observation may reveal other important food species found in the valleys.

It is also possible that the valleys offer specific diet species preferred by the langurs, and of better quality due to the fertility of the valleys and quality of the vegetation (C. Huang et al., 2002). While liana coverage was generally greatest on the slopes of both sites, the most common diet species in the Sanctuary valleys was *Bauhinia ornata*, a large liana. Lianas and vines have been found to be important in other limestone langur diets, for instance, in *Trachypithecus delacouri* vines were found to make up more than on-half of their diet (G. Hu, 2011; Stanford, 1991; Workman, 2010a). In *Trachypithecus margarita*, vines made up 25 per cent of feeding time (V. B. Tran et al., 2019), while for *Trachypithecus johnii* (Roy et al., 2012), *Trachypithecus pileatus* (Solanki et al., 2008) and *Trachypithecus germaini* (H. T. Le et al., 2019) vines, lianas or climbers were the second most consumed plant type after trees.

Other limestone langur species have also been found to prefer valley regions with richer soil than hilly regions, likely due to the higher quality of the vegetation (Burton et al., 1995; C. Huang et al., 2002; Zhaoyuan Li & Rogers, 2006; Manh Ha Nguyen, 2006). The higher quality of the vegetation in the valleys is evidenced by possessing the largest, most established trees compared to the other plot types. Trees in the valleys sampled here have greater diameters and canopy height than trees sampled other plot types. Canopy cover was generally greater in the coastal plots, potentially due to the greater concentration of small young trees in this plot type, compared to valley plots which are predominately recovering from agricultural use including animal grazing. It is recommended that future studies look at the role of valleys in CBL habitat use and feeding behaviour in greater detail.

3.6.3 Habitat compared to other limestone karst species' habitat

Compared to other members of the limestone langur, the CBL within Cua Dong have home ranges of 22 ha and 50 ha (Hendershott et al., 2018), resulting in a seemingly high population

density of approximately 0.2 individuals/km^2 (Hendershott, 2017). However, Hendershott (2017) attributes this to the use of the observed Cua Dong home range in the calculation; it is possible that some parts of the home range may be missing due to the method of tracking the CBL by boat.

The fact that the CBL live in high density despite the degraded nature of their habitat is significant as other Trachypithecus groups such as the closely related white-headed black langur see a decline in population density in fragmented habitat, or a reduction in overall home range as in *Trachypithecus geei* (Gee's golden langur) (Harding, 2009; Srivastava, 2006). Despite their restricted distribution, it might be possible to determine if similar patterns occur with the CBL by undertaking home range studies of the Sanctuary population. While the number of CBL living in the Sanctuary is estimated to be similar to the Cua Dong region, it is possible that the CBL living in the Sanctuary have larger home ranges due to higher quality vegetation.

Habitat degradation and fragmentation is widespread throughout the limestone langur group, with most species experiencing some degree of fragmentation from one or two kilometres to over 100 kilometres separating populations (C. Huang, Li, et al., 2008; Z. Huang et al., 2017). Few species of the limestone group still inhabit primary forest as a result of severe human pressure due to illegal logging, hunting and deforestation (Fan et al., 2015; Mazumder, 2014; Srivastava, 2006). Yet, like the CBL, these groups appear to have adapted to the secondary and disturbed forest that now dominate their habitats (D. Li et al., 2016; Srivastava, 2006). The Cua Dong population of CBL have had births almost every year since regular monitoring began in 2014, suggesting that their current fragmentation is not yet severely impacting their viability as a population (Hendershott, 2017).

The under-study of limestone karst forests has limited our understanding of how species like the CBL and other limestone langurs continue to exist in terrain that appears very unforgiving (Sodhi et al., 2004). In the past, studies have explored whether limestone is a preferred or refuge habitat for these langur groups, yet for the CBL, we must accept that limestone is the only habitat they have ever had access to (Harding, 2009; Li & Rogers, 2005a, 2005b). For other species of the limestone langurs their preferences are less certain. Li and Rogers (2005a)

suggest that for white-headed black langur limestone may not be essential but act as a refuge against encroaching human populations. In contrast, *Trachypithecus laotum* (Laotian langur) appears to prefer limestone karst over the surrounding tropical forest (Duckworth et al., 2010).

In the past, the CBL likely inhabited the entire Cat Ba Island, including the centre of the island. Local community members recall their presence around villages in the north and south of the island. However, the presence of CBL to the west of the island is uncertain as interviews of community members from this region did not recall seeing them in the area. The decline of the CBL across the wider Cat Ba Island and their retreat to the Cua Dong and Sanctuary regions occurred quickly from 1970s, based on the information collected by the interviews. While this may account for why the CBL are now fragmented, it does not necessarily explain why they have remained in these areas noting the availability of the wider National Park area. It is possible that surveys of the wider National Park could provide further insights into the reasons why the CBL have remained in their current distributions.

The lack of permanent expansion deeper into the forest of the National Park, particularly by the Cua Dong population, may indicate a preference for exposed coastal limestone habitats. Analysis by Hendershott et al. (2018), indicates that the Cua Dong CBL were observed predominately on bare rocks and areas of sparse vegetation, cliff faces and exposed slopes during scans. Based on the findings of this analysis, this may be due to the higher number of food species found on slopes and along the coast, indicating these are areas that deserve greater monitoring against human interference and accumulation of pollution such as polystyrene foam.

3.6.4 Conservation implications

Conservation and monitoring of the CBL was funded by the CBLCP and FFI at the time of this study. Since the CBLCP started conservation efforts on the island in 2000, awareness of the langur and promotion of its protection has led to widespread support from the local community (Schrudde et al., 2010). This was further demonstrated by the high level of knowledge demonstrated by interview participants of both the CBLCP and the CBL themselves. Businesses in Cat Ba town also promote the langur and its conservation, and the

CBNP provides rangers to monitor the protected Sanctuary and a ranger who monitors the Cua Dong population daily.

The informal participation of the local community in supporting conservation efforts of the CBL was also during the course of the study. Locals living in the floating village around Cua Dong often provided updates to the ranger about the location of the langurs and any sightings of strangers in the area. Poachers are generally strangers to the island who have come to the island to hunt the langurs (Nadler & Long, 2000; Schrudde et al., 2010). Thus, while the flow-on effects of having humans living so close to the Cua Dong population may negatively impact their habitat in the form of firewood collection and pollution, the local people also assist in helping to reduce the threat of poaching in the area. By involving the community so successfully, the CBLCP has demonstrated the benefits of local involvement in conservation (Dawkins, 2007; Estrada & Coates-Estrada, 1996; Schrudde et al., 2010; T.T.A Nguyen, 2014).

The Sanctuary population has somewhat suffered from its isolation from the local human population despite the benefits it brings to the habitat and growth of the forest. The one or two families occupying floating homes around the edge of the Sanctuary, assist the rangers stationed within the Sanctuary by reporting any sightings of strangers in the area, however in 2015, seven langurs may have been poached from the Sanctuary population of CBL (N. Leonard, personal communication, September, 2015). Such a loss is a severe hit to the threatened species and highlights the need for further investment into monitoring of the region by rangers.

Today, the total population of CBL is approximately 50-60, and the threat of poaching, while still present, is significantly less than in the past. The population has increased since conservation efforts on the island began and babies are born almost yearly, however, the slow growth of the population suggests that now the focus needs to turn to improving and possibly expanding their current habitat to provide additional habitat for new groups, particularly if concerns that the Cua Dong habitat is approaching carrying capacity (Lees et al., 2014; Tien Bui et al., 2016) is occurring. Without data on the habitat of the CBL, it is not possible to monitor whether the current distributions can sustain a growing population or to undertake detailed analysis of areas for potential expansion. The data and subsequent analysis

undertaken in this study, provides conservation groups with information on the structure of the CBL habitat and the spatial distribution of food species, to support area-specific planning for conservation activities (Chapman & Peres, 2001; Knowlton & Graham, 2010).

3.7 Conclusion

The past decade has seen a dramatic increase in our understanding of the CBL through studies of their socio-ecology (Hendershott, 2017; Hendershott et al., 2016; Hendershott et al., 2018), however these studies have exclusively focussed on the Cua Dong population. This study provides the first dedicated analysis of the habitat structure and composition of the CBL in both Cua Dong and the Sanctuary, adding to the growing data on the CBL to assist conservation efforts and identifying opportunities for further investigation.

While there is no significant difference between the two habitats based on vegetation characteristics, the retreat of CBL breeding populations to Cua Dong and the Sanctuary compared to other areas within the National Park, suggest that these areas may offer the CBL access to potential resources that other areas do not, such as access to specific food types, or habitat structure. Using this analysis as a comparison, further surveys of the habitat of other sites within the National Park may offer additional opportunities to expand the habitat of the CBL, as will be further investigated in Chapter Four.

The results of the habitat analysis of the two CBL breeding populations reveals that the CBL live across a relatively homogenous habitat type, which appear to be exhibiting different levels of human disruption. As hypothesised, the sites do not have significantly different topographic or vegetation profiles. Yet, when considering the sites individually, the Sanctuary habitat is much more varied across the coast, slope and valley zones. This means that any future conservation activities in these areas cannot treat the region as a homogenous region – care must be taken to plan for individual zones or plot types. In particular, the habitat of Cua Dong should be monitored against any deterioration of the forest and efforts should be continued to prevent further access by humans collecting firewood or other forest resources.

The two sites do however vary when it comes to the number and density of food species they contain. Cua Dong is home to a higher number of food species, yet the Sanctuary has a greater

density of food stems. It is possible that the langurs in the Sanctuary have a different diet composition compared to Cua Dong. But overall, the number of food species compared to the total number of plant species is quite low. Careful monitoring of CBL food abundances within the two sites should be continued to support their ongoing survival. There should also be special attention paid to the conservation of slopes in both Cua Dong and the Sanctuary to limit degradation of the vegetation there due to its importance as a feeding site for the CBL.

The presence of unmonitored macaque groups living sympatrically with such a high-risk species is also of concern. Observations of the macaques by rangers only began in 2017 after a pilot study on the island for this study and Ruskin (2016). It is recommended that a sister-study on the macaques living in the Sanctuary and their interactions with the CBL is established to gain an understanding of their impact on the CBL.

Chapter 4 Analysis of the viability of a potential corridor between the two main populations of the Cat Ba langur (*Trachypithecus poliocephalus*)

4.1 Introduction

Habitat fragmentation is a critical threat to the ongoing survival of primate populations around the world (Arroyo-Rodriguez & Mandujano, 2009; Blair et al., 2011; Knowlton & Graham, 2010). In biodiversity hotspots like Vietnam, habitat fragmentation has the potential to devastate primate species by isolating populations and reducing their access to critical resources (Blair et al., 2011; Nadler & Streicher, 2004; Norman Myers, 2000; Sodhi et al., 2004). With some of the highest rates of primate endemism in Indochina, a history of deforestation and fragmentation as a result of war and human development has left many Vietnamese primate species on the brink of extinction (Catullo et al., 2008; Eames & Robson, 1993; Sodhi et al., 2004). While the contiguous primary habitat of Vietnam has been gradually encroached upon and broken into smaller remnants on a landscape scale, it is the effects of this fragmentation on a local scale that poses the greatest threat to primate groups (Arroyo-Rodriguez & Mandujano, 2009; Gardner et al., 2007). Fragmentation such as this not only threatens the genetic diversity of primate groups but also threatens the ongoing quality of their habitat due to changes in abiotic factors such as temperature, wind and biotic effects such as plant composition, invasive species and vegetation structure (Arroyo-Rodriguez & Mandujano, 2009).

The CBL, endemic to Cat Ba Island, Hai Phong, has two main breeding populations that are separated from one another as a result of a history of poaching and human interference in the form of logging, fires, and deforestation for agriculture and development on the island (Nadler & Long, 2000; Stenke & Canh, 2004; Tien Bui et al., 2016). The two -populations inhabit two protected areas: Cua Dong and the Sanctuary, both forested peninsulas on the southeast of the island within the boundary of the Cat Ba National Park (CBNP).

Both groups appear to be reproductively but not geographically isolated from one another. A strip of coastline approximately 23km long links the two areas, however, it is not utilised by the CBL. Bachelor males and small groups of two to three langurs from the Cua Dong population have been observed occasionally moving along the coastline towards the

Sanctuary, however the journey is never completed, and the langurs generally turn back after one or two days (pers comm. Mr Cam). There have been no reports of Sanctuary langurs entering this area towards Cua Dong. Although the mid-way point between the two populations is somewhat interrupted by the small Viet Hai port, there do not appear to be any other major obstacles. Macaques have been observed moving along the coastline into the Cua Dong region, presumably from the Sanctuary (pers.com K. Ruskin).

This coastline region, termed the Viet Hai Corridor (VHC), sits within the CBNP boundary, however, it is not immediately clear as to why it is not used more frequently as a true corridor between CBL sites or even inhabited by the Cua Dong population as it appears to extend from the Cua Dong area with no interruptions.

As fragmentation of habitat and populations continues, maintaining or promoting connectivity of at-risk species is becoming an increasing focus of conservation groups to promote gene flow and genetic diversity in declining populations (Beier & Noss, 1998; Damschen et al., 2006; McRae et al., 2008). Increasing landscape connectivity may enhance population viability for many species (Beier & Noss, 1998). Few corridor studies have been conducted with a focus on primates, perhaps due to the scale involved and the difficulty in determining the way in which large animals such as primates may view and use their habitat (Beier & Noss, 1998; Garshelis, 2000; Haddad et al., 2003; Harcourt & Doherty, 2005). Efforts to overcome this are further complicated by the way in which different species respond to habitat fragmentation (Isabirye-Basuta & Lwanga, 2008). Primates in fragmented habitats face a myriad of challenges regarding the changing structure of their preferred habitat, access to suitable resources, as well as access between sub-populations, thereby potentially impacting their reproductive success and social behaviours (Arroyo-Rodriguez & Mandujano, 2009). Each species will respond to these threats in different ways, requiring a species-specific approach to their conservation.

In order to achieve this species-specific approach, it is essential to collect as much data about a species as possible. For primates, research has largely been behaviourally based, however, it is only through studies of a species' habitat and their habitat preferences that researchers can predict their responses and needs in order to undertake meaningful spatial conservation

(R. A. Mittermeier & van Roosmalen, 1981; Pyritz et al., 2010). Until recently, the CBL had only been the focus of behavioural and socio-ecological research (Hendershott, 2017; Hendershott et al., 2016; Hendershott et al., 2018).

Our knowledge and understanding of the habitat of the CBL is limited. For a species at such high risk of extinction, it is critical to establish datasets on habitat structure in order to make meaningful and positive impacts on their future through conservation action and planning. The use of in situ ecological sampling provides important information on species on a local scale, while the use of Maximum Entropy (MaxEnt) modelling allows analysis of primate habitat distribution on a landscape scale (Hansen et al., 2001). Understanding the habitat of fragmented populations using both sampling and distribution modelling can offer greater opportunities to identify connectivity points.

MaxEnt is increasingly preferred to model distribution of species as it is capable of accounting for small sample sizes and complex interactions between variables (Fourcade, Engler, Rödder, & Secondi, 2014; Wisz et al., 2008). By maintaining or re-establishing connections between fragments, it may be possible to improve gene flow between isolated sub-populations and improve the chances of survival for a Critically Endangered species (Arroyo-Rodríguez & Fahrig, 2014; W. Li et al., 2017).

The aim of this chapter is to compare the ecological profiles of the VHC to the habitat of the CBL in Cua Dong and the Sanctuary, to understand if the area is suitable for use by the langurs. It is also the aim to produce a map with the potential habitat distribution of the CBL on Cat Ba Island using MaxEnt modelling of geographic variables. In doing so, it will provide additional insight as to whether the corridor area is suitable for use by the CBL, or whether additional conservation actions are required to improve its ecological profile. By comparing the known home ranges of the CBL to this potential corridor, it might be possible to identify its suitability as a protected link between the two breeding populations or as permanent expanded habitat that should be given additional protections.

I hypothesise that the VHC will show significant differences in the vegetation and plant species composition compared to both Cua Dong and the Sanctuary. It is expected that these ecological differences make the corridor area unsuitable for regular use or settlement as

langurs have not been observed to regularly utilise or permanently remain in the area. The underutilisation of this region may be due to significant differences in the topography or ecological variables such as vegetation density or diversity, or a lack of appropriate diet species that currently makes the area unappealing to the CBL. I further hypothesise that MaxEnt distribution modelling will further demonstrate the unsuitability of the VHC for the CBL. If there is an ecological reason for this lack of use, we may be able to identify ways in which the corridor area can be improved in order to encourage permanent use of the region by the CBL.

This will be the first analysis of a potential corridor to link the two CBL populations and application of a species distribution model of the CBL based on habitat variables.

4.2 Methods

4.2.1 Study site and species

The total wild population of CBL is estimated to be between 50-60 individuals (Fauna & Flora International, 2022), and is endemic to Cat Ba Island, Vietnam; a 140km^2 limestone karst island situated in Ha Long Bay. The CBL population is fragmented across the island into three groups: two main breeding populations inhabiting separate protected zones on peninsulas to the south-east, and a third smaller non-breeding group of an estimated five individuals on a small island off the northern coast of Cat Ba Island, identified as the Hang Cai population. The VHC is a theoretical vegetation corridor, with an estimated area equating to 15km^2 along the coastline, which connects the two main populations in Cua Dong and the Sanctuary (Figure 4.1) bypassing the village of Viet Hai, a popular tourist location.

The Cua Dong population is located on a small peninsular approximately 1.1 km^2, adjacent to a large floating village, and major thoroughfare for fishing and tourist boats. This population has been the main focus of behavioural research (Hendershott, 2017; I. Schneider et al., 2010). The groups in Cua Dong are monitored five days a week by boat by a CBNP ranger funded by Fauna and Flora International (FFI). While this population is not fully habituated to human presence, they do tolerate humans moving around the base of their cliffs and are not immediately startled by the presence of boats and kayaks that maintain an appropriate distance (Hendershott, 2017; Hendershott et al., 2016).

The second breeding group is located within a protected area known as the Sanctuary, an area of approximately 13.1km^2 (Stenke, 2001). While no constant monitoring takes place there as it does in Cua Dong, rangers are responsible for conducting surveys of the region and to report on CBL sightings and other notable events. The Sanctuary is closed to the public, and monitored by CBNP rangers, however despite the best efforts of rangers, there has been at least one serious bout of poaching thought to have occurred in the area in the years before this study (N. Leonard, personal communication, September, 2015).

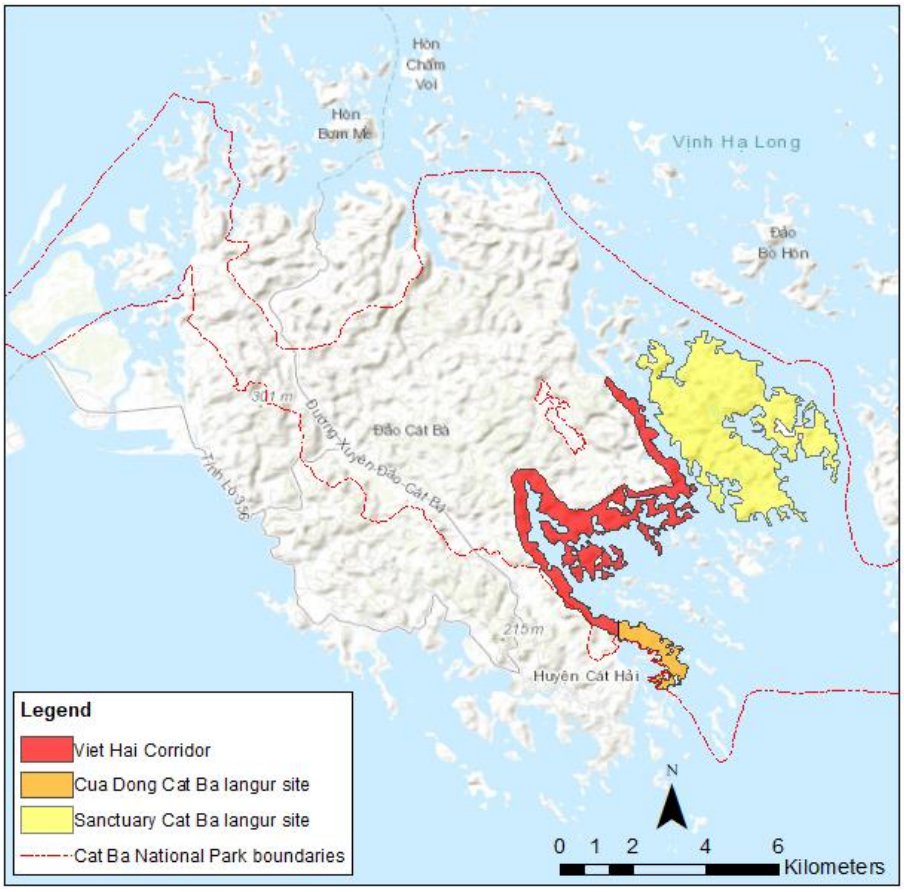


Figure 4.1 Map of main CBL populations and potential corridor. Orange: current locations of main breeding populations of CBL in Cua Dong. Yellow: current location of second breeding group of CBL in the Sanctuary. Red: Viet Hai corridor region. Basemap source: ESRI et al. (2021).

The VHC acts as a theoretical corridor for the CBL between the two sites. Although langurs from Cua Dong travel through the region, they are always observed to turn back after several days. The VHC region is sparsely populated by humans, however the Viet Hai port is situated midway between the two sites and presents a man-made break in the corridor as a result of the road to the port. While this is a popular tourist stop for cruises, it not a built-up area and

while the CBL have not been observed to cross this break, groups of macaques have been seen bypassing the area via the VHC. The coastline between Cua Dong and Viet Hai port has no human settlements, however, there is some infrastructure in the area such as a dam and power cabling. There are also several floating houses in the region but not on the scale seen in the floating village around Cua Dong. The region between Viet Hai port and the Sanctuary has no major infrastructure.

4.2.2 Ecological sampling

To analyse the ecological characteristics the VHC, I established a total of 12 square plots measuring 10x10m. These comprised four coast plots, four slope plots and four valley plots (Figure 4.2) established by stratified random sampling as established by the protocol set out in Chapter 3, section 3.3. Twenty-four plots; 12 from Cua Dong and 12 from the Sanctuary used in Chapter 3 were reused for this analysis.

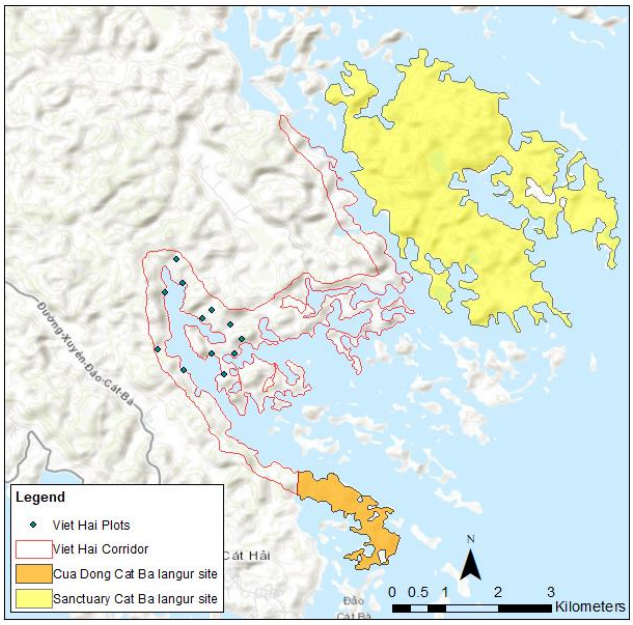


Figure 4.2 Location of plots placed within the VHC. Basemap source: ESRI et al. (2021).

Only a sub-area of the Viet Hai Corridor was sampled due to a number of factors. These included limiting the sampling the region where CBL had been observed by National Park Rangers, which was largely toward the western end of the VHC, potentially due to the corridor break at Viet Hai. Accessibility was also a major factor, as the region was only accessible by boat within the time constraints of the research period. Some consideration was also given to

visibility by the public; noting that the region was off-limits to the public, an effort was made to avoid accessing areas where tourists on cruises or kayaks might interpret our presence as permitting access.

Upon establishing each plot, I took the GPS coordinates in the south-east corner, along with two bearings points. At the SE corner of each plot, I recorded the elevation, aspect, slope, and vegetation type.

All stems within the plots were identified to species level by Dr The Van Pham, botanist and researcher at Van Lang University. All trees and shrubs with a DBH of greater than 2cm were measured with a DBH measuring tape or callipers. The diameter of all lianas over 2cm was also recorded.

Canopy height was estimated to the nearest 50cm; Dr The and I independently estimated heights visually (D. Li et al., 2006), to the nearest 50cm before results were compared and triple checked where estimates differed by over 50cm (S. Cheyne et al., 2013). I recorded the estimated percentage of coverage within the mat, shrub, large shrub, and liana layer (Appendix 1.2). The percentage of canopy cover and general vegetation density score (Appendix 1.3) were recorded for each plot, based on the protocol established in Chapter 3, Section 3.3.

I also estimated the general topography complexity of each plot using a scale where zero indicated no visible limestone within the plot, and five indicated complex, layered limestone that was difficult to traverse (Appendix 1.4).

4.2.3 MaxEnt modelling

4.2.3.1 *Occurrence data*

The CBL has been closely monitored since the early 2000s. The Cua Dong population is monitored by a dedicated National Park Ranger, however, the Sanctuary population is only monitored via National Park Rangers patrols. Ongoing monitoring by Cam (unpublished, 2015), and studies by Luan (2013), Hendershott (2016), and Ruskin (unpublished, 2016) provided a large sample of CBL occurrence points. I also included CBL occurrences collected during a pilot study in 2015 and during my ecological sampling in 2016. I collated these samples and cleaned them to remove inaccurate points. Due to the nature of the CBL ecology,

no true absence points have been collected, and any background points were generated randomly by the MaxEnt program.

4.2.3.1.1 Sampling Bias

Sampling bias associated with the collection of occurrence points for use in MaxEnt modelling has been identified as having a significant potential impact on the model outcomes (Barber, Ball, Morris, & Gilbert, 2022; Low, Zeng, Tan, & Yeo, 2021; Radosavljevic & Anderson, 2014).

Occurrence points of CBL are open to sampling bias largely due to viewshed bias. Due to the difficulty in accessing the limestone habitat most CBL occurrences are recorded from a boat using GPS and a rangefinder to determine distance and angle, which results in a bias for coastal observations. Due to the very small population size of the CBL, this sampling may be compounded by the fact that the Cua Dong population has been sampled significantly more frequently than the population in the Sanctuary (Kiedrzyński, Zielińska, Rewicz, & Kiedrzyńska, 2017). As Cua Dong has a smaller total area compared to the Sanctuary, fewer non-coastal occurrences within the Sanctuary have been captured.

Following the approach undertaken by previous studies (Barber et al., 2022; Elith, Kearney, & Phillips, 2010; Freire Filho & Palmeirim, 2020; Kiedrzyński et al., 2017; Vidal-García & Serio-Silva, 2011), to account for sampling bias I spatially thinned the occurrence records. Using the Spatial Analyst tool in ArcGIS, I filtered the CBL locations to ensure that only one presence record per 30m x 30m raster cell was used in the MaxEnt modelling. As a result, 145 from over 400 records were used as occurrence samples in the modelling.

4.2.3.2 Predictor variables

To model the distribution of the CBL, I selected eleven predictor variables to reflect their geographical spatial and ecological extent. These predictor variables included: a digital elevation model, slope, aspect (Eastness and Northness), normalised difference vegetation index (NDVI), normalised difference moisture index (NDMI), land use data, Terrain Roughness Index (TRI), and the visible bands of the Spot6 satellite multispectral imagery (Appendix 2.3.1). Due to the low geographical spread of the CBL, the resolution of predictor variables was set at approximately 1 second (30 x30m) to capture the highest resolution of the greatest number

of datasets. Typically, climatic datasets are also included, however these were not available at this high resolution.

4.2.3.2.1 Pre-processing and datasets

The eleven predicator variables were clipped as rasters to the geographical extent of Cat Ba Island. This required developing a polygon of the island to enable clipping of all rasters to the exclusion of the surrounding ocean. This was achieved using an initial starting polygon taken from the Vietnam Administrative Boundaries (ESRI 10.8 et al., 2022, accessed 11 November, 2022). All clipping and subsequent calculations were undertaken in ArcGIS Desktop 10.8 using Spatial Analyst and Data Management Tools. I projected all datasets to the Universal Transverse Mercator coordinate system (datum: WGS 1984, zone: 48N).

I used an ASTER Global Digital Elevation Model arc 1 second (ASTGTM v.003) from the United States Geological Survey (NASA, METI, AIST, Spacesystems, & Team, 2019, accessed 15, July 2022), to produce a digital elevation model (DEM) from which I generated slope and aspect rasters using the Spatial Analyst Tool in ArcGIS. The calculated slope raster represents the rate of change of elevation in the direction of deepest descent (Amatulli et al., 2018) in each cell based on the elevation of the DEM.

As aspect is a circular continuous variable ranging from 0 to 360 degrees, I separated aspect into two new continuous variables representing Northness, ranging from 1 (north) to -1 (south) and Eastness ranging from 1 (east) to -1 (west). These two new rasters were created from the aspect raster using the following formula in the ArcGIS raster calculator:

$$Northness = Cos(x * \pi/180)$$

$$Eastness = Sin(x * \pi/180)$$

$$Where\ x = aspect\ raster$$

As the CBL has been observed to socialise and rest in trees throughout the day (Hendershott et al., 2016), I generated a Normalised Difference Vegetation Index (NDVI) from a Landsat 8-9 Operational Land Imager (OLI) and Thermal Infrared Sensor (TIRS) Collection 2 Level-1 downloaded from the United States Geological Survey (USGS & NASA, 2022, accessed November, 2022). The NDVI represents the difference between near-infrared (NIR) and red

reflectance values of satellite imagery normalized by their sum (Rouse, Hass, Schell, & Deering, 1974; Schwager & Berg, 2021). Positive NDVI values are associated with high levels of canopy and vegetation cover, based on visible light absorbance and near-infrared reflectance (Nathalie Pettorelli et al., 2011). The use of NDVI has been found to support the modelling of species distribution modelling for primates (Feilhauer, He, & Rocchini, 2012; Nathalie Pettorelli et al., 2011; N. Pettorelli et al., 2005).

I calculated the NDVI for Cat Ba Island using the raster calculator and the following formula:

$$NDVI = (NIR - RED)/(NIR + RED)$$

$$NDVI = (Band\ 5 - Band\ 4)\ /(\ Band\ 5 + Band\ 4)$$

Due to the low level of water retention in limestone karst, vegetation can provide primates with water in areas with low groundwater availability (Clements et al., 2006). To understand the amount of water available in the canopy at the time of the study (2016), I calculated the Normalised Difference Moisture Index (NDMI) (also, Normalised Difference Water Index; Gao (1996) using Landsat 8-9 Operational Land Imager (OLI) and Thermal Infrared Sensor (TIRS) Collection 2 Level-1 (USGS & NASA, 2022, accessed November, 2022). The NDMI describes moisture level in vegetation or water stress level, using the near infrared and short-wave infrared (SWIR) bands providing values between -1 and 1 (Analytics) with positive NDMI representing higher water absorption and negative values indicating dry vegetation with low water absorption (Gao, 1996; Taloor, Drinder Singh, & Chandra Kothyari, 2021). I calculated the NDMI by

$$NDMI = (NIR - SWIR)/(NIR + SWIR)$$

$$NDMI = (Band\ 5 - Band\ 6)/(Band\ 5 + Band\ 6)$$

Karst limestone is typified by extreme variations in the topography from sunken limestone to high ridges and limestone towers (Clements et al., 2006; Hamilton-Smith, 2001). In order to capture the potential effect of this topographic variation, I generated a Topographic Ruggedness Index (TRI) raster for Cat Ba Island. This dataset measures the total elevation changes across adjacent cells of the DEM (Amatulli et al., 2018; Dilts, Blum, Shoemaker,

Weisberg, & Stewart, 2022; Riley, Degloria, & Elliot, 1999). Using the ASTGTM v.003 DEM, I calculated the TRI using the Focal Statistic Tool and Raster Calculator by

$$TRI = \sqrt{(t + 9x^2 - 2xs)}$$

$where\ x = the\ DEM\ raster$

$t =$ Focal sum (over 3x3 square neighborhoods) of x^2

$s =$ Focal sum (over 3 x 3 square neighborhoods)of x

The land use of Cat Ba Island varies across the island. To capture this variation, I utilised a land use dataset for the island provided by the Earth Observation Research Centre (EORC) ALOS/ALOS-2 Science Project "High-resolution land use cover map" (HRLULC) of the Japan Aerospace Exploration Agency (JAXA, 2020 [version 20.06], accessed December, 2022). The land use map identifies twelve categories: Water, Urban/Built up, Rice, Other crops, Grass/Shrub, Orchard/Crop mosaic, Barren, Evergreen Broadleaf Forest, Coniferous Forest, Deciduous Forest, Plantation Forest, and Mangroves. Categories were identified by JAXA using Landsat data, Sentinel data, ALOS PRISM Digital Surface Model, ground survey data and interpretation of satellite data, and a random-forest-based algorithm (JAXA, 2020).

I also used a commercially available Spot6 unenhanced multispectral satellite image with 6m resolution to prepare separated bands representing: Band 1 (Blue 0.455µm – 0.525µm), Band 2 (Red 0.530µm – 0.590µm), Band 3 (Green 0.625µm – 0.695µm), Band 4 (Near Infrared 0.760µm – 0.890µm). I resampled each raster to 30m using the Resample (Data Management) Tool. The imagery used to support the habitat distribution analysis was archived orthorectified SPOT6 Imagery captured on 26 August, 2016 by Airbus Defence Space. The panchromatic with 1.5m resolution and RGBN multispectral 6m resolution, encompassed 321km^2, to capture the entirety of Cat Ba Island (top left coordinate 696858.00E, 2311776.0N). The image capture date was selected based on the best weather conditions closest to the date the ecological data was collected. The Spot6 images were supplied and processed by GeoImage. I exported the multispectral, pan-chromatic and pan-sharpened imagery to GeoTIFF format for compatibility with ArcGIS 10.8.

All rasters were extracted to the same column (n=759) and row (n=754) length using a Cat Ba Island polygon, via the Spatial Analyst Tool in ArcGIS to allow analysis in MaxEnt.

4.3 Modelling technique

4.3.1 Predictor variable correlation

In order to determine any predictor variables that might be correlated and to reduce the complexity of the subsequent MaxEnt modelling, I used ENMTools in R to conduct a Pearson's correlation analysis. I removed variables which were strongly correlated, based on an *r* coefficient where -0.7<*r*>0.7.

4.3.2 MaxEnt distribution analysis

I used MaxEnt version 3.4.3 (S. J. Phillips, 2017) for all modelling analyses. In order to follow best practice, I undertook an analysis encompassing a combination of feature classes and regularisation multiplier values to identify the best model for the distribution of the CBL (Dorji, Linke, & Sheldon, Preprint 2020; Low et al., 2021; T. V. Nguyen, Man, & Nguyen, 2022).

For the feature classes, I undertook analyses using the following settings: automatic (linear, Quadratic, Product and Hinge) (S. J. Phillips, 2017), Linear-only, Quadratic-only, Hinge, Linear and Quadratic (L+Q) and Linear, Quadratic and Hinge combined (L+Q+H). These were selected based on findings from MaxEnt modelling for other *Trachypithecus* species (Blair et al., 2022; T. V. Nguyen et al., 2022; Phuntsho et al., 2019).

Adjusting the regularisation multiplier can shift the effects of overfitting and model complexity (Radosavljevic & Anderson, 2014; Warren & Seifert, 2011). Values below the default setting of 1 can produce a more localised and complex model, and values higher than 1 can generate less complex, more generalised models (Merow, Smith, & Silander Jr, 2013; Warren & Seifert, 2011). (Blair et al., 2022; T. V. Nguyen et al., 2022; Phuntsho et al., 2019), I chose regularization multiplier settings of 0.5, 1, 2 and 4 (Blair et al., 2022; T. V. Nguyen et al., 2022; Phuntsho et al., 2019). Each feature class combination was run with the four regularization multiplier settings. I set the random test percentage at 50 (Vidal-García & Serio-Silva, 2011), used cross validation as the replicated run type, and used MaxEnt's jackknife feature to measure variable importance for all models (Phuntsho et al., 2019). All other settings, including a maximum number of background points of 10,000, were based on the default settings.

The Area under the Curve (AUC) is produced for each model during the training and testing (S. J. Phillips, 2017). An AUC of <0.5 indicates that the model has no predicative ability greater than randomisation, and an AUC of 1 indicates a perfect model (Elith et al., 2011). For each feature class, I selected the best performing model by the lowest difference (AUC_{DIFF}) between the training (AUC_{TRAIN}) and the testing (AUC_{TEST}) (Low et al., 2021; Warren & Seifert, 2011). Higher AUC_{DIFF} values indicate model overfitting, and do not perform well when extrapolated to the testing data (Low et al., 2021). The best performing model within each feature class was then rerun with the variable contributing least to the model removed.

A total of 30 models were run, and the top performing from each feature class combination, based on the AUC_{DIFF} and AUC_{TEST}, were then rerun with 10 replicates and mean AUC compared to determine the best performing model. The best performing model was selected based on the highest AUC value (Phuntsho et al., 2019).

Based on the best performing model, the total area identified by the MaxEnt modelling as having 90 per cent and greater suitability for the CBL was determined for each target site. This was repeated for the total area identified as having 60 per cent or greater suitability for the CBL.

4.4 Data Analysis

4.4.1 Habitat characteristics

To determine the characteristics of the vegetation of the three sites, I calculated species richness, species diversity, tree area, basal area, average DBH and density of all vegetation types (stems/m^2), and exclusively tree density (stems/m^2) for each plot (Appendix 2.1.1), as established by the protocol in Chapter 3, section 3.4.1.

I used a general linear model to explore the relationships between the variables measured in my ecological plots. To understand differences between the plot types in Viet Hai, I used a one-way analysis of variance (ANOVA) from the linear model to assess significance of effects. To understand differences between Viet Hai, the Sanctuary and Cua Dong, I used a two-way ANOVA. Estimated marginal means based on the linear models were then calculated and compared in a post hoc analysis employing a Tukey adjustment to the p-values.

I undertook a visual inspection of residuals and determined that no transformation was required of variables as residual plots sufficiently satisfied normality constraints, noting a small sample size. Results were reported where $p<0.05$.

I carried out habitat characteristic calculations manually, and linear models, ANOVAs and estimated marginal means calculations were carried out using the VEGAN package in R (4.2.1).

4.4.2 Plant species analysis

I undertook all models and calculations using the VEGAN package and visualisations using GGPLOT2 package in RStudio (2022.07.2) with R (4.2.1).

4.4.2.1 All plant species

As per the protocols established in Chapter 3 Section 3.4.2.1, I used the VEGAN package and METAMDS function in R to undertake a NMDS ordination analyses using the METAMDS function with a Wisconsin double standardisation transformation of the data, and a Bray-Curtis dissimilarity index (Bray & Curtis, 1957) to compare differences in plant species populations based on abundances for: (1) the plant communities within Viet Hai, (2) the plant communities and tree communities between Viet Hai, Cua Dong and the Sanctuary. I used a PERMANOVA using a Bray-Curtis dissimilarity distance matrix to determine whether differences observed in the NMDS were significant.

I then applied intrinsic vectors using the function ENVFIT to determine which species most significantly contribute to plant communities both within and between sites.

4.4.2.2 Food species of the CBL

Food species were taken from a list of 56 food species complied by Ruskin (unpublished, 2016). This list represents the only known compilation of food species for the CBL. Food species were collected by Ruskin (unpublished, 2016), using scans and focals from a distance of >50m.

I repeated the NDMS ordination analysis, PERMANOVA and multiple regression of intrinsic variables analysis on food species reported for the CBL to determine how food abundances vary across coast, valley and slope plots in Viet Hai, and between Viet Hai and the two CBL sites.

4.5 Results

4.5.1 VHC ecological profile

4.5.1.1 Generalised Linear Model, ANOVA and estimated marginal means analysis of VHC

A one-way ANOVA using a generalised linear model shows that elevation, topographic complexity, species diversity, species density, average canopy height, percentage of liana cover, and average DBH all have significant differences across the three plot types in the VHC (Appendix 2.1.8).

The estimated marginal means results (Appendix 2.1.9) show that the topography of the VHC varies significantly across the three plot types. The mean elevation of slope plots (42.75m ±5.09) is significantly greater than both coast (8.25m ±5.09, $p<0.003$) and valley (16.75m ±5.09, $p<0.01$) plot elevations. Valley plots are significantly less topographically complex (1.25 ±0.39) than both coast (3.00 ±0.39, $p<0.03$) and slope plots (3.25 ±0.391, $p<0.014$). Valley plots are also less sloped (5.00° ±3.37) than coast plots (27.75° ±3.37, $p<0.003$) and slope plots (37.50° ±3.374, $p<0.0002$).

The vegetation characteristics of the VHC valleys also significantly differ from the other plot types based on several characteristics. Valley plots have significantly lower species diversity (2.04 ±0.18) than both coast (3.08 ±0.18, $p<0.007$) and slope plots (2.84 ±0.18, $p<0.03$). In contrast, valley plots have significantly greater species density (5.85 ±0.732) than both coast (2.73 ±0.73, $p<0.04$) and slope plots (2.64 ±0.73, $p<0.03$). The valley plots also have significantly higher average tree canopies (6.40m ±0. 55) than that of slope plots (4.13m ±0.55, $p<0.04$), and generally higher than that of coast plots (4.30m ±0. 55).

While not significantly different, the valley plots of the VHC have higher percentages of mat, shrub, large shrub and canopy coverage than both the other type of plots. They also have significantly lower liana coverage (8.75% ±10.59) than coastal plots (42.50% ±10.59, $p<0.03$), and generally lower than that of slope plots (27.50% ±10.59). The average diameter of the trees in VHC valley plots are significantly larger than both coast (5.363 ±0.413, $p<0.0006$) and slope plots (4.900 ±0.413, $p<0.0002$). While not significantly greater, valley plots have greater total basal area than coast and slope plots.

4.5.1.2 VHC Plant Species

4.5.1.2.1 Species composition across VHC plots

Two hundred and forty-two species from 81 families and 4471 stems were identified in the VHC plots (Appendix 2.2.3), however only 34 species are found in all three plot types.

The top ten species across all plots (Table 4.1) account for 47 per cent of all stems and are characterised by herbs and shrubs common to moist forests, ferns, and small trees. The most frequently occurring species is *Ophiopogon latifolius* (n=546), often occurring as a grass-like shrub in moist valleys (Flora of China Project, 2020). Only one species is identified by IUCN Red List: *Amorphophallus interruptus*, classified as Critically Endangered (IUCN, 2022a). This species was previously classified as only occurring on limestone at Ninh Binh (IUCN, 2022a) on the mainland, approximately 150km to the southwest of Cat Ba Island.

Table 4.1 Top ten species found in Viet Hai corridor

Species	**Coastal occurrence (n)**	**Slope occurrence (n)**	**Valley occurrence (n)**	**Total (n)**	**IUCN Red List Status**
Ophiopogon latifolius	9	3	534	546	NE
Thelypteris tonkinensis	0	0	396	396	NE
Rhapis micrantha	0	0	188	188	NE
Drynaria bonii	107	61	1	169	NE
Memecylon edule	3	1	150	154	NE
Cleistanthus tonkinensis	4	133	12	149	NE
Pilea peltata	92	54	0	146	NE
Leptostachya wallichii	0	0	128	128	NE
Derris trifoliata	25	86	3	114	NE
Amorphophallus interruptus	60	38	13	111	CE
Total	**300**	**376**	**1425**	**2101**	

VHC Valley plots

Valley plots had 127 species of plants from 2335 individual stems - over double the number of individual stems than coast and slope plots. The most common species identified is *Ophiopogon latifolius* (n=534), an evergreen perennial grass-like plant native to Southeast Asia (Flora of China Project, 2020). The top ten species (Table 4.2) account for 75 per cent of stems identified within valley plots, and are characterised by shrubs, ferns, and small trees, including *Gironniera subaequalis* (n=71) a tree used for furniture and medicines.

Table 4.2 Top ten species found in Viet Hai valley plots

Species	Valley occurrence (n)	Description*	IUCN Red List Status
Ophiopogon latifolius	534	Grass	NE
Thelypteris tonkinensis	396	Fern	NE
Rhapis micrantha	188	Bamboo	NE
Memecylon edule	150	Evergreen tree	NE
Leptostachya wallichii	128	Herb	NE
Alocasia macrorrhizos	98	Shrub	NE
Ichnanthus pallens var. major	76	Grass	NE
Gironniera subaequalis	71	Tree	LC
Gnetum montanum	59	Climbing shrub	LC
Pterospermum truncatolobatum	55	Tree	NE
Total	**1755**		

*Descriptions from Flora of China Project (2020); POWO (2022)

VHC Coast plots

Across the coast plots, 1092 stems were identified from 126 species. The most common species is *Impatiens halongensis*, a flowering shrub native to the Ha Long Bay region (POWO, 2022). The top ten species identified within the coast plots in VHC (Table 4.3) account for 52 per cent of all stems in coast plots and are characterised by herbs, epiphytes and shrubs, including *Amorphophallus interruptus,* a Critically Endangered shrub at risk due to limestone exploitation (V. D. Nguyen, 2012).

Table 4.3 Top ten species found in Viet Hai coastal plots

Species	Coastal occurrence (n)	Description*	IUCN Red List Status
Impatiens halongensis	108	Flowering shrub	NE
Drynaria bonii	107	Epiphyte	NE
Pilea peltata	92	Herb	NE
Amorphophallus interruptus	60	Shrub	CR
Dioscorea deltoidea	39	Climbing shrub	NE
Pilea hookeriana	39	Herb	NE
Peperomia blanda	37	Herb	NE
Campylotropis bonii	34	Shrub	NE
Impatiens verrucifer	30	Herb	NE
Derris trifoliata	25	Shrub	NE
Total	**571**		

*Descriptions from Flora of China Project (2020); POWO (2022)

VHC Slope plots

Slope plots have the least number of species (n=116), and stems (n=1044) identified. The most common species within the slope plots is *Cleistanthus tonkinensis*, a small shrub common to slopes in Vietnam (POWO, 2022). The top ten species (Table 4.4) found in slope plots in VHC account for 57 per cent of all stems and comprise predominately of shrubs and small trees, climbing shrubs and epiphytes. Two species are recognised by the IUCN Red List, including *Amorphophallus interruptus* listed as Critically Endangered, and *Machilus thunbergia* listed as Least Concern (IUCN, 2022a).

Table 4.4 Top ten species found in Viet Hai slope plots

Species	Slopes (n)	Description*	IUCN Red List Status
Cleistanthus tonkinensis	133	Shrub/Tree	NE
Derris trifoliata	86	Evergreen shrub	NE
Pilea peploides	78	Herb	NE
Drynaria bonii	61	Epiphyte	NE
Pilea peltata	54	Herb	NE
Paraboea halongensis	52	Herb	NE
Amorphophallus interruptus	38	Shrub	CE
Impatiens verrucifer	34	Herb/Shrub	NE
Machilus thunbergii	31	Evergreen tree	LC
Alyxia hainanensis	31	Climbing shrub	NE
Total	**598**		

*Descriptions from Flora of China Project (2020); POWO (2022)

4.5.1.3 Non-metric multi-dimensional scaling analysis of VHC plant communities

NMDS ordination of all the plant species across VHC plots applied a Wisconsin double standardisation and square root transformation. A solution was found within 20 tries and returned a stress value of 0.1, which is considered a good representation of the distances between abundances in two-dimensions.

There is overlap across the three plot types based on their species abundances and compositions of the plant communities (Figure 4.3). Coast plots group closely, with low variation based on its 95 per cent confidence ellipsis. Valley plots group along the NMDS2 axis and display a wide variation and some overlap with coast plots. It appears that much of the overlap is driven by the slope plots, which show high variation across the NMDS1 axis. The

second (VHS2), third (VHS3) and fourth (VHS4) plots group more closely to the coast plots, while the first slope plots (VHS1) groups more closely to valley plots.

A PERMANOVA shows that there is a significant difference between the valleys, slopes and coast plots (R^2=0.24, F=1.46, P=0.013), and that 24 per cent of the variation can be explained by the plot types. This suggests that while the three plot types do have some differences in plant abundances and composition, overall, they are quite similar.

Applying the intrinsic vectors shows that there are a large number of significant (p<0.05) species contributing to the distribution of the plots within the ordination (Figure 4.3). Five species have steep positive gradients *Alpinia chinensis* (p=0.005), *Caryota maxima* (p=0.009), *Celastrus hindsii (*p=0.009), *Combretum sundaicum* (p=0.005), *Dioscorea poilanei* (p=0.021), *Piper saxicola* (p=0.018), *Smilax lanceifolia* (p=0.012), *Sterculia lanceolata* (p=0.002) and contribute to the plant community composition of all plots, particularly valleys. *Lygodium japonicum* (p=0.04) has a negative gradient and contributes to the composition of valley plots. *Allophylus macrodontus* (p=0.04), *Allophylus livescens* (p=0.02), and *Smilax perfoliata* (p=0.01) all have a negative gradient and contribute to the composition of all plots. *Hoya Fungi* (p=0.05), *Pilea peploides* (p=0.03) and *Tetrastigma rupestre* (p=0.03) all have shallow positive gradients and contribute to the composition of the coast and slope plots, particularly slopes.

4.5.1.4 Tree characteristics in VHC

One hundred and ninety-one individual tree specimens from 62 species and 30 families were identified across the three plot types in VHC (Appendix 2.2.4). The most frequently identified tree were *Cleistanthus tonkinensis* (n=18), largely found on slopes (n=16), and *Pterospermum truncatolobatum* (n=18), a tree commonly used for timber and medicinal purposes, found at similar frequencies across all three plot types.

Tree density across all plot types is low. Slopes have the greatest tree density of 0.2/m^2, followed by coasts with 0.15/m^2 and valleys with 0.13/m^2. Of the trees sampled within VHC, the majority had canopy heights of 5m and below, and DBH of 10cm and below (Figure 4.4). The tallest tree was *Bischofia javanica* at 15m, identified in a valley plot. This species is classified as Least Concern, and is typically harvested for timber, fuel and medicinal uses (IUCN, 2022a)

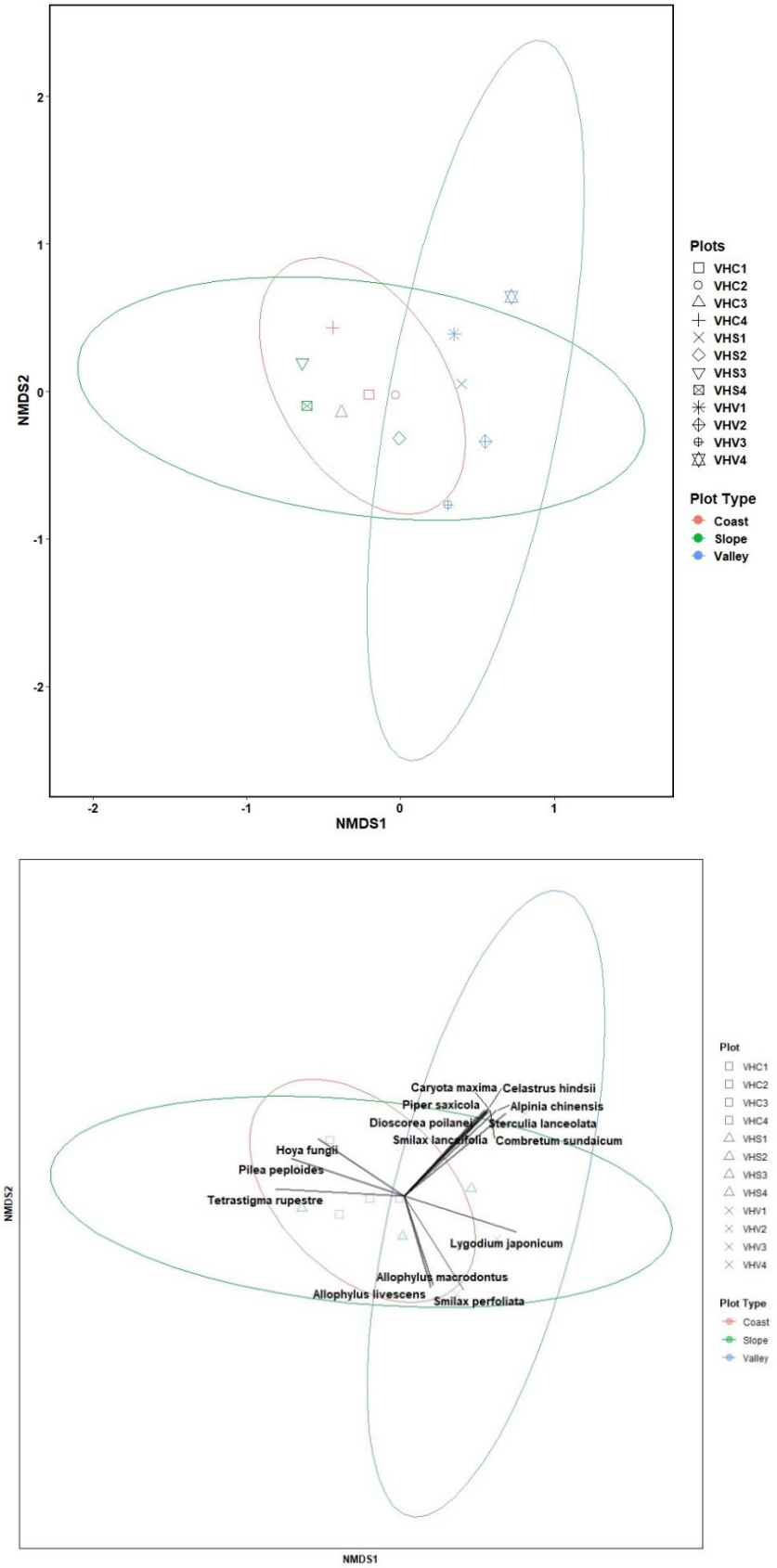


Figure 4.3 NMDS of plants within the VHC. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors.

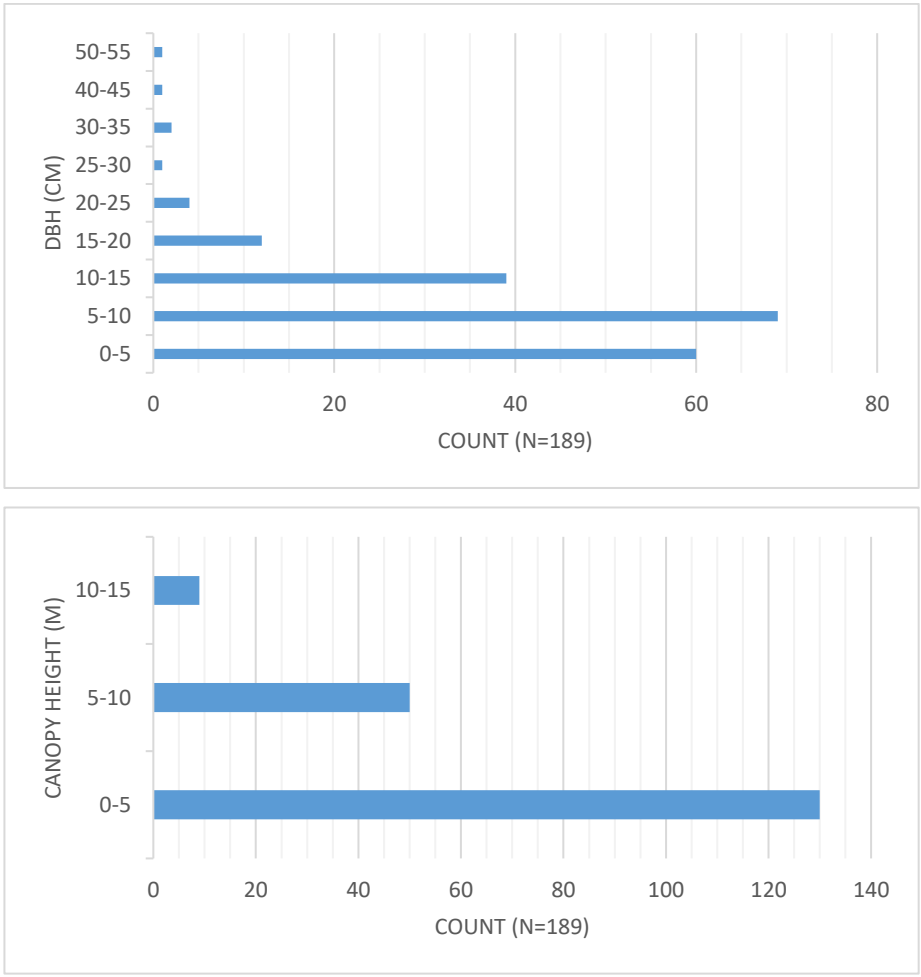


Figure 4.4 Distribution of tree canopy heights and DBH in VHC plots. Top: Distribution of canopy height of trees in VHC plots. Bottom: Distribution of the height of trees in VHC plots.

4.5.1.5 Food species composition and NMDS in Viet Hai

Twenty-nine CBL food species from 408 stems and 21 families were identified across the plots in VHC (Appendix 2.2.5). The top ten species represent 82 per cent of all food species stems (Table 4.5). The most common food species found is *Derris trifoliata* (n=114) a climbing plant (Flora of China Project, 2020), found predominately in slope and coast plots. Slope plots have the greatest distribution of food species (n=25) from 209 stems, followed by coast plots with 19 species and 153 stems, and valleys had the lowest with 16 species and 46 stems.

The NMDS ordination applied a Wisconsin double standardisation to the abundance values, followed by a square root transformation to reduce the effect of high abundances over unique values. A solution was reached within 20 tries and a stress value of 0.06 returned, which is considered a good three-dimensional representation of the abundance relationships.

Table 4.5 Top ten food species in VHC plots

Species	Coast occurrence (n)	Slope occurrence (n)	Valley occurrence (n)	Total (n)
Derris trifoliata	25	86	3	114
Desmos chinensis	13	21	15	49
Pilea hookeriana	39	2	0	41
Primulina drakei	1	24	0	25
Vitex trifolia	14	11	0	25
Tetrastigma rupestre	11	11	2	24
Dracaena cambodiana	9	14	0	23
Alpinia calcicola	11	6	0	17
Sterculia lanceolata	1	3	6	10
Secamone elliptica	3	3	2	8
Total	**127**	**181**	**28**	**336**

There is a high level of overlap between the plots (Figure 4.5), largely driven by the high variation of valley plots, as described by the 95 per cent confidence ellipsis. Coast plots group closely suggesting similar abundances and compositions, with a low variation along the NMDS1 axis. Slope plots appear to split, with the third (VHS3) and fourth (VHS4) slope plots clustering towards the upper variation range of coast plots, and the first (VHS1) and second (VHS2) plots clustering more closely to the lower end of coast variation. All plots fall within the confidence ellipses of the slope plot. The valley plots have a clear spread across both axes, with no close grouping between the plots.

A PERMANOVA shows that there is no significant difference between the plot types (R^2=0.25, F=1.49, P=0.06) and 25 per cent of variation can be explained the different plot types. This is largely a result of the differences in variation found across the plot types. Valley plots exhibit high variation, compared to the low variation found in coast plots.

Applying the intrinsic vectors to the NMDS ordination shows two species significantly ($p<0.05$) contribute to the distribution of the food species compositions across the plots. *Sterculia lanceolata* (p=0.003) has a steep negative gradient and plays an important role in all plot types. *Dracaena cambodiana* (p=0.04) has a steep gradient and contributes to the composition of coast and slope plots along the NMDS2 axis.

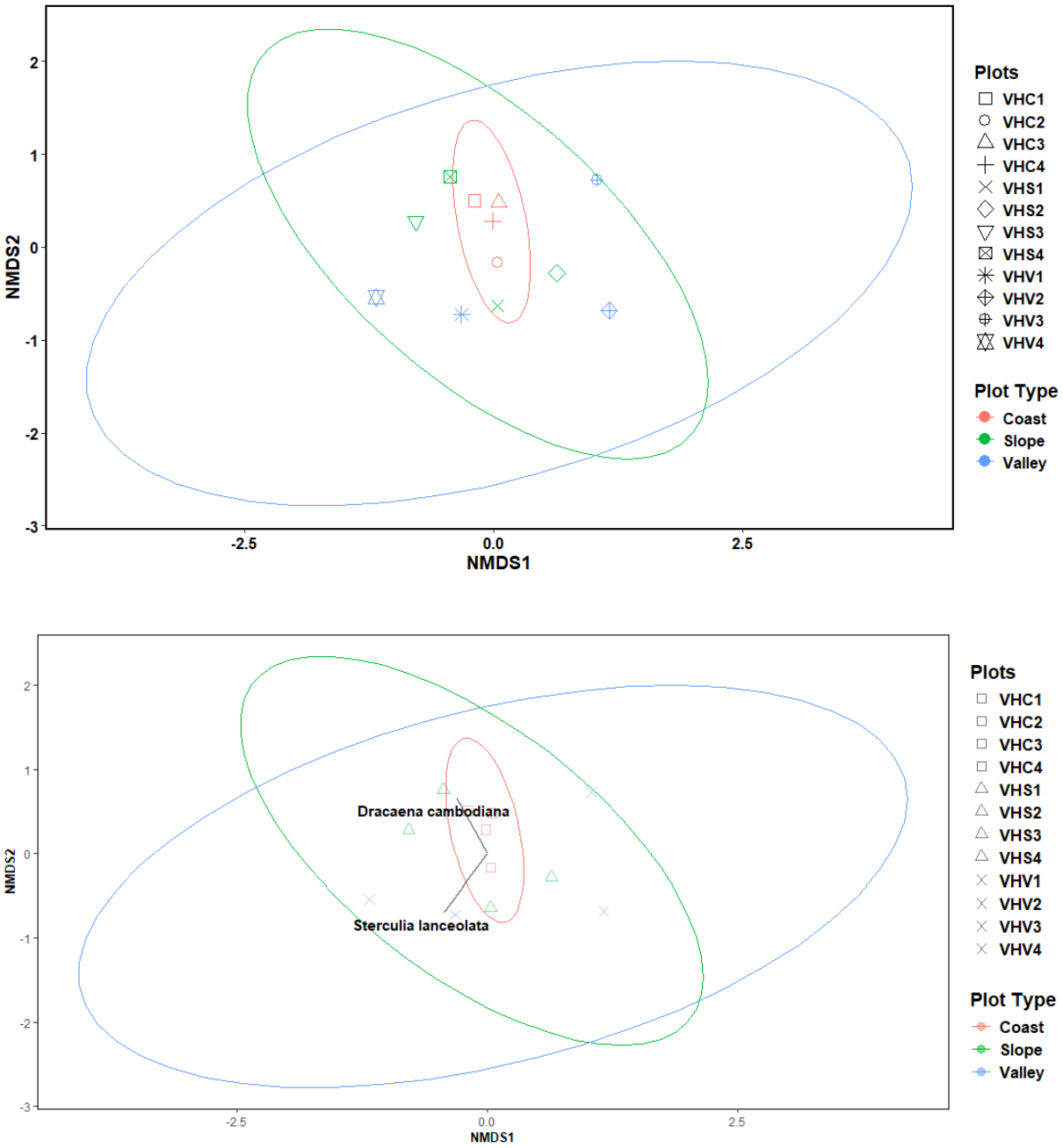


Figure 4.5 NMDS of food species in VHC plots. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors.

4.5.2 Comparison between VHC and CBL habitats

4.5.2.1 Generalised Linear Model, ANOVA and estimated marginal means analysis of the VHC

A two-way ANOVA using a generalised linear model shows that significant ($p<0.05$) differences across the three sites occur in regard to slope, species density, average canopy height, and percentage of mat cover (Appendix 2.1.10).

Estimated marginal means comparing the VHC to the two existing home ranges of the CBL shows few significant differences (Appendix 2.1.11). Of the three sites, it is Cua Dong that appears to be the most different of the three sites. Based on the topographic characteristics, the only significant difference is in the mean slopes for the two langur habitats. Cua Dong slopes (18.66° ±2.40) are significantly shallower than those of the Sanctuary (27.50° ±2.40, $p<0.04$), while the mean VHC slope (23.42° ±2.40) sits in between the two. In terms of elevation and topographic complexity, the VHC does not significantly differ from the other two sites.

Based on the vegetation characteristics of the three sites, the key significant differences lie in the species density, where Cua Dong (1.75 ±0.40) has a significantly lower species density than both VHC (3.74 ±0.40, $p<0.004$) and the Sanctuary (4.87 ±0.40, $p<0001$). VHC also has a significantly higher average canopy height (4.94m ±0.34) than that of Cua Dong (3.72m ±0.34, $p<0.04$), but does not significantly differ from the Sanctuary (3.89m ±0.34). Cua Dong (9.42% ±5.54) also significantly differs from the Sanctuary in terms of percentage of mat cover (33.08% ±5.54, $p<0.015$), but does not significantly differ from the VHC (19.58% ±5.54).

In general, VHC has a greater species diversity, greater general vegetation density greater percentage of canopy cover and liana cover, and greater average tree diameter than both the langur home ranges, though not significantly. For all other characteristics, VHC tends to fall in between the two home ranges.

4.5.2.2 VHC, Cua Dong and Sanctuary plant compositions

4.5.2.2.1 Species composition

A total of 317 species from 104 families and 10,315 stems were identified across the VHC, Cua Dong and the Sanctuary, with only 108 species (34 per cent) common across all three sites. The top ten (Table 4.6) species identified across the three plots accounted for 33 per cent of

all stems. The most frequently occurring species is *Ophiopogon latifolius* (n=879), a perennial grass-like shrub found most frequently across valley plots. The top ten plants shared by the three sites comprise small herbs, ferns, epiphytes, and shrubs. None of the top ten species are classified by the IUCN Red List. The Sanctuary has the greatest number of species (n=236) and stems (n=5844), followed by VHC with 242 species and 4471 stems. Cua Dong has the least number of species (n=186) with 2094 stems.

Table 4.6 Top ten species shared across Viet Hai, Cua Dong, and the Sanctuary

Species	**Viet Hai occurrence (n)**	**Cua Dong occurrence (n)**	**Sanctuary occurrence (n)**	**Total (n)**	**IUCN Red List Status**
Ophiopogon latifolius	546	45	288	879	NE
Leptostachya wallichii	128	1	715	844	NE
Drynaria bonii	169	22	216	407	NE
Pilea peltata	146	81	173	400	NE
Pilea peploides	102	98	164	364	NE
Impatiens halongensis	108	17	163	288	NE
Cleistanthus tonkinensis	149	52	76	277	NE
Adiantum caudatum	33	24	219	276	NE
Streblus ilicifolius	10	193	11	214	NE
Derris trifoliata	114	36	43	193	NE
Total	**1505**	**569**	**2068**	**4142**	

4.5.2.2.2 Non-metric multi-dimensional scaling analysis comparison of plant communities in VHC, Cua Dong and the Sanctuary

The NMDS ordination of all species across the three sites applied a Wisconsin double standardisation followed by a square root transformation. As the stress value returned in two-dimensions was above 0.2, the NMDS was rerun using three dimensions to represent the abundance differences and similarities between the plots. A solution was returned in 20 runs, with a final stress value of 0.14.

There is a high level of overlap between the three sites based on their species abundances (Figure 4.6). None of the sites are showing clear grouping between their plots. There is also minimal grouping between plot types across the three sites, suggesting low differences in the compositions of the three sites. Both the Sanctuary and VHC have outliers, with the first slope plot (SNS1) falling outside the Sanctuary 95 per cent confidence ellipsis, and the fourth slope plot (SNS4) falling outside the VHC 95 per cent confidence ellipsis. It is possible that these two

sites are outliers based on this three-dimensional representation. Cua Dong and VHC have similar variations and spread across the NMDS2 axis, while the Sanctuary is spread across the NMDS1 axis.

A PERMANOVA shows that while there is significant difference between the sites (R^2=0.08, F=1.48, P=0.01), only eight per cent of the variation can be accounted for by location. When testing significance of plot type, there is also only a small difference (R^2=0.11, F=2.09, P=0.001), with 11 per cent of variation explained by the three plot types. Overall, the composition and abundances of plant species are quite similar across the sites.

Applying the intrinsic vectors to the NMDS ordination shows that twenty species contributed significantly (p<0.01) to the distribution and composition of the plots (Figure 4.6). Nine species have positive gradients and contribute to the composition of all plots, with a stronger association with the Sanctuary plots: *Combretum sundaicum* (p=0.001), *Beilschmiedia tsangii* (p=0.004), *Ficus tuphapensis* (p=0.004), *Lygodium japonicum* (p=0.007), *Leptostachya wallichii* (p=0.002), *Machilus bonii* (p=0.006), *Piper saxicola* (p=0.006), *Smilax lanceifolia* (p=0.005), *Wendlandia formosana* (p=0.006).

Three species: *Allophylus livescens* (p=0.008), *Uvaria tonkinensis* (p=0.002), *Pterospermum truncatolobatum* (p=0.007) all have negative gradients and contribute to the composition of primarily VHC and Sanctuary plots.

Alpinia calcicola (p=0.008), *Dracaena cambodiana* (p=0.003), *Pilea peltata* (p=0.002), *Pilea peploides* (p=0.003), *Tetrastigma rupestre* (p=0.003), all have negative gradients and significantly contribute to the composition of all three sites based on their abundances.

The four species *Primulina drakei* (p=0.006), *Secamone elliptica* (p=0.002), *Sterculia lanceolate* (p=0.01), *Wikstroemia indica* (p=0.002) all have positive gradients and are associated with Cua Dong and Sanctuary plots.

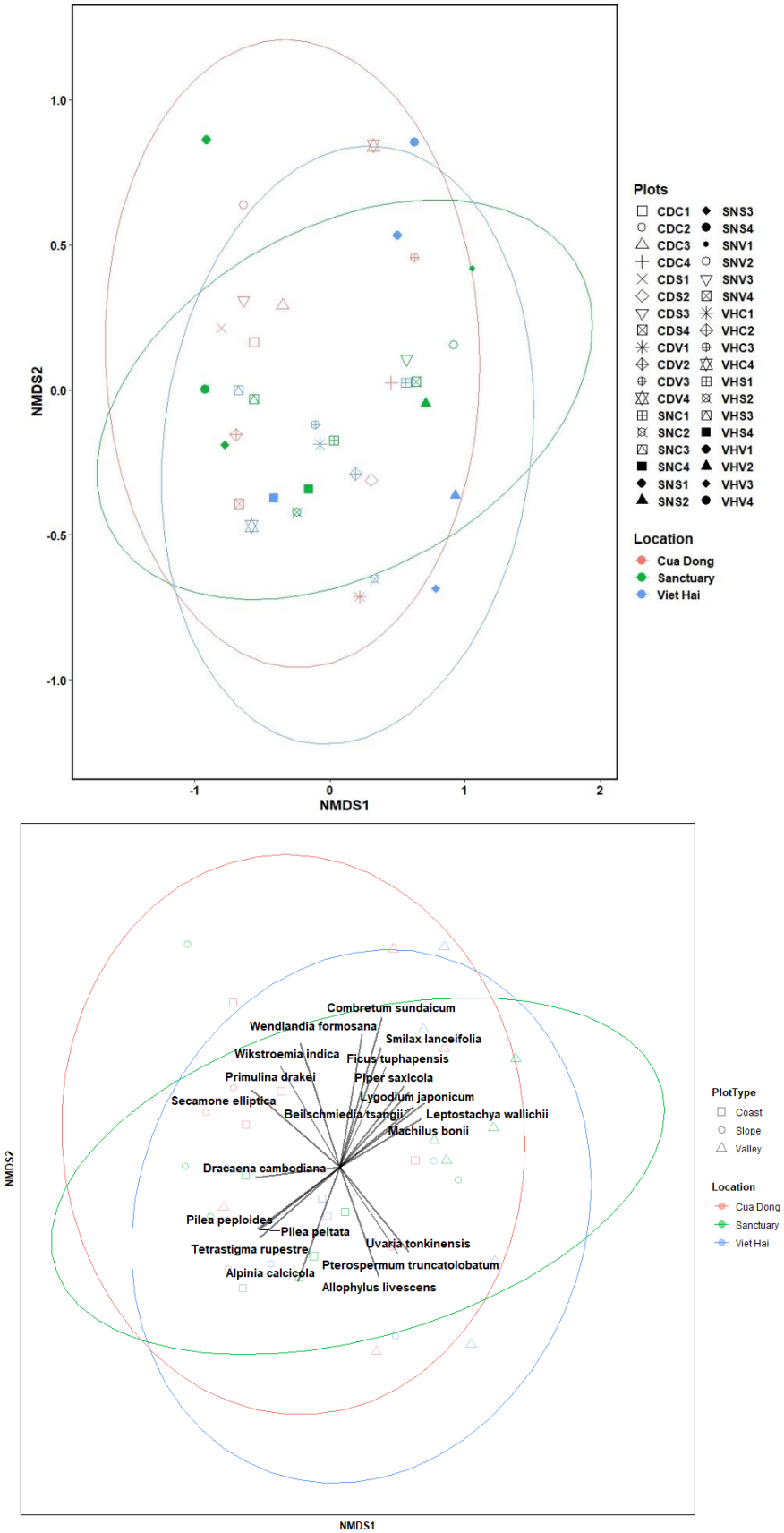


Figure 4.6 NMDS of all species across VHC, Cua Dong, and the Sanctuary. Top: NMDS with 0.95 confidence ellipsis. Bottom: NMDS with intrinsic vectors.

4.5.2.3 Comparison of tree characteristics across VHC, Cua Dong and the Sanctuary

Across the three sites, 640 individual trees were identified, representing 112 species from 44 families (Appendices 2.2.2 and 2.2.4). The top ten tree species account for 44 per cent of all tree stems (Table 4.7). The most common tree species found across the three sites is *Cleistanthus tonkinensis*, a small tree found on forested slopes in Vietnam between elevations of 100-800m (Flora of China Project, 2020).

Table 4.7 Top ten tree species shared across all three sites

Species	Viet Hai occurrence (n)	Cua Dong occurrence (n)	Sanctuary occurrence (n)	Total (n)	IUCN Red List Status
Cleistanthus tonkinensis	*18*	*12*	*44*	*74*	*NE*
Streblus ilicifolius	*4*	*32*	*6*	*42*	*NE*
Dracaena cambodiana	*15*	*11*	*15*	*41*	*NE*
Pterospermum truncatolobatum	*18*	*5*	*9*	*32*	*NE*
Bridelia balansae	*11*	*11*	*6*	*28*	*LC*
Machilus thunbergia	*13*	*1*	*5*	*19*	*LC*
Microcos tomentosa	*9*	*5*	*4*	*18*	*LC*
Diospyros mollis	*2*	*1*	*10*	*13*	*NE*
Aglaia elaeagnoidea	*1*	*7*	*1*	*9*	*LC*
Tarenna attenuata	*1*	*2*	*5*	*8*	*LC*
Total	***92***	***87***	***105***	***284***	

4.5.2.4 Food species composition and NMDS comparison across VHC, Cua Dong and the Sanctuary

Of the 56 food species identified by Ruskin (unpublished, 2016) across the sites at Cat Ba Island, a total of 41 food species were identified as part of this ecological sampling, and 20 species were found in all three sites, from a total of 1198 food species stems (Appendix 2.2.5).

The top ten shared food species (Table 4.8) account for 71 per cent of all stems identified. The most commonly occurring species shared across all three sites is *Derris trifoliata* (n=193), a climbing shrub found distributed across moist monsoon forests (Flora of China Project, 2020). Cua Dong has the greatest number of food species (n=34), followed by the Sanctuary (n=30) and then VHC (n=29).

Table 4.8 Top ten food species shared across all three sites

Species	Viet Hai occurrence (n)	Cua Dong occurrence (n)	Sanctuary occurrence (n)	Total (n)
Derris trifoliata	114	36	43	193
Pilea hookeriana	41	18	57	116
Dracaena cambodiana	23	31	59	113
Primulina drakei	25	18	41	84
Tetrastigma rupestre	24	23	25	72
Desmos chinensis	49	10	11	70
Vitex trifolia	25	1	35	61
Sterculia lanceolata	10	49	2	61
Alpinia calcicola	17	11	14	42
Breynia fruticosa	0	14	21	35
Total	**382**	**211**	**308**	**847**

The NMDS ordination for food species found across the three sites applied a Wisconsin double standardisation and a square root transformation. A solution was found after 20 runs for a stress value of 0.15, which is considered a good three-dimensional representation of the plots. A two-dimensional solution returned a stress greater than 0.2, thus a three-dimensional solution was sought.

There is a high level of overlap with all three sites (Figure 4.7) and a grouping in the centre of the plot, comprising a mix of plot types and sites. Generally, Sanctuary and Viet Hai plots appear to cluster more closely but the Sanctuary plots have a greater variation based on the 95 per cent confidence ellipsis. There are two potential outliers in the NMDS ordination: Sanctuary valley plot one (SNV1), the fourth VHC valley plot (VHV4) both fall outside their respective confidence ellipses.

A PERMANOVA shows that there is only a low level (seven per cent) of difference explained by the site location, and it is not significant (R^2=0.07, F=1.23, P=0.15). Plot type accounts for similar levels of variation (10 per cent) however, the difference according to plot type is significant (R^2=0.10, F=1.88, P=0.004).

Applying the intrinsic vectors to the NMDS ordination found nine species that significantly ($p<0.05$) contribute to the distribution of the plots (Figure 4.7). *Severinia monophylla* (p=0.02) has a steep positive gradient and contributes predominately to Cua Dong food species

composition. *Vitex trifolia* (p=0.002) has a negative gradient and contributes to the food species compositions in the Sanctuary and Viet Hai. *Aristolochia indica* (p=0.03) has a negative gradient and contributes to both the Cua Dong and Viet Hai compositions. *Wikstroemia indica* (p=0.007) has a similar gradient to that of *Secamone elliptica,* however, it primarily contributes to the compositions of Cua Dong and the Sanctuary.

Pilea hookeriana (p=0.007), *Tetrastigma rupestre* (p=0.002) and *Dracaena cambodiana* (p=0.02) have steep negative gradients and contribute to all three sites. *Primulina drakei* (p=0.003) and *Secamone elliptica* (p=0.003) also have negative gradients and contribute to the food species compositions of all three sites.

4.5.3 Distribution analysis for Cat Ba langur

4.5.3.1 Pearson's correlation of predictor variable results

The Pearson's correlation identified four strongly correlated variables: Spot6 Band 1, Band 2 and Band 3, and Slope (-0.7<*r*>0.7) (Appendix 2.3.2). Following their removal, seven continuous variables were left in the MaxEnt modelling: Eastness, Northness, NDMI, NDVI, DEM, TRI, and Spot6 Band 4 (near infrared). The categorical land use variable was also included in the MaxEnt analysis.

4.5.3.2 MaxEnt modelling results of feature class and regularization multiplier variations

Of the feature class combinations analysed (Appendix 2.3.3.1), the Quadratic-only models performed the worst with low AUC_{TEST} values of 0.79. The predictor variables contributing most to the Quadratic-only modelling were predominately DEM, land-use and Spot6 Band4 (NIR), while Eastness contributed the least. A jackknife of the test gain shows that Quadratic-only models performed better without the Eastness variable. An additional model, based on the highest performing Quadratic-only model with a regularisation multiplier of 4 (Test 4: AUC_{TEST}=0.799, AUC_{DIFF}=0.014), and without the Eastness variable only performed marginally better (Test 5: AUC_{TEST} = 0.800, AUC_{DIFF}=0.013).

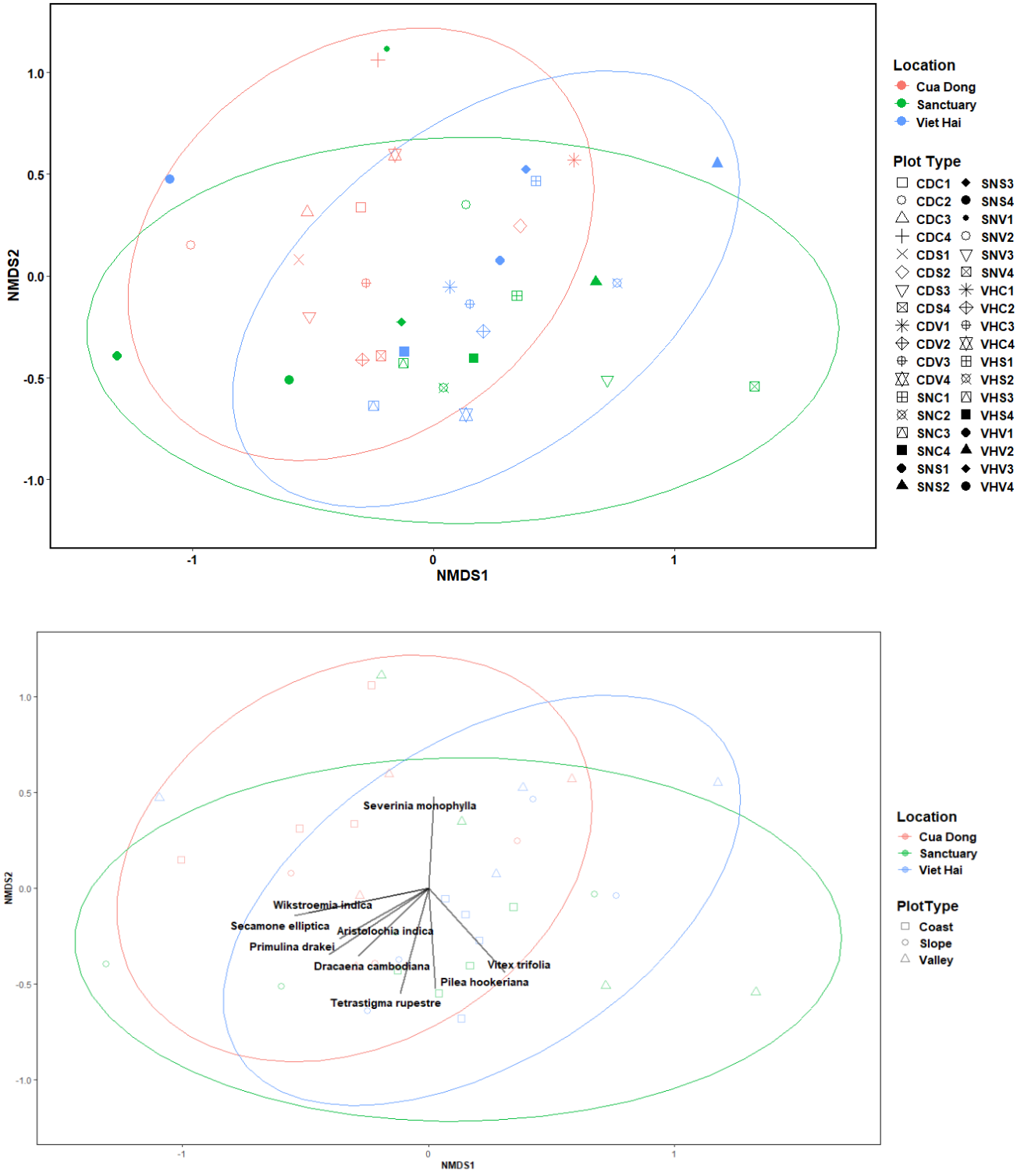


Figure 4.7 NMDS of food species across VHC, Cua Dong, and the Sanctuary. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors.

Linear models were only marginally better, with AUC_{TEST} values of 0.801 and below. The predicator variables contributing the most to all models were DEM, Spot6 Band4 (NIR), and land use. The TRI and Eastness had the lowest contribution and based on the jackknife, all models performed better without the Eastness variable. Removing this variable from an additional run, based on the best performing variation with a regularization multiplier of 4 (Test 9: AUC_{TEST}=0.791, AUC_{DIFF}=0.017), again performed only slightly better (Test 10: AUC_{TEST}=0.792, AUC_{DIFF}=0.015). The Linear and Quadratic combination (L+Q) performed better than the Linear- and Quadratic-only models based on AUC_{TEST} values. AUC_{TEST} values of over 0.82 indicate a strong model, and the multiplier regularization of 0.5 variation performed the best (Test 14: AUC_{TEST}=0.841, AUC_{DIFF}=0.02). The predicator variables contributing the most to this model was the DEM, Spot6 Band 4 (NIR), land use and NDVI. The least contributing variable was Eastness, and the model consistently performed better without it included. To test this, the model was rerun based on the highest performing L+Q model (Test 14) without Eastness and the resulting model performed better than other L+Q models, with no difference between the training and test AUC values (Test 15: AUC_{TEST}=0.842, AUC_{DIFF}= 0.0).

The Hinge-only, Linear, Quadratic and Hinge (L+Q+H) and Auto feature class combinations all performed similarly, with AUCs ranging from 0.83 to 0.85. For all three model types, the most contributing predictor variables was the DEM. Eastness was the least contributing variable, reducing the test gain, and all model-types performed better without it based on the jackknife function.

The best performing Hinge-only model had regularization multiplier of 4 (Test 18: AUC_{TEST}=0.842, AUC_{DIFF}=0.021). To test the impact of Eastness, the model was rerun. The resulting model performed much better than previous variations (Test 20: AUC_{TEST} = 0.844, AUC_{DIFF} = 0.0.002).

For the Linear, Quadratic and Hinge (L+Q+H) model, the best performing model again had a regularization multiplier of 4 (Test 24, AUC_{TEST}=0.840, AUC_{DIFF}=0.022). Running this model again with the Eastness variable removed, showed that the model performed much better with an almost identical AUC for both training and testing models (AUC_{TEST}=0.844, AUC_{DIFF}=0.001).

In the Automatic functions model, the best performing model had a regularisation multiplier of 4 (Test 29: AUC_{TEST}=0.845, AUC_{DIFF}=0.021). The rerun of this model with Eastness rerun performed slightly worse (Test 30: AUC_{TEST}=0.843, AUC_{DIFF}=0.021), as the AUC_{DIFF} remained the same, but both the training and test AUC values declined though only slightly.

4.5.3.3 Top performing model comparison

Based on the AUC_{DIFF}, the top performing model from each feature class was rerun with 10 replications (Appendix 2.3.3.2). With the exception of the Linear and Quadratic (L+Q) model, which had a regularization multiplier of 0.5, all other top performing models had a regularization multiplier of 4.

The best performing model based on the highest mean AUC was the Automatic feature type where AUC=0.85 ±0.033, indicating excellent discrimination in modelling suitability for the Cat Ba langur. The worst performing model was the Quadratic-only (AUC=0.791 ±0.042), followed closely by the Linear-only (AUC=0.800 ±0.052). The Linear and Quadratic model (L+Q) performed better (AUC=0.835 ±0.03) than the individual models. The Hinge (AUC=0.84 ±0.026), and Linear, Quadratic and Hinge (L+Q+H) (AUC=0.841 ±0.028) models performed almost identically, just behind the top model.

Based on the comparison of top model performance, it appears that the Automatic feature class produced the best model regardless of other possible combinations, however, the regularization multiplier of 4 performed better than the default setting of 1.

4.5.3.4 Cat Ba langur distribution

Based on the top performing model, the distribution of the Cat Ba langur can be predicted based on habitat suitability derived from the seven predictor variables (Appendix 2.3.3.3).

The DEM was the highest contributor to the model (36 per cent) and suggests that CBL occurrence declines as the elevation increases; over 75m above sea level, the probability of CBL occurrence declines below 50 per cent.

Land use was the next highest contributor (19.3 per cent), indicating that CBL presence is most strongly associated with the land use and cover categories representing water and bare limestone (barren). The high association with water is likely due to the resolution of the

variable datasets and association of the CBL with cliff faces, making accurate land use categories difficult to determine for these locations. Evergreen broadleaf forests, and grass or shrub cover have the lowest associations with CBL presence. The categories for deciduous forest and coniferous forests are not present in the land use map for Cat Ba Island.

The TRI had a moderate contribution (16.7 per cent), with the presence of CBL most strongly associated with nearly level terrain. The suitability of terrain for the CBL only gradually decreases as terrain becomes more rugged, indicating the presence of the CBL could be associated with nearly level to highly rugged limestone karst.

The contribution of NDMI (10.7 per cent) and NDVI (7.9 per cent) to the model were similar. NDMI values of between -0.05 and 0.20 indicates a 50 per cent probability of the CBL distribution. This suggests only areas with vegetation with very low moisture levels are suitable for the CBL, possibly due to the presence of saltwater absorption by plants consumed by the langurs. The association between CBL-suitable habitat and NDVI values, suggests that the sparse, poor-quality vegetation is suitable for the langurs and an increase in quality does not impact the suitability of an area. This is also reflected in the low contribution of Spot6 Band 4 (NIR), which suggests that as vegetation density increases, the presence of the CBL decreases.

The contribution of Northness to the model was lowest of all predictor variables (3.9 per cent), suggesting that the CBL are more likely to be found on southern aspects but that it acts as a very low predictor for the presence of CBL.

The resulting habitat suitability map, showing the expected distribution of the CBL across Cat Ba Island, suggests that very little of the island is associated with high probabilities of the CBL presence (Figure 4.8). The CBL is most expected to be found around the coastline, and along areas associated with humans, including built up areas and roads.

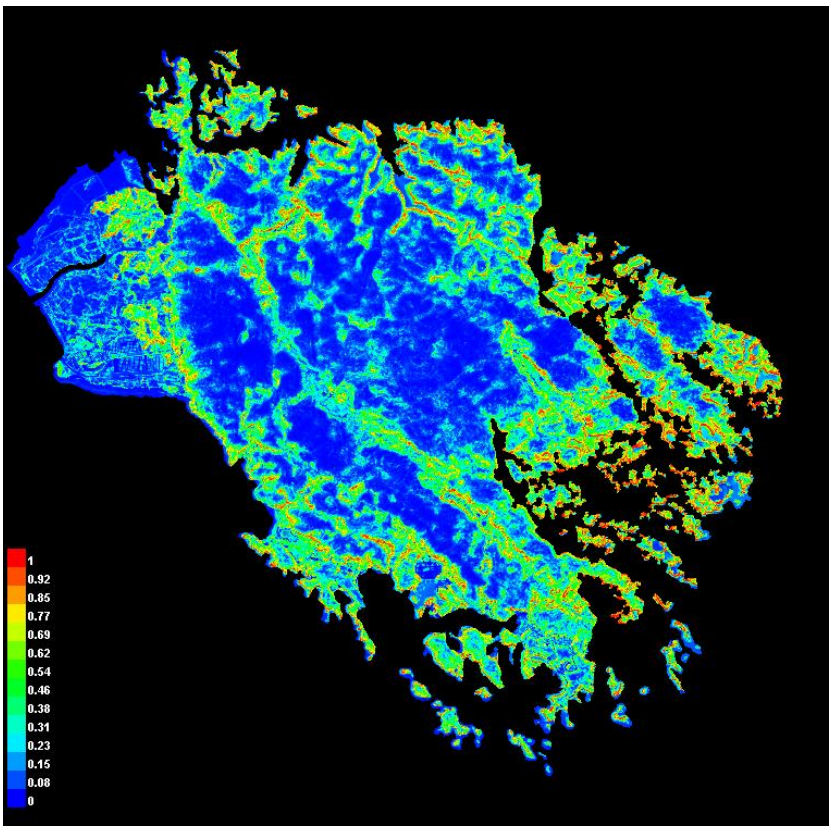


Figure 4.8 Median summary of CBL distribution across Cat Ba Island. Map output from MaxEnt [v 3.4.4]

Areas with a suitability for the CBL, with a probability of 90 per cent or greater, represents an area of 4.92km^2 or four per cent of the total area of Cat Ba Island (Figure 4.9). Within the two main ranges of the CBL this represents 0.15km^2 (13.5 per cent) of Cua Dong's 1.1 km^2 total area, and 1.05 km^2 (8.0 per cent) of the Sanctuary's total 13.1 km^2 area. Within the VHC, approximately 0.62 km^2 (4.0 per cent) was identified as having a suitability probability for the distribution of the CBL of 90 per cent or higher.

Areas of 60 per cent suitability account for 29km^2 or 20 per cent of the total area of Cat Ba Island. In Cua Dong, 0.53km^2 (48 per cent) and in the Sanctuary, 4.68km^2 (35.7 per cent) was identified as having a 60 per cent probability of being suitable for the CBL. Within VHC, 2.56 km^2 (17 per cent) was found suitable.

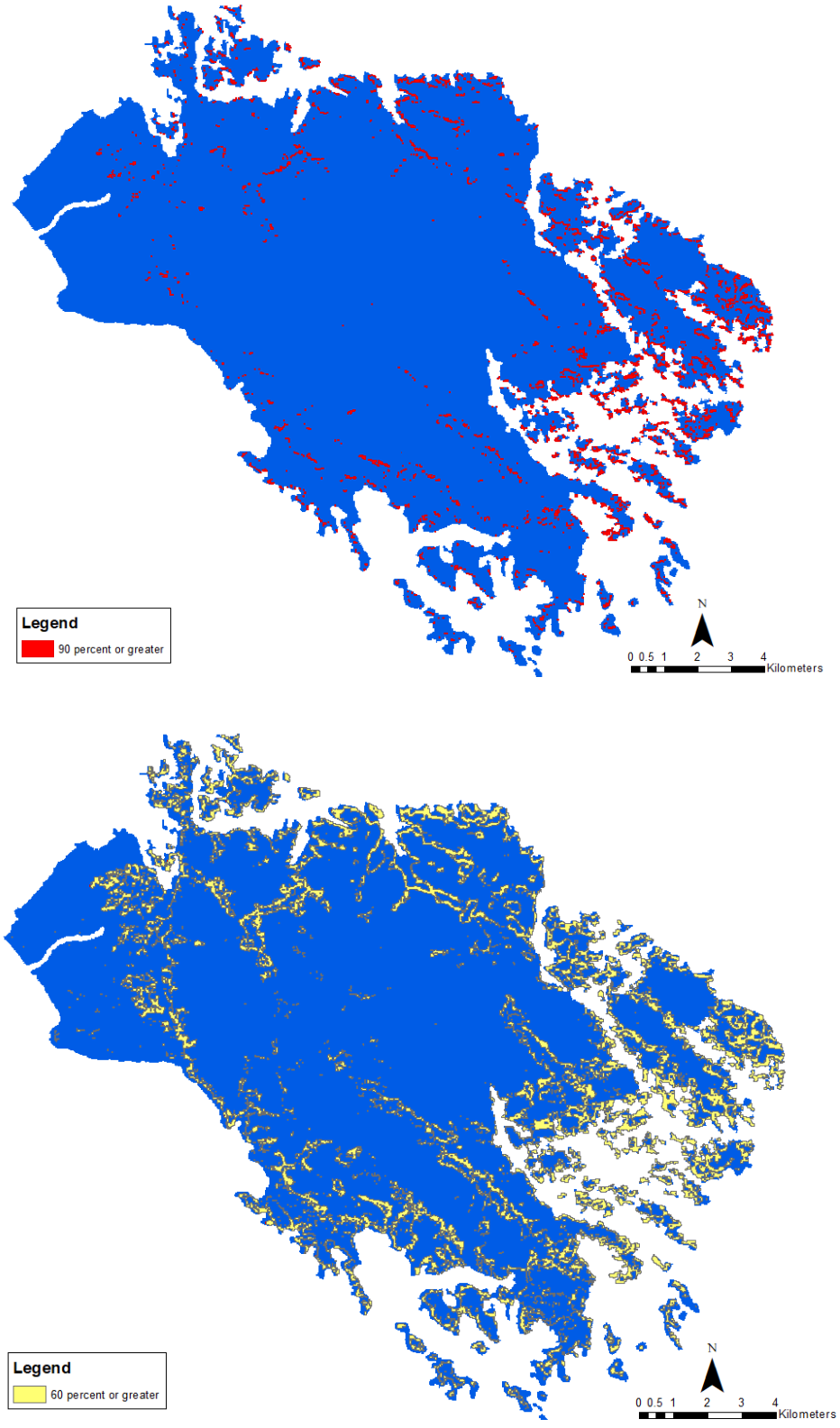


Figure 4.9 Potential distribution of the CBL at 90 per cent and 60 per cent habitat suitability. Top: Habitat with 90 per cent or greater probability of suitability. Bottom: Habitat with 60 per cent or greater probability of suitability.

The majority of the island, including most of the CBNP, appears to have low suitability across both 90 per cent and 60 per cent modelling, despite representing the most established forest and lowest human activity.

The coastline along the Viet Hai corridor suggests only medium probability of CBL presence, with small patches indicated pockets associated with high suitability located closer to the Sanctuary. A major pocket of suitable habitat appears to the west of Cat Ba Island, in a region that was identified as having low historical association with the CBL based on interviews with the local community (Chapter 3, section 3.5.1).

4.6 Discussion

4.6.1 VHC ecology

Overall, the ecological sampling does not support the hypothesis that the VHC is significantly different to the Cua Dong or Sanctuary habitat. VHC, based on general vegetation composition and tree compositions is more similar to that of Cua Dong rather than the Sanctuary. In terms of species density and average canopy height, however, VHC is more similar to the Sanctuary.

While VHC may not significantly differ overall from the current CBL habitats, results show that the VHC has a greater general vegetation density, with a higher canopy height and more canopy cover than the other two sites. This suggests a less disturbed overall vegetation profile than either habitat site. The site characteristics suggest that VHC has the lowest elevation and topographic complexity means, however, this may be a result of limited accessibility for plots due to the high cliffs that border a large portion of the coast between Cua Dong and the VHC areas sampled. While this was a limitation for sampling, the cliffs do not act as a barrier to the movement of langurs along this stretch; as limestone langurs such as the CBL travel predominantly via limestone (Hendershott, 2017; Workman & Schmitt, 2011; Xiong, Gong, Qiu, & Li, 2009).

The VHC ecological analysis reveals that the valley plots are significantly distinct from coast and slope plots. The overall topography of valley plots is less complex than the slope and coastal plots and they were predominately in the process of undergoing regeneration, as indicated by the high levels of small, medium and large shrub coverage recorded within the

plots. The state of VHC valleys is not an unusual pattern across the three sites; in Cua Dong and the Sanctuary, many valleys are still regenerating from historical use for farming or plantations.

Valleys also have higher species density, but lower species diversity compared to the slopes and coasts. This is due to valley plots being largely covered in dense mat or shrub layers of the same species such as *Ophiopogon latifolius*, a grass-like species found predominately in the valley plots in the VHC. Although VHC valleys have the lowest density of trees (0.13 stems/m^2), trees are more established and have greater mean DBH, higher mean canopy heights, greater mean canopy coverage and greatest mean basal area than both slopes and coasts.

Like other limestone langurs, CBL have been found to preference valleys and areas of dense vegetation when foraging (Hendershott et al., 2018; Huang et al., 2008; Schneider et al., 2010; Zhou et al., 2013;). Based on the vegetation profile of the VHC, particularly its valleys, this suggests that the region might align with the habitat usage observed in Cua Dong. Yet as a foraging site, this only holds if the valleys in VHC support CBL food species in high enough quantities.

The VHC (n=29) falls just short of Cua Dong (n=34) and the Sanctuary (n=30) in terms of food species availability. Food species are most frequently found on the slopes of Cua Dong and the Sanctuary, with the fewest number of species expected to be found in the valleys (Chapter 3, sections 3.5.2.2.3 and 3.5.3.2.4). This pattern is reflected in the food species distribution across plot types in VHC. In VHC, slopes had the highest number of food species (n=25), and highest tree density (0.2 stems/m^2) compared to the coast (n=19, tree density=0.15 stems/m^2) and valley plots (n=16, tree density=0.13 stems/m^2). This is promising in terms of the VHC being suitable for CBL use; Hendershott et al. (2018) found that for the CBL foraging was most likely to occur on slopes, particularly in trees and areas of dense vegetation. Slopes (or hillsides) have also been found to be important region for both white-headed black langurs and François' langurs for travel, resting and feeding (C. Huang, Wu, et al., 2008; F. Liu et al., 2022). The distribution of food species on slopes in VHC appears to reflect that found in Cua Dong and the Sanctuary.

As found in Cua Dong and Sanctuary sampling, valleys in the VHC display a lower availability of food species compared to slopes and coastal plots. Previous studies of the CBL have suggested that both valleys and slopes represent important foraging sites for the CBL (Hendershott, 2017; Hendershott et al., 2018). The preference of the CBL to forage in valleys may indicate that these areas provide a preferred food type such as fruit, as in the case of *Trachypithecus shortridgei* (Geng et al., 2020), or that foods in the valleys are of a higher quality than those on the coasts, despite the decreased variety. Valleys are likely to provide greater quality soils for growth than the slopes of coasts due to soil runoff from greater elevations and the porous nature of limestone karst to hold water (Clements et al., 2006). This may impact the use of the VHC by the CBL as many of the valleys in the VHC immediately surrounding Viet Hai village are still used for farming, thereby reducing the available forest in the region available to the langurs.

Of the 377 plant species identified across the three sites, 16 are listed on the IUCN Red List (2018). Only 56 species have been identified as CBL foods (Ruskin, unpublished 2016) and 41 were captured within sampling across all three sites, which represents only 11 per cent of the total number of species sampled. The low number of diet species in comparison to the species profile of the sites suggests that that the CBL are highly selective in their food choices (Geng et al., 2020; C. Huang, Wu, et al., 2008). Other *Trachypithecus* species are also selective in their food choices, and do not appear to select food species based on how abundant they are within their habitat (Geng et al., 2020; C. Huang, Wu, et al., 2008; Youbang Li, Ding, Huang, Jiang, & Wood, 2009; Qihai Zhou, Wei, Li, Huang, & Luo, 2006). This pattern of selectivity appears to hold even in fragmented habitats when certain food species may be limited (Y. Li et al., 2009).

Access to suitable food resources is a critical factor in determining species' home ranges and distribution (Carl, 2009; D. Li et al., 2011; Onderdonk & Chapman, 2000; Qihai Zhou et al., 2007) perhaps more so than other environmental factors. It is surprising then that the VHC has a similar density of food species (0.34 stems/m^2) than both the Sanctuary (0.34 stems/m^2) and Cua Dong (0.32 stems/m^2), and yet it does not appear to be regularly utilised by the langurs. Further study on the composition of food species making up the two CBL habitats

may reveal a deficit in the quality or mixture of food resources found in VHC compared to Cua Dong and the Sanctuary.

For now, it does not appear that the VHC is significantly different from the current CBL ranges based on general vegetation profiles or food species availability. This suggests that a lack of food species or altered habitat structure in the VHC are not preventing the Cua Dong CBL from expanding into the area. Based on the habitat characteristics and species distribution across the three sites, there is no obvious factor that suggests that the VHC area would not make a suitable corridor or habitat expansion for the CBL.

4.6.2 VHC use and wider CBL distribution

Based on the MaxEnt modelling, only a small percentage of the total area of Cat Ba Island is predicted to have habitat suitable for the presence of the CBL (four per cent). When expanding the suitability probability to include areas of 60 per cent or greater, the total potential distribution of the CBL increased five times, to include 20 per cent of the total Cat Ba Island area. The current area of the CBL protected zones in Cua Dong and the Sanctuary currently represent 14.2km^2, representing only 10 per cent of the island's area. Despite these areas being considered the extent of the CBL ranges (Hendershott et al., 2016; Hendershott et al., 2018), the MaxEnt modelling suggests that not all areas within Cua Dong and the Sanctuary are suitable for the langurs.

The Cua Dong population comprises two main groupings, with occasional fluctuations (Hendershott et al., 2018). The home ranges for these two groups have been found to be 0.55km^2 and 0.22km^2, with 0.05km^2 overlap (Hendershott et al., 2018). This suggests that CBL within Cua Dong are using approximately of 0.72km^2 based on polygon calculation of home ranges (Hendershott et al., 2018). Based on this, even at 60 per cent predicted habitat suitability (0.53km^2), within Cua Dong the CBL are using areas identified as having low suitability based on the factors accounted for in this analysis.

The presence of CBL is associated with elevations below 75m, and level to medium rugged terrain. The distribution of the langurs based on the MaxEnt modelling is highly fragmented and concentrated around the coastlines, including in areas highly populated by humans. While this may be at odds with the current behaviour of the CBL, local members of the community

recalled memories of langurs around villages and even occasionally interacting with humans. The current Cua Dong population is somewhat habituated to human activity, however, they do move away if humans get too close to their groups. Based on current behaviours, these areas close to humans do not support langurs and it is not recommended that these areas are pursued as potential habitat.

It is possible that the sampling bias for occurrence data is impacting the results of the MaxEnt modelling and may account for the model's identification of coastlines and areas of elevation below 75m. As discussed previously, samples are biased towards the Cua Dong population, which has been the focus of most previous studies of the CBL (Hendershott et al., 2016; Hendershott, 2017; Hendershott, et al., 2018). The Cua Dong population occupies a smaller area and is characterised as a peninsula, further compounding the risk of sampling bias, occurrence data collected from the Cua Dong region are predominately collected from researchers in boats, a common method used by researchers studying limestone langur species near water (Agmen, 2014; Hendershott, 2017; Hendershott et al., 2018; Thuc et al., 2014; Schneider et al., 2010; Workman 2010). While this was attempted to be accounted for by spacing the occurrence points (Kiedrzyński, Zielińska, Rewicz, & Kiedrzyńska, 2017), it is unlikely this influence was entirely removed from the model. The low population size of the CBL and the difficult topography of the inner regions of the CBL distributions makes it difficult to account for this bias, however, future studies may benefit from increasing the representation of the Sanctuary population.

The results of the MaxEnt modelling also suggests that large sections of the Viet Hai Corridor do not have high suitability for the presence of the CBL. Only the coastal borders of VHC appear are classified by the model as suitable area for the presence of CBL.

Despite the conflict between the findings of the in situ ecological surveys and the MaxEnt, the behaviours of the CBL and other limestone langur species may support the fragmented patches identified by the MaxEnt modelling. A key driver for suitability of areas in the model appears to be the negative relationship between the CBL and evergreen broadleaf forests with high canopy densities. As noted, the VHC has higher mean tree canopies, greater canopy coverage and larger trees than the other two sites. Based on the MaxEnt modelling, this type

of dense vegetation found in VHC and the wider CBNP is predicted to have low suitability for the CBL.

Unlike other canopy specialists, canopy connectedness may not be a significant deciding factor for CBL habitat (Das et al., 2009; Hankinson et al., 2021; Islam, 2014). As with other limestone langurs, the CBL are at least partially terrestrial, prefering to move along the limestone rather than through the canopies (Hendershott, 2017; Nadler & Long, 2000; Stenke & Canh, 2004; Workman & Schmitt, 2011). François' langurs (C. Huang, Wu, et al., 2008) and white-headed lack langur (F. Liu et al., 2022) like the CBL have been observed to spend a significant amount of time on bare limestone (Hendershott et al., 2018). Like most limestone langurs, the CBL also use caves and ledges on cliff faces as sleeping sites (Hendershott, 2017; C. Huang & Li, 2005; C. Huang, Li, et al., 2008). These behaviours could indicate that the high number of observations along coastlines do reflect the habitat use by the CBL and are accurately demonstrated in the results of the modelling.

A lack of suitable valleys within the VHC, as identified by the MaxEnt modelling, may also make the region less suitable for longterm use by the CBL. Although the CBL spend large amounts of their time in areas with sparse vegetation and on exposed slopes and cliffs, valleys play an important role in their foraging behaviours (Hendershot et al., 2018). Limited access to valleys in this region, particularly during the dry season (Hendershott et al., 2018), may reduce the viability of this region as an alternative to the Cua Dong region.

As a result, the observations of langurs moving through this VHC region and failing to permanently remain may indicate that it acts only as a coastal highway for lone langurs, particularly for bachelor males. Based on the length, it may prove too long a journey for langurs despite the availability of food species. Fragmented habitats have been found to restrict langur habitats and reduce the amount of time spent moving in favour of feeding (Z. Huang et al., 2017). This could indicate why the CBL groups are not moving into the VHC region more frequently as their activity budgets reflect those of other limestone langurs (Hendershott et al., 2016), which are often also inhabiting fragmented habitats. Instead, despite the possibility of conflict with other groups, CBL groups remain close to known food patches.

It appears that while the ecological sampling suggests that the VHC region should be suitable for the CBL, the MaxEnt modelling appears to reflect the current status of the Cua Dong and Sanctuary as core habitat areas, surrounded by fragments of suitable habitat. Other core areas indicating the presence of the CBL across the main part of Cat Ba Island are already highly associated with humans, making it unlikely that the areas would also support the CBL. Further study into the diet of the CBL in both Cua Dong and the Sanctuary may provide greater insights into their preferences, allowing for further exploration of the VHC as a connecting corridor between the groups. Further study of the Sanctuary population may also provide greater insight into the suitability of the VHC.

4.6.3 Other potential factors impacting corridor use

It is possible that factors beyond the vegetation charcateristics of the VHC are influencing its use by the CBL. Predation and competing species may be a critical factor in species habitat selection (Carl, 2009; M. F. Schneider, 2001). Cat Ba Island is not known to have any large predators remaining (Abramov & Kruskop, 2012), however, rangers and locals did report historical observations of CBL predation by pythons and possibly large birds. These events appear to be rare, not just for CBL but for the limestone langurs across Vietnam and Southeast Asia (Harding, 2010; Manh Ha Nguyen, 2006; Standford, 1989).

Today, the main threats faced by the CBL, include the many domestic dogs introduced to the area by humans. In Cua Dong, every house in the floating village living alongside the CBL, has at least one dog. In at least one area, the introduction of dogs at a household in Cua Dong has seen a group of CBL bachelors reduce their former range and they no longer pass near the house (pers comm, Mr Cam). This aversion to domestic dogs has also been reported in other langur species such as Gee's langur (Chetry et al., 2010). In the VHC, the farmed valleys around the region are home to dogs, which may make the area less appealing to the CBL when they enter this region.

Variation in the availability of sleeping sites between the regions may also be dictating their current distribution and limiting long-term use of the VHC. It appears that sleeping sites are not randomly chosen, and that langur groups may have a finite number that are cycled through depending on the travel each day or depending on the season (Burton et al., 1995).

Groups of *Trachypithecus hatinhensis* (Hatinh langur) reportedly used the same sleeping sites between 1998 and 2006 (Manh Ha Nguyen, 2006), suggesting that sleeping sites are established and not easily changed.

A previous study by Huang et al. (2008) also suggested that the availability of sleeping sites for the closely related white-headed black langur may be affecting population numbers; if langurs are reluctant or unable to establish new sleeping sites, it may restrict their ranging and ability to colonise or remain in new areas (Huang et al., 2008). Thus, it is possible that the wider dispersal of the CBL as their population grows and groups fracture is somewhat limited by their ability to find new suitable sleeping sites. Observations made by Ruskin (personal communication, June 2017) and Hendershott (2017) noted that some sleeping sites in Cua Dong continue to be shared by groups despite the breakdown of larger groups, causing groups to alternate use of the sites. This suggests a reluctance or inability to establish new sleeping sites for the CBL.

Yet it seems difficult to understand why new sleeping sites could not be found within the VHC. The region is surrounded by high cliffs facing the water that would appear appropriate for sleeping sites, and small groups of langurs have been observed to stay out in the VHC region for several nights, which indicates they are able to find somewhat suitable sites during their stay. Furthermore, the sleeping sites themselves appear to vary greatly from actual caves in the limestone, to tiny ledges on cliff faces that appear to offer little protection (Hendershott, 2017; Nadler & Long, 2000). Further study of the structure and characteristics of sleeping sites may reveal how sites are selected by CBL.

Knowledge of food locations may also be a limiting factor in CBL dispersal. Limestone langurs living within fragmented habitats have been found to reduce time moving in favour of increasing time feeding (Z. Huang et al., 2017). Uncertainty regarding food distribution within the VHC may be limiting the capacity of Cua Dong langurs to move beyond their current ranges due to energy conservation strategies (Z. Huang et al., 2017).

While they were once distributed across most of the island, the fragmentation of the CBL population may also have ensured that they are reluctant to move out into territory that may be associated with high levels of perceived or actual predation either from animals or humans.

Their familiarity with their current area means that they know the locations of sleeping sites and the patterns of potential predators (Isbell, 1994). Thus, this may partly explain the observations that mainly lone male langurs are observed to temporarily enter the region; while a bachelor male may enter the region in search of potential mates, groups of langurs may not be under any pressure to leave the Cua Dong region. This may change in the future, however, if the population continues to grow and the Cua Dong region reaches carrying capacity.

Competition with other species may also be a deterrent for langur expansion into the corridor area (Erinjery et al., 2017; Mackey & Lindenmayer, 2001). Small group sizes and the threat of an unfamiliar area may explain why the VHC is also not regularly used or permanently inhabited. A lack of familiarity of with the VHC and smaller group sizes may also make CBL more vulnerable to predators or confrontations with macaque groups. Macaques, which largely reside in the Sanctuary, have been seen around the outskirts of the Cua Dong area (K., Ruskin, personal communication, June 2017) and may also pose a threat to langur expansion. The small number of langurs observed moving around and temporarily staying in the Viet Hai area are almost always reported to be single males, with the occasional group of two or three langurs. This suggests that perhaps males are moving into this region in search of territory or mates, but it might also make them reluctant to encounter any large macaque groups.

The current population size of the Cua Dong CBL may not yet be encouraging the permanent dispersal of groups into VHC. Hendershott (2017) observed two main groups within Cua Dong; Group A, a larger group of one adult male, five adult females and four to seven young langurs and Group B, a small group consisting of one adult male, two adult females, two subadults, and two young langurs (Hendershott et al., 2018). Both groups were found to have distinct home ranges with some overlap, however, the smaller langur group's home range was smaller than the other group and somewhat constrained towards the tip of the peninsula (Hendershott, 2017; Hendershott et al., 2018). Based on these group structures, the Cua Dong area appeared to be sustaining the Cua Dong population and ongoing births were being recorded (Hendershott et al., 2018).

During this study, it was observed ad hoc that there had been a fracture of Group B, resulting in two smaller group. The compositions of the new groups consisted of at least one adult male and one adult or subadult female. Due to the home range of Group A limiting their ability to disperse, these two new groups appeared to be sharing the original home range of Group B. As result, these groups were found to overlap in their ranging and bouts of conflict or avoidance were observed. This suggests that the Cua Dong region may not support growing or changing compositions of CBL in the long term. It also makes it unlikely new groups of langurs can establish themselves in the area. It also may account for the movements of male langurs in the VHC as they seek out mating opportunities. The VHC then becomes an important region to consider if not for habitat expansion, but as a connection to link the two major breeding populations of the Cua Dong and the Sanctuary.

4.6.4 Corridor viability

The population of CBL has been predicted to grow slowly to an estimated population of 86 individuals by 2050, however, this may increase further if the reproductive isolation of the Cua Dong and Sanctuary groups is overcome (Thuc et al. 2014). Population viability modelling has also shown that that best outcomes for CBL population growth is linked to a population where there is regular movement between sites compared to isolated sub-populations currently observed (Lees et al., 2014). Thus, any efforts to improve connectedness between the two langur habitats, may positively contribute to population growth of the entire species.

Based on in situ ecological modelling, the VHC region appears to have no significant differences overall from the Cua Dong and Sanctuary habitats in terms of vegetation, species distribution and food distribution. Yet it is not regularly utilised by the CBL despite its connection to the Cua Dong population. This suggests that long-term expansion into the VHC may not be expected based on the factors considered in this analysis.

Habitat studies, particularly those which represent sub-areas of the historical distribution, can suffer from the human interpretation of habitat; where we seemingly observe suitable habitat, the study species may only see hot spots of suitable pockets in a landscape of non-habitat (Garshelis, 2000). This is demonstrated by the MaxEnt analysis, which identifies only small patches along the VHC associated with high suitability for the presence of CBL,

suggesting the VHC is less suitable for long-term CBL usage than their current home ranges. The number and frequency of these suitable patches increase further along the coast around Viet Hai, towards the Sanctuary. This is unexpected as this area represents higher human activity due to the Viet Hai village and the Viet Hai port – a popular stopping point for tourist cruises.

If the VHC does not represent habitat for the CBL, then it may serve more appropriately as a linkage between the two main breeding populations. Corridors may act as convenient connectors between patches of habitat viewed as suitable for breeding or foraging (Knowlton & Graham, 2010). However, in its current state, the VHC may also not represent a true corridor for langurs, due to the break caused by Viet Hai port and the associated roads. While macaques have been observed to make their way along the coast via the corridor, langurs have not been observed making the complete journey.

A major issue with the creation of corridors is encouraging their use by the target species (Beier & Noss, 1998). In the case of the VHC region, observation has demonstrated that individuals from the Cua Dong area are partially entering the region, though the connection is never completed. As discussed earlier, the lack of utilisation of the VHC may be a result of energy conservation in the face of fragmented habitat and a lack of food distribution (Z. Huang et al., 2017), predator avoidance, or due to a lack of resources related to sleeping sites and/or food. The distance between the Cua Dong and Sanctuary populations may be too great for groups to travel and despite observations of inter-group conflict within Cua Dong, there may not be any current pressure for groups to seek out new ranges.

Instead, it is possible that the corridor may function to encourage the movement of individuals, particularly bachelor males, seeking to access mating opportunities thereby establishing genetic exchanges between the two main breeding groups (Hilty et al., 2019). Fragmented habitats and populations give rise to increased extinction risk (Isabirye-Basuta & Lwanga, 2008) but improving connectivity between groups across the Cat Ba Island landscape can work to counteract the negative effects of small populations as a result of habitat fragmentation (Beier & Noss, 1998; Haddad et al., 2003; Hilty et al., 2019).

The development of corridors to link habitat fragments requires species specific planning to allow for the greatest chance of success and while few corridor studies have focussed on primates, there is a growing interest in their use to offset the effects of population fragmentation (Huang et al., 2017; Panagoda & Weerasinghe, 2019; Chan et al., 2020). Until more detailed studies of the diet of the CBL in both Cua Dong and the Sanctuary, it is difficult to know how best to characterise the CBL.

In terms of vegetation and species, there is little reason not to encourage the VHC as a means of linking the two main breeding populations of CBL. The potential benefits of an interconnected population of CBL could be the key to maintaining or even preserving this species. While the vegetation in these areas may not be as pristine as the small segments of primary forest in the centre of the National Park, nor as protected from human interference, the CBL have shown that, like other langur species, they can successfully breed and survive in habitat fragments (Estrada & Coates-Estrada, 1996; Hendershott, 2017; D. Li et al., 2016). Efforts should be made to support this adaptability and maintain or re-instate connections between fragmented groups to support their survival.

While there is a clear gap in our knowledge of the way in which the CBL uses this VHC, we know that the area is used, even if only by a small number of individuals, which is critical in corridor development and success (Beier & Noss, 1998). The port and road in Viet Hai do pose a potential obstacle to the successful connection of the Cua Dong and Sanctuary region. While CBL have been observed to locomote on rocks and occasionally beaches (Hendershott, 2017), roads represent an unacceptable risk to such a Critically Endangered population. The introduction of structures to allow species to cross roads safely, is a common approach to overcome the barrier effect roads can present (B. D. Taylor & R. L. Goldingay, 2010).

It is highly recommended that as part of further study of the VHC is undertaken, consideration of a structure to support movement safely across the VHC port road is prioritised, particularly in light of its potential to connect the two groups of langurs and enhance the viability of the global CBL population (Beier & Noss, 1998; Carrete et al., 2009; Damschen et al., 2006).

4.7 Conclusion

Based on the ecological sampling of the VHC, the region is not significantly different from the CBL habitat in Cua Dong or the Sanctuary. The profiles of the general plant species and food species across the three sites are also not significantly different and the VHC has a similar density of food specimens than the other two sites. The general differences in canopy and vegetation differences between VHC and the CBL habitats, however, may contribute to the low utilisation of the region. MaxEnt modelling suggests that the VHC has only marginal areas of suitability of 60 per cent or greater, restricted largely to the coast. Further study of the Sanctuary is recommended to provide a less biased dataset and to provide greater understanding of the preferences of the CBL.

In the absence of any obvious ecological impediment, it appears that a corridor encouraging an interconnected population will provide greater benefits to the species and its future than a continuation of highly fragmented groups (Ahmed Sadia E., 2014; Beier & Noss, 1998). Further study into the VHC and its usage is critical for the CBL's future and offers a relatively low-cost option to help the species compared to expensive widespread translocation of entire groups (Beier & Noss, 1998). It is recommended that behavioural monitoring of langurs using this region is undertaken to compare activity budgets to the CBL in Cua Dong and the Sanctuary. Differences in CBL behaviour in this region may provide greater insight into its potential as a connecting corridor.

With current fragments used by primates often too small to ensure their ongoing survival (Harcourt & Doherty, 2005), any opportunity to expand the current langur habitat should be embraced (Z. Huang et al., 2017). Thus, it is also recommended that this stretch of potential corridor should be protected against any planned development, similar to the protection given to the Sanctuary habitat even before further study is undertaken, to ensure that the area retains its potential as a region of habitat expansion or as a connection between the two main home ranges. Opportunities for enrichment of the area should also be considered (P.A.B.G. Panagoda & V.P.A. Weerasinghe, 2019) to encourage the use of the corridor with the aim of establishing genetic exchanges between the two breeding populations (Lees et al., 2014).

Part two: *Rhinopithecus avunculus* (Tonkin snub-nosed monkey)

Abstract

The Tonkin snub-nosed monkey (*Rhinopithecus avunculus*) (TSNM) is one of the most endangered primates, with only an estimated 200 individuals surviving in the wild. It has been listed as Critically Endangered by the IUCN since 1996 (IUCN, 2019) and is also listed in CITES Appendix I (CITES, 2019; UNEP-WCMC, 2022). Originally thought to be extinct since 1986 (Russell A. Mittermeier & Cheney, 1987), small populations were rediscovered in Tuyen Quang Province and then again in Khau Ca, Ha Giang Province (Covert et al., 2008; Ratajszczak et al., 1992; Thach, 2009).

Today, due to ongoing hunting, habitat destruction and human development, significant populations are only believed to still exist in Tung Vai, with 42-53 individuals and Khau Ca, with approximately 150 individuals (Dine, 2012; Fauna & Flora International, 2020; Quyet & Covert, 2010). The Tonkin Snub-nosed Monkey Species/Habitat Conservation Area at Khau Ca (Khau Ca), is an island of limestone karst forest of approximately 20.4km^2, which includes a core area used by the TSNM of approximately 10km^2, bordered by three communes and extensive agricultural land (N. X. Dang et al., 2014; Hai, 2008). The population in Khau Ca is not only the largest breeding population in the world, representing 80 per cent of the total population, but is also the only fully protected group remaining in Vietnam (Fauna & Flora International, 2020; C. Schwitzer, Mittermeier, R.A., Rylands, A.B., Chiozza, F., Williamson, E.A., Byler, D., Wich, S., Humle, T., Johnson, C., Mynott, H., and McCabe, G., 2019).

In 2015, it was announced that the Khau Ca National Park would be merged with the larger Du Gia Nature Reserve to the north and northeast to form the Du Gia National Park (An et al., 2018). While these two regions were once a single area of forest, they have become separated through decades of human growth in the region, conversion of land to agricultural land, and the establishment of mines, making the Du Gia Forest potentially unsuitable for the TSNM.

The following chapter will provide an analysis of the TSNM habitat and a sample of the larger Du Gia Nature Reserve to assess potential as an area of future habitat expansion. This provides first insights into the suitability of the Du Gia region as TSNM habitat and assist conservation planning.

Chapter 5 A comparison of the habitat of the Tonkin snub-nosed monkey in Khau Ca and Du Gia National Park, Ha Giang Province.

5.1 Introduction

The endemic primates of Vietnam continue to face ongoing threats from habitat destruction, degradation, and fragmentation as a result of direct and indirect human influence (Arroyo-Rodriguez & Mandujano, 2009; Blair et al., 2011).

The TSNM is the only member of the *Rhinopithecus* genus endemic to Vietnam, with other members of the genus endemic to China and Myanmar (Geissmann et al., 2011; Groves, 2001; Grueter et al., 2017; Yang et al., 2019). While all snub-nosed monkey populations are currently under threat, the TSNM faces the greatest uncertainty as to its future (Anh et al., 2014; N. X. Dang et al., 2014). The fate of the TSNM has been intertwined with decades of human growth and intervention into its habitat, leading to highly fragmented populations across Northern Vietnam (Thach, 2009). By the 1990s, the TSNM was thought to be extinct due to hunting and loss of habitat until its rediscovery by Quyet (2004).

Once believed to inhabit limestone forests across northern Vietnam (Le & Boonratana, 2006), today the largest population of TSNM inhabits a small fragment of limestone karst forest in Khau Ca, Ha Giang Province Northern Vietnam (N. X. Dang et al., 2014; Dine, 2012). This region, the focus of conservation efforts since 2003 (Covert et al., 2008; Quyet, 2014), is an island of primary and secondary limestone karst forest surrounded by three communes and set within an agricultural and urban landscape.

The loss of the TSNM in other areas of Vietnam stems from ongoing damage to their habitats from local human populations, destruction by the development of dams and mines, and deforestation for urban settlement or agriculture (Le & Boonratana, 2006; Martin, 2004; Thach, 2009). Several pockets of populations have been discovered and lost over the past 20 years (Knight, 2019; Le & Boonratana, 2006; Thach, 2009). Today we can be sure of only two sites supporting breeding populations: Tung Vai and Khau Ca in Ha Giang province (Dine, 2012; Thach, 2009).

Khau Ca is home to the largest population of TSNM in the world, with an estimated 150 individuals inhabiting the approximately 21km^2 region of protected forest (Fauna & Flora International, 2020; Knight, 2019). Although this population appears to be growing, mitochondrial (MtDNA) genetic testing suggests that there is very little MtDNA genetic variation within the population, suggesting greater susceptibility to extinction events (Ang et al., 2016). With no significant captive population, this may put the TSNM at greater risk to the effects of disease, natural disasters, and human expansion. The small size of their available habitat will also eventually limit their population growth, if it has not already.

The Tonkin Snub-Nosed Monkey Species/Habitat Conservation Area at Khau Ca (Khau Ca) was established in 2009 (Decision No. 3115/QDUBND) (Dung & Tho, 2015; Quyet, 2014). It is located roughly 300km outside of Du Gia Nature Reserve, within the designated buffer zone of this larger forest (Covert et al., 2008; Thach, 2009).

Several ecological studies have been made of the Khau Ca region since 2004 (Anh et al., 2014; Covert et al., 2008; Quyet, 2014; Quyet, 2004; Quyet et al., 2007), which have been key in providing a baseline understanding of the TSNM habitat. These studies focussed predominately on the diet of the TSNM and phenology of the trees within Khau Ca – an important focus for arboreal primates as it provides clues as to forest productivity and food availability (Anh et al., 2014). However, it only allows for minimal quantification of the wider terrestrial habitat and future food supply. My study builds on this work by surveying the wider vegetation structure to determine the characteristics of the habitat of the TSNM and to understand the overall profile of their habitat.

This opportunity to compare more recent habitat data to baseline data collected during the initial rediscovery period of the TSNM is rare for many of Vietnam's primates, where ecological studies are often limited. While the baseline data for this study is not very old, it does provide a valuable resource to allow an assessment of the change in TSNM habitat over several years. Such a comparison will provide conservation groups with the ability to track the health and composition of the Khau Ca area and assist in their continued monitoring and planning for this highly at-risk species (Pyritz et al., 2010; Y. Zeng et al., 2013). This will not only help to protect the TSNM but also the wider ecosystem of Khau Ca (Kirkpatrick, 1995; Kirkpatrick & Grueter,

2010). It will also continue to contribute to our growing, yet still limited, knowledge base for *Rhinopithecus* (Nüchel et al., 2018).

In 2015, the Vietnamese government announced the creation of the Du Gia National Park (approximately 150km^2), a result of merging the Du Gia Nature Reserve (Du Gia) and Khau Ca Species and Habitat Conservation Area (Tourism, 2015). Since 2008, researchers (Covert et al., 2008) have recommended this linkage partly due to speculation of the potential for Du Gia harbour additional populations of TSNM (Quyet, 2004), which could potentially improve the outlook for the TSNM – however, to date, there has been no observation or identification of TSNM in Du Gia (Le & Boonratana, 2006). There also yet to be a study of the suitability of the Du Gia Forest as a potential habitat for the TSNM.

The amalgamation of Du Gia and Khau Ca into the Du Gia National Park (Figure 5.1), established by the Vietnamese government in 2015 (2286/BVHTTDL-DSVH), was intended to promote both protected areas, reduce administration and promote ecotourism to the area (pers comm. Anon). Ecotourism within Du Gia already exists. It is a popular destination for forest walks and excursions for domestic travellers.

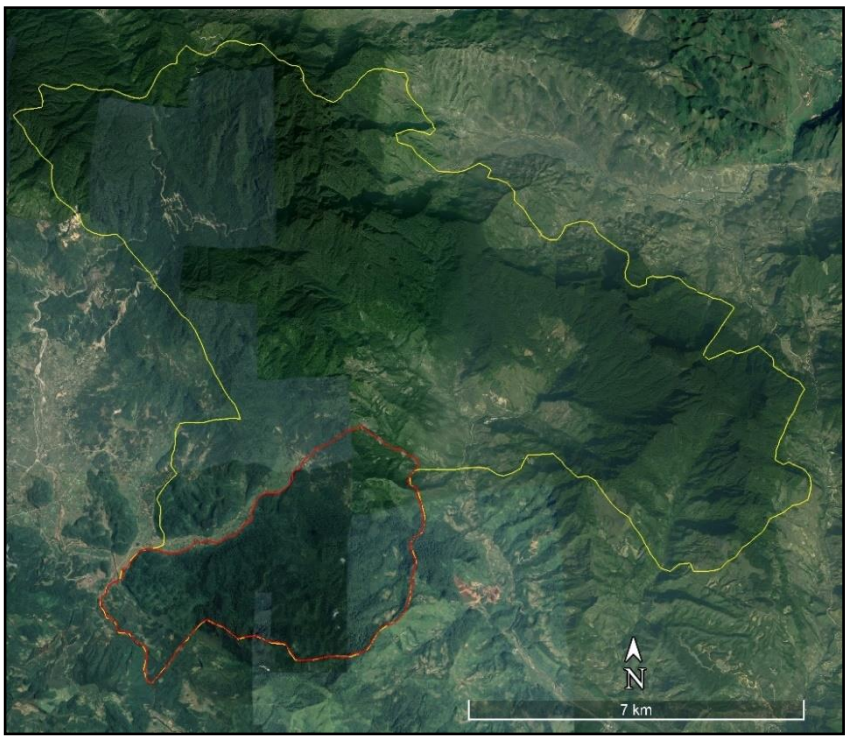


Figure 5.1 Satellite image of the boundary of the Du Gia National Park (yellow) with Khau Ca (red) within. Satellite image: Google Earth Pro (Airbus, 2025; CNES/Airbus, 2025; Max ar Technologies, 2025).

Khau Ca and Du Gia are reportedly linked by a small corridor and buffer zone (Truong & Linh, 2017). In 2014 (N. X. Dang et al., 2014) noted that a strip of limestone forest within Du Gia could be a suitable for corridor for the TSNM, to move between the two areas. Further study of this region is critical for the future of the TSNM. In particular, it is necessary to understand the vegetation profile of the Du Gia region to understand if it is capable of supporting the TSNM (Gardner et al., 2007). The aim of this chapter is to compare the ecological profiles of Khau Ca to the larger Du Gia protected reserve to, for the first time, provide a measure of its suitability as habitat for the TSNM. By comparing Du Gia to Khau Ca, we can better determine how different the primary forests of the areas are to each other or to any linking corridors. These results will have conservation implications as they will allow conservation groups and the Vietnamese local government to determine how successful the merger might be for the future of the Khau Ca TSNM population.

I hypothesise that Du Gia will have a similar profile to the Khau Ca habitat as the two regions were historically joined and part of the same primary forest (Kempinski et al., 2009). Due to the close presence of humans and farmland around Khau Ca, I also predict that the corridors joining the two areas will be of poorer quality exhibited by less contiguous canopy, fewer trees and lower species richness and diversity.

5.2 Methods

5.2.1 Study species

The global population of the TSNM is estimated to contain 200 individuals (Fauna & Flora International, 2020). The largest breeding population of approximately 150, is located in the limestone karst forest island of Khau Ca. Based on a census of the TSNM in Khau Ca in 2017, the population here has seen an increase of 25 per cent (Fauna & Flora International, 2020). This growth is encouraging for the Critically Endangered species; however, genetic analysis suggests that while births have been observed over the last decade, the mitochondrial genetic variability of the group is the lowest reported for a wild population of primates (Ang et al., 2016). The closest known population of the TSNM to Khau Ca is an estimated 42-53 individuals over 40 km away in Tung Vai Forest, Quan Ba District, Ha Giang Province (Dine, 2012; Knight, 2019). With the total wild population of TSNM highly fragmented and with no chance of natural migration between these groups, the ongoing protection and study of TSNM is critical.

The TSNM is known to historically overlap with the Endangered Francois's langur (IUCN, 2019), however today the only main point of contact between the two species is thought to be in Na Hang Nature Reserve, where both may still be locally extant (Paul Insua-Cao, 2012). Within Khau Ca, the TSNM are believed to be sympatric with two species of loris and potentially three species of macaques identified by N. X. Dang et al. (2014). While Thach (2009) suggests that the TSNM actively attack macaques that encroach upon their territory, macaque groups were heard and observed several times throughout this study and no interactions with the TSNM were witnessed.

5.2.2 Study site

Khau Ca Protected Zone (Khau Ca) is located in Ha Giang Province in northwest Vietnam (22˚49' - 22˚52' N and 105˚05' - 105˚09'E). It consists of approximately 21 km^2 of primary and secondary forest, roughly 300km outside Du Gia Nature Reserve, but considered within the buffer zone of this forest (Figure 5.2) (Covert et al., 2008; Thach, 2009). Khau Ca currently exists as an island of forest surrounded by agricultural land, plantations, and villages (Kempinski et al., 2009), 15km east of Ha Giang city. Three communes border the forest: Minh Son and Yen Dinh in the Bac Me District, and Tung Ba in the Vi Xuyen District (N. X. Dang et al., 2014; Hai, 2008).

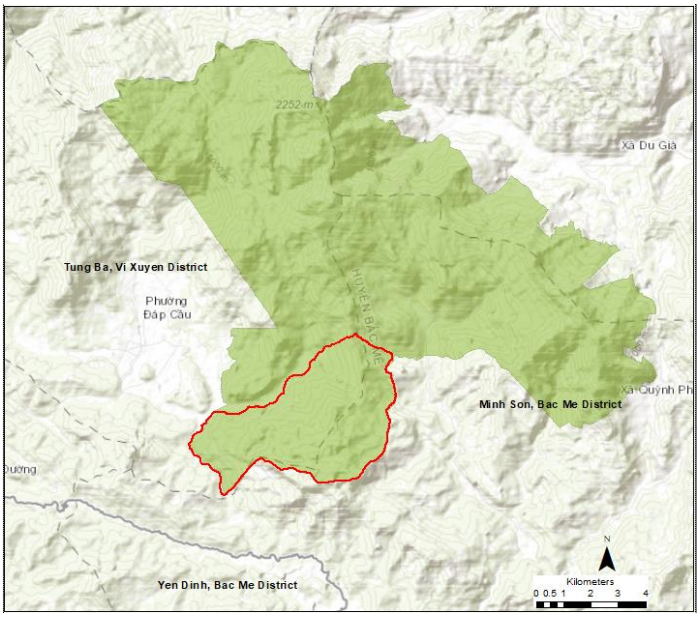


Figure 5.2 Map of Khau Ca as part of Du Gia National Park Red outline indicates Khau Ca boundary. Green indicates proposed Du Gia National Park including Khau Ca. Three surrounding communes: Minh Son, Bac Me District; Yen Dinh, Bac Me District; Tung Ba, Vi Xuyen District. Base map: Esri (2021), proposed national park polygon: UNEP-WCMC (2023) .

Public access to Khau Ca is prohibited and the TSNM are regularly monitored by community rangers employed by the Ha Giang National Park and supported by FFI. Part of the core forest was once used as grazing land for farms, however, today the entire area is protected from farming and hunting. Two small farms are located just outside the Khau Ca boundary, which results in the occasional movement of goats into the core area (Figure 5.3).

Figure 5.3 Regeneration of Khau Ca and surrounding farmland. Top left and right: regenerating former farmland within Khau Ca core zone. Bottom left and right: farm and goats bordering Khau Ca. Photos: K. Apthorp, 2016.

Khau Ca has been the main focus of TSNM conservation for the last 14 years (Quyet et al., 2020). Locating and observing the TSNM within Khau Ca is challenging due to the difficult limestone terrain and the shyness of the TSNM (Boonratana & Canh, 2013; Hai, 2008). Despite this, the area has been the subject of previous ecological and behavioural surveys (Anh et al., 2014; Hai, 2008, 2011; Quyet, 2014; Quyet et al., 2007).

Prior to its amalgamation, Khau Ca bordered the southwest edges of the Du Gia Nature Reserve (NR) (22°48'30''-22°58'00''N; 105°3'00''-105°20'30''E). Du Gia NR was established in 1994 and includes approximately 117.95m^2 of protected primary forest (N. X. Dang et al.,

2014) across portions of Yen Minh district, Bac Me District and Vi Xuyen district, in Ha Giang Province (Birdlife International, 2001). Only small areas in the centre and east of the reserve are limestone, with the rest largely sandstone (N. X. Dang et al., 2014; Birdlife International, 2001). As a result, the reserve supports limestone forest, montane evergreen forest and lowland evergreen forest (Birdlife International, 2001).

To date, very little research has been undertaken within the Du Gia (Covert et al., 2008; N. X. Dang et al., 2014), however, some TSNM researchers have speculated that TSNM may persist in the area, as Khau Ca was historically part of the larger Du Gia Forest (Kempinski et al., 2009). A 2013 survey (N. X. Dang et al., 2014) of Du Gia identified 58 species of mammals in the region. This included a number of members of Carnivora including three species of cat species: *Catopuma temminckii* (Asian golden cat), *Prionailurus bengalensis* (the leopard cat) and *Neofelis nebulosa* (the clouded leopard). Other carnivores included civets, mongooses, and weasels identified by through specimens, interviews or traces of footprints or faeces; (N. X. Dang et al., 2014).

Although N. X. Dang et al. (2014) did not find evidence of TSNM during the Du Gia survey, six other primates were identified through direct observation, poached specimens or via interview with locals. These included the Francois' langur, three macaque species (*Macaca arctoides*, *Macaca assamensis* and *Macaca mulatta)* and two loris species (*Nycticebus bengalensis* and *Nycticebus pygmaeus*) (N. X. Dang et al., 2014). Primate species were identified through collection of specimens, hunting specimens or observation (N. X. Dang et al., 2014).

Due to the size and limitations in accessing the centre of Du Gia, sampling of the forest was undertaken in Minh Son commune (22°50'56" N, 105°12'24"E), Bac Me District, Ha Giang. The patch of Du Gia Forest sampled (22°53'5" N, 105° 10' 40" E) was approximately 5.5 km north-east of Khau Ca. For the purposes of this study, this site is referred to as Du Gia.

Data collection for this study was undertaken between September 2016 and October 2016 in an attempt to avoid disruptions from extensive rain or the threat of snow later in the year. Temperature averages were captured for Ha Giang, the closest town to the study site (Table 5.1).

Table 5.1 Average temperature, rainfall and humidity in Ha Giang during data collection

Month (2016)	Average temperature (˚C)	Average rainfall (mm)	Average humidity (%)
September	18	55.55	86
October	19	32.18	87

All weather information for Ha Giang is collected from 'World Weather Online' https://www.worldweatheronline.com/lang/en-au/ha-giang-weather-averages/vn.aspx

5.2.3 Interviews

During fieldwork, thirteen interviews were undertaken in Tung Ba, the closest commune to Khau Ca, and communes along the border of Du Gia Nature Reserve in October 2016 with the support of FFI translators. Interviewees were selected with assistance from FFI translators, who identified candidates based on established relationships, and with regard to the following criteria that they should be adults, residents of the Communes bordering Khau Ca, and a cross section from the surrounding Communes.

Information collected included historical and current encounters with TSNM and macaques, forest health and changes, local use of the forest, and awareness of the TSNM conservation efforts. To establish reliability of the information collected, only information that was common across multiple interviews was reported unless otherwise noted, as per Fan et al. (2011). Unlike Fan et al. (2011), information was not confirmed across interviews to avoid influencing responses (interview questions: Appendix 1.1).

Ethics approval was granted by the Australian National University Human Ethics Committee (protocol number: 2015/761) for the period of 1/2/2016 to 1/2/2018 to undertake interviews with community members local to each of the national parks under investigation.

5.2.4 Ecological sampling

Ecological sampling in Khau Ca and Du Gia for this study, was conducted using 12 square ecological plots at each site (Figure 5.4), across three habitat types: slopes, valleys and ridges (Table 5.2). Each plot measured 10x10m. The dangerous nature of the limestone karst within Khau Ca made it necessary to keep the plots small as demonstrated in previous studies of TSNM by Hai (2008).

When establishing plots in Khau Ca, they were placed within the core area used by the TSNM as advised by rangers responsible for monitoring the TSNM. In 2002, a 10km trail system was established covering the day and home homes ranges of the TSNM within Khau Ca (Covert et al., 2008; Kirkpatrick, 1995; Quyet, 2014). Four phenology transects (named A to D), each measuring 1 km in length and four metres wide, were also established along the trails to enable regular sampling while minimising disruption to the surrounding forest (Covert et al., 2008). These transects and additional plots were regularly sampled and supported further research undertaken by Quyet (2014).

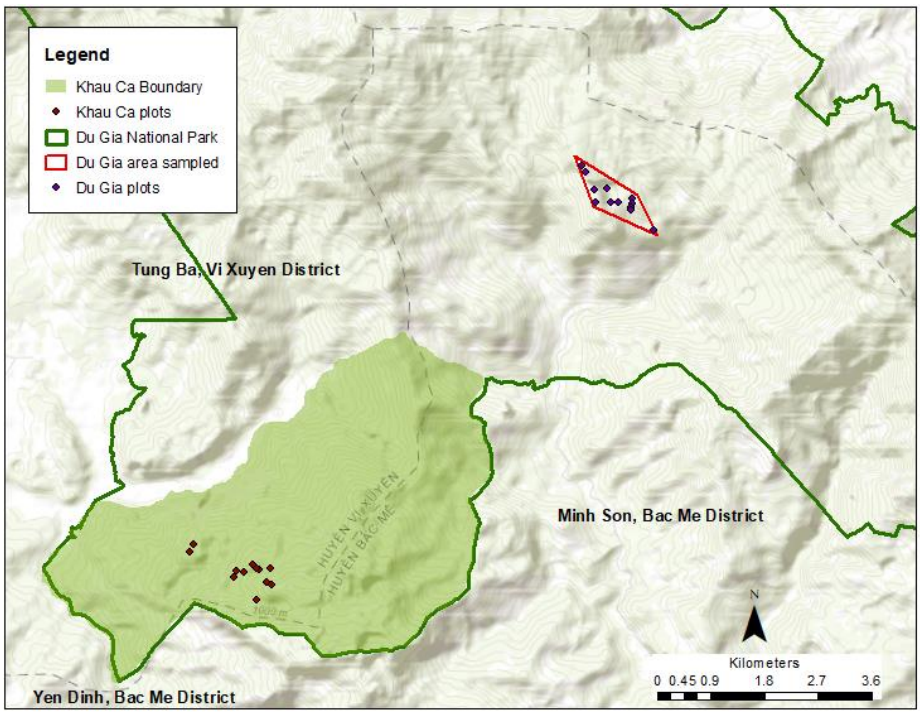
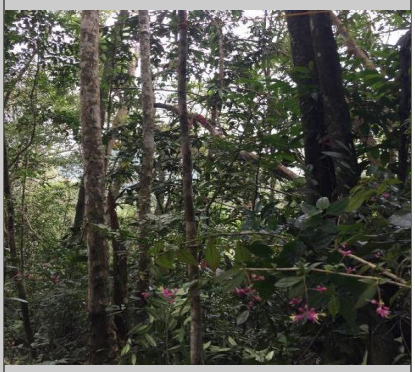


Figure 5.4 Location of plots within Khau Ca and Du Gia

Using a map setting out the trail system, I identified areas representing valley, slope and ridges, and randomly selected plot positions. Due to the difficulty in accessing deeper areas of Khau Ca and to limit disruption to the forest, plots were randomly placed adjacent to the trails. By locating plots within five to 10 metres adjacent to the trails/transects, I could ensure that damage to vegetation was reduced – a consideration to be made when undertaking ecological sampling in the habitats of at-risk species (Covert et al., 2008). In instances where the chosen location for plots was inaccessible due to the nature of the limestone, plot locations were shifted to nearest safe area, while still sampling the designated 'plot type' vegetation.

Table 5.2 Vegetation stratum types identified in the TSNM habitat

Habitat type	Description	Number of plots sampled	Example
Valley	Valley floor.	4	
Slope	Between 400- 1300m in elevation.	4	
Ridge	Ridge and summits of limestone, typically 900m – 1300m in elevation.	4	
Ex-agricultural	Valley floor outside the areas used by the TSNM – formerly farmland. Vegetation is largely scrub and grass as the area regenerates.	n/a	

Photos: K. Apthorp, 2016.

Although previous studies had also established plots within Khau Ca (Covert et al., 2008), the ongoing use of these sites and the focus on tree phenology meant that these plots were not suitable for sampling all stems within the plot due as the lower levels of vegetation were likely to have been trampled.

A similar approach was taken with the plots established within the Du Gia forest. Access was granted to an area of the forest with the guidance of a National Park ranger. Plot sites were selected randomly according to the three plot types, 5 to 10 metres from the established trails to minimise the impact of the trail and the impact of the team on the wider forest.

All stems were identified to species level by Dr Vu Anh Tai, a botantist from the Department of Bio-Geography, Institute of Geography Vietnamese Academy of Science and Technology. Dr Tai had extensive experience identifying species within Khau Ca and Du Gia, having participated in several research studies previously, including as part of research undertaken by Quyet (2014).

I recorded the DBH for all trees and shrubs where DBH≥2cm using a DBH measuring tape or callipers. Crown size for all trees and shrubs where DBH≥2cm and height > 1m, was determined by estimated diameter measurements taken along the maximum and minimum axes of the tree crown. Where the diameter of lianas was greater than 2cm, this was also recorded.

Heights of tree canopies were independently estimated by me and Dr Tai to the nearest 50cm before results were compared. In rare instances where measurements disagreed significantly, a third measurement by a clinometer was attempted. While the clinometer was used where possible, the difficulty of the terrain often made it impractical to use. Estimation of canopy heights follows previous protocols used for surveys (D. Li et al., 2006). Canopy coverage was determined using a qualitative assessment of the percentage of the total coverage within each plot by tree crowns with zero per cent indicating no canopy present in the plot and 100 per cent indicating full coverage with high density allowing little light to reach the plot floor. This is necessarily a qualitative estimate as tree crowns are not uniform in the density of their leaves or coverage within the circumference of their crowns (Bonham, 2013).

As established in the protocols in Chapter 3, Section 3.3, I recorded the composition and density of all vegetation layers within each plot (Appendix 1.2). The understory was divided into four parts: a mat layer, comprising of small herbs, plants and seedlings measuring ≤20 cm; a shrub layer comprising small plants, ferns and seedlings measuring between 20 cm and 1.5m; and large shrubs comprising larger plants, shrubs and saplings measuring between 1.5m and 2m, or above where DBH<2cm (Smith et al., 2012); and a canopy layer estimated for trees and shrubs where DBH≥2cm and deemed to be contributing to the canopy.

Using these layers, I estimated a general vegetation density based on a scale of one to five (Stickler & Southworth, 2008), with one being easily passable and absent of significant visible vegetation beyond small herbs in rock crevices, and five being largely impenetrable due to vegetation (Appendix 1.3). As plots may have patches of impenetrable vegetation due to dense shrubs and lianas, as well as empty patches, an average of vegetation density based on ease of access around the plot was taken. To obtain a full picture of the species composition of the TSNM habitat, the percentage of the liana cover was also recorded (G. Hu, 2011; Stanford, 1991).

A similar scale was used to determine topographic complexity (Appendix 1.4), where one indicated no visible limestone within the plot and five indicated non-uniform and layered limestone sheets, making the plot difficult to move around, and requiring some climbing within the plot.

I also recorded environmental variables such as slope and elevation using a range finder and GPS. I collected GPS coordinates to allow replication in future studies, with the southeast corner acting as the GPS designator. Due to the inaccuracy of GPS that can occur in limestone terrains (K. A. Phillips et al., 1998), some GPS recordings were corrected post-field work using Google Earth Pro.

5.2.4.1 Study limitations

5.2.4.1.1 Differences to earlier studies

As my study design included trees and all stems within plots, the number of plots is less than in previous studies where only trees were sampled. This will provide a clearer understanding of the vegetation profile of Khau Ca, capturing all levels of the TSNM habitat. This level of

detail has not previously been undertaken in previous studies of the TSNM habitat (Covert et al., 2008; Hai, 2008; T. M. Hoang & Covert, 2010; Quyet et al., 2007; Thach, 2009). As a result, sample sizes were smaller to accommodate the extra level of detail. Time available to sample the two sites was also significantly reduced due to issues around accessibility.

While earlier studies had lower limits of 10cm and 6cm when recording DBH, this study's lower limit was 2cm. Sampling trees with a DBH above 10cm misses out on capturing seedlings and new tree growth that will provide conservation groups with a clearer understanding of the health and structure of the Khau Ca region. This information is important when considering the long-term suitability of the region to continue to support the Khau Ca.

5.2.4.1.2 Corridor and buffer zone sampling

My initial planning included ecological sampling of the corridor described as connecting the Khau Ca and Du Gia forests (N. X. Dang et al., 2014), however, on the ground observations and discussions with Ha Giang national park officials revealed that this corridor no longer existed in a meaningful way.

Between Khau Ca and the Du Gia area sampled, the absence of any potential corridor was abundantly clear. This particular region is inhabited by approximately 33 households, including H'Mong families. The area between the two forests has been farmed for over 40 years, with key crops including corn, cassava and livestock (Figure 5.5). This represents one of the closest points between Khau Ca and Du Gia, with only 5-6km separating the two forests, however due to farmland, the only remaining forest remains on the summits of the surrounding hills and ridges.

Other potential connection points between the two areas are also highly degraded. During sampling in Du Gia, officials from the National Park for Ha Giang Province made a trip to the remaining corridor area and reported that due to extensive cardamom plantings, the corridor area had largely been converted into cropland and as a result, the biodiversity corridor between Khau Ca and Du Gia no longer existed (pers comm. Mr Tue). Regeneration of this area is expected to take many years, and without careful planning may not be appropriate for passage by the TSNM. As a result, no sampling of a corridor connection was undertaken as well established natural connections reportedly no longer existed at the time of the study.

Due to the separation between Khau Ca and Du Gia, no additional species distribution modelling was undertaken.

Figure 5.5 Example of farmland within the corridor between Khau Ca and Du Gia Top left and right: deforested slopes and ridge tops used as farmland. Bottom left: rice fields in the valleys and slopes. Bottom right: looking from corridor back to Khau Ca Forest. Photos: K. Apthorp, 2016.

5.3 Data analysis

5.3.1 Habitat characteristics

To establish the general habitat characteristics of each site and plot type, several vegetation measures were calculated including the species richness, species diversity, tree area, basal area, average DBH and density of all vegetation types (all stems/m^2), and tree density (tree stems/m^2) (Appendix 3.1.1) as per the protocol in Chapter 3, section 3.4.1.

I used a linear model to explore the relationship between my ecological plots and various outcomes of the variables. To understand differences between plots at each site, I used a one-way ANOVA from the linear model to assess significance of effects. To understand differences

between sites, I used a two-way ANOVA. Estimated marginal means based on the linear models were then calculated and compared in a post hoc analysis employing a Tukey adjustment to the p-values.

I also undertook a visual inspection of residuals and determined that no transformation was required of variables as residual plots sufficiently satisfied normality constraints, noting a small sample size. Results were reported where $p<0.05$.

Habitat characteristic calculations were carried out manually. General linear models, ANOVAs and estimated marginal means calculations were carried out using the VEGAN package in R (4.2.1).

5.3.2 Plant species analysis

All models and calculations were carried out using the VEGAN package and visualisations using GGPLOT2 package in RStudio (2022.07.2) with R (4.2.1).

5.3.2.1 All plant species

Using the protocols established in Chapter 3, Section 3.4.2.1, I used the VEGAN package and METAMDS function in R to undertake NMDS ordination analyses and graphically represent relationships between (1) all plant and tree communities within the Khau Ca plots; (2) the plant and tree communities within the Du Gia plots; (3) the plant communities between Khau Ca and Du Gia. I also used a PERMANOVA using a Bray-Curtis dissimilarity distance matrix to determine whether differences observed in the NMDS were significant.

I applied a multiple regression of intrinsic vectors using the function ENVFIT to determine which species most significantly contribute to plant communities both within and between the two sites.

5.3.2.2 Food species

To understand the abundances and food species across the current TSNM habitat in Khau Ca and in Du Gia, I repeated the same NMDS ordination analysis, PERMANOVA and multiple regression of intrinsic variables analysis using food species captured within the plot sampling for: (1) TSNM food species across plot-types; (2) Du Gia food species across plot-types; and (3) food species comparison between the TSNM and Du Gia.

Collection of food species consumed by the TSNM was beyond the scope of this study due to limitations around time, staff availability and finances, which did not allow for prolonged access to the site to capture long-term food identifications. Previous studies of the diet of the TSNM have identified 156 species of plants from 106 genera consumed (Appendix 3.3.1) (Covert et al., 2008; Hai, 2011; Quyet, 2014; Quyet et al., 2007).

Despite sampling subsections of previously sampled areas of the habitat, only 11 species recorded as food species of the TSNM were captured within the plots of this study, yet many of the same genera were captured. This could be due to several reasons, including differences in diet identification methods across previous studies. Of the five previous studies encompassing food species, there was very little overlap in the species identified as consumed by TSNM. It could also be due to misclassification of species of the same genera in the field in this study, or due to the methods employed in previous studies where food observations were predominately made from a distance due to difficult terrain, and to reduce disturbance of the TSNM.

Thus, to compare the presence of diet plants for the TSNM, I have used a genera-level comparison (Appendix 3.3.2). This approach was also used by Quyet et al. (2007) when considering food genera consumed by the TSNM. While this may limit the strength of the comparison, so little is understood of the TSNM and its habitat, that it still provides a novel and useful comparison for future studies of the TSNM.

5.4 Results

5.4.1 Interviews

Interviewees came from a range of occupations; however, a majority were connected to the national park or conservation work in some way. In conducting interviews I attempted to cover a cross-section of the local community (Table 5.3), however, it was difficult to contact people without connection to local governance or the national parks, thus the sample may not be an accurate representation of the local population.

Seventy-five per cent of interviewees have lived in their villages since birth but only 50 per cent had seen a TSNM in the wild. All sightings of TSNM have only occurred within known sites

such as Khau Ca or in Na Hang Province – there have been no sightings from the Du Gia Forest area. Over 58 per cent of interviewees have seen macaques in the region, particularly around their villages raiding crops and fruit trees for food, however several participants note that this behaviour has declined in recent years as macaque sightings had become rarer outside of Khau Ca.

Table 5.3 Demographics of interviewees from communes surrounding Khau Ca

	Demographics	Response, % (N=13)
Sex	Male	76.9
	Female	23.1
Years living in local area	0-15 years	23
	16-30	7.7
	31-45	7.7
	46-60	23
	61-75	7.7
	Unknown*	30.7
Occupation	Linked to National Park or TSNM Conservation	30.8
	Teaching	15.4
	Farming	15.4
	Local governance	38.5

*Lived in area since birth but exact age unknown. Estimated all to be over 35 years of age.

The condition of forests within Khau Ca and Du Gia is generally reported to be improving because of protections and restoration efforts, although while cultivation activities had ceased in Khau Ca, some cultivation of other adjacent forest areas for business (interpreted as cash crops) continues. Reports from national park officials differ over the status of the buffer zone: some community patrol members suggest that forest and vegetation remained within the buffer zone, however officials involved with TSNM protection report that any remaining connection or buffer zone could not support TSNM to travel through as a result of cardamom and other cash crop farming. The presence of other forest wildlife is reported to have increased since protections were imposed.

While some interviewees indicate that the climate had improved as a result of forest restoration and plantations have increased around the Du Gia-side of the buffer zone, most suggest that temperatures in recent years have become more irregular, with hotter temperatures in summer, colder in winter, and unpredictable rain patterns.

The conservation efforts at Khau Ca are predominately considered positive, however several interviewees noted that the cessation of cultivation within the area has impacted incomes and that greater financial support for local families should be increased and more evenly spread across the community, particularly around the buffer zone. Generally, this is followed by a suggestion that ecotourism in the area could improve the financial position of local communities. Some participants also suggested that the Khau Ca region was not secure at night, allowing people to enter to collect forest resources unrelated to the TSNM.

The merging of the Khau Ca and Du Gia Nature Reserve into a national park is widely considered a positive opportunity to reduce government costs and improve funding, however, those more closely involved with the TSNM conservation effort suggest that the Du Gia forest was inferior and could not support TSNM, even if a viable corridor remained, which by all accounts it no longer did in any meaningful way. Furthermore, the presence of mines around the edges of Du Gia in Minh Son was noted as a major risk to the health of the forest and TSNM future.

5.4.2 Khau Ca habitat characteristics

5.4.2.1 Generalised linear model, ANOVA and estimated marginal means analysis of Khau Ca

For the ANOVA analysis, I compared the vegetation characteristics measured within the ecological plots. The ANOVA analysis (Appendix 3.1.2) shows that elevation, topographic complexity, slope, species density, and percentage of large shrub cover has significant differences across the three plot types within the Khau Ca site.

The estimated marginal means analysis (Appendix 3.1.3) shows topography of Khau Ca is one of extremes, with significant differences ($p<0.05$) in the elevation of valleys (695m ±58.60) utilised by the TSNM compared to the ridges (974m ±58.6, $p=0.02$). Slope plots (810m ±58.60) do not significantly differ from either valley or ridge plots in terms of elevation. The slope of valley plots (5.8 degrees ±5.39) are also significantly flatter than both slope plots (33.80 degrees ±5.39, $p=0.01$) and ridge plots (27 degrees ±5.39, $p=0.05$). Valley plots within the TSNM habitat are also characterised by significantly less limestone complexity (1.5 ±0.67) than slope plots (3.5 ±0.67, $p=0.03$) but not ridges (3 ±0.67, $p=0.12$).

In terms of vegetation characteristics, valley plots have significantly greater species densities (4.51 ±0.66) than slope plots (2.54 ±0. 66, p=0.04), while ridge plots (3.78 ±0.66) fall between the two. Valleys also exhibit significantly greater percentages of large shrub coverage (35 ±9.54) than slope plots (6.25 ±9.54, p=0.04). Slope plots have significantly greater percentage liana coverage (4 ±0.601) than both valley plots (1 ±0.601, p=0.02), and ridge plots (1 ±0.601, p=0.04).

The species richness and species diversity of valleys is generally lower than that of both slopes and ridges, however, the density of species is much higher than both other plot types. While the density of trees within the valleys is lower than that of slope plots and ridge plots, valleys exhibit much higher densities of mat, shrub, and large shrub coverage. Despite possessing a lower tree density than other plot types, the trees within valleys are larger, with greater average diameters, greater canopy coverage and greater total basal area, suggesting that the trees are more established than those found on slopes or ridges.

5.4.2.2 Khau Ca Plant species analysis

5.4.2.2.1 Plant species composition in Khau Ca

A total of 4326 stems from 29 species and 82 families were identified across all plots sampled in Khau Ca (Appendix 3.2.1). Ridge plots have the largest number of unique species (n=55) compared to both valley (n=30) and slope (n=31) plots. The most commonly found species across all plots is the shrub *Psychotria tonkinensis* (n=253), a shrub native to Vietnam. The top ten most common species found within Khau Ca (Table 5.4) represent 34 per cent of all stems and are all low-lying shrubs, herbs and grasses.

Table 5.4 Top ten species found in Khau Ca plots

Species	Ridge occurrences (n)	Slope occurrences (n)	Valley occurrences (n)	Total occurrences (n)
Psychotria tonkinensis	11	15	227	**253**
Elatostema monandrum	152	22	27	**201**
Aspidistra typica	43	5	134	**182**
Adiantum caudatum	0	0	172	**172**
Asplenium normale	48	12	63	**123**
Diplazium maximum	56	22	38	**116**
Asplenium confusum	3	28	83	**114**
Arundinaria sat	103	0	0	**103**
Phlogacanthus colainae	0	0	98	**98**
Begonia caobangensis	25	37	35	**97**
Total	**441**	**141**	**877**	**1459**

Khau Ca Ridge plots

Ridge plots have the greatest species richness with 123 plant species identified from 1510 stems. Ridge vegetation is largely characterised by bamboo, ferns, shrubs, epiphytes and tree species. The most frequently occurring species is the herb, *Elatostema monandrum* (n=152) (Table 5.5).

Table 5.5 Top ten species identified within Khau Ca ridge plots

Species	Occurrence (n)	Description*	IUCN Red List Status
Elatostema monandrum	152	Herb	NE
Arundinaria sat	103	Bamboo	NE
Neocheiropteris sapaensis	70	Fern	NE
Liparis macrantha	58	Orchid	NE
Allophylus caudatus	57	Small trees or shrubs	NE
Garcinia fagraeoides	56	Tree	NE
Diplazium maximum	56	Fern	NE
Psychotria montana	52	Shrub	NE
Asplenium normale	48	Epiphyte	NE
Aspidistra typica	43	Shrub	NE
Total	**695**		

*Descriptions taken from Flora of China Project (2020); POWO (2022)

Khau Ca Slope plots

Slope plots contain 114 species from 1014 stems. Slope plot vegetation is largely characterised by shrubs and epiphytes. The most frequently occurring species (Table 5.6) is *Aglaonema*

siamense (n=51), found throughout south-east Asia and classified by IUCN Red List as a species of Least Concern due to logging and clearing of trees for agriculture (Allen, 2011).

Table 5.6 Top ten species identified within Khau Ca slope plots

Species	Occurrence (n)	Description*	IUCN Red List Status
Aglaonema siamense (syn. A. simplex)	51	Shrub	LC
Antrophyum callifolium	39	Epiphyte	NE
Asplenium nitidus	39	Fern	NE
Diospyros sp.	38	Tree	NE
Begonia caobangensis	37	Shrub	NE
Lasianthus hookeri	33	Large Shrubs	NE
Phlogacanthus annamensis	30	Flowering shrub	NE
Dipteris chinensis	29	Shrub	NE
Asplenium confusum	28	Epiphyte	NE
Colocasia gigantea	28	Shrub	NE
Total	**352**		

*Descriptions taken from Flora of China Project (2020); POWO (2022)

Khau Ca Valley plots

There were 98 species identified within the valley plots from 1802 stems; the lowest number of species but greatest number of individual stems found in any of the three plot types. Valley vegetation is characterised by shrubs and epiphytes (Table 5.7), and the most frequently identified species is the shrub *Psychotria tonkinensis* (n=227). The top ten species in valley plots represent over 58 per cent of all stems identified.

Table 5.7 Top ten species identified within Khau Ca valley plots

Species	Occurrence (n)	Description*	IUCN Red List status
Psychotria tonkinensis	227	Shrub	NE
Adiantum caudatum	172	Epiphyte	NE
Aspidistra typica	134	Shrub	NE
Phlogacanthus colainae	98	Shrub	NE
Ophiorrhiza japonica	96	Small shrub	NE
Asplenium confusum	83	Epiphyte	NE
Alpinia tonkinensis	76	Small shrub	NE
Asplenium normale	63	Epiphyte	NE
Asarum caudigerum	55	Herb	NE
Phlogacanthus annamensis	46	Flowering shrub	NE
Total	**1050**		

*Descriptions taken from Flora of China Project (2020); POWO (2022)

5.4.2.2.2 Non-metric multi-dimensional scaling analysis of Khau Ca plants

The non-metric multi-dimensional scaling analysis of all plant species found in Khau Ca was undertaken in two dimensions and a Wisconsin double standardisation was applied to standardise the abundance values. A square root transformation was also applied to reduce the impact of high abundances over unique counts before applying a Bray Curtis dissimilarity distance to the model. The best solution was reached in 20 runs and returned a stress value of 0.144, which is considered suitable as it fell below 0.20.

Based on the abundances of species across the plot, there is a large overlap of all plot types (Figure 5.6). The slope plots group together with a narrow spread, however there is overlap with ridge plots due to similarity with the first (KCR1) and third (KCR3) ridge plots. Slope plots also overlap with valley plots due to similarity with the plant community within valley plot 1 (KCV1). Based on the confidence ellipses, ridge communities have the largest variation.

A PERMANOVA shows that there is no significant difference between the three plot types (R^2=0.20, F=1.16, P=0.16) based on their plant abundances and compositions. This suggests that despite the variation observed, they are quite similar in composition.

Applying the intrinsic species vectors reveals that there are twelve species contributing significantly ($p<0.05$) to the composition of the NMDS ordination. *Stephania rotunda* (p=0.026), *Vernica montana* (p=0.009), *Illicium parvifolium* (p=0.009), *Liparis macrantha* (p=0.009*), Garcina fageoides* (p=0.002), and *Sinosideroxylon wightianum* (p=0.026) all have negative gradients and are associated with ridge plot plant compositions. *Ficus villosa* (p=0.035) and *Syzygium zeylancium* (p=0.027) have positive gradients and are also associated with ridge plots. Lasianthus hookeri (p=0.046) and *Sterculia lanceolata* (p=0.021) have negative gradients and are associated with slope plots. *Lithocarpus sp*. (p=0.037) is associated ridges and valleys, but particularly typical of valleys.

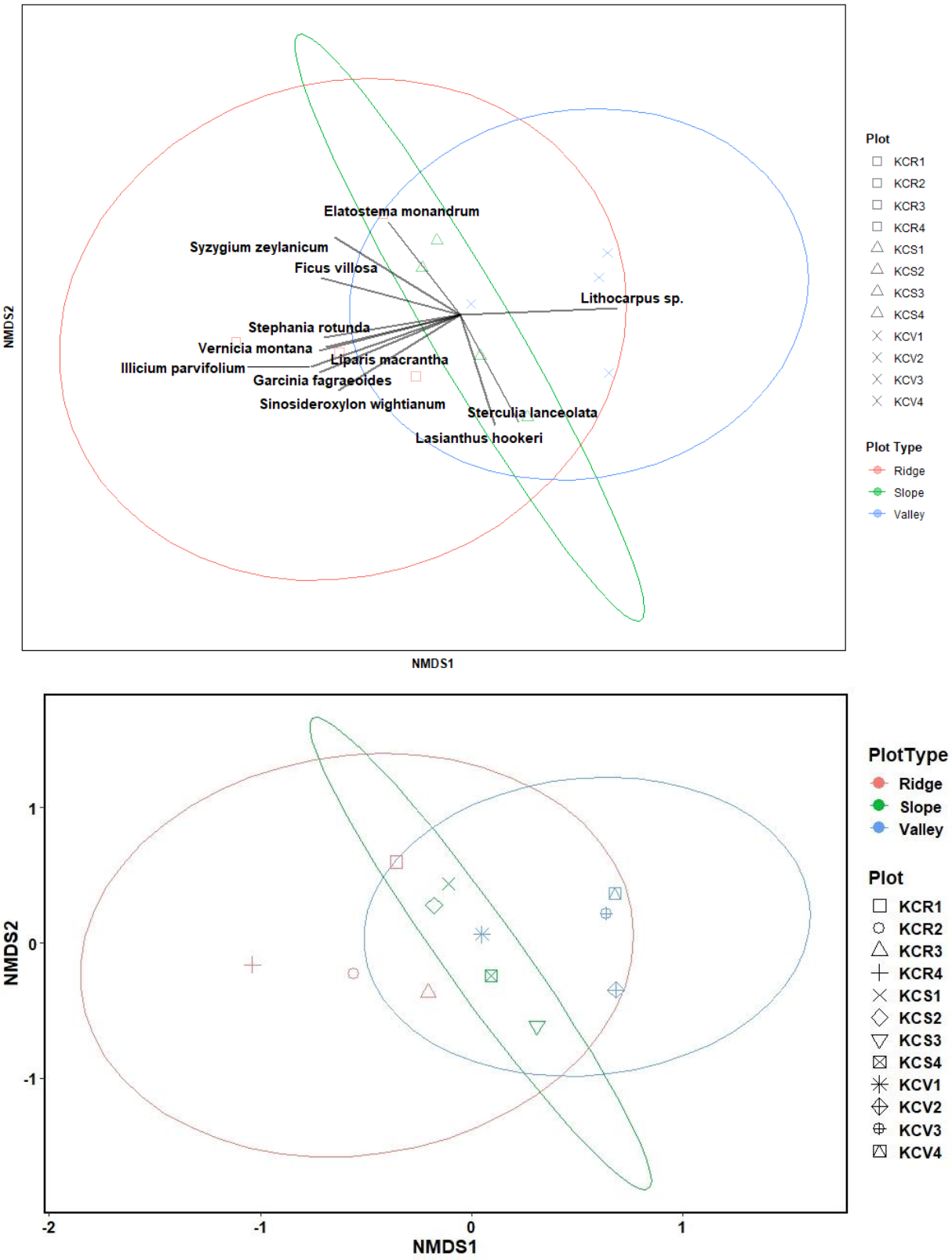


Figure 5.6 NMDS of plants in Khau Ca. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors.

5.4.2.3 Khau Ca Trees and NMDS analysis

Eighty tree species from 42 families were identified in Khau Ca plots from 296 tree stems counted across the twelve plots (Appendix 3.2.2). Eleven species were shared across all three plot types. The most frequently occurring tree species (Table 5.8) is *Polyalthia laui* (n=21) found predominately in Vietnam in forests on slopes (Flora of China Project, 2020). Only one species is listed on the IUCN Red List, *Aphanamixis polystachya* assessed as Least Concern. While no direct threats have been assessed for this species, its timber is widely used in construction (Barstow, 2018).

Table 5.8 Top ten tree species identified within Khau Ca plots

Species	Ridge occurrence (n)	Slope occurrence (n)	Valley occurrence (n)	Total
Polyalthia laui	14	6	1	21
Villebrunea integrifolia	10	5	0	15
Diospyros buxifolia	2	5	5	12
Phlogacanthus annamensis	2	0	9	11
Garcinia fagraeoides	7	3	0	10
Wendlandia laotica	7	1	1	9
Psychotria rubra	5	0	4	9
Aphanamixis polystachya	2	4	2	8
Olea rosea	2	3	3	8
Phyllanthus ruber	1	5	2	8
Total	**52**	**32**	**27**	**111**

Ridge plots have the greatest number of trees (n=143) from 51 species, followed by slopes (n=86) from 37 species and valleys (n=67) from 33 species. Trees across the plots have DBHs from less than 5cm to 240cm, and canopy heights from 1.9m to 37.1m (Figure 5.7). Over 75 per cent of trees have a DBH of no greater than 10cm, and 82 per cent of canopy heights are 10m high or less. The majority of trees with DBH less than 5cm and canopy height less than 5m are captured within ridge plots. The trees with the largest DBH and canopy heights are found in valleys, the largest being a specimen of *Burretiodendron hsienmu* (240cm DBH, 37.1m canopy height).

To undertake an NMDS, a Wisconsin double standardisation was applied to the raw data, and reached a solution within 20 tries, and returned a stress score of 0.15, which is considered a good representation of the tree communities across the plots.

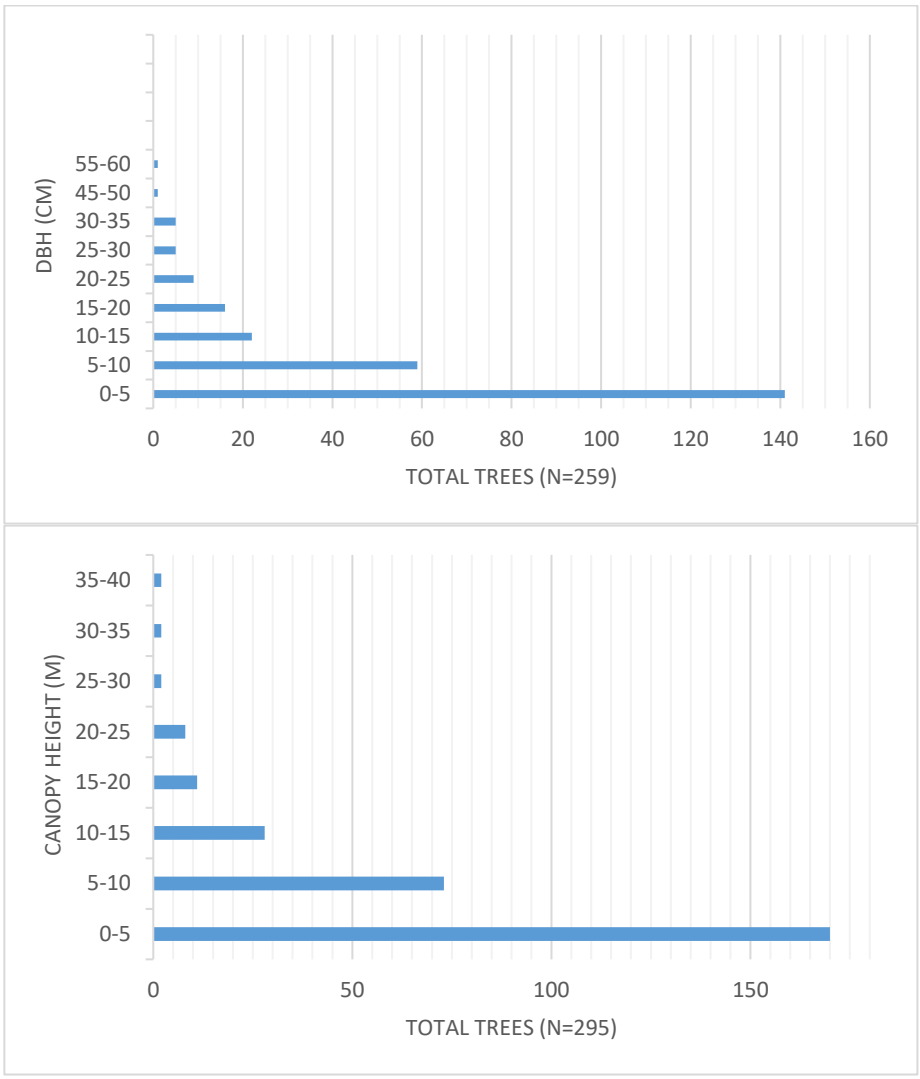


Figure 5.7 Tree metrics across plots in Khau Ca plots Top: Frequency of DBH across plots. Bottom: Frequency of tree heights across plots.

There is a high level of overlap across the plots based on tree species abundances (Figure 5.8), indicating high similarity between them. Most of the valley plots group tightly based on tree species abundances, however, the first valley plot (KCV1) groups more closely to slope plots and the third slope plot (KCS3) groups more closely to the other valley plots. Ridge plots also show this mixing of plots: all ridge plots group closely however, the first ridge plot (KCR1) groups more closely to other slope plots based on their similar tree species abundances. As a result of this mixing between plots, the confidence ellipses show that there is a high level of overlap based on the expected spread of 95% of plot observations.

A PERMANOVA shows that there is no significant difference between the plot types (R^2=0.19, F=1.09, P=0.32). All plot types have similar shapes and variation, with different directions along the axes.

Applying the intrinsic vectors to the NMDS ordination shows that seven tree species contribute significantly (p<0.05) to the composition of the tree communities within Khau Ca plots. The species *Sinosideroxylon racemosum* (p=0.006) and *Phyllanthus ruber* (p=0.05) have steep positive gradients and contribute to the composition of slope plots. *Sterculia lanceolata* (p=0.3) is also significantly contributing to slope plots along the NMDS2 axis. Ridge plots are influenced significantly by species of *Sinosideroxylon wightianum* (p=0.03), *Illicium parvifolium* (p=0.01), *Litsea brevipes* (p=0.006), and *Quercus sp*. (p=0.2) which have steep negative gradients. *Sterculia lanceolata* (p=0.3) is the only species contributing to composition of the valley plots.

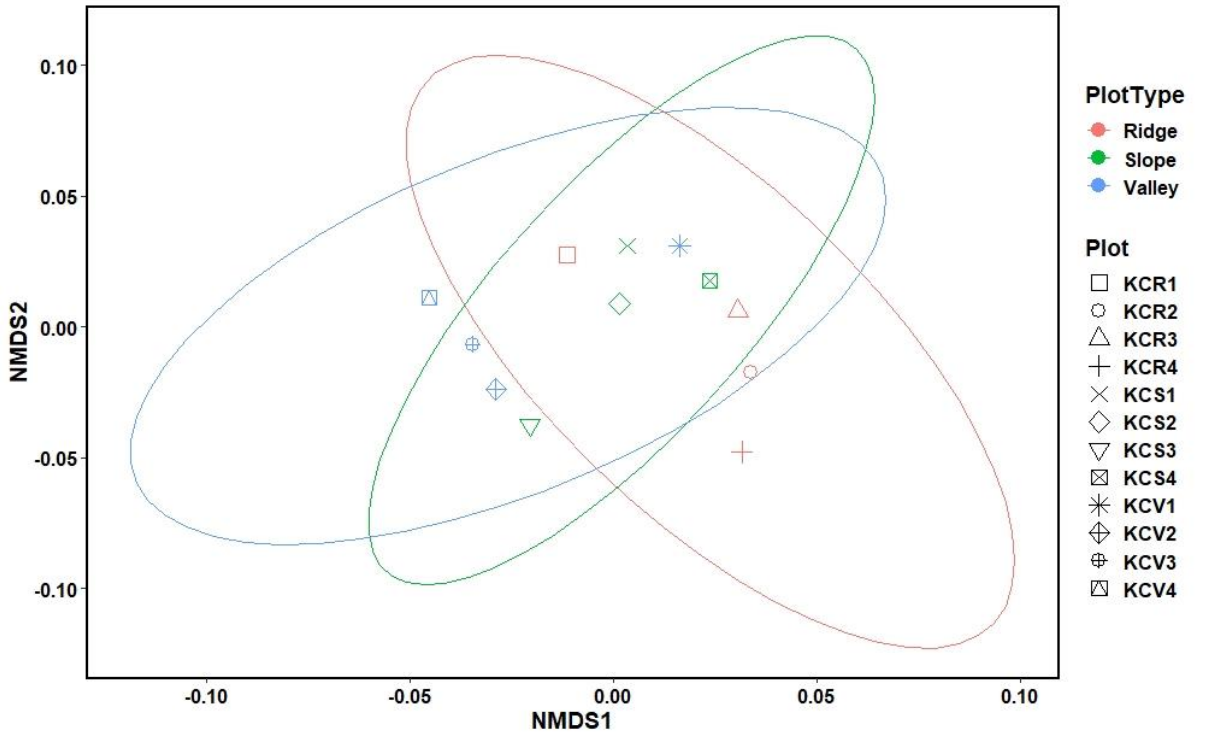


Figure 5.8 NMDS of trees in Khau Ca with 0.95 confidence ellipses.

5.4.2.4 Food species and genera in Khau Ca and NMDS analysis

Only seven of the 158 species previously identified as part of the TSNM diet (Covert et al., 2008; Hai, 2011; Quyet et al., 2007; Pham, Mai, & Tay, 1993/4), were identified in the Khau Ca plots in this study (Appendix 3.3.1). All seven have been identified as the most common species consumed by the TSNM in Quyet et al. (2007) and Hai (2011) (Table 5.9). These species occur most frequently in ridge plots (n=75). Only one species has a status of concern on the IUCN Red List 2022 - *Syzygium zeylanicum var. ellipticum* (a synonym of *Syzygium zeylanicum*), classified as Endangered (IUCN, 2022a; World Conservation Monitoring Centre, 1998b). The species is a small tree, found throughout Southeast Asia, India, and Madagascar (POWO, 2022), threatened due to extensive loss through forest fires, conversion of land for agriculture or plantations, and collection for fuel (World Conservation Monitoring Centre, 1998b).

Table 5.9 TSNM food species captured in Khau Ca plots

Species	Ridge (n)	Slope (n)	Valley (n)	Total (n)	IUCN Red List Status
Acer tonkinensis	12	0	0	**12**	NE
Garcinia fagraeoides	56	5	0	**61**	NE
Iodes seguini	0	0	1	**1**	NE
Pometia pinnata	0	3	2	**5**	LC
Premna flavescens	1	0	0	**1**	NE
Syzygium zeylanicum (syn. Syzygium zeylanicum var. ellipticum)	6	3	0	**9**	EN
Trevesia palmata	0	4	1	**5**	LC
Total	**75**	**15**	**4**	**94**	

Of the 104 genera identified in previous studies of the diet of TSNM (Covert et al., 2008; Hai, 2011; Quyet et al., 2007; Pham et al., 1993/4), 35 were also captured within the Khau Ca plots (Appendix 3.3.2). The top ten genera captured (Table 5.10) make up over 73 per cent of stems of TSNM food genera within Khau Ca plots. All three plot types have similar numbers of food genera; however, ridges have the greatest occurrence of food stems (genera=23, stems=264), compared to slopes (genera=24, stems=217) and valleys (genera=25, stems=171).

An NMDS analysis of food consumed by the TSNM at the genera-level, applied a Wisconsin double standardisation and achieved a solution within 20 tries, returning a stress of 0.15,

which is considered a good two-dimensional representation of the food genera relationships across the plots.

There is little separation between the ridge and slope plots based on the abundances of food genera captured within the plot types (Figure 5.9), suggesting these two may be very similar based on size of variation. While the ridge and slope plots show variation along the NMDS2 axis, valley plots have a large variation along the NMDS1 axis.

Table 5.10 Top ten food genera for TSNM in Khau Ca plots

Genera	Ridge occurrences (n)	Slope occurrences (n)	Valley occurrences (n)	Total (n)
Tetrastigma	41	23	39	**103**
Diospyros	19	46	12	**77**
Polyalthia	24	18	31	**73**
Garcinia	56	5	0	**61**
Acer	40	0	0	**40**
Sapindus	1	25	3	**29**
Pavetta	6	0	21	**27**
Ficus	12	13	1	**26**
Burretiodendron	7	13	5	**25**
Sinosideroxylon	10	6	4	**20**
total	**216**	**149**	**116**	**481**

A PERMANOVA shows that despite the difference seen between the valley plots, and the ridge and slope plots, there is no significant difference between the plots (R^2=0.19, F=1.1, P=0.30). The overall shape and variation exhibited by the three plots is very similar but is influenced differently along the axes.

Applying the intrinsic vectors shows that five genera significantly contribute to the composition and distribution of the plot types (Figure 5.9). *Lisea* (p=0.01) has a steep gradient and contributes to all three plot types but is typically found in ridge plots. The genus *Phyllanthus* (p=0.003) has a steep negative gradient and also contributes to all three plots, particularly slope plots. The grouping *Camellia* (p=0.01)*, Tetrastigma* (p=0.05) both have negative gradients and contribute predominately to valley plots, but also the other two plot types. *Iodes* (p=0.04) has a negative gradient and contributes to the composition of slope and valley plots.

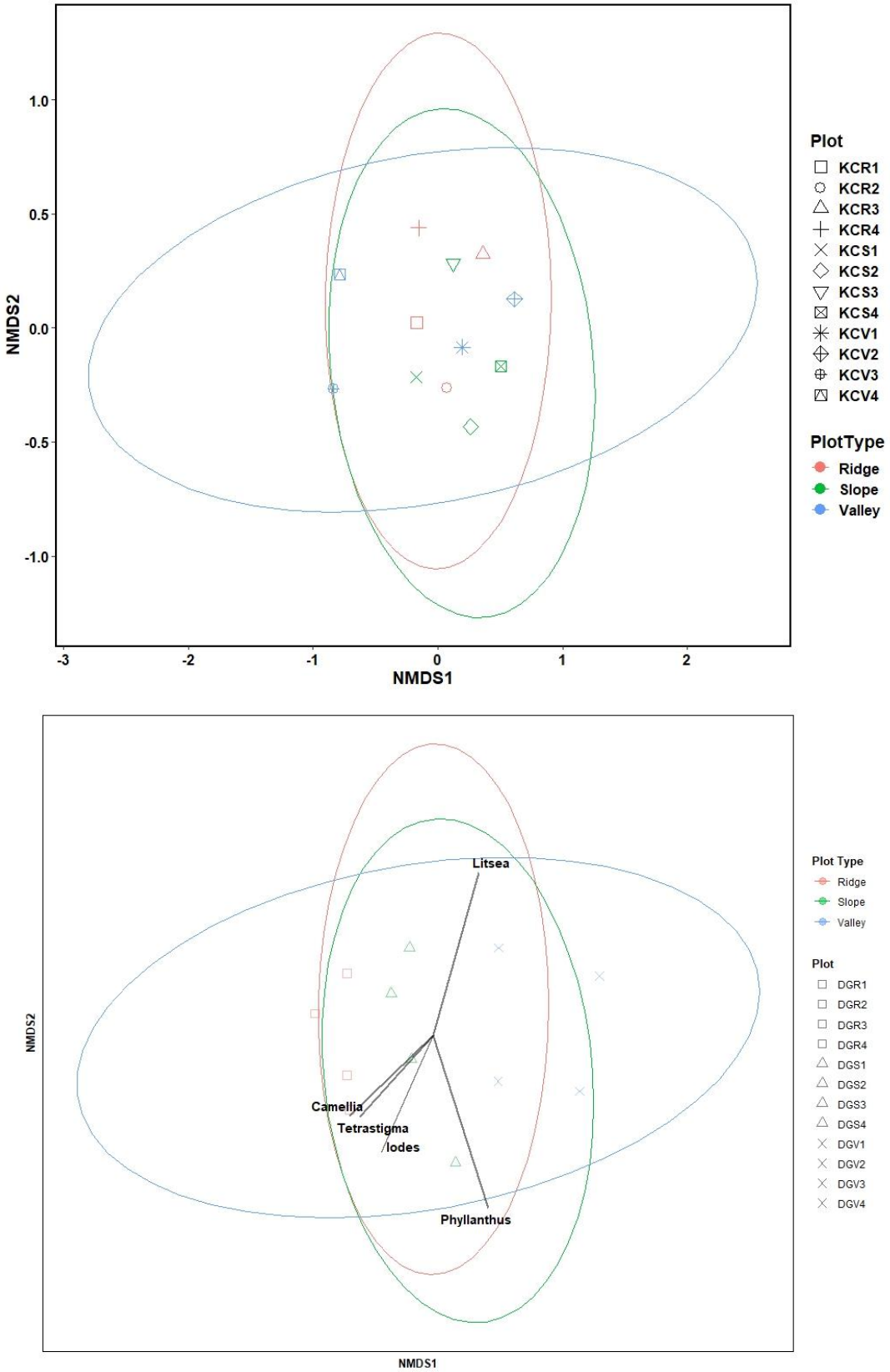


Figure 5.9 NMDS of diet genera within Khau Ca plots. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors.

5.4.3 Du Gia habitat characteristics

5.4.3.1 Generalised linear model, ANOVA and estimated marginal means analysis of Du Gia

I used an ANOVA to compare the vegetation characteristics across valley, slope, and ridge plots captured through the ecological sampling. An ANOVA analysis (Appendix 3.1.4) demonstrates that elevation and slope are the only significant variables across the three plot types.

The estimated marginal means shows that topography of plots across Du Gia vary significantly based on mean elevation and mean slope (Appendix 3.1.5). Valley plots (896m ±25.1) are significantly lower than both slope plots (1026m ±25.1, $p=0.01$) and ridge plots (1200m ±25.1, $p<0.0001$). Ridge and slope plots also vary from one another significantly ($p=0.002$). On average, ridge plots (4.5˚ ±3.71) have significantly flatter slopes than valley plots (27.8˚ ±3.71) and slope plots (29.2˚ ±3.71). The overall topographic complexity of all three plot types, however, are the same (1 ±0.27) due to low levels of limestone karst and high levels of fertile soil on sandstone substrate.

Based on vegetation characteristics, the three plot types are relatively homogenous, with no significant differences. In general, valley plots have greater mean general vegetation density, species richness, species density, tree height, percentage of mat, shrub, large shrub and liana cover, and larger average diameter and total basal areas than both slope and ridge plots. All three plot types also share roughly the same mean large shrub cover (approximately 24.5 per cent) and canopy cover (approximately 45 per cent).

5.4.3.2 Du Gia Plant Species analysis

5.4.3.2.1 Plant species composition in Du Gia

A total of 199 species from 82 families were identified across the Du Gia plots from 4108 stems (Appendix 3.2.1), with the fern *Cyclosorus angustipinnata* (n=486), the most frequently occurring species within the plots, predominately in valley plots (Table 5.11). The top ten species are mainly captured within the mat, shrub and large shrub layers. Three of the top species are also represented in tree form: *Elaeocarpus petiolatus* (as trees n=20), mainly found on ridges, *Macaranga henryi* (as trees n=24), found on ridges and slopes, and *Donella lanceolate* (as trees n=49), mainly found on ridges and slopes. In Du Gia, valley plots have the highest number of unique species (n=67) compared to ridges (n=33) and slope (n=26).

Table 5.11 Top ten species found in Du Gia plots

Species	Ridge occurrences (n)	Slope occurrences (n)	Valley occurrences (n)	Total occurrences (n)
Cyclosorus angustipinnata	35	75	376	486
Asplenium normale	14	355	6	375
Antrophyum callifolium	0	202	4	206
Elaeocarpus petiolatus	204	1	0	205
Macaranga henryi	133	51	1	185
Adiantum philippense	94		86	180
Cyathea gigantea	4	10	161	175
Alpinia globosa	119	0	0	119
Prunus wallichii	106	0	0	106
Donella lanceolata	44	36	1	81
Total	**753**	**730**	**635**	**2118**

Du Gia Ridges

Ridge plots have the lowest species richness with 86 plant species identified from 1377 individual stems. The evergreen tree Elaeocarpus petiolatus is the most commonly found species (n=205) (Table 5.12), predominately captured within the mat level as a seedling (n=153). This species is classified as being of Least Concern by the IUCN Red List and has a wide geographic range across Southeast Asia (L. Zhao & Yu, 2019).

The top ten species comprised over 61 per cent of all stems captured within ridge plots. Ridge vegetation is predominately made up of shrubs and tree species, none of which had an IUCN Red List status higher than Least Concern.

Table 5.12 Top ten species identified within Du Gia ridge plots

Species	Occurrence (n)	Description*	IUCN Red List Status
Elaeocarpus petiolatus	204	Tree	LC
Macaranga henryi	133	Tree	LC
Alpinia globosa	119	Shrub	NE
Prunus wallichii	106	Large shrub or small tree	LC
Adiantum philippense	94	Lithophyte	NE
Donella lanceolata	44	Tree	LC
Lasianthus hookeri	42	Shrub or tree	NE
Psychotria montana	40	Shrub	NE
Cyclosorus angustipinnatus	35	Fern	NE
Cinnamomum loureirii	33	Tree	NE
Total	**850**		

*Descriptions taken from Flora of China Project (2020) and POWO (2022)

Du Gia slopes

There were 90 species identified within slope plots from 1273 individual stems. The top ten species in slope plots (Table 5.13) make up over 68 per cent of stems identified. The most commonly found species is the lithophyte fern, *Asplenium normale* (n=355). Slope vegetation is mainly characterised by ferns and trees. The tree species *Diospyros quaesita* (n=55) is listed as Vulnerable on the IUCN Red List; it is also listed as being endemic to Sri Lanka, however, no distribution data is available, and the last assessment was made in 1998 (World Conservation Monitoring Centre, 1998a). The climbing vine species *Pothos scandens* (n=19) is used medicinally in Yunnan, China for traumatic injuries and joint stiffness (Flora of China Project, 2020).

Table 5.13 Top ten species identified within Du Gia slope plots

Species	**Occurrence (n)**	**Description***	**IUCN Red List Status**
Asplenium normale	355	Lithophyte fern	NE
Antrophyum callifolium	202	Epiphyte fern	NE
Cyclosorus angustipinnatus	75	Fern	NE
Diospyros quaesita	55	Tree	VU
Macaranga henryi	51	Tree	LC
Donella lanceolata	36	Tree	LC
Carex baccans	28	Flowering shrub	LC
Psychotria rubra	25	Tree	LC
Psychotria montana	20	Shrub	NE
Pothos scandens	19	Climbing vine	NE
Total	**866**		

*Descriptions taken from (2020) and (POWO, 2022)

Du Gia valleys

Valley plots have the largest number of identified species (n=116) compared to other plot types, with a total of 1458 individual stems. The top ten valley species (Table 5.14) make up over 63 per cent of all stems. The most commonly occurring species is the fern *Cyclosorus angustipinnata* (n=376). The flowering shrub *Camellia tsai* is listed as being of Least Concern by the IUCN Red List and is one of the first species to establish itself following recovery from agriculture (Rivers, 2015). The vegetation of Du Gia valleys is primarily characterised by shrubs, with *Saurauia roxburghii* the only tree species identified in the top ten.

Table 5.14 Top ten species identified within Du Gia valley plots

Species	Occurrence (n)	Description*	IUCN Red List Status
Cyclosorus angustipinnata	376	Fern	NE
Cyathea gigantean (syn. Gymnosphaera gigantean)	161	Shrub or tree	NE
Adiantum philippense	86	Lithophyte	NE
Elatostema eurhynchum	76	Perennial shrub	NE
Saurauia roxburghii	51	Tree	LC
Colocasia gigantean (syn. Leucocasia gigantean)	43	Flowering shrub	NE
Homalomena tonkinensis (syn. Homalomena cochinchinensis)	42	Perennial shrub	NE
Camellia tsai	30	Flowering shrub	LC
Pollia japonica	30	Shrub	NE
Pilea melastomoides (syn. Pilea hispaniolana)	26	Herb or shrub	NE
Total	**921**		

*Descriptions taken from Flora of China Project (2020) and POWO (2022)

5.4.3.2.2 Non-metric multi-dimensional scaling analysis of Du Gia plants

The NDMS for Du Gia plants applied a Wisconsin double standardisation and a square root transformation and reached a solution within the 20 tries with a stress value of 0.076. As the stress was well below 0.1 it is considered to produce a very good two-dimensional representation of the tree communities across plots.

Based on abundances of species, the NDMS with 95 per cent confidence ellipses (Figure 5.10) there is clear separation between the plot types. Valley plots are dissimilar to slope and ridge plots within Du Gia, potentially as a result of the much greater variation in number of species and stems. There is also clear grouping between ridge plots, suggesting high similarity of plant communities, however the 95 confidence ellipses suggests that slope plots overlap with ridge plot communities indicating similarity of community compositions between the two plot types. Slope plots group tightly with the exception of the fourth slope plot (DGS4).

A PERMANOVA shows that there is a significant difference between the plots, 42 per cent of the variation in the distances is explained by the plot types (R^2=0.42, F=3.3, P=0.001), particularly distances between ridges and valleys, based on the variation and separation they exhibit.

Applying the intrinsic vectors (Figure 5.10) show that 23 species significantly ($p<0.05$) contribute to the plot types. The species *Alpinia tonkinensis* (p=0.01), *Gnetum montanum* (p=0.008), *Psychotria rubra* (p=0.02), *Lasianthus tonkinensis* (p=0.05), *Polyalthia lauii* (p=0.01), all have steep positive gradients and are typical of slope plots, contributing to their composition.

The species *Archidendron tonkinensis* (p=0.02), *Phlogacanthus annamensis* (p=0.01), and *Pothos repens* (p=0.03) all have shallower positive gradients and are typical of valley plots in Du Gia. Similarly, *Saurauia roxburghii* (p=0.02), *Colocasia gigantean* (p=0.003), *Piper brevicaule* (p=0.004), *Paraboea multiflora* (p=0.02), *Piper cubeba* (p=0.01), *Glyptopetalum poilanei* (p=0.03), and *Lithocarpus fenestratus* (p=0.02) area all typical of valley plots, however they have negative gradients.

The species *Alpinia globosa* (p=0.04), *Macaranga henryi* (p=0.004), *Prunus arborea* (p=0.02), *Maranta arundinacea* (p=0.03), *Olea rosea* (p=0.02) have steep negative gradients and contribute to the composition of ridge and slope plots but are more typical of the former.

The species *Machilus oreophila* (p=0.03) and *Engelhardtia roxburghiana* (p=0.022) have shallow negative gradients and contribute to both slope and ridge plots.

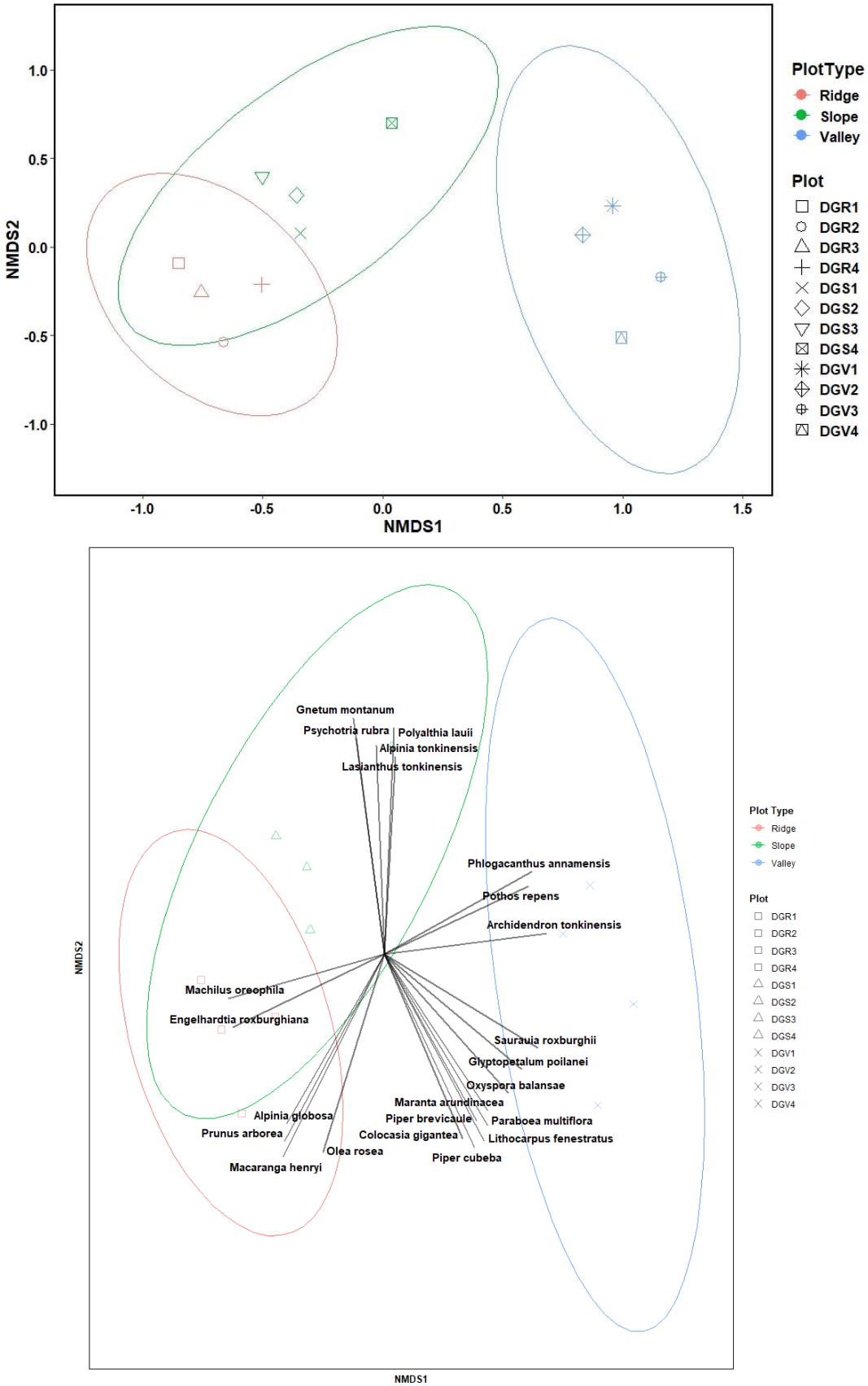


Figure 5.10 NMDS of plants within Du Gia species. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors.

5.4.3.3 Du Gia Trees and NMDS analysis

There were 81 species of trees (37 families) identified from 419 individual tree stems counted within the Du Gia plots (Appendix 3.2.2). The top ten tree species (Table 5.15) account for only 38 per cent of all tree stems as there is a high number of unique counts (n=26). Slope plots have the highest number of tree species (n=42), followed by valleys (n=38) and ridges (n=33). Only five species were shared across all three plot types. In terms of tree stems counted, the highest number were captured within ridge plots in Du Gia (n=172), followed by slope plots (n=161) and then valleys (n=86). The most commonly occurring tree species is Donella lanceolate (n=49), most commonly found in ridge plots.

Table 5.15 Top ten species of tree identified within Du Gia plots

Species	Ridge occurrences (n)	Slope occurrences (n)	Valley occurrences (n)	Total (n)
Donella lanceolata	33	15	1	49
Macaranga henryi	11	13	0	24
Diospyros quaesita	0	17	4	21
Elaeocarpus petiolatus	19	1	0	20
Cinnamomum loureirii	13	3	2	18
Prunus arborea	11	5	0	16
Syzygium zeylanicum	13	0	0	13
Camellia tsai	0	0	11	11
Machilus oreophila	7	3	0	10
Litsea balansae	0	8	1	9
Decaspermum parviflorum	2	7	0	9
Lithocarpus sp.	2	6	1	9
Total	**78**	**63**	**19**	**160**

The majority of trees in Du Gia are small with DBH under 10cm and canopy heights under 10m (Figure 5.11). Over 83 per cent of trees have a DBH below 10cm and over 86 per cent of trees in all three plot types have canopy heights ten meters or under. Valley plots have the highest number of tall trees, with three trees measuring over 20m: *Actinodaphne elliptibacca* (28.1m)*, Cinnamomum loureirii* (24.8m) and *Saraca dives* (23.6m). Slope plots have no trees over 20m; however, they have the greatest frequency of trees in the 10-20m height range (n=22). Ridge plots have only a single tree over 20m, identified as *Castanopsis fabrei* (24.2m), as well as a high number of trees in the 10-20m (n=18).

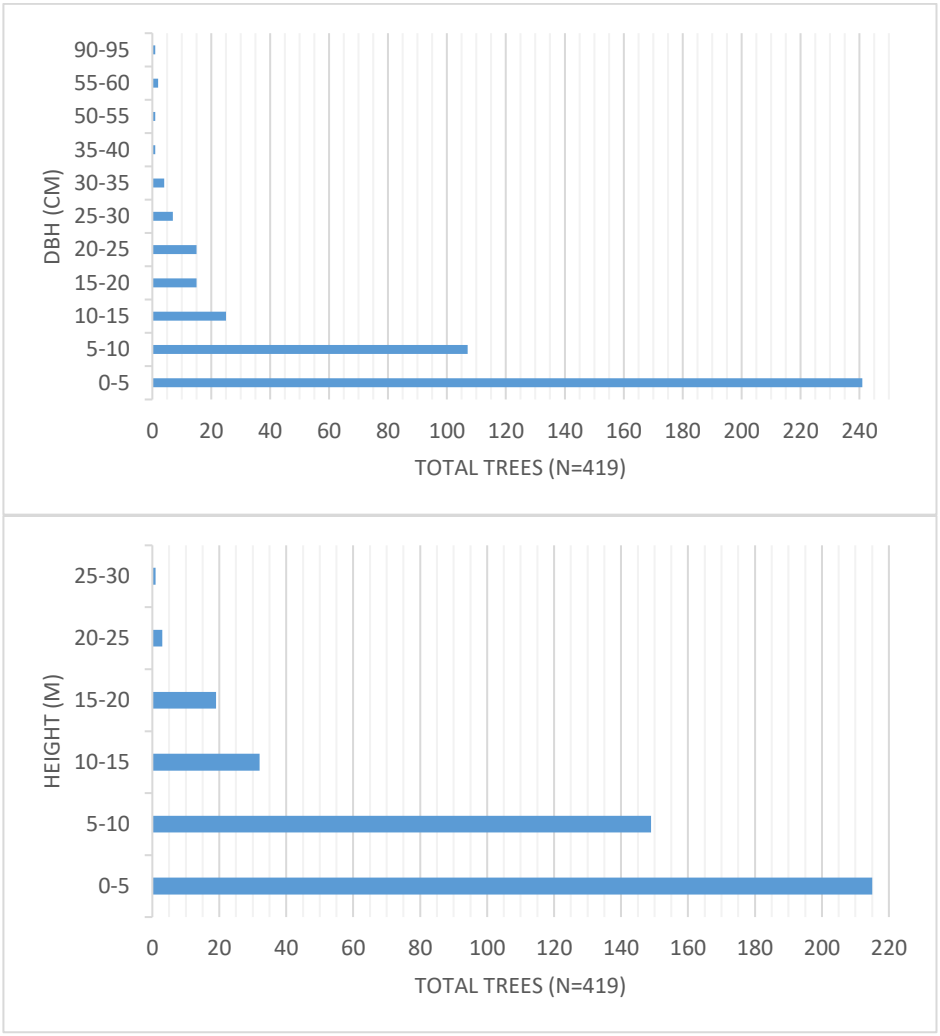


Figure 5.11 Du Gia tree DBH and height distributions Top: Distribution of tree DBH across Du Gia plots. Bottom: Distribution of tree heights across Du Gia plots

Undertaking an NDMS exclusively on the mature tree communities within each plot type applied a Wisconsin double standardisation and reached a solution within 20 tries. A stress value of 0.093 was returned, indicating a very good two-dimensional representation of the similarities between the tree communities within plots.

There is strong overlap between plot types based on their 95 per cent confidence ellipses (Figure 5.12). There is a grouping of valley plots, however, the confidence ellipse indicates there is a wider variation in expected values than represented within these four plots, potentially due to the reasonably high species numbers but low occurrence of individual tree stems. Ridge plots have a close grouping and smaller variation based on confidence ellipses,

suggesting low similarity to valley plot tree communities. Slope plots overlap with both valley and ridge plots based on their tree communities.

A PERMANOVA shows that there is a significant difference between the plots, with 41 per cent of the variation explained by the plot type grouping (R^2=0.41, F=3.09, P=0.001). The differences are particularly strong between the ridge and valley plots.

Applying the intrinsic vectors shows that four species are significantly (p<0.05) contributing to the distribution of plots (Figure 5.12). *Lithocarpus fenestratus* (p=0.02) has a shallow gradient and is contributing to the composition of valley plots. The species *Phylogacanthus annamensis* (p=0.02) has a steep negative gradient and contributes to the distribution of the slope and valley plots. *Donella lanceolata* (p= 0.02) and *Machilus oreophila* (p=0.03) and is typical of ridge plots.

5.4.3.4 Food species and genera in Du Gia and genera NMDS

Only seven of the food species identified by previous studies of the TSNM in Khau Ca (Covert et al., 2008; Hai, 2011; Quyet et al., 2007; Pham et al., 1993/4), were captured within plots in Du Gia (Table 5.16). Except for *Elaeocarpus petiolatus*, food at the species level were captured in very small abundances.

Table 5.16 Food species captured in Du Gia

Species	Ridge occurrences (n)	Slope occurrences (n)	Valley occurrences (n)	Total (n)	IUCN Red List Status
Canarium album	0	2	0	2	NE
Elaeocarpus petiolatus	204	1	0	205	LC
Garcinia bracteata	0	0	1	1	LC
Garcinia fagraeoides	1	7	0	8	NE
Gnetum montanum	0	12	0	12	LC
Saraca dives	0	0	1	1	NE
Syzygium zeylanicum	13	0	0	13	EN
	218	**22**	**2**	**242**	

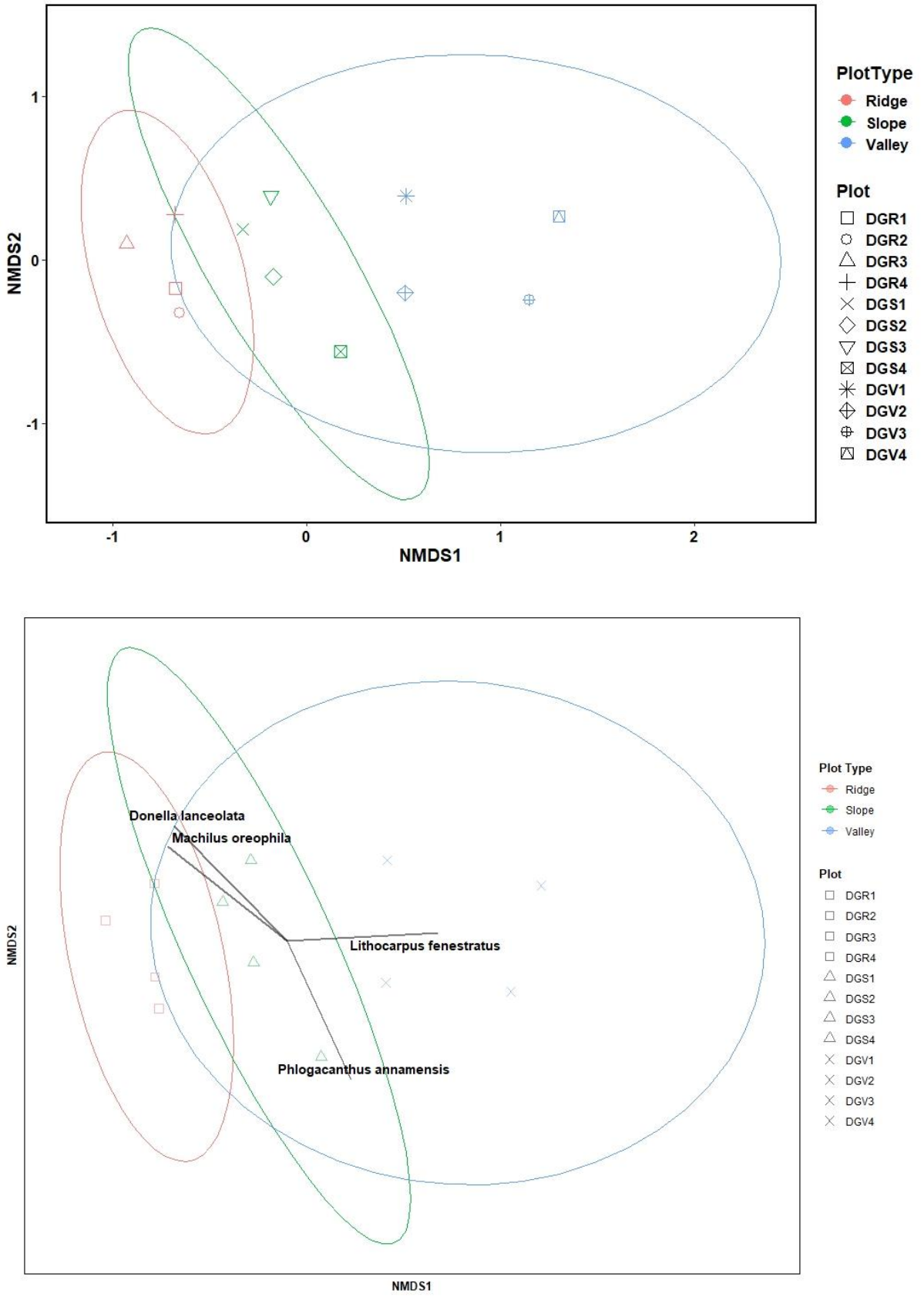


Figure 5.12 NMDS of trees in Du Gia plots. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors

At the genera level, 33 genera of food plants were identified in the Du Gia plots (Appendix 3.3.2). All three plot types have similar numbers of genera; however, ridges have the greatest number of genera stems (genera=19, stems=350), followed by slopes (genera=22, stems=179) and valley plots (genera=21, stems=152). The top ten genera identified across plots (Table 5.17) is *Elaeocarpus*, a flowering tree with at least 491 species (POWO, 2022), found predominately within ridge plots in Du Gia.

Table 5.17 Top ten food genera identified in Du Gia plots

Genera	**Ridge occurrences (n)**	**Slope occurrences (n)**	**Valley occurrences (n)**	**Total (n)**
Elaeocarpus	219	2	0	**221**
Diospyros	0	57	18	**75**
Litsea	41	26	8	**75**
Archidendron	9	4	24	**37**
Camellia	0	0	34	**34**
Syzygium	13	6	12	**31**
Tetrastigma	8	2	18	**28**
Machilus	11	6	0	**17**
Polyalthia	0	13	4	**17**
Gnetum	0	12	3	**15**
Sapindus	3	11	1	**15**
Total	**304**	**139**	**122**	**565**

An NMDS analysis on the food genera captured within Du Gia applied a Wisconsin double standardisation and square root transformations on the raw data. A solution was reached after 20 tries and a stress value of 0.17 was returned, which is considered a reasonable two-dimensional representation of the food genera across plot types in Du Gia.

While there is a large overlap between the plot types based on their 95 per cent confidence ellipses (Figure 5.13), there is a large degree of variation between the plot types. Ridge and slope plots show the greatest variation along NMDS1 axis and valley plots have the greatest variation along the NMDS2 axis. Slope plots are the closest grouping of the plot types. Valley and ridge plots group more closely with plots from other plot types. The fourth valley plot (DGV4) groups more closely with slope plots based on the composition of its food genera. The ridge plots have some separation into two subgroups, with the first and second ridge plots

(DGR1, DGR2) group more closely with the second valley plots (DGV2) than with the other two ridge plots.

A PERMANOVA shows that there is a significant difference between the three plots (R^2=0.4, F=3.06, P=0.001), with 40 per cent of the variation in the differences is explained by the plot types.

Applying the intrinsic species vectors shows that six genera have significant correlations to the NMDS ordination (Figure 5.13). *Ardisia* (p=0.006) has a negative gradient and an association with ridge plots, particularly the grouping of DGR3 and DGR4, the only two plots that had occurrences of this genus. *Schefflera* (0.039) also has a shallow negative direction, and an association with ridge plots, particularly the grouping of DGR1 and DGR2, and also valley plots such as DGV2. *Ficus* (0.004) also has a negative gradient; however, it has a closer association with valley plots, which had greater occurrences of the genus than other plot types.

The genera *Gnetum* (p=0.012) and *Phyllanthus* (p=0.016) have positive gradients and are more closely associated with slope plots due to their greater occurrence within this plot type. *Castanopsis* (p=0.013) has a positive gradient and is also associated with slope plots but also ridge plots due to similar occurrences.

5.4.4 Comparison of Du Gia to Khau Ca

5.4.4.1 General linear model, ANOVA and estimated marginal means analysis comparison of Du Gia and Khau Ca

I applied an ANOVA analysis to compare the overall vegetation characteristics between the two sites. The ANOVA analysis (Appendix 3.1.6) shows that the significant variables are elevation, topography complexity, canopy cover, and liana cover that suggest a difference between the two sites.

The estimated marginal means analysis (Appendix 3.1.7) shows that the topography of Du Gia differs significantly from that of Khau Ca in terms of elevation and topographic complexity. Du Gia has significantly greater mean elevations (1040m ±26m, p<0.0001) than that of Khau Ca (826m ±26m). The topographic complexity of Du Gia (1.25 ±0.22) is also significantly smoother than that of Khau Ca (2.67 ±0.22, p<0.0003).

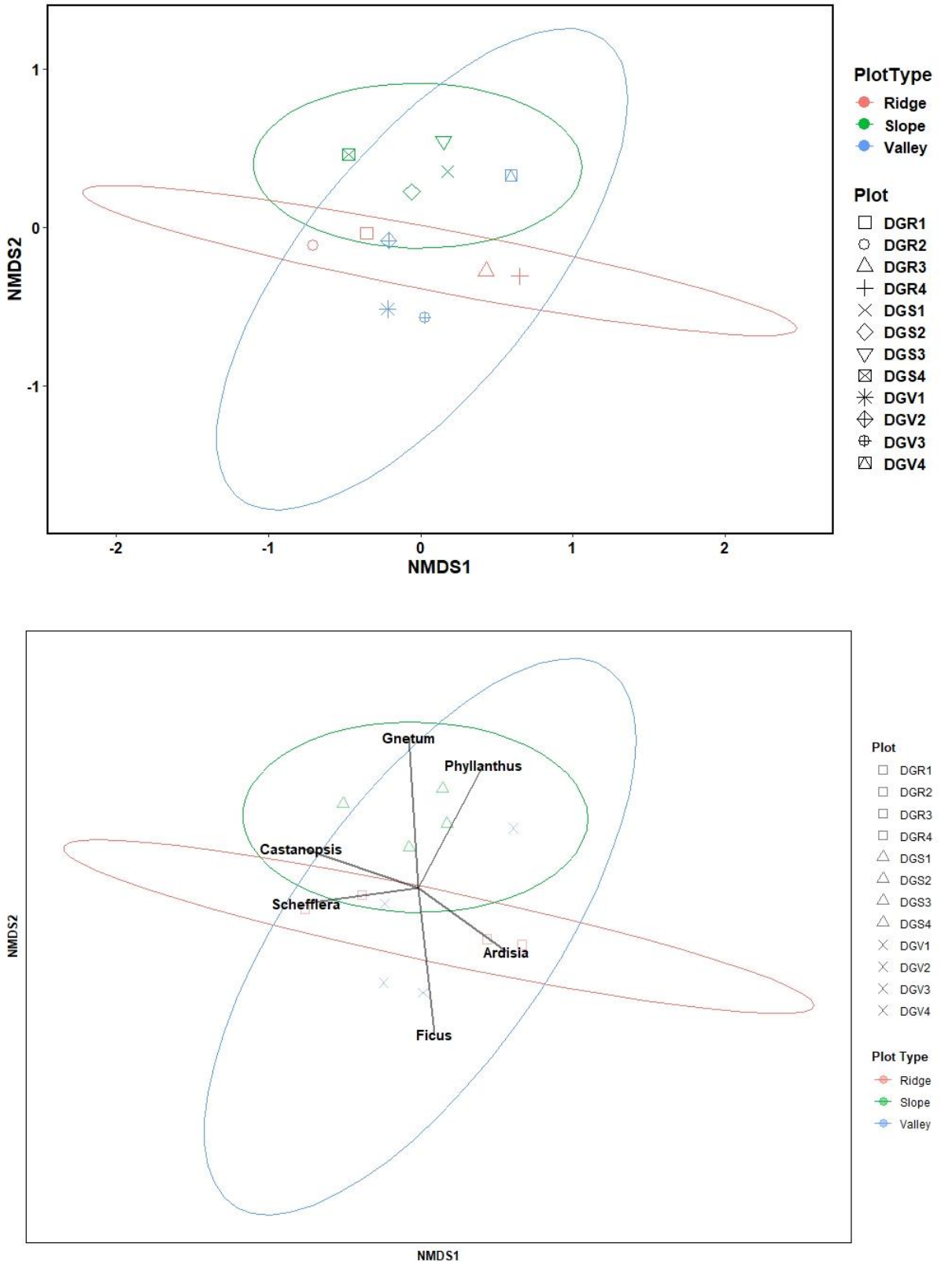


Figure 5.13 NMDS of food genera identified in Du Gia plots. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors p<0.05).

Based on vegetation characteristics, the two sites were largely homogenous across the vegetation measurements. In general, Khau Ca was found to have, taller trees (6.92m ±0.697m) with greater average diameters (10.21cm ±1.32cm) and greater mean total basal area (74.40 ±28.36) than that of Du Gia (6.59m ±0.69m; 8.49cm ±1.32cm; 3386 ±2836). Khau Ca also had a greater mean species diversity (3.05 ±0.116) and mean mat cover (27.1% ±0.697), than those found in Du Gia (2.73% ±0.116 and 18.3 ±5.34).

5.4.4.2 Plant species comparison of Du Gia and Khau Ca

5.4.4.2.1 Species composition comparison

The two sites share 104 species from a total of 304 species. A total of 199 species comprising 4108 stems were recorded within the Du Gia sample. In Khau Ca, 209 species were identified, and 4326 stems counted (Appendix 3.2.1). The most abundant species in Du Gia is a fern *Cyclosorus angustipinnata* (n=486), while in Khau Ca, *Psychotria tonkinensis,* a flowering shrub, is the most commonly found species (n=253). The majority of the top ten shared species (Table 5.18) have not been assessed by the IUCN Red List 2022, however, one species, *Diospyros quaesita* (n=121) is listed as Vulnerable (World Conservation Monitoring Centre, 1998a). Though, as mentioned in section 6.4.4.2.1, this is considered endemic to Sri Lanka (though more recent data is missing) (IUCN, 2022a).

Du Gia has less tree height diversity than Khau Ca and seventy per cent of tree canopies in Du Gia are 10m or less. In comparison, in Khau Ca, only 54 per cent of tree canopies are 10m or less. Du Gia also has trees with smaller DBHs – over 83 per cent of trees have a DBH under 10cm compared to Khau Ca (75.5 per cent). The largest DBH in Minh Son belongs to *Cinnamomum loureirii* (DBH = 92cm) compared to Khau Ca with *Burretiodendron hsienmu* (DBH = 240cm).

An NDMS ordination applied a Wisconsin double standardisation and a square root transformation to the raw count data. It reached a solution after 20 tries and returned a stress value of 0.17, which indicates a reasonable two-dimensional representation of the plant community dissimilarities.

Table 5.18 Top ten shared species between Du Gia and Khau Ca

Species	Du Gia occurrences (n)	Khau Ca occurrences (n)	Total (n)	IUCN Red List Status
Asplenium normale	375	123	498	NE
Psychotria tonkinensis	21	253	274	NE
Antrophyum callifolium	206	50	256	NE
Adiantum philippense	180	34	214	NE
Aspidistra typica	11	182	193	NE
Cyathea gigantea	175	8	183	NE
Psychotria montana	68	67	135	NE
Diospyros quaesita	73	48	121	VU
Psychotria rubra (syn. Psychotria asiatica)	37	77	114	LC
Prunus wallichii (syn. Prunus undulata)	106	7	113	LC

The NMDS ordination shows that the two sites do not group together based on their 95 per cent confidence ellipses (Figure 5.14). This suggests that the two plant communities between the two sites are dissimilar to one another based on their respective species abundances.

A PERMANOVA shows that the two sites are significantly different (R^2=0.12, F=3.17, P=0.001), however only 12 per cent of the variation is explained by the sites. Instead, it is possible that the differences being observed in the ordination are a result of plot type differences.

Over 60 species contribute significantly ($p<0.05$) to the composition of plant communities across the two sites (Figure 5.14). These grouped into three main species groupings, the first group including *Cyclosorus angustipinnata* (p=0.008) have positive gradients and associations with Du Gia plots particularly valley plots. Grouping two including *Diplazium maximum* (p=0.01) have negative gradients and are associated with Khau ca plots. Grouping three includes *Smilax bracteata* (p=0.02) and has mainly positive gradients and associations with Du Gia.

5.4.4.3 Food species composition and NMDS comparison between Khau Ca and Du Gia

Of the diet genera captured within the Du Gia and Khau Ca plots, 44 genera were represented total, with the two sites sharing only 24 genera (Appendix 3.3.2). Khau Ca had the greatest number of diet genera (n=35), with 652 stems identified across plots. The most commonly found diet genus across Khau Ca plots was *Tetrastigma*, a liana from the grape family. In contrast, 33 diet genera were identified in Du Gia, with 681 stems counted. The most commonly identified diet genus across the Du Gia plots was the flowering genus *Elaeocarpus*.

An NMDS ordination of the food genera consumed by the TSNM across the two sites applied a Wisconsin double standardisation and a square root transformation. The NMDS was set to three-dimensions as the two-dimensional ordination returned a stress greater than 0.2. Using a three-dimensional representation, a solution was achieved after 20 tries and a stress of 0.14 was returned.

There is only some overlap between the two sites based on the composition of food genera (Figure 5.15) suggesting low similarity. The Khau Ca plots appear to mostly group closely to one another, however the DGS2 plot falls outside the 95 per cent confidence ellipses, suggesting a difference in genera abundances compared to other plots when represented in a three-dimensional representation.

A PERMANOVA shows that there is a significant difference (R^2=0.12, F=2.9, P=0.001), however only 12 per cent of variation is explained by the location of the plots. This suggests that the Khau Ca and Du Gia plots are fairly similar based on their compositions according to site variables.

Seven genera significantly contribute to the composition of food communities in the NMDS ordination in three-dimensions (Figure 5.15). *Archidendron* (p=0.009) and *Gnetum* (p=0.002) have negative gradients and associations with Du Gia plots, as it is neither genus is found in Khau Ca plots. *Phyllanthus* (p=0.002), *Burretiodendron* (p=0.008), *Celtis* (p=0.001), *Sinosideroxylon* (p=0.001) and *Tetrastigma* (p=0.009) all have positive gradients and associations with Khau Ca plots. Of these four genera, only *Tetrastigma* appears in Du Gia, however, it occurs in lower frequencies than in Khau Ca.

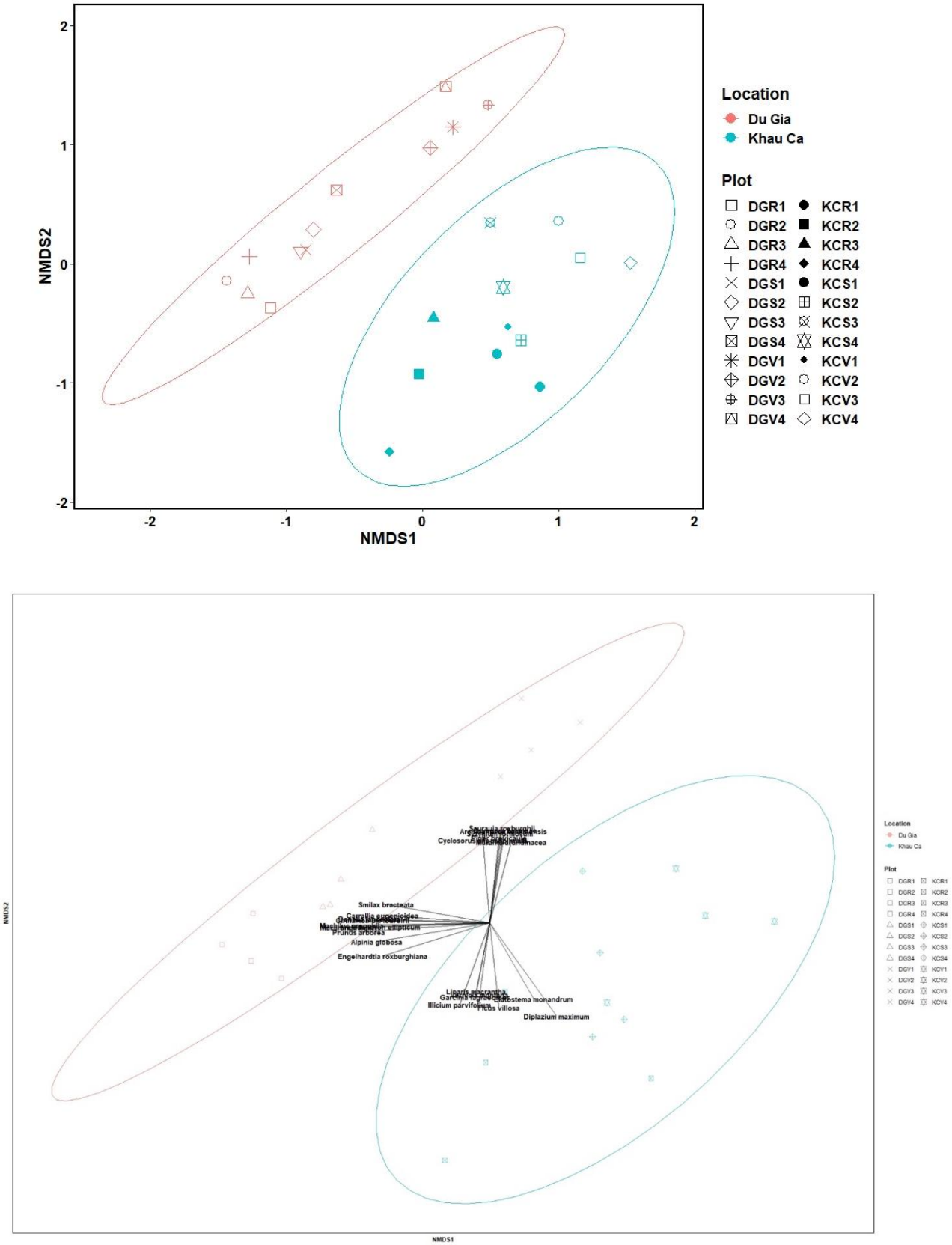


Figure 5.14 NMDS of plant species identified across Du Gia and Khau Ca. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic species vectors where p<0.01 – over 63 species contribute to the differences between the site tree communities.

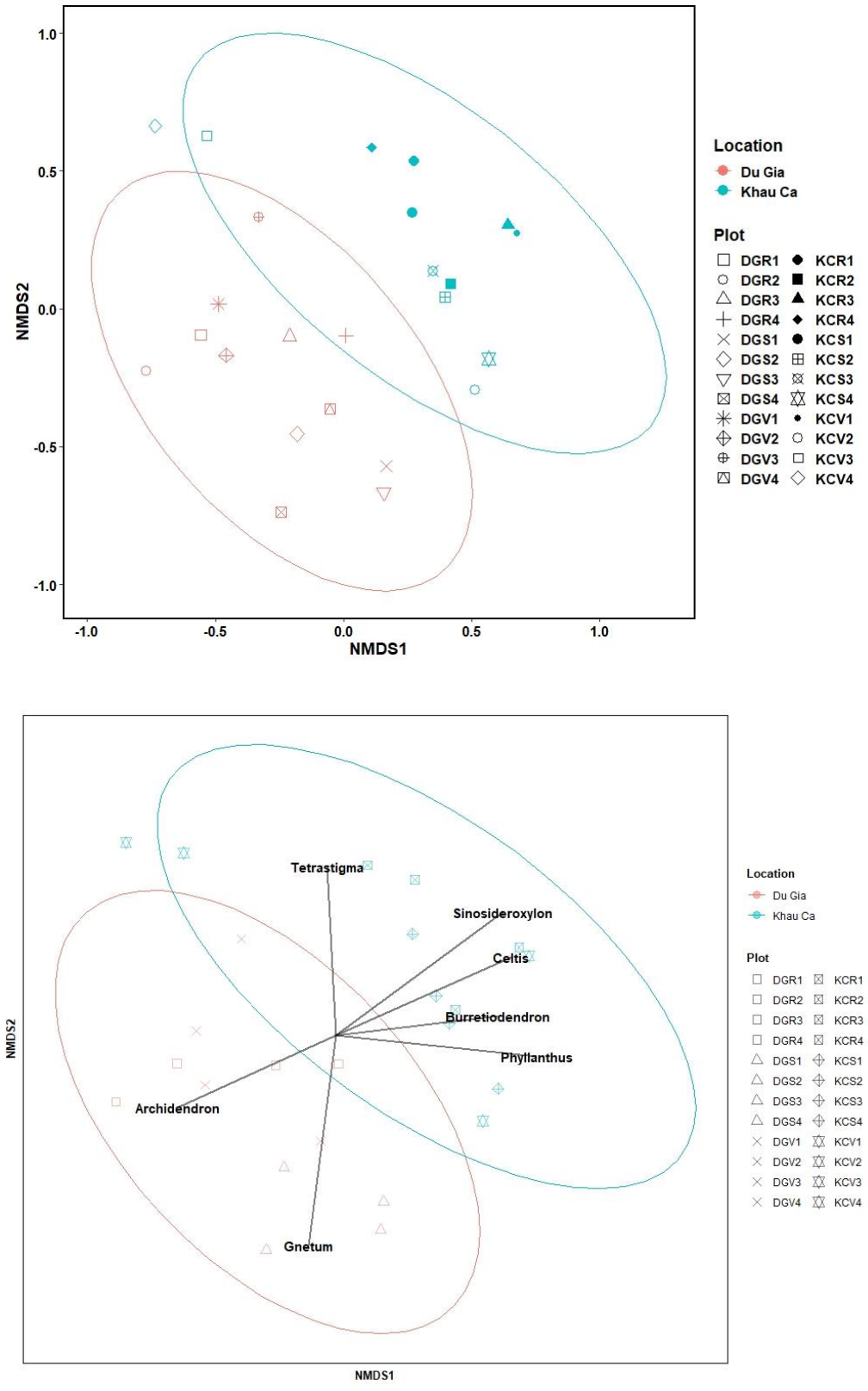


Figure 5.15 NMDS of food genera identified in Du Gia and Khau Ca plots. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors p<0.05.

5.5 Discussion

5.5.1 Khau Ca habitat

5.5.1.1 Composition

The results of this research provide a detailed analysis of the vegetation profile of the TSNM core habitat, complementing previous studies that primarily focussed on tree phenology (Covert et al., 2008; Hai, 2011; Quyet, 2014). The use of a broader profile of the region can support monitoring and planning for the health and management of the protected area across valleys, slopes and ridges, including tracking the introduction of invasive species and the density of future supplies of food species for the TSNM.

The habitats of *Rhinopithecus* are increasingly under pressure from human activities and development (Dine, 2012). Both the habitats of the black-and-white snub-nosed monkey and the TSNM are now island remnants of a once-wider distribution (Liu et al., 2009). Unlike the other sites covered in this thesis, the structure of the Khau Ca habitat is that of an 'island-bowl' of primary forest surrounded on all sides by farmland (Kempinski et al., 2009) and plantations of *Acacia.*

The structure of Khau Ca's 'bowl' of forest is emphasised by the steep ridges and slopes encircling the interconnected valleys, which are typified by little visible limestone, and a mean elevation of 695m. Within Khau Ca, the TSNM are reported to heavily use approximately 7-10km^2 of 'core area' (Thach, 2009) within the total 21km^2 of protected forest. The sampling I undertook was primarily located within this core area based on advice from local rangers responsible for monitoring the TSNM.

Significant differences apparent in the three plot types are primarily topographical rather than based on vegetation. As elevation increases, the topography becomes more complex, and less stable, extending dramatically from shallow valleys to steep sided mountains and narrow ridges. Elevation tends to increase from the shallower northwest end up to the steeper southeast side of the protected area (Hai, 2011).

The vegetation of Khau Ca is dominated by small species of plants such as epiphytes including *Asplenium confusum, Asplenium normale* and *Adiantum caudatum*; herbs and ferns such as *Diplazium maximum, Elatostema monandrum*; shrubs such as *Begonia caobangensis,*

Psychotria tonkinensis, Phlogacanthus colainae, and Aspidistra typical; and bamboo including *Arundinaria sat*. No trees are represented in the top ten species, indicating the diversity of the lower forest layers within Khau Ca.

Based on the plant species abundances within the three plot types in Khau Ca, they appear to be relatively homogenous, as the NMDS suggests no significant differences between the plot types. Slope plots act as a transition between valley and ridge plots as exhibited by their overlap in variation between the two extremes. Most of the difference in plant communities was driven by species that were identified within ridge plots in higher frequencies than the other plots. Ridges are characterised by a higher species richness than the other habitat types. This is likely due to the fact that ridges provide a greater surface area for plants to attach – the crevices between limestone acts as traps for soil and provide shelter for small herbs and small plants (Clements et al., 2006).

Khau Ca vegetation has a gradual transition from valley to ridge plots, with slope plots intermediate in terms of vegetation composition. The greater species diversity exhibited by slope plots compared to valley and ridge plots, may be due to gradual transition from valley to more ridge like vegetation. Other characteristics of slope plots reflect the steep gradient between valley plots and ridge plots. Slope plots also exhibit a greater level of topographic complexity, even though Khau Ca slopes are generally well covered in soil compared to other limestone forest areas. The differences found between the habitat types are likely reflected in the behaviour of the TSNM with different regions being used for different behaviours.

The overall tree density for all trees over 2cm in DBH identified in Khau Ca for this study is 2500 stems/ha – substantially greater than the tree densities identified in Khau Ca by Quyet (2014), 513 stems/ha, and by Hai (2011), 882/ha. This is also greater than the density of trees Hai (2011) recorded in the Na Hong TSNM habitat (956 stems/ha). This variation is partly due to the differences in DBH selected by each study; Hai (2011) collected measurements only for trees with a DBH greater than 6cm, and Quyet (2014), collected measurements for trees greater than 10cm. However, as over half of trees captured in my sampling had a DBH of under 10cm, the use of a higher DBH may miss an important snapshot of the TSNM habitat.

Most of these trees contributed to the overall canopy, and demonstrates the high proportion of saplings and younger trees within the environment, indicating that the secondary forest within Khau Ca is continuing to grow, but may also increase the profile of available food species within Khau Ca. The most commonly found tree is *Polyalthia laui*, which can grow up to 25m (Flora of China, 2020).

Primate habitats are often depicted only within the context of the large trees (M. Spicer et al., 2022), however, the growth of new trees, particularly within the valley areas which have predominately seen some level of disturbance in Khau Ca, suggests that the area is regenerating – a positive indicator for the TSNM – but also highlighting the opportunity to provide a guiding hand as to what species might best serve a growing population of TSNM in these areas. Understanding the variation across the Khau Ca habitat can improve efforts to preserve the vegetation and ensure the best habitat for the TSNM regardless of the limited size of the area.

5.5.1.2 Sleeping sites

As primates have been found to sleep for roughly half their lives (J. R. Anderson, 1998; Kappeler, 1998; Z.-F. Xiang et al., 2010), sleeping sites are critical components of their habitat (J. Anderson, 1984). With the exception of the limestone karst langurs, including the CBL, members of the Colobine family sleep in trees (D. Li et al., 2006). In other *Rhinopithecus* species, the size of the trees plays an important role in sleeping tree choice. The black-and-white snub-nosed monkey has been found to prefer the tallest trees on slopes, with large DBH and crowns (L. W. Cui, Quan, & Xiao, 2006; D. Li et al., 2006; Z.-H. Liu & Zhao, 2004). Similar preferences for taller trees with a large DBH have been found in golden snub-nosed monkeys (Chu, Sha, Kawazoe, & Dong, 2018). In gray snub-nosed monkeys the size of sleeping trees does not appear to differ significantly from the surrounding trees in the area, however a connected canopy is important (Z.-F. Xiang et al., 2010).

Current understanding of TSNM suggests that they do not use regular sleeping sites like many other primates but instead have a preference for sleeping towards the lower levels of trees in the 5-10m range (Hai, 2008; Thach, 2009). If size and canopy coverage is important to TSNM, based on the findings of this analysis, it is unlikely that ridges play any role as sleeping sites.

Trees sampled on the ridges in this study were found to be generally smaller and had less canopy cover than those found on slopes and valleys.

According to Hai (2008), TSNM prefer sleeping sites in valleys. This is supported by Thach (2009) who found that TSNM prefer sleeping sites in low-lying forests with larger established trees rather than those found at higher elevations. Based on the sampling undertaken here, the trees in Khau Ca valleys areas were found to be more established, with higher canopies, greater DBH and greater basal area than those in slope and ridge plots.

The quantity of available sleeping sites in an area is likely to be important to TSNM (and other SNM) as fission/fusion of AMUs and OMUs has been observed to occur at sleeping sites, with groups coming back together to rest at the end of the day (Dong, Hua, & Boonratana, 2011; Thach, 2009; Z.-F. Xiang et al., 2010). Observations of rest-huddling where one or more TSNM embrace each other while resting on branches (Hai, 2011), suggests that larger trees with strong branches are likely to be required based on the size of the TSNM. Such trees were largely found within valley plots. A requirement for larger established trees may also suggest safe sleeping sites out of the reach of predators are a driving factor for sleeping site selection for TSNM (Hai, 2008; T. M. Hoang & Covert, 2010), and/or protection from inclement weather, as these established trees are more protected within the valleys.

Other factors suggested to impact sleeping tree choice for *Rhinopithecus* include maintaining social ties, thermoregulation and hygiene (J. R. Anderson, 1998; Chu et al., 2018; Z.-F. Xiang et al., 2010). Black and white snub-nosed monkey has been found to prefer sleeping sites at lower altitudes during the winter months, suggesting weather might also drive their sleeping preferences (L. W. Cui et al., 2006). The TSNM has similarly been observed choosing sleeping sites low to the ground between 5 to 10m above the ground by Hai (2008), while Thach (2009) suggest that they have highly flexible sleeping selection including tall trees and bamboo bushes. Valleys in Khau Ca have very low levels of bamboo shrubs, however, they are more abundant along the ridges.

Based on the vegetation profile from my sampling, valleys in Khau Ca, as found in other limestone regions, have greater vegetation density with higher coverage from mat species, shrubs, and large shrubs. These layers contribute to the cycling of nutrients (F.S. Gilliam,

2007), higher abundances may indicate greater nutrient supply to the trees, resulting in the higher DBH and higher canopy heights found in the valley plots. While tree density is lower in valleys, the trees are, on average, larger and more established than those found on slopes and ridges.

The lack of larger, established trees elsewhere in Khau Ca means that valleys are an essential resource for the TSNM in terms of providing sleeping sites. The high representation of shrubs and herbs within valleys also makes them appealing to invasive species such as goats. During data collection, ad hoc observations were made of goats wandering into the protected area of Khau Ca from the adjacent farm. While the goats were retrieved and occurrences were reported to be low, the value of valleys to TSNM means that access should be tightly controlled to further minimise the risk of incursions by goats and other invasive animals or plants. It is recommended that the valleys within the core protected area are prioritised for ecological monitoring.

5.5.1.3 Feeding sites

Ridge plots had the greatest number of food species suggesting that they may be important for TSNM for feeding. This appears to be at odds with the findings of Hai (2011), who observed TSNM feeding trees to have 'medium to large' DBH that could support many individuals or whole groups at a time (Hai, 2011). While the ridges of Khau Ca have the greatest density of trees, they were typically smaller, with DBH less than 5cm and heights less than 5m, and less established than those found in the valleys or slopes.

This suggests that the trees found on ridges are likely to be less suitable for regular use by the large bodied TSNM for extended periods. However, the use of lower vegetation such as lianas on ridges may be underestimated by previous studies such as Hai (2011), due to the distance observations were made at – Hai (2011) notes that line of sight was often lost below the upper canopy. My results suggest that ridges may be important sites for feeding and further investigation as to the utilisation of these areas could offer greater insights into the feeding behaviours of the TSNM.

In addition to ridges, slopes are also likely to be important feeding locations for TSNM, as both ridges and slopes have higher frequencies of preferred food genera, including lianas, which

have been identified by Quyet (2014) as a key component of TSNM diets. *Diospyros*, the most selected food choice identified by Hai (2011), was also found predominately on slopes in this study. Slopes also had on average, larger trees than those found on ridges, indicating that feeding trees may be better to support TSNM groups for feeding bouts, which may indicate that these areas may see common usage by the TSNM when foraging.

5.5.1.4 Availability of food species

Studies of the TSNM show that they prefer to consume fruits, seeds and young leaves (Boonratana & Le, 1998; Hai, 2011; Quyet, 2014; Pham et al., 1993/4) and they are highly selective in their choice of diet species. In an analysis of the nutrient content of plants consumed by the TSNM, Anh et al. (2014) found that they selected plants with high water, lipid, protein, non-fibrous carbohydrates, ash, and digestible energy along with low levels of fibre, total phenol, tannin contents. Based on this selection, the TSNM have been found to avoid the most commonly occurring species within Khau Ca due to high levels of phenol and tannin found within them (Anh et al., 2014). Instead, the TSNM prefer to consume leaves with high water content, likely as a result of the lack of water available within Khau Ca. This may explain why the diet of the TSNM has been noted to be dominated by less common species of Khau Ca (Hai, 2011).

This study only captured 10 species of the approximately 158 food species identified by previous studies within the ecological plots sampled. The absence of food species in the ecological plots appears to be a common occurrence, likely due to the TSNM preferring the rarer species in Khau Ca. Despite this, six of the most common diet species – three identified by Hai (2011) and three identified by Quyet et al. (2007) were captured in the ecological plots in this study (Table 5.19). Only *Garcinia fagraeoides* was identified to be amongst the most commonly eaten species across both studies. The limited overlap between diet studies of the TSNM could be a result of this selective feeding due to the climatic conditions or availability of certain food species during each study period.

It is concerning that one of the most commonly consumed species is also Endangered *Syzygium zeylanicum* var. *ellipticum* (World Conservation Monitoring Centre, 1998b). While the distribution of this species is not well known, additional conservation assessment of its occurrence within Khau Ca should be considered due to its importance to the TSNM.

Table 5.19 Key food species captured in this study

Species	Occurrence within my study (n)	Study
Acer tonkinensis	12	Quyet et al. (2007)
Diospyros sp.	77	Hai (2011)
Garcinia fagraeoides	61	Quyet et al. (2007); Hai (2011)
Iodes seguini	1	Quyet et al. (2007)
Syzygium zeylanicum	9	Hai (2011)
Trevesia palmata	5	Hai (2011)

Several studies have attempted to determine the diet of the TSNM (Anh et al., 2014; Boonratana & Le, 1998; Covert et al., 2008; Hai, 2011; Quyet, 2014; Quyet et al., 2007; Le & Boonratana, 2006), however, there appears to be a limited amount of overlap in identified food species between studies (Hai, 2011). It is very likely that this is a result of the TSNM adjusting its diet and feeding strategy based on the vegetation composition of their habitat (Hai, 2011) and general availability of certain species seasonally and year-to-year.

Variations between studies may also be due to differences in methodologies and timing of sampling (Altmann, 1974; Hai, 2011; Rothman, Chapman, & Soest, 2012). For instance, Pham et al. (1993/4) collected diet information from a collection of interviews of local villagers, field observations and examination of stomach contents (Hai, 2011), while Boonratana and Le (1998) identified diet species via observations from high peaks and ridgetops – only two samples were directly collected. Covert et al. (2008) similarly made observations of the TSNM from distances of 200-300m across ravines. Hai (2011) appears to have made the closest observations from 30 to 100m, however, these still largely occurred from hills opposite TSNM groups across two sites. Of all diet studies, Quyet et al. (2007) appears to be the only diet study that took direct samples for post hoc identification.

The distance of observations common across many of these studies is due to the difficulty of close observation of the TSNM in Khau Ca (and other sites) due to the monkeys' shyness and lack of habituation (Hai, 2011). The limestone terrain also makes close follows of the monkeys

very difficult (Boonratana & Canh, 2013; Boonratana & Le, 1998; Hai, 2008; Thach, 2009). Due to the identification of diet species occurring largely from distant observations or identification of plants after the fact, that is, once the TSNM had moved on from an area, it is possible that the list of diet species is not entirely accurate. As noted by Boonratana and Le (1998) and Hai (2011), due to the poor visibility of the monkeys in the canopy and exactly what they were eating, it is possible there has been some mixed identification, particularly at the species level. Overcoming this uncertainty is not clear due to the difficulty in close follows of the TSNM due to a lack of habituation and the difficulty of the terrain. The only way to improve our consistency in collecting food data is to increase the number of longitudinal studies.

5.5.2 Du Gia habitat

5.5.2.1 Composition

The vegetation characteristics across Du Gia plots were largely homogenous, as seen in Khau Ca, with no significant differences captured between the valley, slope and ridge plots. This is likely due to the high level of soil accumulation and low levels of limestone apparent across all plot types. This is somewhat surprising due to the high variation within elevations present across the sample. Elevation ranged from 855m to 1236m, with the mean valley elevation of 896m, steeper than both the mean valley (695m±58.6m) and slope plots (810m ±58.6m) of Khau Ca, yet the presence of soil in plots was much greater, with very little limestone apparent, suggesting less runoff of soil, allowing established root systems from plants to maintain the soil layers.

The general vegetation of Du Gia is dominated by smaller plants such as epiphytes and ferns including *Cyclosorus angustipinnata, Asplenium normale, Antrophyum callifolium, Adiantum philippense,* and *Cyathea gigantea*) and shrubs including *Macaranga henryi, Alpinia globosa,* and *Prunus wallichii*. Medium sized trees including *Elaeocarpus petiolatus, Donella lanceolata* also dominate the landscape in Du Gia. *Donella lanceolata*, a fruiting tree, is the most frequently occurring tree species in Du Gia and can reach heights of 30m (Flora of China, 2020).

Based on the NMDS ordinations and analysis of the variation on display, the vegetation of Du Gia is not homogenous across the ridges, slopes and valleys in contrast to the fairly homogenous nature of Khau Ca. The valleys are distinct from the other plot types based on

the composition of the plant communities (Figure 5.16) and the presence of distinct groups of species typical of the valleys but not the ridges and slopes. Valleys in general had greater vegetation density, species richness, species density but lower tree density. This is because valley plots tended to have low numbers of larger, taller, well-established trees resulting in a higher total basal area, and high levels of mat, shrub and large shrub cover, including lianas. In comparison, ridges and slopes had smaller, shorter trees with a lower total basal area. This is difference is repeated in the analysis of the tree species and food species of the TSNM.

Figure 5.16 Plot types in Du Gia Left: Ridge plot (DGR3). Middle: Slope plot (DGS3). Right: Valley plot (DGV3). Photos: K.Apthorp, 2016.

5.5.2.2 Comparison to Khau Ca

Overall, Du Gia and Khau Ca the two sites vary only a little based on the vegetation characteristics. This is to be expected based on the historical linkage between the two areas (Birdlife International, 2001; N. X. Dang et al., 2014; Kempinski et al., 2009). The key differences between Khau Ca and Du Gia are apparent in the significantly higher mean canopy cover evident in Khau Ca. The high level of canopy cover here suggests greater canopy connectedness across the plots, likely important for both TSNM feeding and movement. Hai (2011) observed that the TSNM spends 92 per cent of their time feeding in the middle and high canopy. Quyet (2014) also found that the TSNM used branches and boughs most commonly over trunks, lianas and twigs. While flexible branches are used during feeding due to the location of most preferred foods in the fringes of trees (Quyet, 2014), the size of the TSNM as one of the largest Asian colobines, suggests they require larger trees to support their use. This could suggest that Khau Ca offers more secure feeding sites in the canopy than that

in Du Gia. The higher density of trees found in Du Gia, is due to the large number of small tree stands found there.

Higher canopy coverage also maintains pathways for arboreal primates – this is a potentially important factor for species such as the TSNM, which have been described as being habitually arboreal (Boonratana & Le, 1998; Hai, 2011; Quyet, 2014; Thach, 2009). The preferred locomotion of the TSNM is quadrupedal walking and running (53.31%), mainly along horizontal tree branches (Quyet, 2014). Leaping and climbing accounted for a total of 28.30%. This suggests that overlapping trees large enough to support their weight is the preferred environment (Fleagle & Mittermeier, 1980). Khau Ca trees had on average, larger DBH, higher canopies, a greater total basal area and significantly more canopy coverage than trees in Du Gia.

Higher canopies and greater canopy connectivity also offers greater protection from terrestrial predators, though the level of TSNM predators within Khau Ca appears low (Kirkpatrick & Grueter, 2010). The presence of three cat species has been recorded for both Khau Ca and Du Gia (N. X. Dang et al., 2014), however none were reported in the Khau Ca Forest during this study. In Du Gia, the much larger patch of available forest means that large predators could still persist, suggesting that taller canopies may offer greater protection, while greater canopy connectivity may offer more escape routes for climbing predators. As quadrupedal walkers and runners, more horizontal continuous connections in the canopy are important (Fleagle & Mittermeier, 1980) to facilitate the TSNM movement.

Du Gia was found to have a higher density of trees compared to Khau Ca, however the trees in Khau Ca had a larger mean DBH and mean height, suggesting the trees in Khau Ca were more established than those of Du Gia. The trees of Khau Ca are on average, taller, larger and maintain greater canopy connection than those found in Du Gia, however little is known about the preferred structure of TSNM sleeping trees. The TSNM do not appear to have established sleeping sites (Hai, 2008; Thach, 2009), they reportedly prefer to settle in valleys, on branches low to the ground (5 to 10m) potentially as predator avoidance (Quyet, 2014; Thach, 2009) or to protect from harsh weather such as wind and rain (Boonratana & Le, 1998; L. W. Cui et al., 2006). Unlike the wider Du Gia Forest, Khau Ca no longer appears to have major terrestrial

predators (N. X. Dang et al., 2014; Kirkpatrick, 1995), which could indicate sleeping choice is largely focussed on thermoregulation or based on a cultural memory of heavy predation in the past (Z.-H. Liu & Zhao, 2004; Nishida, 1987). If the latter, this memory could be important for their survival should they be able to disperse into the Du Gia Forest. Further research is required to better understand TSNM sleeping tree choices.

Khau Ca and Du Gia also differ topographically. As demonstrated within the Du Gia plots, there is very little limestone due to high levels of soil. As a whole, Du Gia predominately sits on sandstone and only limited portions are limestone (N. X. Dang et al., 2014). The lack of limestone coupled with lower canopy coverage demonstrated in Du Gia could impact the way TSNM potentially adapt to the wider Du Gia Forest. Currently, the TSNM are restricted to the limestone karst forest of Khau Ca and have been for several decades if not longer. As a result, they may have retained their ecological niche or adapted to the food species available within Khau Ca (Anh et al., 2014) that are conditioned to survive the harsh conditions of the limestone karst. Due to differences in the geology of Du Gia, being a mix of both limestone karst and sandstone, it may then impact the composition and availability of certain food species in Du Gia.

It remains unclear whether the limestone itself is an important substrate for the TSNM. In other species such as the CBL, the limestone karst is important stratum for many social behaviours, locomotion and as a sleeping site (Hendershott, 2017; Hendershott et al., 2018) though usage of the limestone varies across other limestone langurs (C. Huang & Li, 2005; Workman & Schmitt, 2011; Xiong et al., 2009; Q. Zhou, Luo, Wei, & Huang, 2013). While observations of the TSNM on the ground are limited, they have been observed by Hai (2011) to utilise the ground occasionally for travelling, feeding and resting. The extent of terrestrial behaviour for the TSNM may be significantly underestimated due to the difficulty in observing the primates (Boonratana & Le, 1998; Hai, 2011; Quyet, 2014). As a result, the extent of the use of the limestone karst by the TSNM is not fully resolved and should be further investigated to determine whether Du Gia with its geological mix of substrates may impact TSNM behaviours.

Other *Rhinopithecus* species, collectively considered arboreal, have also been found to exhibit terrestrial behaviours to varying degrees for resting, movement across open patches (Bao-Qi, 1993; Bleisch et al., 1993; Kirkpatrick, 1996; Long, Kirkpatrick, Xiao, & Zhong, 1998; Su et al., 1998). Until we can fully understand how the TSNM interacts (or doesn't interact) with the limestone karst, it is unclear how they may adapt to forests on sandstone. This, coupled with limited understanding of TSNM terrestrial behaviours, suggests that future studies should seek to fill this gap to complete our understanding of how the TSNM use their habitat.

5.5.2.3 Availability of food species

The presence of feeding sites may also impact the sleeping locations of the TSNM (D. Li et al., 2013). Previous studies (Covert et al., 2008; Hai, 2011; Quyet et al., 2007; Pham et al., 1993/4) have identified 158 species consumed by the TSNM, however my sampling captured just 12 across the two sites (Table 5.20), and only two of those were found in both Khau Ca and Du Gia. All of the species found in Khau Ca were classified as the most commonly consumed by the TSNM. In contrast, only two highly consumed species were found in Du Gia. To account for the low capture of ecologically important components of the TSNM habitat, I instead used a genera-level analysis of the availability of plants consumed.

Table 5.20 Food species found in Khau Ca and Du Gia

Species	Du Gia occurrence (n)	Khau Ca occurrence (n)	Total occurrence (n)	IUCN Red List Status
*Acer tonkinensis**	0	12	12	NE
Canarium album	2	0	2	NE
Elaeocarpus petiolatus	205	0	205	LC
Garcinia bracteata	1	0	1	LC
*Garcinia fagraeoides**	8	61	69	NE
Gnetum montanum	12	0	12	LC
*Iodes seguini**	0	1	1	NE
*Pometia pinnata**	0	5	5	LC
*Premna flavescens**	0	1	1	NE
Saraca dives	1	0	1	NE
*Syzygium zeylanicum**	13	9	22	EN
*Trevesia palmata**	0	5	5	LC
	242	**94**	**336**	

*Indicates the most commonly consumed species as identified by Hai (2011) and Quyet et al. (2007).

Of the 104 food genera identified in previous studies by Boonratana and Le (1998); Covert et al. (2008); Hai (2011); Quyet (2014); Quyet et al. (2007), only 44 were captured within Khau Ca and Du Gia (Table 5.21). Similar numbers of food genera were captured across the two plots: 35 genera in Khau Ca and 33 were found in Du Gia. *Diospyros* was the second most common food genus identified in Du Gia, which was also one of the top food choices of the TSNM as observed by Hai (2011). *Syzygium* was similarly found as a common food genus in Khau Ca, and the sixth most common food genera sampled in Du Gia. This represents diet genera across all strata (seedlings, small shrubs, shrubs, large shrubs, trees and liana) of the Khau Ca and Du Gia plots.

Food tree genera were more abundant within Khau Ca (n=30) compared to Du Gia (n=23). The total basal area of the top ten food genera was over two times greater than that found in Du Gia. As basal area was measured for trees only, this shows that a large proportion of food species found in Du Gia were at the mat, shrub or large shrub layer. As Quyet (2014) observed the majority of feeding activities occurring in trees, or larger structures, it appears that Khau Ca offers a greater range of available feeding trees than Du Gia.

Table 5.21 Top ten food genera captured across Du Gia and Khau Ca

	Du Gia				Khau Ca				
Genus	**Ridge (n)**	**Slope (n)**	**Valley (n)**	**Basal area* (m^2)**	**Ridge (n)**	**Slope (n)**	**Valley (n)**	**Basal area* (m^2)**	**Total (n)**
Elaeocarpus	219	2	0	14.98	4	3	7	5.18	235
Diospyros	0	57	18	20.34	19	46	12	84.20	152
Tetrastigma	8	2	18	0	41	23	39	0	131
Litsea	41	26	8	7.85	8	7	2	4.09	92
Polyalthia	0	13	4	6.35	24	18	31	37.90	90
Garcinia	1	7	1	0.71	56	5	0	0.95	70
Syzygium	13	6	12	4.99	6	5	5	4.98	47
Sapindus	3	11	1	1.51	1	25	3	1.51	44
Acer	1	0	0	0	40	0	0	5.98	41
Camellia	0	0	34	10.53	0	0	5	0.03	39
Total	**286**	**124**	**96**	**67.26**	**199**	**132**	**104**	**144.82**	**941**

*Basal area of trees only, other totals include other vegetation layers.

Based on the feeding behaviour of the TSNM observed by Hai (2011), 82 per cent of feeding occurred in the middle canopy (10 to 17m), with feeding trees characterised as 'medium to large size in diameter,' supporting multiple individuals. While Hai (2011) does not elaborate on what constitutes medium or large diameters, this study applied the following breakdown: small trees with a DBH of 10cm and less, medium trees with DBH 11-30cm and large trees with a DBH over 30cm. Based on this, over 35 per cent of potential diet trees were medium or large in Khau Ca and less than 20 per cent of potential feeding trees within Du Gia plots could be classified as medium or large.

Based on the capture of genus and species-level food choices in Khau Ca compared to Du Gia, it appears that more frequently consumed species and a large range of food general are to be found in Khau Ca. Yet this may not make Du Gia unfit for the TSNM, as they appear to be capable of adapting their dietary requirements based on the composition of their immediate habitat (Hai, 2011). Studies of TSNM diet suggest that the composition of their diet is related to availability, with a preference for leaves with a high protein and lipid concentration, and low in fibre (Anh et al., 2014; Hai, 2011; Quyet et al., 2007). While certain species may be preferred (Hai, 2011; Quyet, 2014), they may be able to adapt their diet as required.

Such adaptability has been observed in other snub-nosed monkeys; the black-and-white snub nosed monkey and the golden snub-nosed monkey consume high levels of lichen in winter as a fallback food (Grueter, Erb, Ulibarri, & Matsuda, 2022; Grueter et al., 2009; S. Guo, Li, & Watanabe, 2007; Kirkpatrick, 1996; Kirkpatrick et al., 1999; Yiming Li, 2001; H. Zhao et al., 2020). In one population of black and white snub-nosed monkey, lichens were recorded as making gup 95 per cent of their diet (Z. F. Xiang, Huo, Xiao, Quan, & Grueter, 2007). The nutritional value of lichens is low in proteins, fibre and tannins but higher in sugars and starch (Kirkpatrick, 1996; X. Liu, Stanford, Yang, Yao, & Yiming, 2013; H. Zhao et al., 2020).

Currently, over 158 food species have been identified across several studies (Appendix 3.3.1) with little overlap: Boonratana and Le (1998); Covert et al. (2008); Hai (2011); Quyet (2014); Quyet et al. (2007). This represents a much higher variety in the TSNM diet than has been demonstrated in other *Rhinopithecus*: 59 plant species for black-and-white snub-nosed monkey (Ding & Zhao, 2004); 51 species for the golden snub-nosed monkey (B. Li, Chen, Ji, &

Ren, 2000); 104 species for gray snub-nosed monkeys (Y. Guo et al., 2018), and 14 species for the Myanmar snub-nosed monkey (Yang et al., 2019). It is worth noting that when presented with additional species from their natural home range, a captive group of Myanmar snub-nosed monkey consumed 170 species (Yang et al., 2019).

Based on the dietary profiles of the black-and-white snub-nosed monkey and Myanmar snub-nosed monkey, the TSNM list may not be entirely inflated. Yet due to the lack of consensus across studies on the makeup of the TSNM diet, it is hard to determine whether Du Gia has enough dietary variety to maintain a healthy TSNM population. The wide variety of genera identified by Boonratana and Le (1998); Covert et al. (2008); Hai (2011); Quyet (2014); Quyet et al. (2007), could suggest that the TSNM has a generalist approach to their preferred diet species. It could suggest that the TSNM have a wide-ranging diet that may vary widely in any given year based on the availability of certain food species, therefore accounting for variation reported.

Overall, the vegetation characteristics sampled within Du Gia do not suggest a significant difference between the two sites. This is to be expected due to the historical linkage between Du Gia and Khau Ca (Birdlife International, 2001; Kempinski et al., 2009). The two sites do, however, display a reasonable level of dissimilarity based on plant communities, though the exact cause for this difference is not clear. It is possible that it could be due to differences in the substrate particularly between limestone and more soiled components of the forest. It could also be a result of climatic or environmental health due to human interactions at each site. The latter is of particular concern when comparing the suitability of Du Gia as a potential habitat for the Critically Endangered TSNM.

5.5.2.4 Habitat protection and human interaction

Approximately 160 TSNM persist in Khau Ca (Fauna & Flora International, 2020), protected by a dedicated mix of community rangers, national park officials and conservation groups. Community rangers have relatively high pay compared to other local employment options (Anh et al., 2014) and carries a level of prestige within the local community. The core team of community rangers tasked with monitoring the TSNM within Khau Ca, are highly skilled and have become talented research assistants. During the course of this study, the team assisted as guides and with ecological sampling. The success of Khau Ca is in no small part due to these

rangers and conservation efforts to raise community awareness of the TSNM. The TSNM have become a point of pride, and many locals support the need to protect the Khau Ca zone for the TSNM. There is, however, conflicted opinions amongst the community at to the potential benefit of the introduction of ecotourism to the area.

The isolation and success of Khau Ca is in stark contrast to what was observed in Du Gia Forest during this study. The Du Gia Forest sampled in sat within Minh Son, roughly 2 km from Khau Ca and is frequently used by locals and visitors to the area. A zinc and aluminium mine (Hai, 2011) sits a few hundred metres further along a dirt road, heavily trafficked by large trucks travelling back and forth from the mine. Mining is a key factor in the loss of forest in Vietnam (N. X. Dang et al., 2014; Hai, 2011; Le & Boonratana, 2006). Mining destroys the landscape, produces pollution, noise and the presence of large trucks (N. X. Dang et al., 2014). In addition to this large-scale interruption on the very edge of the forest, a significant amount of logging was observed within the forest of Du Gia (Figure 5.17). The constant evidence of logging was observed during every visit to the forest in this area, despite the area being protected under law.

Figure 5.17 Evidence of logging in Minh Son Photos: K.Apthorp, 2016.

Rangers responsible for monitoring and protecting the forest around Minh Son, do not have the same relationship with the forest observed in Khau Ca. The ranger responsible for assisting with this study was new to the area had never been in this area of forest. A lack of regular patrolling by rangers from the Du Gia Nature Reserve is clearly evident by the high levels of logging observed just around the sample site. The loggers did not appear to be concerned about being caught – at several logging sites, the wood had been laid out for further cutting over the next few days. Part of the reason for this is due to the consequences of being caught. Logging is likely carried out by the local people – prior to the establishment of the Du Gia Protected Reserve, approximately 7,310 ethnic Hmong, Tay, Dao and Kinh ethnic groups inhabited the area (Birdlife International, 2001). At the time of the study, approximately 130 families lived around the reserve in the Minh Son commune (Anon, personal communication, November, 2016).

Punishment for logging includes a fine of approximately US$200 and includes court, however given that the average monthly income for the region is US$243 (Data, 2021), rangers report that this rarely happens due to the poverty of local households (pers comm, Anon). While legislation exists to prevent illegal logging and poaching, enforcement of these laws can be weak and therefore have little effect (Lippold & Thanh, 1998). The strong social connection within communes makes it difficult for rangers to prosecute lawbreakers (Lippold & Thanh, 1998) and the potential of corruption amongst law enforcement adds an additional layer to an already complex relationship between protected forests and the remote and often poor communities that rely upon them (International Fund for Agriculutural Development, 2004; Lippold & Thanh, 1998).

These issues make the connection between Khau Ca potentially disastrous for the Critically Endangered TSNM, the threats of the mine, widespread logging and use of the forest could prove fatal for the future health of the TSNM, and any potential link could have the potential to provide easy access to the TSNM for poachers or invasive species via the newly established Du Gia National Park.

5.5.3 Corridor

The issues of connecting the Du Gia Nature Reserve and Khau Ca as part of the Du Gia National Park are unlikely to be an issue in the near future due to the lack of viable connecting corridor between the two areas. The land surrounding Khau Ca consists of agricultural areas and acacia plantations, however, reports on the presence of a corridor between Khau Ca and Du Gia have varied over the years. Previous studies of the TSNM in Khau Ca have noted the possibility of a vegetation corridor linking Khau Ca and Du Gia (Covert et al., 2008; N. X. Dang et al., 2014). Other studies have been less confident in the continued existence of any corridors (Kempinski et al., 2009; Truong & Linh, 2017). During this study, it became apparent that the existence of this corridor was no longer a viable option to link the two regions.

The uncertainty as to the status of the corridor is likely due to its condition. While a 5km vegetation connection was thought to remain at the beginning of this study, during sampling of Du Gia, the head of the Ha Giang National Park visited the corridor to assess viability and reported that the corridor was no longer intact. This was due to the widespread destruction of the under canopy for cardamom and Lysimachus cultivation, both of which grow well on limestone slopes and valleys (Trinh Dinh Hoang et al., 2015; James, 2016) (Figure 5.18).

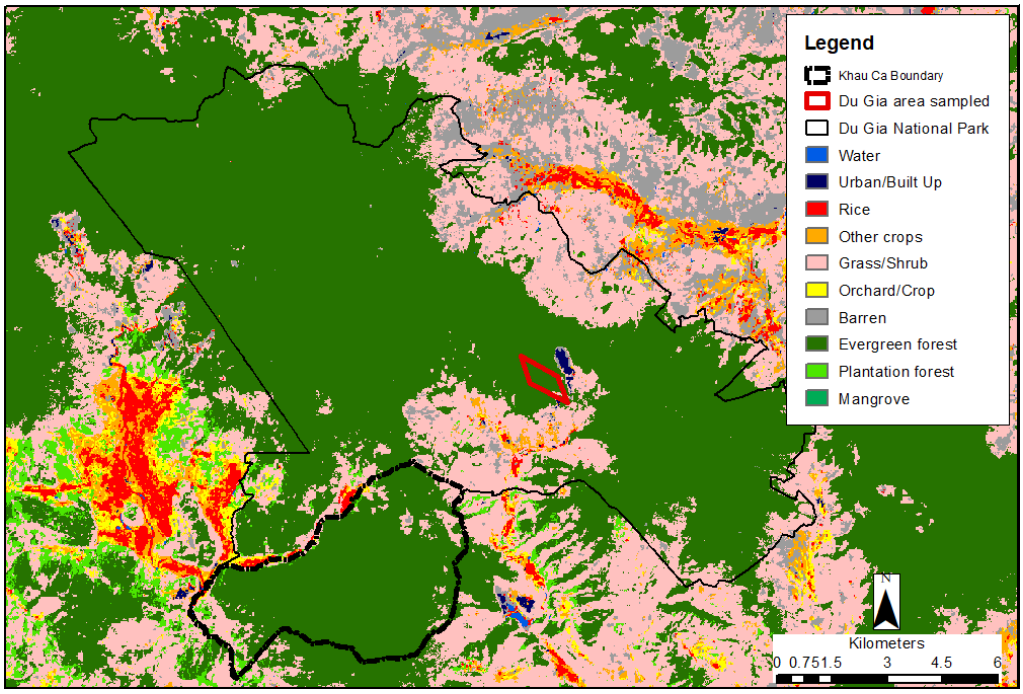


Figure 5.18 Land-use map showing high level of disturbance around Khau Ca and Du Gia. Land use layer: Earth Observation Research Centre (EORC) ALOS/ALOS-2 Science Project "High-resolution land use cover map" (HRLULC) of the Japan Aerospace Exploration Agency (JAXA, 2020 [version 20.06]).

The farming of these crops results in canopy thinning to reduce canopy cover (Trinh Dinh Hoang et al., 2015), thereby reducing the arboreal pathways available for any potential TSNM movement. While FFI are working to reduce the farming of these cash crops in other TSNM areas, including Tung Vai (Trinh Dinh Hoang et al., 2015), the income provided to households makes it a difficult task, and it continues to threaten the future of the small TSNM population within the area (Knight, 2019).

Based on the lack of a clear, established corridor connecting the two regions, the expansion of the Du Gia National Park to include Khau Ca may not offer any additional habitat for the TSNM. While this may be a good thing for the TSNM based on the current high levels of logging, low law enforcement and presence of mining in the Du Gia region, it also potentially ensures that the TSNM in Khau Ca will never be able to expand the population beyond the capacity of their current habitat. This problem is shared by other snub-nosed monkeys such as black-and-white snub-nosed monkey (L. Li et al., 2009), for which a lack of viable vegetation corridors continues to restrict any population growth. For the TSNM of Khau Ca, with their limited genetic diversity, a larger habitat is unlikely to solve their population struggles. Yet, the discovery of new populations of Myanmar snub-nosed monkeys (Long YC, 2012) does provide some hope. The size and difficult terrain of Du Gia has the potential to hide an as yet undiscovered population of TSNM (Covert et al., 2008; N. X. Dang et al., 2014). Based on the findings of this study, it is suggested that serious work is needed to improve the quality and safety of the Minh Son Forest closest to Khau Ca for the TSNM, and a dedicated and protected corridor established before there is any hope for the survival or even presence of the Khau Ca TSNM in Du Gia. While this work is underway, extensive surveys of Du Gia are necessary to determine if there is any possibility of undiscovered TSNM, which could have significant positive impact on the future of the TSNM.

5.6 Conclusion

The results of this study provide some of the first analyses to consider the broader vegetation profile of the habitat of the TSNM. Understanding the herb and shrub layer can reflect the previous use of the area as a result of anthropogenic activities such as agricultural practices

and support ongoing planning for a habitat as whole and (Spicer et al., 2022; M. Vellend & M.A. Geber, 2005).

Based on the compositions of the plots and their vegetation characteristics, it is recommended that ridge and slope plots are monitored as critical sites for food species, while valley compositions should be managed as the only areas available within Khau Ca with suitable sleeping sites for the large-bodied TSNM. Understanding the vegetation profile can assist conservationists in monitoring habitat health and planning for the future. In forest fragments like Khau Ca, the isolation can lead to low genetic diversity, not just for the TSNM but also the vegetation (Gilliam, 2007). This can result in plant communities that are unable to adapt to changes such as altered environmental conditions due to climate change, anthropogenic activities, or the introduction of invasive species (Gilliam, 2007).

The findings of this study also suggest that, in light of the high levels of human activity through logging and hunting and low levels of enforcement reported in Du Gia (N. X. Dang et al., 2014), any efforts to improve forest connections between Khau Ca and Dua Gia should be carefully considered. The TSNM are best served by the protection provided by their current forest island and trained community rangers. If rehabilitation of a connection is sought, a major survey of the use and human threats to the Du Gia Forest should be undertaken in an effort to mitigate the risks any TSNM might face should the larger Du Gia forest become accessible. It is also recommended that a major survey of the existing species, particularly primate species that may still inhabit Du Gia. In doing so, we can reach a better understanding of the potential risks and benefits such an expansion to the TSNM habitat would offer.

In addition, further study, extensive training, increased enforcement and education, and TSNM-preferred vegetation cultivation is needed in surrounding communes if they are to ever successfully venture beyond the safety of Khau Ca into Du Gia.

Part three: *Nomascus nasutus* (cao vit gibbon)

Abstract

The CVG is one of the world's most Critically Endangered primates, with only 135 individuals known to inhabit a patch of limestone karst forest that sits on the Vietnamese-Chinese border (Fauna & Flora International, 2021; IUCN, 2022a). Until its rediscovery of in Vietnam in 2002 and across the border in China in 2006, the CVG had been considered extinct since the 1950s (Fan et al., 2011; B. Tan, 1985). The CVG has been categorised as Critically Endangered since its rediscovery (IUCN, 2022a).

Historically, the CVG are reported to have had a distribution throughout southern China and northern Vietnam (Trung & Hoang, 2004). Today, the CVG inhabit a transboundary patch of monsoon limestone karst forest that straddles the Vietnam-China border. The majority of this population live within the Cao Vit Gibbon Conservation Area (CVGCA) in Trung Khanh, Cao Bang Province, Vietnam. A smaller number of individuals mainly inhabit the Bangliang National Nature Reserve (BNNR) in Jingxi County, Guangxi, China. The two contiguous protected zones are home to the only population of CVG in the world (C.-Y. Ma et al., 2020).

Major threats to the CVG have included hunting, and habitat loss and degradation (Dat et al., 2008a; Insua-Cao et al., 2012). Within Trung Khanh, forests have been subjected to high levels of degradation through collection of forest resources and logging, conversion of land for agricultural use and expanding human populations (Trung & Hoang, 2004). Efforts of conservation groups, including the FFI have had success through education programs highlighting the need for protection for the CVG and its habitat, and implementing programs to reduce reliance on forest resources such as firewood (Tatarski, 2017).

To date, most published studies have focussed on gibbons from BNNR. The following two chapters will provide an analysis of the CVG habitat within the CVGCA and a comparison to an area identified by Fan et al. (2013) as having potential for habitat expansion for the CVG. The first chapter will cover traditional in situ ecological sampling and analysis, and the subsequent chapter will present the results of MaxEnt modelling of the CVG distribution, using GIS and satellite imagery.

Chapter 6 Analysis of the Cao Vit Gibbon Conservation Area (CVGCA) habitat of the cao vit gibbon (*Nomascus nasutus*) and potential for expansion.

6.1 Introduction

All members of the Hylobatidae family are currently experiencing some type of population pressure (J. Zhou et al., 2008). Of the 20 recognised species within the Hylobatidae family, 95 per cent are classified as Endangered or Critically Endangered by the IUCN Red List (IUCN, 2022a). All gibbon species have experienced habitat loss and fragmentation due to human expansion, poaching, over exploitation of forest resources and land conversion for agricultural or urban development within their historic ranges. They have managed to endure these environmental changes throughout their ranges despite having slow life histories and expected fragility to any habitat change that reduces food availability (Jablonski & Chaplin, 2009; Ping Li et al., 2022; Lootvoet, 2015). It has, however, come at a cost; all gibbon species are currently experiencing some form of population fragmentation or stagnation (IUCN, 2022a; Turvey et al., 2015).

For the CVG, its survival in the face of extreme habitat disruption and anthropogenic threats was unexpected. By the 1960s, the species was thought to be extinct throughout Vietnam and China (Fan et al., 2010) until its rediscovery in 2002 (Trung, Hoang, Long, & Geissmann, 2002). Today, the CVG is one of the most endangered apes in the world with a global population of 135 individuals inhabiting a transboundary limestone forest fragment in northern Vietnam and southern China (Fauna & Flora International, 2021; IUCN, 2022a).

The habitat of the CVG poses a distinct challenge for researchers due to the rugged limestone karst forest and the international border that bisects the forest fragment. The majority of CVG (17-19 groups) reside exclusively within the Vietnamese forest in the protected Cao Vit Gibbon Conservation Area (CVGCA), established in 2007 (Fan et al., 2013; Insua-Cao et al., 2012; C.-Y. Ma et al., 2020). Three groups are also known to live within the Chinese forest in the protected Bangliang National Nature Reserve, established 2009 and promoted to a national nature reserve in 2013 (C.-Y. Ma et al., 2020). At least two of the Chinese-based groups have also been observed to move across into the Vietnamese forest (Fan et al., 2010; C.-Y. Ma et al., 2020).

Studies of the CVG have primarily focussed on the Chinese-based gibbon groups in the BNNR, despite the fact that the majority of CVG inhabit the Vietnamese forest in CVGCA. The CVGCA is home to up to 22 groups (C.-Y. Ma et al., 2020) and has had many unpublished surveys as part of FFI's extensive work in the region but is somewhat underrepresented as the study population in published works. This is a common bias in primatological studies, where behavioural and ecological analyses often focus repeatedly on single study sites. This can allow the collection of highly detailed data (Willems & Hill, 2009); however, it can also lead to results from specific sites being applied to the entire distribution of a species, without consideration of site-specific interactions. Although the BNNR and CVGCA are contiguous forest patches, it is possible that key insights as to the CVG behaviour, diet and ecology are missing due to this sampling bias.

While protected areas are important to conserving at risk environments and species, it is also important to consider habitat and forest composition on a landscape scale to capture the full use of a region by a target species (Arroyo-Rodriguez & Mandujano, 2009). The focus of only monitoring and protecting core areas, defined as specific areas within a home range where concentrated activity occurs (Samuel, Pierce, & Garton, 1985), can be problematic. Focusing on this core can obscure the role that surrounding forest can play and risk under-preserving adjacent forest patches (Asensio, Brockelman, Malaivijitnond, & Reichard, 2014; Buchanan, Fredrickson, & Seaman, 1998). The degradation of surrounding forest patches beyond cores can then further limit the movement and expansion of species.

The core CVG habitat within the CVGCA is linked to regenerating forest to the southeast, and efforts to restore parts of this forest within the protected area in Vietnam, have included the plantation of CVG food trees across six valleys (3.23 km^2 in total) at sites previously used for grazing or agriculture (C.-Y. Ma et al., 2020). Gibbons have been observed to enter this region in search of fruit (particularly fruit trees) but do not remain in the area for prolonged periods (pers. comm CVGCA National Park Rangers).

On both sides of the international border, the CVG habitat is surrounded by villages, infrastructure including roads, and agricultural land. While the protected area appears to retain some degree of linkage to forest fragments in China and along the border, the true

nature of these linkages is not clear. As gibbons are canopy dwellers and travel predominately by brachiating, their ability to traverse breaks in forest continuity and obstacles such as roads, rivers or clearings is limited and can put them at greater risk of predation or death (Fan et al., 2013; Umapathy & Kumar, 2003). Failure to act to investigate opportunities to expand the CVG habitat may result in an island forest fragment, similar to that experienced by the TSNM in Khau Ca. Without the opportunity to disperse to new habitat, the growth of the CVG population is likely limited (Fan et al., 2013).

An assessment of the current CVG transboundary habitat and surrounding forest patches using remote sensing by Fan et al. (2013), considered five forest zones (Zones I to V) that surrounded both the Chinese and Vietnamese CVG protected areas, in an effort to identify areas that could be suitable as additional habitat. Zone I included the current distribution of the CVG within the protected BNNR and CVGCA forest; Zones II and III were forest fragments adjacent to the BNNR, located on the Chinese side of the border (Fan et al., 2013). Zones IV and V were forest fragments that bordered the Vietnamese CVGCA to the south (Fan et al., 2013).

The findings of the evaluation identified Zone I, consisting of the combined BNNR and CVGCA habitat, as an area of high-quality habitat and a conservation priority (Fan et al., 2013). Through their analysis, Zone I was found to be of high-quality based on tree coverage and had the current capacity to support approximately 120 gibbons (Fan et al., 2013). Ongoing management and forest rehabilitation of this zone would support a further 36 individuals according to Fan et al. (2013).

Zone IV was also recommended as a conversation priority as two areas within this region were identified as potential habitat expansions, with pre-existing corridor linkages to the CVGCA (Fan et al., 2013). Habitat restoration of these two areas was predicted to support an additional 132 gibbons (Fan et al., 2013), more than doubling the carrying capacity of the current CVG distribution in Zone I.

The fragments in Zone II, III and V were found to contain predominately scrub vegetation and due to their separation from the core CVG habitat by road and river barriers, were not identified as candidates for potential habitat expansions (Fan et al., 2013). Analysis was

undertaken using land cover mapping and remote sensing data; no ecological sampling was undertaken within Vietnam (Fan et al., 2013).

The findings of Fan et al. (2013) provide an opportunity to further investigate the opportunity to expand the current habitat of the CVG to promote further population growth. Noting the findings by Fan et al. (2013) that the current CVG habitat within the BNNR and CVGCA combined areas is approaching carrying capacity, without action now, researchers may miss the opportunity to contribute to the long-term recovery of a Critically Endangered species.

It is thus the aim of this study to use in situ sampling to determine the ecological profile of both the core CVG habitat within the CVGCA and the primary forest fragment identified within Zone IV as an area of high conservation priority. A comparison between the two areas will aim to identify whether the Zone IV area varies significantly from the habitat of the CVG to provide further data on the suitability of this area as a potential habitat extension.

In analysing the suitability of Zone IV habitat for the CVG, I hypothesise that Zone IV has a similar general plant community composition and food species composition to the CVGCA based on species abundances, as they were historically part of the same forest patch. However, based on the lack of dedicated protections compared to the CVGCA, I also hypothesise that Zone IV will have lower quality vegetation composition reflected by lower mean canopy height, canopy cover and species richness and diversity indices compared to the CVGCA, requiring significant conservation efforts for rehabilitation.

6.2 Methods

6.2.1 Study site

6.2.1.1 Site one: Cao Vit Gibbon Conservation Area

The only remaining population of the CVG is restricted to an area of forest straddling the northern Vietnamese and Chinese border (Figure 6.1). Due to the difficulty in accessing the entire CVG habitat due to the international border, this study was undertaken wholly within the Vietnamese portion, in the CVGCA (22˚53’-56.4’N, 106˚30’-33’E), Trung Khanh, Cao Bang in northern Vietnam. The CVGCA was established by the Ministry of Agriculture and Rural Development based on recommendations by the Cao Bang Provincial People’s Committee in 2007 (Anon, 2007; Dat et al., 2008b; Insua-Cao et al., 2012) and covers approximately 16.56

km^2 of disturbed primary and secondary forest. An additional 65.3 km^2 of forest contiguous with the CVGCA, forms the BNNR – the Chinese component of the CVG distribution established in 2009 (Insua-Cao et al., 2012). I was unable to access the BNNR area to undertake as part of fieldwork.

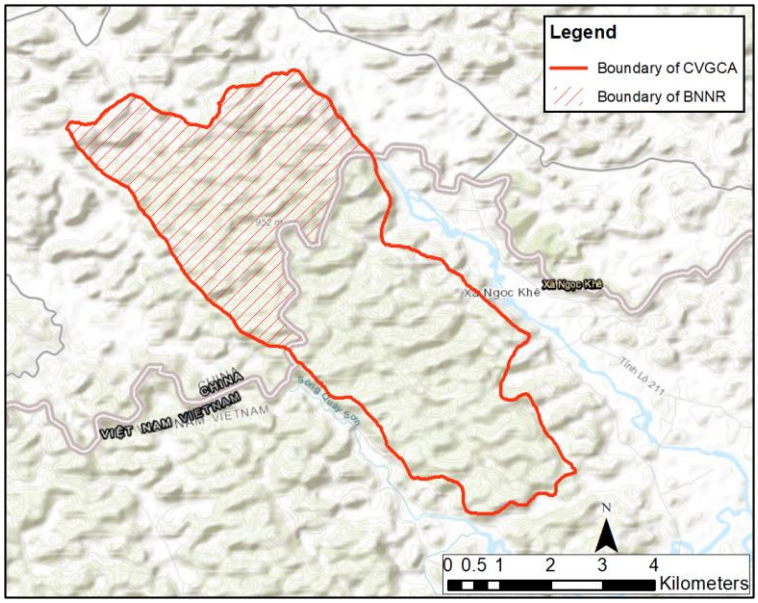


Figure 6.1 Boundaries of the CVGCA and BNNR protected zones. Basemap source: (ESRI et al., 2021)

The terrain of the CVG habitat is limestone karst (Figure 6.2), supporting tropical monsoon limestone karst forest that has undergone significant degradation due to logging and expanding agricultural activities since the 1980s (Dat et al., 2008b; Insua-Cao et al., 2012). The topography of the CVGCA is characterised by steep limestone mountains with elevations of 400m to 950m (C.-Y. Ma et al., 2020).

Figure 6.2 Terrain of the CVGCA. Photos: K. Apthorp, 2016.

The Vietnamese CVGCA is surrounded by three communes: Ngoc Con, Ngoc Khe and Phong Nam, and bounded to the north and south by the Quay Son River (Insua-Cao et al., 2012). A road also bounds the eastern border of the CVGCA. Due to these major boundaries, the CVG are limited in their ability to expand their existing habitat within Vietnam (Figure 6.3).

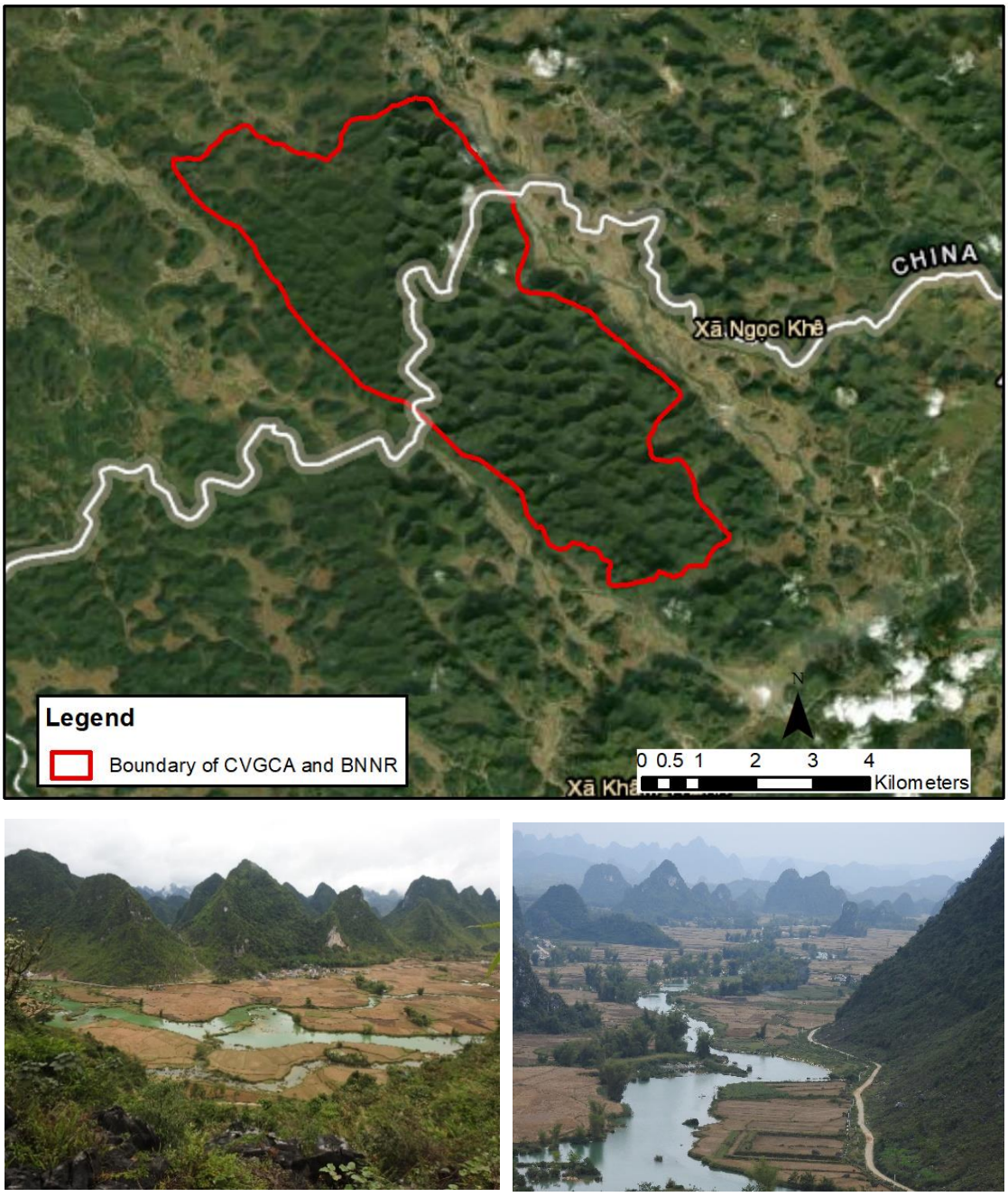


Figure 6.3 Boundaries of CVG protected zones. Top: map showing boundaries of river and roads surrounding CVGCA and BNNR. Bottom: Quay Son River and farmland surrounding the CVGCA. Basemap: Esri (2009). Photos: K. Apthorp 2016.

The CVGCA was historically used by the surrounding communes for farming and hunting. The base camp for this study was located within the core area of the CVGCA in a former corn plantation. Many of the surrounding valleys are ex-crop sites are currently undergoing regeneration (Figure 6.4). This area was also still visited by large mammals, including sun bears, which had destroyed the original basecamp water tank months prior to the study. The vegetation on the slopes and ridges of the CVGCA displayed less disturbance from historical farm use, due to the difficulty in navigating the limestone karst.

Figure 6.4 Base camp in CVGCA. Photos: K. Apthorp, 2016.

6.2.1.2 Site two: Zone IV

Sampling was also carried out within a region identified by Fan et al. (2013) as a second-tier conservation priority area after the CVGCA as it could be a potential habitat extension for the CVG (Figure 6.5). This region, within an area labelled Zone IV (Fan et al., 2013), sits southwest to the CVGCA, and was reportedly once home to the CVG prior to 2000 (Dat et al., 2008b).

This forest region is dominated by limestone karst, similar to that of the CVGCA region, however in some areas, soil accumulation is much greater. Zone IV has been protected since 2012 (Fan et al., 2013); however, it is still accessible by grazing livestock, including cattle. The boundary of this area is surrounded by valleys converted to cropland, with bamboo plantations along the edges.

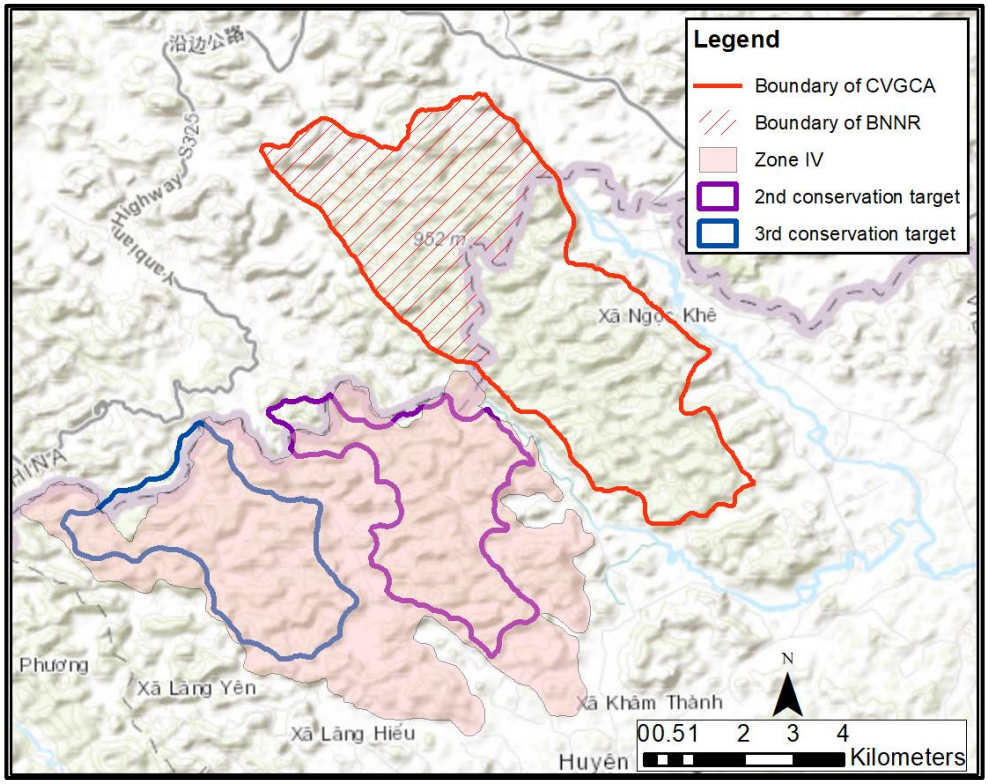


Figure 6.5 Map of potential habitat expansion for the CVG in Zone IV. Map shows Zone IV with the second and third areas of conservation priority (after the CVGCA and BNNR region) as identified by Fan et al. (2013). Basemap: Esri (2021). Zone IV and Conservation target polygons: Fan et al. (2013).

Local farmers and rangers also reported the presence of macaques in this region between 2011 and 2016, raiding farms for food. The last reported sighting of macaques prior to this study was only a few weeks earlier, suggesting ongoing activity in the region. No macaque sightings were made during fieldwork collection.

CVGCA and Zone IV are separated by a 'corridor area' and a larger expanse of actively farmed agricultural land in the valleys (Figure 6.6). Forest in this region is restricted to the steep slopes and peaks of the limestone karst, with valleys extensively used for crops and cattle and goat grazing. Transition zones from valley to slope in the corridor area are largely characterised by scramble vegetation.

Figure 6.6 Limestone karst and topography of Zone IV and surrounding farmland. Top: limestone karst in Zone IV. Bottom: surrounding farmland. Photos: K. Apthorp, 2016.

The corridor area linking the two regions is a narrow belt of forest along the Vietnam and China international border (Figure 6.7). This forest had been heavily degraded at the time of sampling. In some sloped parts of the corridor, rangers noted the potential for undiscovered landmines within the forest, making it too dangerous to traverse. The corridor region was also bisected in parts by unofficial pathways crossing the border, which interrupted the forest for several metres with scramble vegetation. The river bordering the CVGCA to the south-west disappears underground for 900m at the corridor (Fan et al., 2013), reappearing on the Chinese side of the border.

6.2.2 Study species

Following their rediscovery in 2002, 26 individuals in five groups were identified in Vietnam, having been thought extinct in the country since the 1960s (Geissmann et al., 2002; Geissmann et al., 2003; Trung et al., 2002). Surveys between 2004 and 2006 estimated the population had increased, suggesting the presence of at least eight groups and confirming the

presence of the CVG in China (Chan et al., 2008; Trinh Ding Hoang, 2004; Trung, 2005; Vu Ngoc, Nguyen Xuan, Nguyen Manh, Luu Tuong, & Nguyen Thi, 2005).

Figure 6.7 Corridor belt along Vietnamese and Chinese International border. Top left and right show signage marking international border along the corridor valley and on ridge, respectively. Bottom left shows path crossing border with scramble vegetation interrupting forest canopy. Bottom right shows river on valley floor prior to going underground. Photos: K. Apthorp, 2016.

A census in 2007 carried out by FFI researchers estimated 110 individuals across 18 groups, with only three groups found to cross between China and Vietnam and another single group found to remain entirely within the Chinese forest (Dat et al., 2008b; Fan et al., 2010). In 2012, 129 individuals were identified (Dat & Oanh, 2007; Dat et al., 2008b; Insua-Cao et al., 2012), however in 2016, this was revised to 104-116 gibbons across 15 groups as recorded through auditory surveys (Fauna & Flora International, 2016). Another sampling study of the CVG in 2016 further revised this figure to 107-136 (C.-Y. Ma et al., 2020), and most recently FFI (2021) estimated 135 individuals. This variation may be explained by differences in gibbon survey methods (see Chapter 7, Section 7.2.2). The current home range of the CVG is 1.3km^2 (Fan et al., 2011), making it one of the largest home ranges of the crested gibbons.

6.2.3 Interviews

I conducted seventeen interviews with locals from surrounding villages and communes in November 2016, with support from FFI translators. Interviewees were selected with assistance from FFI translators and local National Park staff. Criteria for interviewees included that they should be adults, local long-term residents, and represent a cross-section of the Communes surrounding the CVG protected forest.

Interviews gathered information on recent historical distribution, changes observed in the area in regard to forest use and health, local awareness of the CVG and efforts for its conservation. Interviewees were all adults, chosen randomly from a cross section of the community to capture a range of viewpoints. To establish reliability of the information collected, I have only reported information that was common across multiple interviews unless otherwise noted, as per Fan et al. (2011). However, unlike Fan et al., (2011), I did not confirm information across interviews to avoid influencing responses (interview questions in Appendix 1.1).

Ethics approval was granted by the Australian National University Human Ethics Committee (protocol number: 2015/761) for the period of 1/2/2016 to 1/2/2018 to undertake interviews with community members local to each of the national parks under investigation.

6.1.1 Ecological sampling

I sampled the CVGCA habitat and Zone IV potential habitat with a total of 12 square ecological plots at each site, evenly distributed across the three habitat types: slope plots, valley plots and ridge plots (Table 6.1). I also established three transects, consisting of a slope, valley and ridge, at each site (Figure 6.8). Each plot measured 10x10m, and each transect measured 4x50m. Transects were established along lines following the plot type; from the starting point, a tape measure was wound out to maintain a straight line and ensure the correct measurements.

The location of plots and transects were selected by random sampling. Within the CVGCA, a map of the core area used by the CVG was divided into areas of slope, valley and ridge zones and locations were randomly selected within areas known to be used by the CVG, based on information provided by previous FFI surveys and rangers. A similar approach was used to

select plot sites within Zone IV, however, due to a lack of familiarity with the area, plots were sometimes moved due to accessibility issues or to reduce disruption to the vegetation in order to reach certain points. If chosen plots were deemed unsafe due to the limestone karst, plots were moved from their randomly selected position to the nearest safest point while remaining within the same vegetation type.

I also sampled three transects measuring 4x50m within the Corridor area, one slope, valley and ridge transect, as this area has been identified by Fan et al. (2013) as a potential link between the CVGCA and Zone IV potential habitat sites. Locations were selected within a sub-area of the total Corridor area, based on accessibility and safety due to concerns of undiscovered landmines on certain slopes. I chose the location of transects under guidance of rangers and guides to ensure the safest areas accessible. As this area was sampled as a potential dispersal path, sampling focussed on tree metrics.

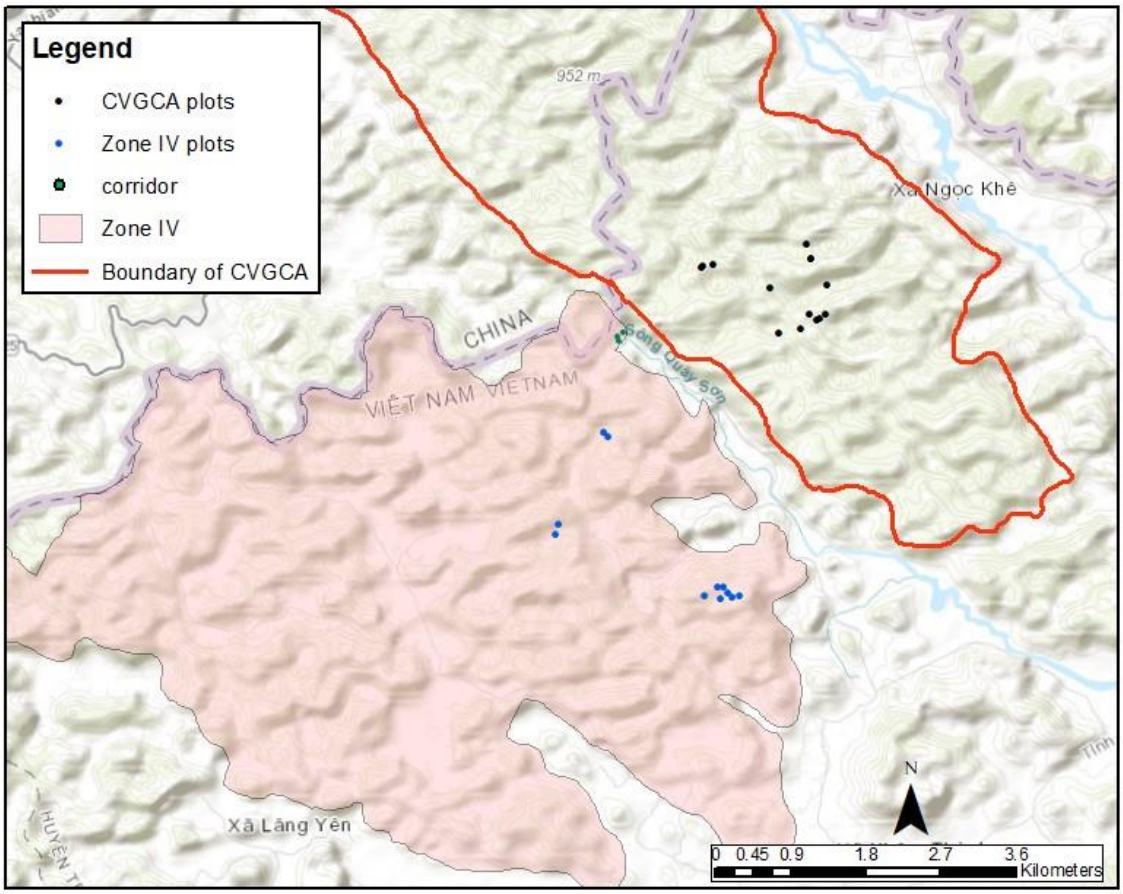


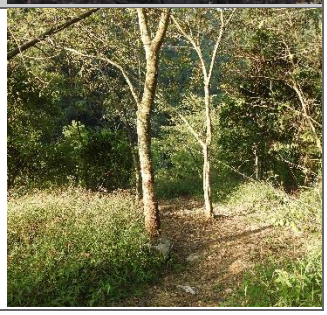
Figure 6.8 Location of plots across CVGCA, Zone IV and corridor. Basemap: Esri (2021). Zone IV polygon: Fan et al. (2013).

The karst made it difficult to set out larger plots, particularly along the narrow ridges, thereby restricting the size of plots (Tanja Haus, Vogt, & Forster, 2012). While previous studies of the CVG habitat in both Vietnam and China, have utilised larger plots e.g. of 20x20m (Fan et al., 2011) and 10x50m (Insua-Cao et al., 2012) and 50x10m (Tai & Tu, 2007), this study was focussed on sampling the different habitat types within the gibbon habitat. Due to the nature of the limestone karst, larger plots would result in capturing more than one habitat type at a time. For instance, even plots with a width of 10m were difficult and dangerous within many of the ridge/summit plots, and plots of a larger width in these areas would begin to capture slope habitat.

Field identification of all stems was identified within each plot and transect by Dr Vu Anh Tai, a botantist from the Department of Bio-Geography, Institute of Geography Vietnamese Academy of Science and Technology. The measurement of non-tree stems within gibbon studies is rare due to their strictly arboreal nature. I sampled the total composition of each plot to assist in understanding the structure of the CVG forest (Tai & Tu, 2007). These insights may provide a point of comparison for future studies and assist conservation groups looking to understand the health and growth of the forest to assist planning for the CVG.

The GPS location for each plot was taken in the SE corner, with two bearings also recorded. For transects, the GPS location was taken at 0m, 25m, and 50m. Two bearing points were also recorded at the 0m GPS point. At the SE corner of each plot and at 0m for transects, I recorded the elevation, aspect, slope, vegetation type. In the case of transects, the elevation was determined by averaging the elevation taken every 10m along the 50m length. I also recorded the general topographic complexity of the limestone based on the scale developed as set out in (Appendix 1.3). Unless otherwise stated, I undertook all measurements to maintain consistency across plots.

Table 6.1 Habitat types sampled for plots and transects

Habitat type	Description	Total number of plots sampled across all sites	Example of plot type
Valley	Valley floor	8 Plots 3 Transects	
Slope	Between 400- 1300m in elevation.	8 Plots 3 Transects	
Ridge	Ridge and summits of limestone, typically 900m – 1300m in elevation.	8 Plots 3 Transects	
Ex-agricultural	Vegetation is largely scrub and grass as the area regenerates. Typically in non-gibbon use areas	n/a	

Photos: K. Apthorp, 2016.

Within the plots and transects, I recorded the DBH for all trees and larger shrubs where DBH≥2cm and/or height≥2m using a DBH measuring tape or callipers. I also measured the crown size for all trees where DBH≥2cm and height ≥2m using visual diameter measures of the maximum and minimum axes of the tree crown. As at the other two primate (CBL, TSNM) sites, the use of a clinometer was not always possible. As such, estimates of tree heights were made visually (D. Li et al., 2006), independently simultaneously by myself and Dr Tai, to the nearest 50cm and triple checked where estimates differed by over 50cm. Visual estimation of tree heights using height categories has been employed in other studies (S. Cheyne et al., 2013).

Data collection was undertaken in October and November 2016, to avoid the peak of the rainy season. Temperature averages were captured for Cao Bang city, the closest city to the CVGCA where the study was undertaken (Table 6.2).

Table 6.2 Average temperature, rainfall and humidity in Cao Bang city during data collection

Month (2016)*	**Average temperature (˚C)**	**Average rainfall (mm)**	**Average humidity (%)**
October	28	326.9	82
November	25	522.48	89

*All weather information for Cao Bang is collected from 'World Weather Online' https://www.worldweatheronline.com/lang/en-au/ha-giang-weather-averages/vn.aspx

6.3 Data analysis

6.3.1 CVG habitat characteristics and potential habitat characteristics

I calculated the following vegetation characteristics using the protocol set out in Chapter 3, Section 3.4.1: species richness, species diversity, tree area, basal area, canopy coverage, mean DBH, vegetation density (stems/m^2) and tree density (tree stems/m^2) (Appendix 4.1.1).

I used a General Linear Model (GLM) to explore the relationship between my ecological plots and various outcomes of the variables. To understand differences between plots at each site, I used a one-way analysis of variance (ANOVA) from the linear model to assess significance of effects. To understand differences between sites, I used a two-way ANOVA. I then calculated the estimated marginal means based on the linear models were then calculated and used a Tukey adjustment to the p-values as a post hoc analysis. Transects were not included in this

component of the analysis of the CVGCA and Zone IV habitats due to the difference in the total plot areas represented in the vegetation characteristics.

To compare the CVGCA, Zone IV and the Corridor area, I used only topographic and tree metrics from the transect data collected across all three sites. I undertook a GLM, and two-way ANOVA based to assess significance. I then calculated the estimated marginal means based on the linear models and compared them in a post hoc analysis, employing Tukey adjusted p-values. No plot data was utilised in this analysis due to the limitations in undertaking enough plots within the narrow Corridor on the Vietnamese side of the border.

I undertook a visual inspection of residuals and determined that no transformation was required of variables as residual plots sufficiently satisfied normality constraints, noting a small sample size. Results were reported where $p<0.05$.

I carried out habitat characteristic calculations manually and used the VEGAN package in R (4.2.1) to undertake the GLM, ANOVAs and estimated marginal means analysis.

6.3.2 Plant species analysis

All models and calculations were carried out using the VEGAN package and visualisations using GGPLOT2 package in RStudio (2022.07.2) with R (4.2.1).

6.3.2.1 Analysis of plant species

Using the protocols established in Chapter 3, Section 3.4.2.1, I used the VEGAN package and METAMDS function in R to undertake a NMDS ordination analyses using the METAMDS function. I did this using a Wisconsin double standardisation transformation of the data, and a Bray-Curtis dissimilarity index (Bray & Curtis, 1957) to compare differences in plant species populations based on abundances for: (1) the plant and tree communities within CVGCA plots and transects; (2) the plant and tree communities within Zone IV potential habitat plots and transects; (3) the plant and tree communities between CVGCA and Zone IV; (4) the tree communities within the Corridor transects to determine whether it offered a potential travel path for the CVG between the two main areas sampled. I then used a PERMANOVA using a Bray-Curtis dissimilarity distance matrix to determine whether differences observed in the NMDS were significant.

I then applied a multiple regression of intrinsic vectors using the function ENVFIT to determine which species most significantly contribute to plant communities both within and between sites.

6.3.2.2 Food species analysis for the CVG

In order to understand the abundance of food species across the current CVG habitat and Zone IV potential habitat, I repeated the same NMDS ordination analysis, PERMANOVA and multiple regression of intrinsic variables analysis using food species captured within the plot and transect sampling on: (1) CVGCA food species across plot-types; (2) Zone IV food species across plot-types; and (3) food species comparison between the CVGCA and Zone IV. A visual analysis of the food species present in the Corridor transects was also undertaken but no further analysis was conducted due to the small sample size; only three transects were sampled within the small corridor area and a small number of food species were captured.

Collection of food species consumed by CVG in the CVGCA area was beyond the scope of this study due to site access, personnel availability, time and financial constraints. To overcome this limitation, a list of food species consumed by the CVG in the CVGCA and BNNR was compiled from Insua-Cao et al. (2012), Fan et al. (2011), Fan et al. (2015), B. P. L. Chan and Ng (2006), and (Thien & Dine, 2012) (Appendix 4.3.1). Due to the extensive food data available, I was able to compile a large list of items consumed by the CVG for inclusion in this analysis.

A large proportion of these foods have been identified down to species; however, a few items were only identified down to genus level. As a result, for food items identified to only genus level, all species under that genus, were included in the diet analysis. While this may conflate the number of food species captured in my study, the methods used to identify items consumed by the CVG often include observation from distances of over 50m using binoculars (Insua-Cao et al., 2012), making the species identification in some instances potentially less certain. Based on the current methods to identify food species, the inclusion of species under genera-level identification is not assumed to make a significant difference to the NMDS ordination analysis.

6.4 Results

6.4.1 Interviews

All interviewees have lived in the villages and communes around the CVGCA since at least the 1980s, with the majority born in the region (Table 6.3). Most interviewed have only ever seen or heard CVG within the current CVGCA, and no one reported ever hearing or seeing the CVG within the Zone IV area or surrounding area.

Table 6.3 Demographics of interviewees from communes surrounding CVGCA

Demographics		Response, % (N=17)
Sex	Male	82.4
	Female	17.6
Years living in local area	0-15	0
	16-30	11.8
	31-45	23.5
	46-60	41.2
	61-75	11.8
	76-90	11.8
Occupation	Linked to National Park or CVG Conservation	11.8
	Teaching	5.9
	Farming	64.7
	Local governance	17.6

A majority of participants report that the current condition of the CVGCA forest has significantly improved in the last 20-15 years stemming from protection management. These reports were based on perceived growth of taller, larger trees and increased sightings of wildlife including, primates, bears and pheasants. Prior to the establishment of the CVGCA, the forest was largely utilised for logging and grazing livestock, however, since the introduction of electricity, and efficient stoves and biogas initiatives by Fauna & Flora International, local people no longer had a reason to rely on forest resources. All participants report that the climate has become warmer but also more unpredictable, noting snowfall occurring in 2015 – few could ever remember seeing snow in the region before.

Older participants recalled hunting of the CVG and macaques for food and medicinal purposes prior to the border wars with China in the 1970s. Today, macaques are viewed as a pest, who regularly raid crops to eat corn. The prevailing opinion is that local government should compensate farmers for lost corn due as the protection resulting improved health of the forest

has seen macaque numbers grow and crop raids increase. It was also noted that *Trachypithecus francoisi* (François langurs), identified based on physical descriptions and confirmation from FFI staff, once lived in the region, however no sightings have been made since the 1980s.

While conservation efforts for the CVG were well known and generally viewed positively, there are suggestions that greater educational drives or educational propaganda should be pursued to remind and inform local people of the need to protect the CVG and its habitat. It was also recommended that rangers should do more to prevent people from accessing the CVGCA. Improved funding for local livelihoods and increased engagement with local communities to support conservation activities is also recommended by participants.

6.4.2 CVGCA habitat characteristics

6.4.2.1 Generalised Linear Model, ANOVA and estimated marginal means analysis of the CVGCA

I undertook an ANOVA to compare the vegetation characteristics, captured through sampling, between valley, slope, and ridge plots within the CVGCA. A one-way ANOVA shows that elevation, species density, canopy height, and percentage of canopy cover have significant differences between plot types based on the linear model applied (Appendix 4.1.2).

Based on the estimated marginal means (Appendix 4.1.3), the topography of the CVGCA is complex. The valleys have significantly lower elevations (691m ±15.2m) compared to the slopes (753m, p=0.043) and ridges (806m, p=0.0013), reflecting the extreme peaks and mountains present throughout the region.

The vegetation characteristics of the three plot types have few significant differences. Valleys are characterised as having significantly greater species density (5.38 ±0.582) than both slope (1.99, p=0.006) and ridge plots (3.02, p=0.044). In general, they also have greater species richness (43.45 ±3.16) compared to slope (32.5 ±3.16) and ridge vegetation (34.25 ± 3.16). The higher overall density of valley plots is a result of greater mat cover (30% ±6.21), shrub cover (52% ±11.68) and liana cover compared to the other two plot types.

Tree metrics vary across the three plot types. Ridge plots have the greatest density of trees (0.838 ±0.337) and slopes the lowest (0.23 ±0.337). However, ridge plots have significantly

lower canopy height (3.21m ±0.58) than both slopes (7.32m, p=0.0019) and valleys (6.51m, p=0.0079), and the smallest mean total basal area (1036.32 ±569.19) compared to slopes (2480.39 ±569.19) and valleys (2693.45 ±569.19). Ridge plots also have the greatest large shrub cover percentage (25% ±5.14) compared to both the valley and slope plots (12.5% ±5.14).

Slope plots have a significantly greater per cent of canopy coverage (63.75% ±4.77) than valleys (47.5%, p=0.004) and ridges (17.5%, p=0.0002), and the tallest trees out of the three plot types.

6.4.2.2 CVGCA Plant Species

6.4.2.2.1 Species composition of plots in CVGCA

A total of 7795 stems were identified within the CVGCA plots and transects from a total of 84 families, and 249 species (Appendix 4.2.1). The flowering herb *Impatiens arrensii* (n=946) is the highest occurring species – found exclusively within the valley transect. The top ten species identified across both plots and transects accounted for over 50 per cent of the total stems (Table 6.4).

Table 6.4 The top ten species across CVGCA

Species	**Ridge (n)**	**Slope (n)**	**Valley (n)**	**Total (n)**
Impatiens arrensii	0	0	946	946
Pilea notata	58	203	661	922
Epipremnum pinnatum	0	38	274	312
Pilea melastomoides	0	3	293	296
Aspidistra typica	0	3	284	287
Liparis balansae	246	9	7	262
Aglaonema siamense	0	21	215	236
Chirita speciosa	236	0	0	236
Bulbophyllum ambrosia	0	229	0	229
Cephalomappa sinensis	0	123	52	175
Total	540	629	2732	3901

CVGCA Valleys

Within the CVGCA valleys, 153 plant species were identified from 4586 stems. Valley vegetation is largely characterised by perennial flowering herbs, shrubs, bamboo, ferns and several species of lianas (Table 6.5). In addition to *Impatiens arrensii*, the most frequently identified perennial herbs include *Pilea notata* (n=661), *Pilea melastomoides* (n=293), and *Alpina malaccensis* (n=172). Flowering shrubs also dominate the vegetation profile, including *Aspidistra typica* (n=284), *Epipremnum pinnatum* (n=274), and *Aglaonema siamense* (n=215). Bamboo*, Arundinaria amabilis* (n=168) is also frequently occurring, as is *Ophiopogon reptans* (n=119), a grass-like perennial plant.

Table 6.5 Top 10 species identified within CVGCA valleys

Species	Occurrence (n)	Description*	IUCN Red List status
Impatiens arrensii	946	Flowering herb	NE
Pilea notata	661	Perennial herb	NE
Pilea melastomoides	293	Perennial herb	NE
Aspidistra typica	284	Flowering perennial shrub	NE
Epipremnum pinnatum	274	Flowering plant	NE
Aglaonema siamense	215	Evergreen shrub	NE
Alpinia malaccensis	172	Large herb	NE
Arundinaria amabilis	168	Bamboo	NE
Ophiopogon reptans	119	Grass-like perennial	NE
Angiopteris yunnanensis	81	Fern	NE
Total	**3213**		

*Descriptions from Flora of China Project (2020)

CVGCA Slopes

Slope vegetation within the CVGCA is home to 115 distinct species from 1598 stems, and is characterized predominately by herbs, epiphytes, trees, and lianas. The most frequently identified species (Table 6.6) characterising slope vegetation include *Bulbophyllum ambrosia* (n=229) a creeping epiphytic rock orchid, and perennial herbs including *Pilea notata* (n=203) *Elatostema cuneatum* (n=87), *Pellionia griffithiana* (n=26), and *Alpinia chinensis* (n=23). Dominant tree species include *Cephalomappa sinensis* (n=116), *Trigonostemon thyrsoideus* (n=45) *Burretiodendron hsienmu* (n=35) and *Acer tonkinensis* (n=23). Lianas also occurred at high frequencies including *Tetrastigma beauvaisii* (n=61), *Hoya balansae* (n=57) and the climbing shrub *Epipremnum pinnatum* (n=38).

Table 6.6 Top 10 species identified within CVGCA slopes

Species	Occurrence (n)	Description*	IUCN Red List Status
Bulbophyllum ambrosia	229	Creeping/epiphytic rock orchid	NE
Pilea notata	203	Perennial herb	NE
Cephalomappa sinensis	116	Evergreen tree	VU
Elatostema cuneatum	87	Herbaceous perennial	NE
Tetrastigma beauvaisii	61	Liana	NE
Laportea violacea	59	Herb	NE
Hoya balansae	57	Liana	NE
Trigonostemo thyrsoideus	45	Shrub/small tree	NE
Epipremnum pinnatum	38	Shrub	NE
Burretiodendron hsienmu	35	Tree	VU
Total	**930**		

*Descriptions taken from Flora of China Project (2020)

CVGCA Ridges

Ridges in the CVGCA are home to 90 identified species from 1611 stems, characterized by small plants (Table 6.7) including orchids *Liparis balansae* (n=246), *Coelogyne lactea* (n=132), herbs *Pilea notata* (n=58) and *Elatostema monandrum* (n=48), and shrubs *Chirita speciosa* (n=236), *Crotalaria pallida* (n=69), *Boeica porosa* (n=66), *Breynia diversifolia* (n=55). Ridges also have high frequencies of bamboo *Sinarundinaria floribunda* (n=66) and ferns including *Selaginella delicatula* (n=32).

Table 6.7 Top 10 species identified within CVGCA ridges

Species	Occurrence (n)	Description*	IUCN Red List Status
Liparis balansae	246	Orchid	NE
Chirita speciosa	236	Perennial flower shrub	NE
Coelogyne lactea	132	Epiphyte orchid	NE
Crotalaria pallida	69	Perennial flowering shrub	NE
Boeica porosa	66	Shrub	NE
Sinarundinaria floribunda	66	Bamboo	NE
Pilea notata	58	Perennial herb	NE
Breynia diversifolia	55	Shrub	NE
Elatostema monandrum	48	Herb	NE
Selaginella delicatula	32	Fern	NE
Total	**1008**		

*Description taken from Flora of China Project (2020)

6.4.2.2.2 Non-metric multi-dimensional scaling analysis of CVGCA plants

The NMDS was undertaken in two dimensions, and a Wisconsin double standardisation was applied to standardise the abundance values, followed by a square root transformation to reduce the effect of high counts over unique counts when applying the Bray-Curtis dissimilarity distance. A solution was reached after 20 tries, and a stress of 0.09 was returned; as this fell below 0.1, it is considered a very good 2-dimensional arrangement of the plots and transects to show their similarities.

Based on abundances and distances, there is a clear distinction between the ridge plots and the other plot types (Figure 6.9). There is some overlap between slope and valley plots, partly due to the third slope plot (tks3) falling closer to the first (tkv1) and fourth valley (tkv4) plots than the other slope plots. This overlap suggest that the plant communities in valley and slope plot are not significantly different. Valley plots have the largest spread across their plant community similarities, while ridge plots had the smallest spread. All three plot types show most of their variation along the NMDS2 axis.

A PERMANOVA shows that there is a significant difference, with 35 per cent of variation can be explained by plot type (R^2=0.35, F=3.26, P=0.001). This variation can clearly be seen in the separation between the ridge plots and the other two plot types.

Applying the intrinsic vectors shows that seven species significantly (p=0.01) contribute to the composition of the three plots (Figure 6.9). Three species *Dendrocnide urentissima* (p=0.001), *Asplenium nitidus* (p=0.002) and *Phaius indochinensis* (p=0.006), have steep positive gradients and all contribute to the composition of valley plots, however, *Asplenium nitidus* also contributes to the slope plots.

The remaining four species: *Chirita speciosa* (p=0.001), Tirpitzia sinensis (p=0.001), *Tetrastigma chapaense* (p=0.007), and *Triadica rotundifolia* (p=0.009) all have shallower positive gradients and area all typical of CVGCA ridge plots.

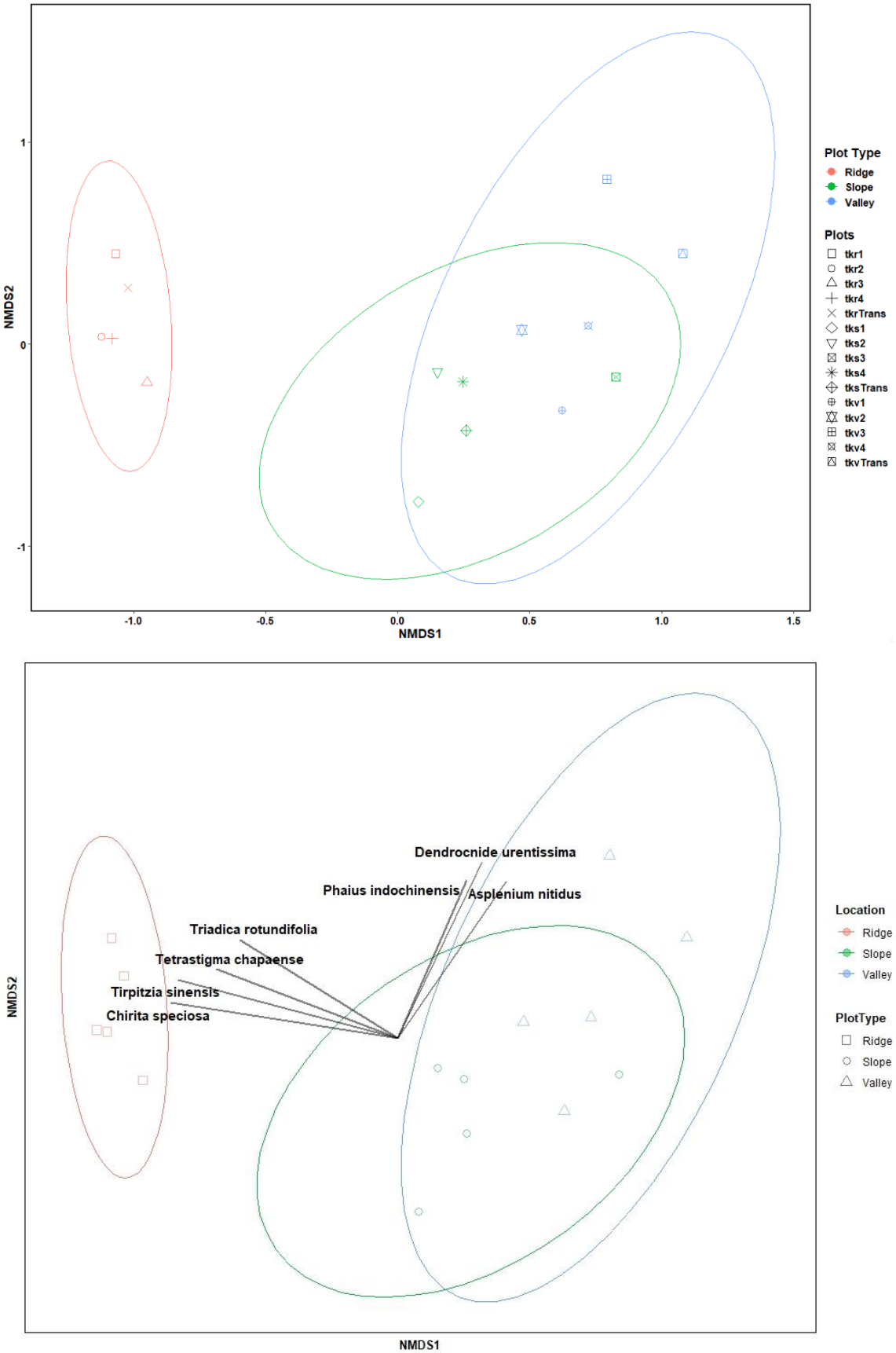


Figure 6.9 NMDS of plants in CVGCA Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors where p<0.05.

6.4.2.3 Tree characteristics in CVGCA and NMDS analysis

Four hundred and forty-six trees from 90 species of trees (41 families) were identified across the CVGCA region (Appendix 4.2.3), the most commonly identified being *Cephalomappa sinensis* (n=73) a karst tree species (Geekiyanage, Goodale, Cao, & Kitajima, 2018), most frequently identified within the slope plots (n=45) and valleys (n=28).

Most tree species within the CVGCA had small DBH of 1.5cm to 10 cm (Figure 6.10). The largest DBH recorded was for a *Celtis tetrandra* (47.8cm) sampled within a valley plot. Tree canopies are generally within the 2-10m range, with the tallest tree a specimen of *Bridelia ovata* (23.7m) – usually found as a smaller tree in plots – identified here in a slope plot.

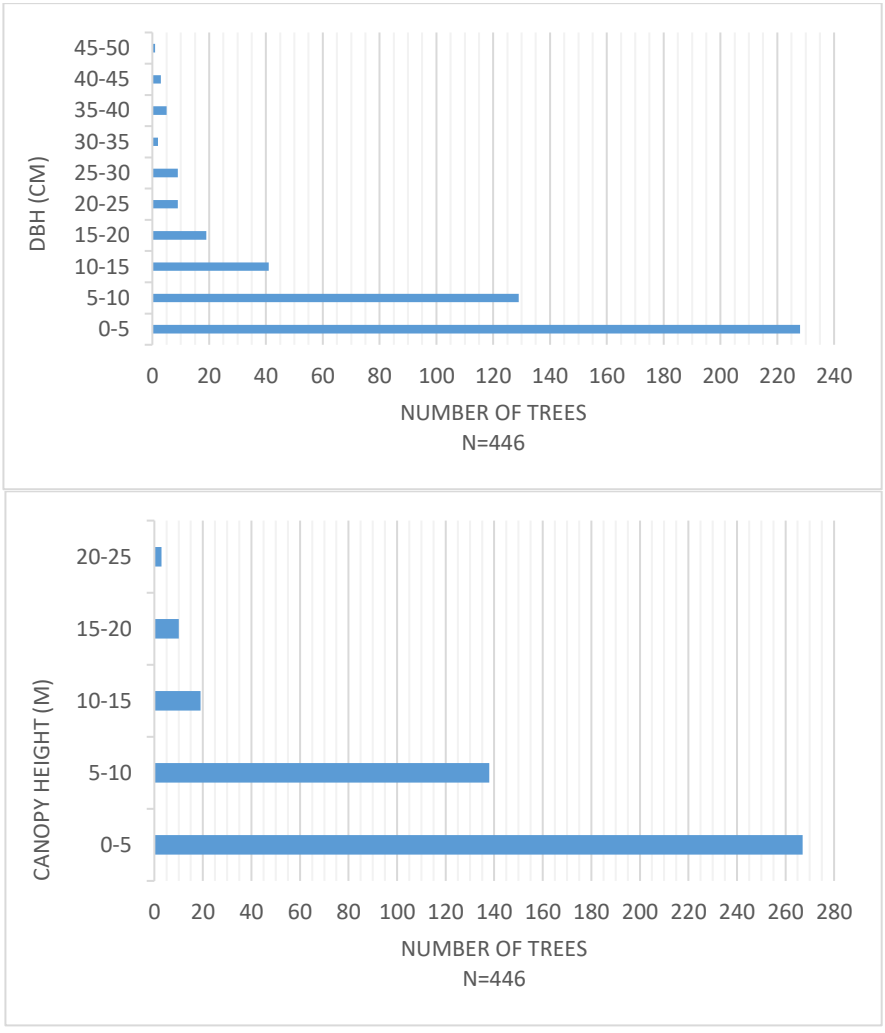


Figure 6.10 Tree metrics across plots and transects in CVGCA Top: Frequency of DBH across plots and transects. Bottom: Frequency of tree canopy heights across plots and transects.

The NDMS applied a Wisconsin double standardisation and reached a solution after 20 tries. A stress of 0.12 was returned; as this fell below 0.2, it is considered a good 2-dimensional arrangement of the tree communities within plots and transects to show their similarities.

There is some overlap across all three plot types based on tree species abundances (Figure 6.11), however, ridge plots are more distinct from other plot types, while valley and slope plots have greater overlap. The valley transect appears to be increasing the dissimilarity across the valley plots, while slope plot 3 (tks3) is most dissimilar of the valley plots.

A PERMANOVA shows that there is a significant difference in the variation between plot types (R^2=0.38, F=3.63, P=0.001) and 38 per cent of the variation observed is explained by the plot types and ridge plots are the most dissimilar.

Applying the intrinsic vectors to the NMDS tree ordination (Figure 6.11) shows that eight species of tree are significantly ($p<0.05$) contributing to the distribution and composition of the plot types in CVGCA. The species *Radermacheta sinica* (p=0.02), *Dendrocnide urentissima* (p=0.002) have very steep positive gradients and contribute to the valley plots. *Schefflera pesavis* (p=0.03) also has a steep positive gradient and contributes to all three plot types, particularly ridges and valleys. *Celtis tetrandra* (p=0.03) has a shallow negative gradient and it typical of valleys and slopes.

Crotalaria pallida (p=0.007), *Breynia diversifolia* (p=0.04) *Tirpitzia sinensis* (p=0.009) and *Pistacia weinmannifolia* (p=0.003) all have negative gradients and are all typical of ridge plots.

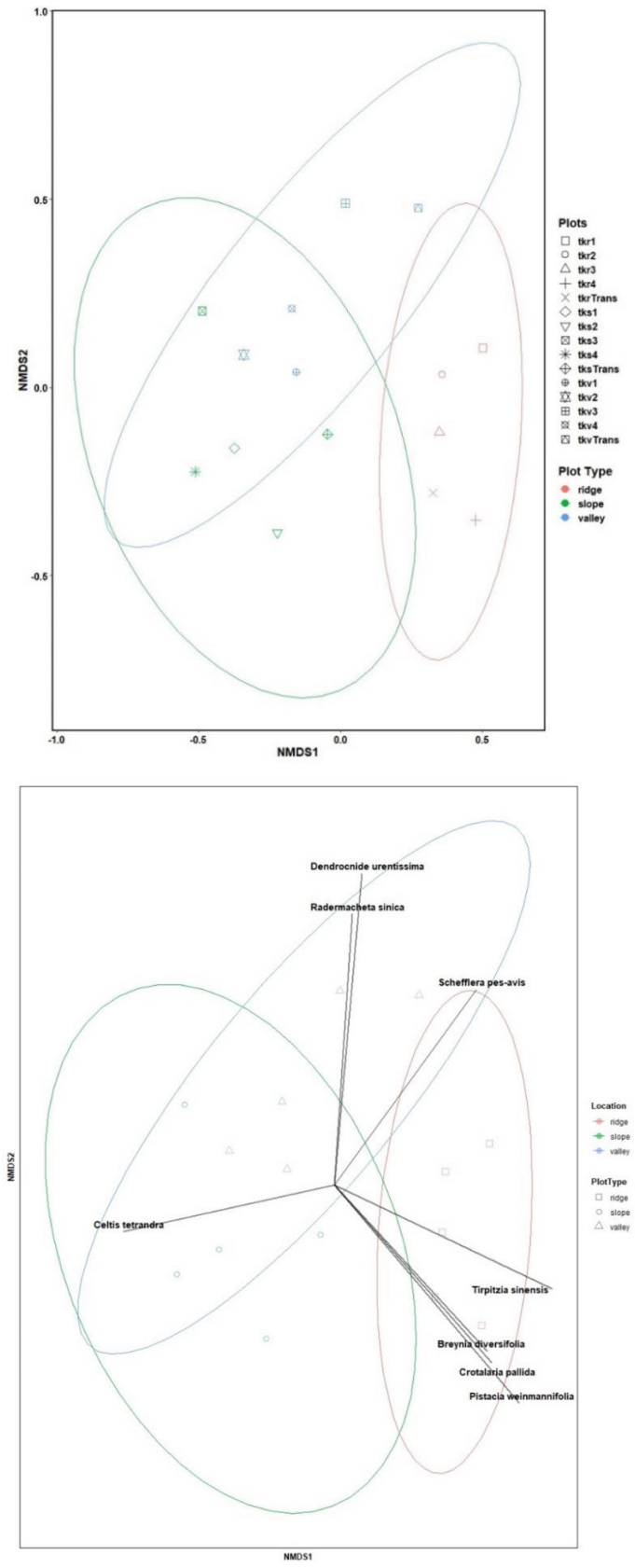


Figure 6.11 NMDS of trees in CVGCA. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors where p<0.05

6.4.2.4 Food species composition and NMDS across CVGCA plots

Of 118 food species identified in previous studies of the CVG in the CVGCA and BNNR sites (B. P. L. Chan & Ng, 2006; Fan et al., 2011; Insua-Cao et al., 2012; Thien & Dine, 2012; Vu Ngoc et al., 2005), 17 species from 14 families were captured within the ecological plots and transects (Appendix 4.3.2). Slopes have the greatest occurrence of diet species, with 217 specimens from 11 species. Valleys have 121 specimens from 11 species, and ridges 53 specimens from six species.

The NDMS applied a Wisconsin double standardisation and reached a solution after 20 runs. A stress of 0.08 was returned, and as this falls below 0.1 is it considered a strong representation of the food species community similarities within the plots and transects in the CVGCA.

There is a large overlap between the plot-types based on a 0.95 confidence ellipse (Figure 6.12), suggesting little difference between the plant communities across the three plot types. Based on their confidence ellipses, ridges and valleys demonstrate the greatest variance in the plant communities within their plots rather than between each other. The second (tks2) and fourth (tks4) slope plots are most similar to the first (tkv1), second (tkv2) and fourth (tkv4) valley plots, indicating high similarities in species and abundances captured by sampling.

A PERMANOVA shows that there is no significant difference between the variation observed as a result of plot types (R^2=0.06, F=0.82, P=0.58).

Applying the intrinsic vectors shows that three species are significantly contributing to the distribution and abundances of the plant communities in each plot type ($p<0.05$) (Figure 6.12). *Tetrastigma planicaule* (0.02) has a steep positive gradient and contributes to slope and valley plots. The species *Allophylus caudatus* (0.02) has a negative gradient and also contributes to slope and valley plots. *Sinosideroxylon wightianum* (p=0.04) had a negative gradient and contributes to the ridge and slope plots.

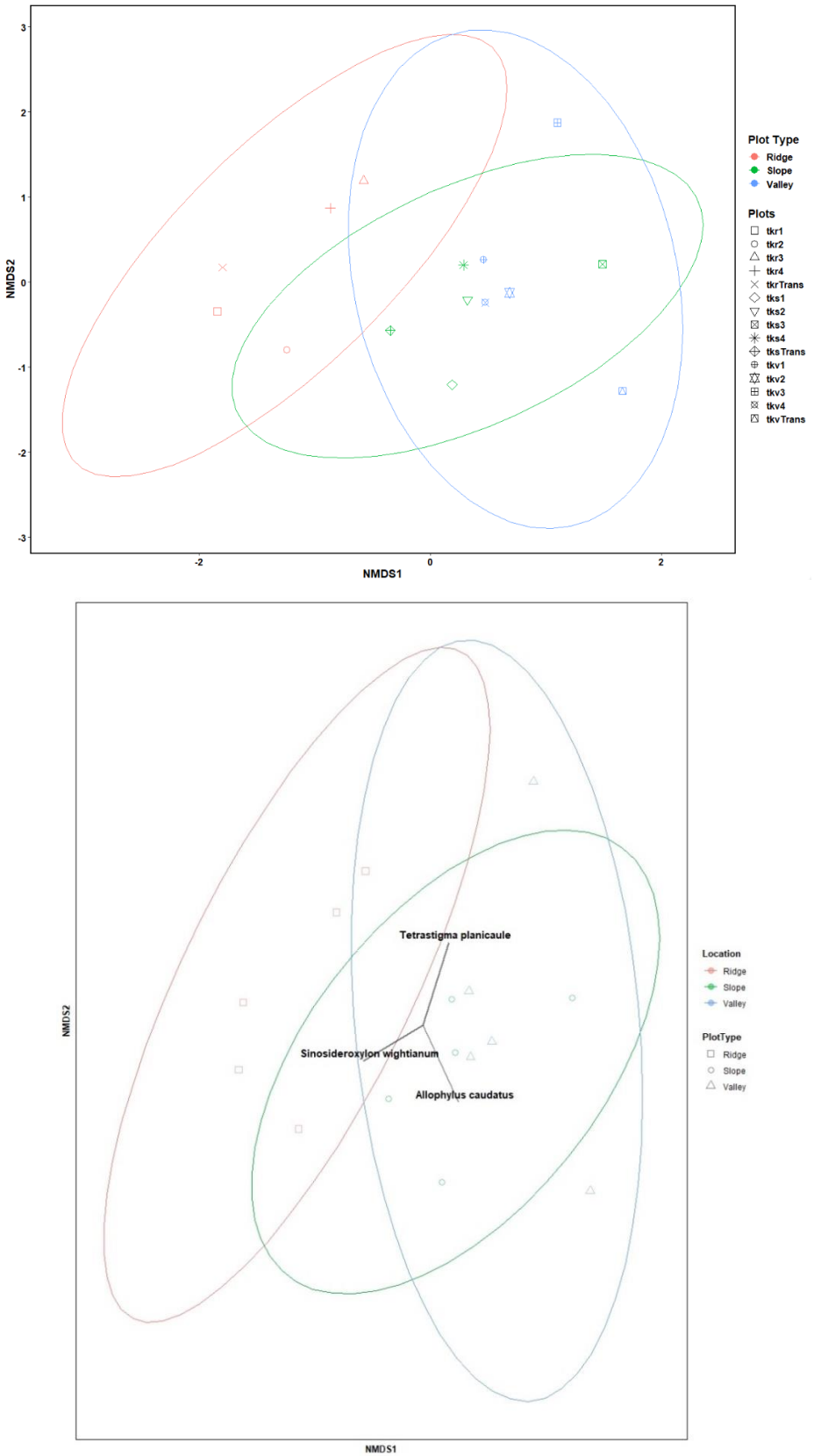


Figure 6.12 NMDS of food species in CVGCA. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors where p<0.05

6.4.3 Zone IV Potential Habitat characteristics

6.4.3.1 Generalised Linear Model, ANOVA and estimated marginal means analysis of Zone IV

I undertook a one-way ANOVA on the vegetation characteristics of the valley, slope and ridge plots in Zone IV. The ANOVA shows that elevation, topographic complexity, slope, canopy cover and total basal area have significant differences across the plots based on the linear model applied (Appendix 4.1.4).

Based on the estimated marginal means, the topography of the Zone IV potential habitat varies significantly across the three plot types (Appendix 4.1.5). The mean elevation varies significantly across the region, with ridges (857.3m ± 47.36m) significantly greater than valleys (670.3m ±47.36, $p=0.05$) and the mean topographic complexity of the limestone karst also significantly greater in ridges (3.5 ±0.42) than valleys (1.25 ±0.42, $p<0.05$).

The change in mean slope across the three plots also increased significantly from valleys (9˚ ±3.19) to slopes (34.5˚ ±3.19, $p<0.01$) and valleys to ridges (31.25˚ ±3.19, $p<0.001$).

The vegetation characteristics across the three plot types does not vary significantly, with no significant differences found across the density, species richness or density, or across the mat, shrub, canopy or liana cover measured in each plot type. Slopes have the greatest values across all metrics compared to both valleys and ridges, however the difference is not significant.

Tree-related metrics were also comparatively uniform; however, the mean tree coverage was significantly different between valleys (23.75 ±9.45) and slopes (63.75 ±9.45, $p<0.05$). The mean total basal area was also significantly greater in slope plots (1933.0.3 ±266.37) compared to valleys (783.66 ±266.37, $p<0.05$), but not slope plots (1256.13 ±266.37). Slopes also exhibit the tallest mean tree heights (4.7m ±0.4) compared to valleys (4.47m ±0.4) and ridges (32.5m ±0.4), though this is not a significant difference. Trees found in ridge plots exhibit the greatest mean DBH (6.85cm ±0.55) compared to valleys (5.56 ±0.55) and ridges (6.78 ±0.55).

6.4.3.2 Zone IV Plant Species

6.4.3.2.1 Species composition of plots in Zone IV

A total of 9886 stems were identified within the Zone IV potential habitat plots and transects sampled, from a total of 89 families and 271 species (Appendix 4.2.1). The fern *Diplazium maximum* (n=928), an edible fern traditionally consumed by tribes in western Himalayas (Sareen, Bhattacharya, & Srivatsan, 2021), is the highest occurring species, predominately in valleys and occasionally on slopes. The top ten occurring species found across both plot types account for almost 49 per cent of the total stems (Table 6.8).

Table 6.8 The top ten species across Zone IV potential habitat

Species	**Ridge (n)**	**Slope (n)**	**Valley (n)**	**Total (n)**
Diplazium maximum	0	62	866	928
Erigeron canadense	0	0	828	828
Pilea notata	38	630	21	689
Pyrrosia bonii	322	245	0	567
Asplenium normale	295	68	69	432
Eragrostis unioloides	0	76	333	409
Ficus hirta	0	2	340	342
Laportea violacea	138	108	18	264
Chirita speciosa	71	5	138	214
Arachniodes hasseltii	0	87	79	166
Total (n)	**864**	**1283**	**2692**	**4839**

Zone IV Valleys

The valleys in Zone IV potential habitat had 131 species identified from 4851 stems, characterised by flowering shrubs, seedling mats of grasses and small herbs, and evergreen flowering trees (Table 6.9). The seedling mat is dominated by the small flowering plant *Erigeron canadense* (n=764). This small flowering plant is native to North America and considered an invasive weed in South America, Europe, Africa and Asia (Trust, 2022). The most frequently identified tree species in valleys include *Itoa orientalis* (n=28) and *Oxyspora paniculate* (n=28).

Table 6.9 Top ten species found in valleys in Zone IV potential habitat

Species	Occurrence (n)	Description *	IUCN Red List Status
Diplazium maximum	866	Edible fern	LC
*Erigeron canadense^*	828	Herb	NE
Ficus hirta	340	Shrub or small tree	NE
Eragrostis unioloides	333	Grass or herb	LC
Centella asiatica	161	Herb	LC
Itoa orientalis	150	Tree	LC
Oxyspora paniculata	143	Tree	NE
Chirita speciosa	138	Flowering herb	NE
Urena lobata	135	Shrub-like herbs	LC
Polygonum posumbu	113	Herb	NE
Total	**3207**		

^Weed species often found in open areas, Flora of China Project (2020)
*Description taken from Flora of China Project (2020)

Zone IV Slopes

Within slopes plots and transects, 172 species from 2890 stems were identified. The slopes within Zone IV potential habitat are characterised by shrub species, including herbs and ferns, dominated by *Pilea notata* (n=630), a flowering succulent herb and *Pyrrosia bonii* (n=245), a fern with a significant medical applications (Cai et al., 2018) (Table 6.10). The fern *Arachniodes hasseltii* (synonyms *Acrorumohra hasseltii* and *Dryopteris hasseltii*) is considered Endangered as a result of habitat loss (IUCN, 2022a). No lianas or trees were identified within the top ten slope species.

Table 6.10 Top ten slope species in Zone IV potential habitat

Species	Occurrence (n)	Description *	IUCN Red List Status
Pilea notata	630	Herb	NE
Pyrrosia bonii	245	Fern	NE
Laportea violacea	108	Shrub	NE
Staurogyne brachystachys	95	Herb	NE
Arachniodes hasseltii	87	Fern	EN
Zanthoxylum laetum	84	Shrub	NE
Eragrostis unioloides	76	Grass or herb	LC
Asplenium normale	68	Fern	NE
Elatostema monandrum	65	Herb	NE
Diplazium maximum	62	Edible fern	LC
Total	**1520**		

*Description taken from Flora of China Project (2020)

Zone IV Ridges

There were 121 species from 2145 stems identified in ridge plots and transects. Ridges within the Zone IV potential habitat are characterised by shrub and seedling mat species (Table 6.11), dominated by ferns including *Pyrrosia bonii* (n=322) and *Asplenium normale* (n=295), the latter is often found on steep banks and rocks. Small flowering shrubs and herbs are also well represented; however, no large shrub or tree forms are represented in the top ten species.

Table 6.11 Top ten ridge species in Zone IV potential habitat

Species	Occurrence (n)	Description (2020)	IUCN Red List Status
Pyrrosia bonii	322	Fern	NE
Asplenium normale	295	Fern	NE
Laportea violacea	138	Shrub	NE
Neocheiropteris sapaensis	96	Fern	NE
Satureja confinis	89	Herb	NE
Chirita drakei	80	Shrub	LC
Chirita speciosa	71	Shrub	NE
Elatostema monandrum	66	Herb	NE
Epipremnum pinnatum	49	Shrub/climber	NE
Pilea notata	38	Herb	NE
Total	**1244**		

6.4.3.2.2 Non-metric multi-dimensional scaling analysis of Zone IV plants

The NDMS was undertaken in two dimensions and a Wisconsin double standardisation and square root transformations were applied prior to a Bray-Curtis dissimilarity distance. A solution was achieved after 20 runs and a stress of 0.14 returned. As this is less than 0.2, it is considered a good two-dimensional arrangement of the plant community similarities of the plots.

There is a large overlap in the confidence intervals for all plot types (Figure 6.13), however each plot has different variations. Ridge plot variation runs roughly equally along both axes, while valley plots show most of their variation along NMDS2 axis. Slope plots, with the greatest variation, show most of their variation along the NMDS1 axis. Slope plots appear to be responsible for most of the overlap due to wide variation in plant communities, as the fourth (ZR4) and the transect (ZRTrans) falling closely to the second (ZR2) ridge plot, while the third (ZS3) slope plot groups more closely to valley plots. Ridge plots and valley plots indicate some dissimilarity in plant communities due to very little overlap of groupings.

A PERMANOVA shows that there is a significant difference (R^2=0.27, F=2.27, P=0.002). Twenty-seven per cent of the variation observed can be explained by the plot types.

Applying the intrinsic vectors shows that there are eight vectors that significantly contribute to the composition of the plots and their distribution (Figure 6.13). The species *Clematis loureiriana* (p=0.003), *Centella asiatica* (p=0.002), *Diplazium maximum* (p=0.004), *Lygodium japonicum* (p=0.004) and *Ocimum gratissimum* (p=0.008) all have steep positive gradients and are typical of valley plots. *Pyrrosia lanceolate* (p=0.007) has a steep negative gradient and contributes to all plots, particularly slope plots. *Satureja confinis* (p=0.007), *Asplenium normale* (p=0.01) both have positive gradients and contribute to all plots, particularly ridge plots.

6.4.3.3 Tree characteristics in Zone IV and NMDS analysis

Ninety-seven tree species representing 43 families were identified from 438 individual trees (Appendix 4.2.3). The most frequently identified are *Maesa montana* (n=40), a small multi-stemmed, tree native across mainland Southeast Asia (2020), classified as Least Concern by the IUCN Red List (IUCN, 2022a). It is predominately found across valleys (n=34) and a few specimens are also found on slopes (n=6). The majority of trees in Zone IV potential habitat have canopies of 10m or lower, and a DBH 10cm or lower (Figure 6.14). Slope plots have the mean tallest trees and greatest mean canopy, however, trees within the ridge plots have the greatest mean DBH. The tallest tree identified was *Elaeocarpus balansae* with a height of 26.2m and DBH of 19.1cm identified in a slope plot.

The NDMS applied a Wisconsin double standardisation transformation and reached a solution after 20 runs. A stress of 0.09 was returned, which as it is below 0.1, produces a good two-dimensional representation of the tree communities across the plots.

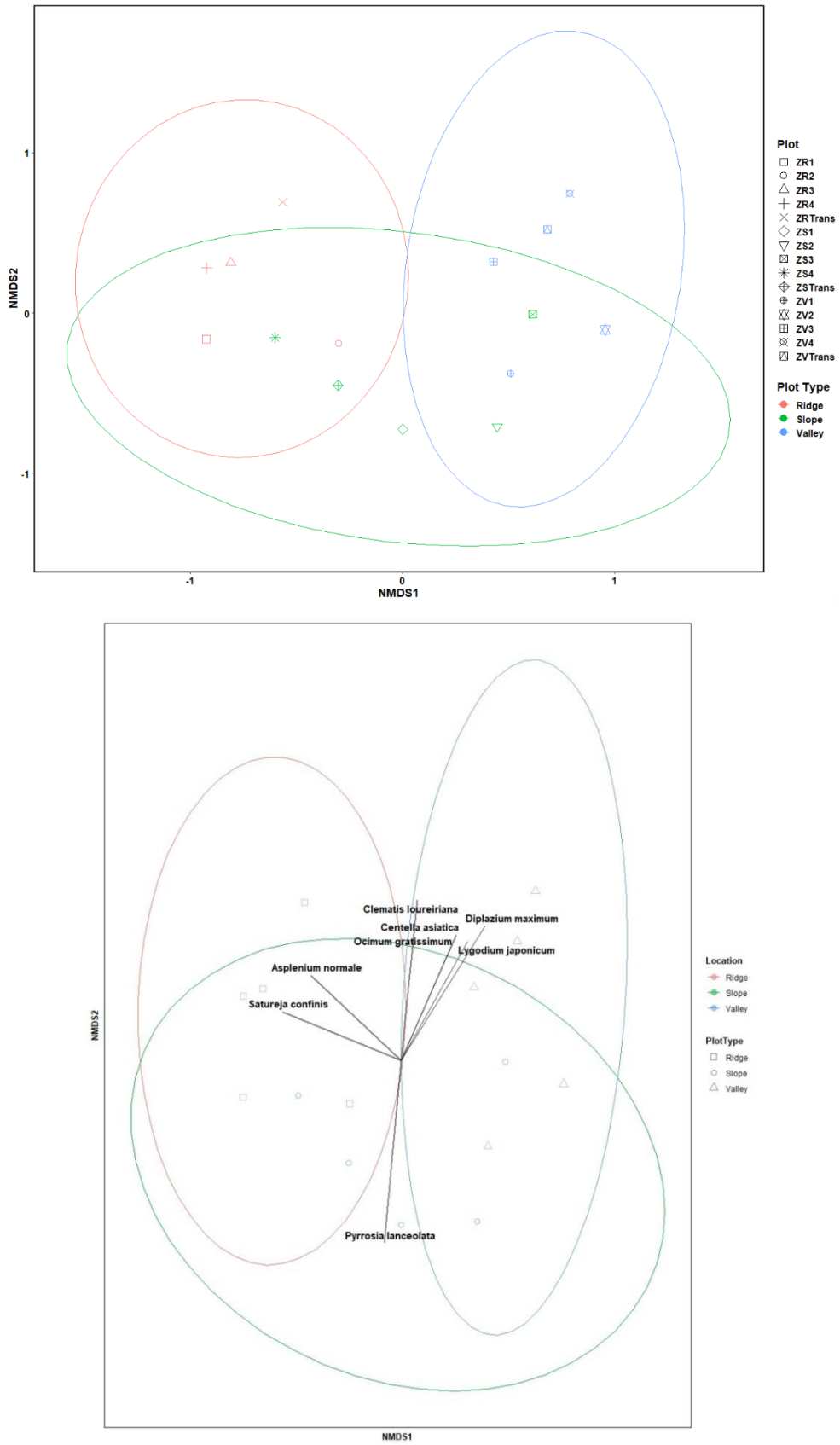


Figure 6.13 NMDS of all species in Zone IV. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors p<0.05.

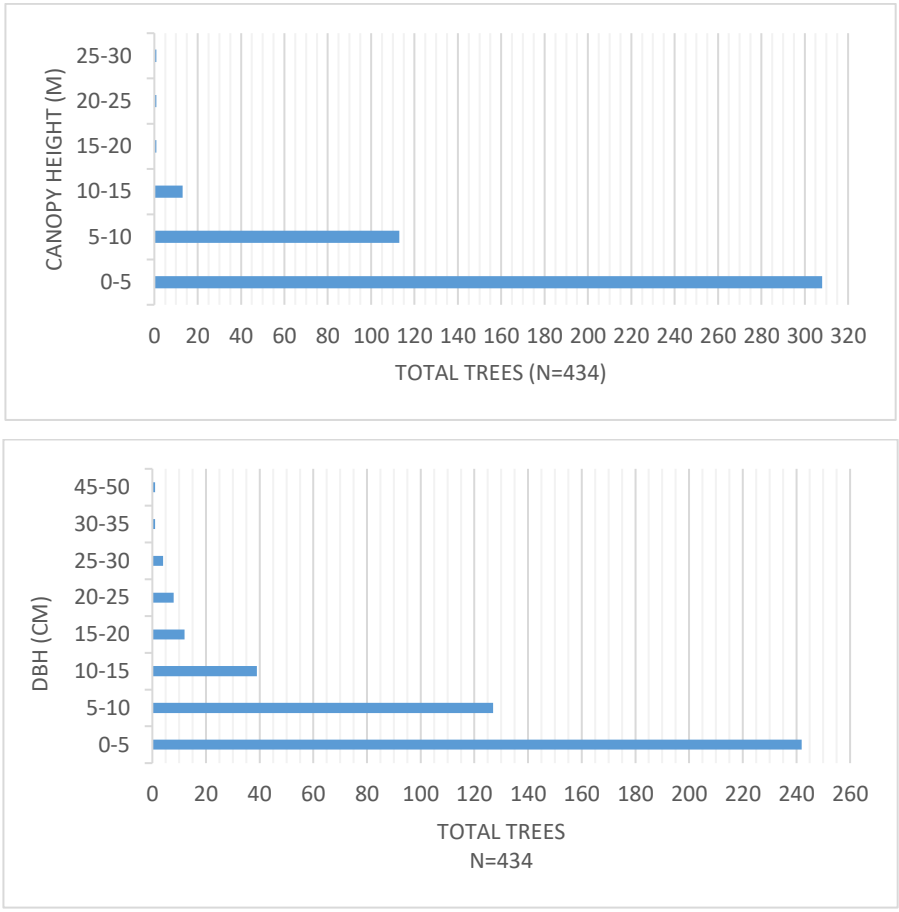


Figure 6.14 Tree DBH and canopy height distribution in Zone IV

There is a degree of overlap between plots based on confidence ellipses (Figure 6.15), largely driven by a wide variation in ridge and slope plots. Valley plots are closely grouped, suggesting that plant communities are more similar between valley plots than to other plot types.

A PERMANOVA shows that there is a significant difference (R^2=0.27, F=2.25, P=0.001), with 27 per cent of the variation explained by the plot types. In particular, differences between valleys and ridges appear to be very marked.

There are nine significant intrinsic vectors contributing to the composition and distribution of the plots (Figure 6.15). *Alangium chinensis* (p=0.03) has a step positive gradient and contributes to valley plots. *Itoa orientalis* (p=0.04) has a negative gradient and contributes to slope plots. *Ficus cyrtophylla* (p=0.01) and *Alchornea trewiodes* (p=0.04) contribute to slope and ridge plots in low abundances. The species *Euonymus balansae* (p=0.01), *Litsea brevipes* (p=0.01) and *Tirpitzia sinensis* (p=0.01) all have shallow negative gradients and are typical of ridge plots. *Elaeocarpus balansae* (p=0.04) has a steep positive gradient and contributes to

ridge and slope plots, while *Mallotus philippinensis* (p=0.03) has a near vertical gradient and is found across all three plot types.

6.4.3.4 Food species composition and NMDS analysis across Zone IV

Eighteen food species were captured within the ecological sampling of the Zone IV potential habitat area from 264 stems (Appendix 4.3.2). Slopes have the greatest occurrence of food species, with 133 stems from 15 species. Ridges have 62 occurrences of 11 food species, and valleys have 69 occurrences from 10 food species. Ony seven species were shared across the three plot types.

The NDMS applied a Wisconsin double standardisation transformation and achieved a solution after 20 runs, with a stress of 0.16. There is extreme overlap between all plot type confidence ellipses (Figure 6.16), suggesting that there is a high level of similarity between the food plant communities across all plots. Slope and ridge plot variation is greater along the NMDS1 axis, while the valley variation is greater along the NMDS2 axis. Based on shape and orientation, valleys appear to be the most different of the plot types.

A PERMANOVA shows that there is a significant difference (R^2=0.25, F=1.96, P=0.02), and 25 per cent of the difference can be explained by the plot types. This is expected to largely be a result of valley variation.

Applying the intrinsic vectors shows that only three species significantly contribute to the composition of the plots (p<0.05) (Figure 6.16). *Acer tonkinensis* (p=0.03) has a steep negative gradient and contributes to all three plots but is predominately found in ridge plots. *Burretiodendron hsienmu* (p=0.03) has a shallower negative gradient and contributes to both ridge and slope plots in low abundances. The species *Mallotus barbatus* (p=0.003) has the steepest negative gradient and contributes to all three plots.

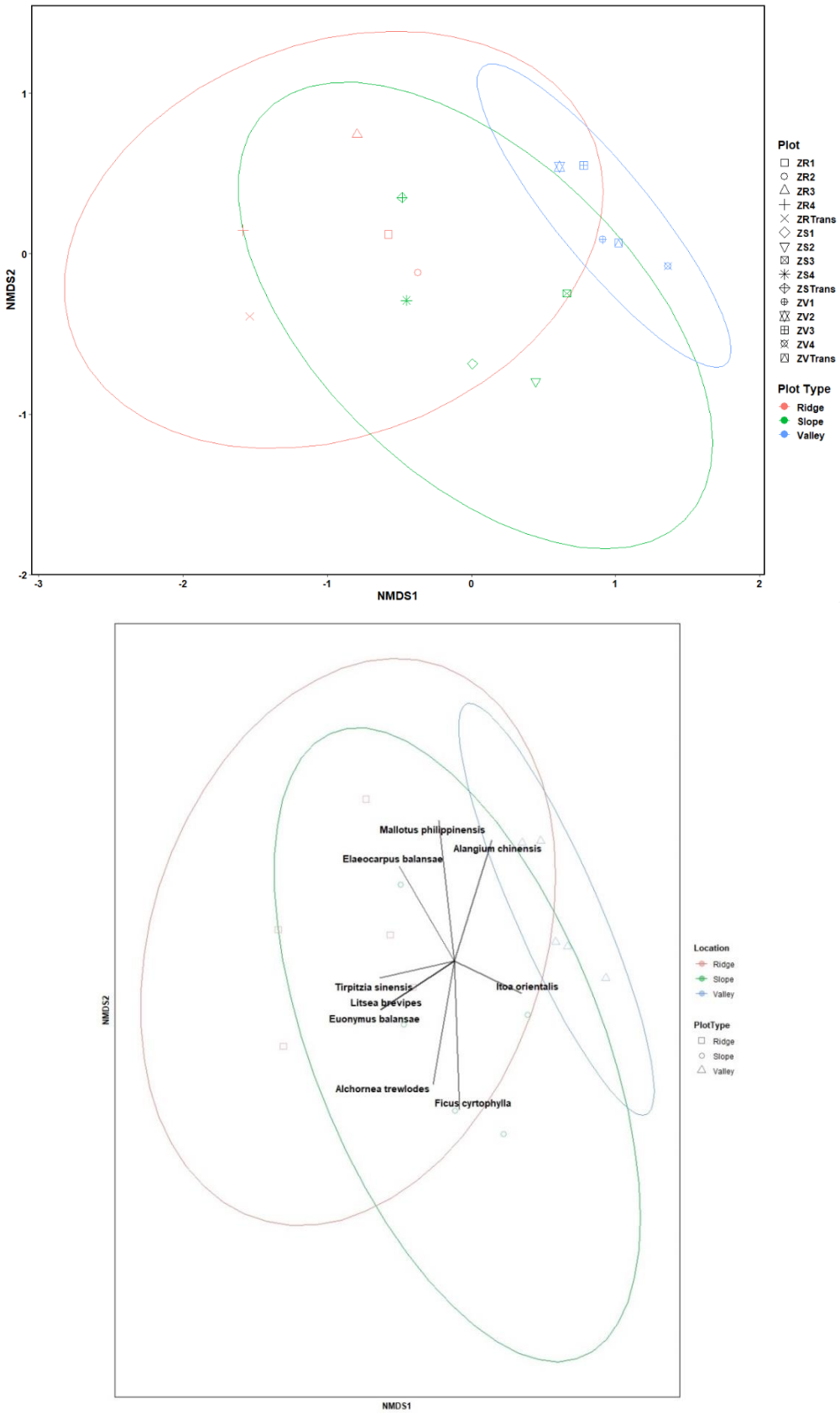


Figure 6.15 NMDS of trees in Zone IV. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors where p<0.05

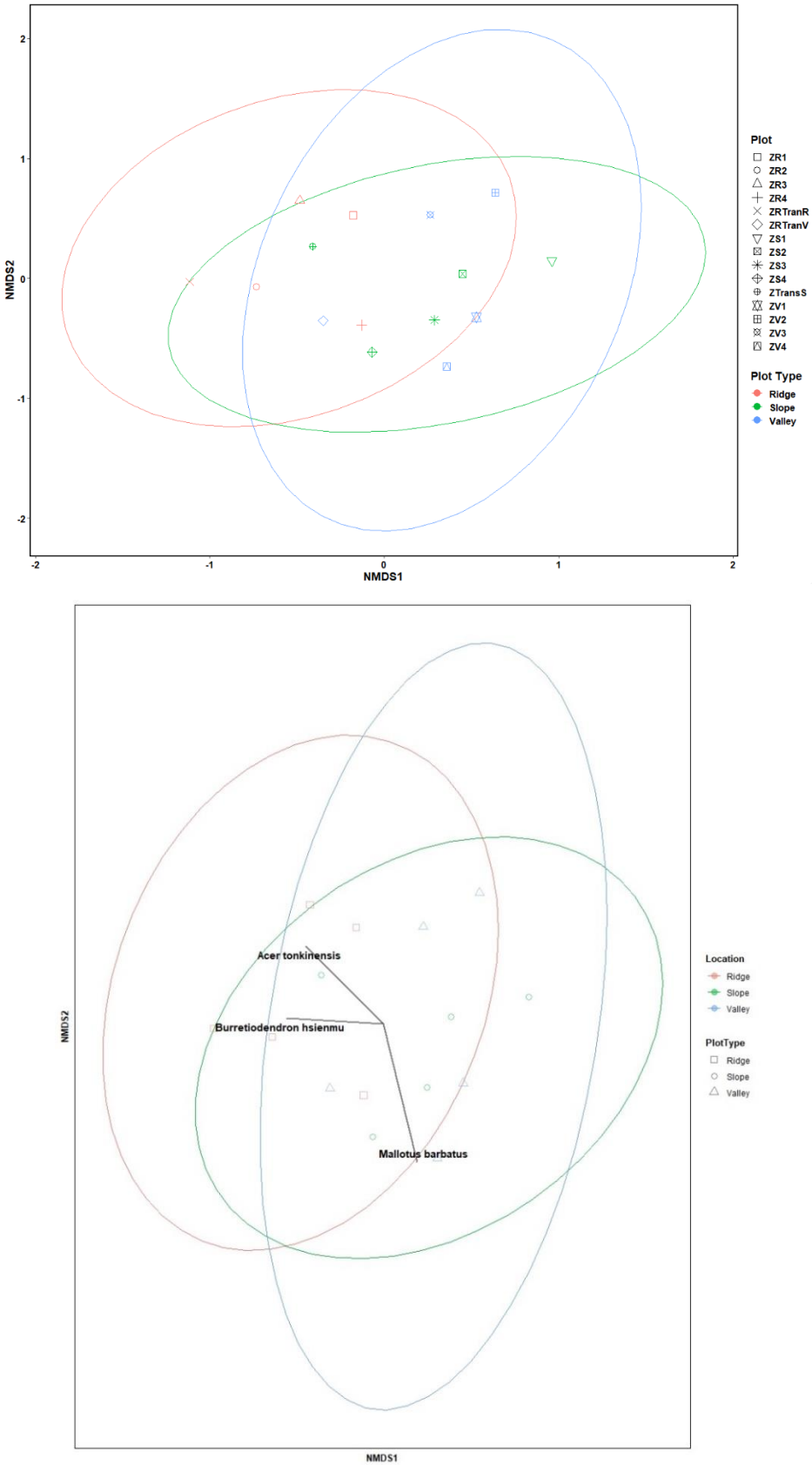


Figure 6.16 NMDS of food species in Zone IV. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors.

6.4.4 CVGCA habitat and Zone IV potential habitat comparison

6.4.4.1 Generalised Linear Model, ANOVA and estimated marginal means analysis of CVGCA and Zone IV comparison

I undertook a two-way ANOVA analysis based on a general linear model, on the vegetation characteristics between the CVGCA and Zone IV potential habitat. The ANOVA shows that topographic complexity, species richness, species density, canopy height, shrub cover, liana cover, DBH, and total basal area have significant differences across the sites based on the linear model applied (Appendix 4.1.6).

The estimated marginal means reveal that topographic complexity of CVGCA (3.42 ±0.26) is significantly greater than that of the Zone IV potential habitat (2.5 ±0.26, $p<0.05$) (Appendix 4.1.7). Across other topographic metrics the two sites do not vary significantly. While the CVGCA has a higher mean elevation, the mean slope values across the two sites are very similar.

The vegetation metrics across both sites differ significantly in terms of mean species richness, species density, and liana cover. Zone IV potential habitat has significantly greater species richness (45.8 ±2.12) and species density (4.98 ±0.42) compared to the CVGCA (36.7 ±2.12, $p<0.01$ and 3.47 ±0.42, $p<0.01$ respectively). The shrub cover of Zone IV potential habitat (77.5 ±5.6) and liana cover (29.2 ±4.2) is also significantly greater than that of the CVGCA (35.0 ±5.6, $p<0.0001$; and 13.5 ±4.2, $p<0.01$). The mat cover and large shrub cover measured in the Zone IV habitat is also greater that that found in the CVGCA, but not significantly so.

In contrast, the mean canopy height of the CVGCA (5.68m ±0.29) is significantly greater that canopy height in Zone IV (4.38m ±0.29, $p<0.005$). The mean diameter of the CVGCA trees (13.5cm ±0.53) is also significantly greater than the trees in Zone IV (6.4cm ±0.53, $p<0.01$). The total mean basal area of the CVGCA trees is also significantly greater (2070 ±257) than Zone IV (1327 ±257, $p<0.05$). The average canopy cover of the CVGCA habitat is also greater than the canopy cover in Zone IV, however not significantly.

6.4.4.2 Plant species comparisons

6.4.4.2.1 Species composition comparison of CVGCA and Zone IV

Three hundred and eighty-six plant species from a total of 17,681 stems were identified in plots and transects sampled across both the CVGCA and Zone IV areas (Appendix 4.2.1). There were 134 shared species represented by 11,102 stems, which accounted for 63 per cent of the total stems sampled across the two areas. The top ten shared species (Table 6.12) represented 33 per cent of the total stems identified across both sites. These were all identified within the mat, shrub, large shrub and liana layers, with the exception of *Ficus hirta* (hairy fig) for which its tree form was also sampled twice in each area; none of the top ten species are listed on the IUCN Red List.

Table 6.12 Top ten shared species in CVGCA and Zone IV

Species	CVGCA stems (n)	Zone IV stems (n)	Total (n)	IUCN Red List status
Pilea notata	922	676	1598	NE
Diplazium maximum	75	928	1003	NE
Pyrrosia bonii	13	556	569	NE
Asplenium normale	94	421	515	NE
Chirita speciosa	236	214	450	NE
Epipremnum pinnatum	312	104	416	NE
Ficus hirta	12	342	354	NE
Laportea violacea	91	245	336	NE
Pilea melastomoides	296	4	300	NE
Aspidistra typica	287	3	290	NE
TOTAL	**2338**	**3493**	**5831**	

6.4.4.3 Non-metric multi-dimensional scaling analysis comparison of CVGCA and Zone IV

The NMDS was undertaken in two dimensions, a Wisconsin double standardisation followed by a square root transformation was applied, and a Bray-Curtis dissimilarity distance undertaken on the sites, with a solution reached after 20 tries. A stress of 0.16 was returned, as this fell below 0.2, it is considered a good two-dimensional arrangement of the plots and transects to show their similarities.

Based on the abundances of the plant species captured within the two sites, there is some distinction between the CVGCA plots and the Zone IV plots (Figure 6.17). The Zone IV plots appear group most closely to ridge plots from the CVGCA site, suggesting more similar plant

communities. The slope plots of both sites are more similar to one another than the valley plots of each site, which are very dissimilar. Confidence ellipses shows that there is some overlap, suggesting that the two sites share some similarity in their plant communities, largely driven by ridge and slope plant communities.

The PERMANOVA show that while there is a significant variation (R^2=0.08, F=2.58, P=0.001) between the two sites, the variation explained is only eight per cent, indicating that the CVGCA and Zone IV sites are fairly similar based on their plant communities. Plot types explain more of the variation observed (R^2=0.15, F=2.4, P=0.001), explaining 15 per cent of variation observed.

Applying the intrinsic vectors shows that 34 species are significantly (p<0.01) to the composition of the plant communities within the sites (Figure 6.17). A large cluster of species including *Amorphophallus tonkinensis* (p=0.005) have steep positive gradients and while they contribute to both plots in both sites, they are more typical of CVGCA than Zone IV based on their abundances.

A second grouping with steep negative gradients includes *Diplazium maximum* (p=0.001), all of which all have the strongest contribution to Zone IV plots. The species *Chirita speciosa* (p=0.007) has a negative gradient and strong contributions to both sites

The fourth grouping including *Sinarundinaria floribunda* (p=0.005), have negative gradients and contribute to both plots at similar abundances, as does *Ardisia crenata* (p=0.006), which has a positive gradient.

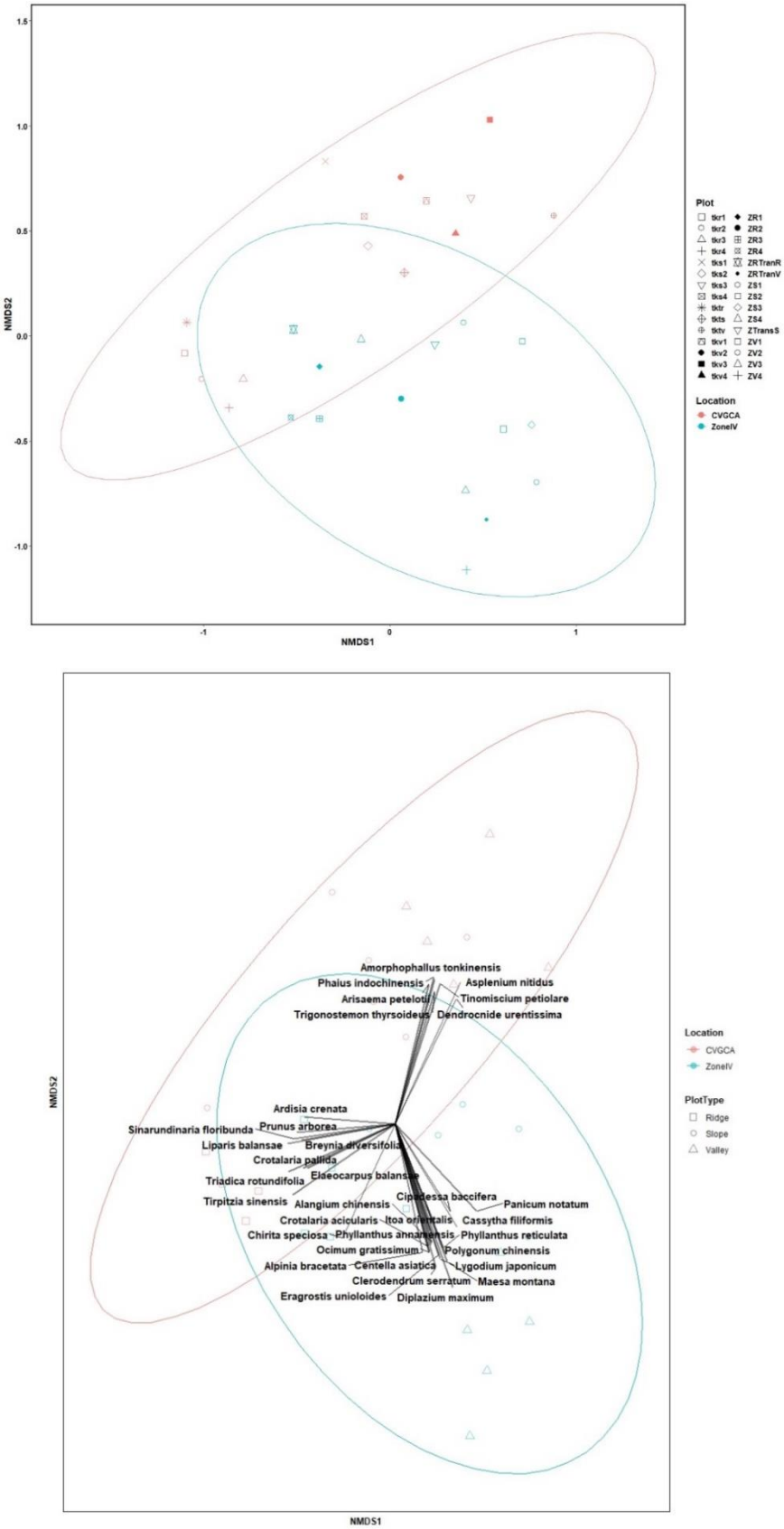


Figure 6.17 NMDS of CVGCA and Zone IV sites Top: NMDS with confidence ellipses (0.95). Bottom: NMDS with intrinsic vectors where p<0.05.

6.4.4.4 Tree comparison between sites

There were 145 tree species from 51 families captured 884 times across the CVGCA and Zone IV sites, 42 species of which are shared by both sites (Appendix 4.2.2). The top ten species shared by both sites account for over 28 per cent of all tree stems captured (Table 6.13). The top three shared tree species are all listed by the IUCN Red List. The most frequently sampled shared tree was *Cephalomappa sinensis,* listed as Vulnerable by the IUCN Red List ("Cephalomappa sinensis.," 1988) due to overuse as forage for cattle and a lack of wild regeneration without human intervention through plantations.

Table 6.13 Top ten tree species shared by CVGCA and Zone IV sites

Species	Occurrence CVGCA (n)	Occurrence Zone IV (n)	Total (n)	IUCN Red List Status
Cephalomappa sinensis	73	10	83	VU
Tirpitzia sinensis	17	13	30	LC
Acer tonkinensis	11	14	25	NT
Crotalaria pallida	19	3	22	NE
Burretiodendron hsienmu	17	1	18	VU
Radermacheta sinica	4	14	18	NE
Schefflera pes-avis	11	5	16	NE
Villebrunea integrifolia	2	13	15	NE
Sinosideroxylon wightianum	11	3	14	NE
Ardisia tinctoria	4	10	14	NE
Total	**169**	**86**	**255**	

The NDMS applied a Wisconsin double standardisation transformation and reached a solution after 20 runs. A stress of 0.15 was returned, which as it is below 0.2, produces a good two-dimensional representation of the tree communities across the two sites.

There is a large overlap between the two sites based on their tree compositions (Figure 6.18), with ridge plots of both sites grouping closely. The CVGCA slope and valley transects group more closely with the Zone IV slope plots and ridge plots respectively, than with their own CVGCA plots. The CVGCA site shows more variation along the NMDS2 axis than Zone IV.

A PERMANOVA shows that while there is a significant difference (R^2=0.08, F=2.72, P=0.001), only eight per cent of the variation seen can be explained by location of the sites. Instead, 19

per cent of variation can be explained by plot type across the sites (R^2=0.07, F=19, P=0.001). This however is still low and suggests that the two sites are quite similar.

Applying the intrinsic vectors shows 13 species significantly contribute to the composition of the plots (Figure 6.18). *Radermacheta sinica* (p=0.007), *Maesa montana* (p=0.001), *Itoa orientalis* (p=0.001), *Callicarpa macrophylla* (p=0.002), *Cipadessa baccifera* (p=0.004) all have shallow positive gradients and contribute to the composition of Zone IV plots. The species *Alangium chinensis* (p=0.001), *Phyllanthus reticulate* (p=0.003) have shallow negative gradients and also contribute to Zone IV plots.

Crotalaria pallida (p=0.003), *Breynia diversifolia* (p=0.009), *Tirpitzia sinensis* (p=0.003) have negative gradients and while they are found across both plots, contribute more to the CVGCA plots. The species *Trigonostemon thyrsoideus* (p=0.007), *Cephalomappa sinensis* (p=0.009), *Celtis tetrandra* (p=0.006) have very steep negative gradients and predominately contribute to CVGCA plots.

6.4.4.5 Food species composition and NMDS comparison between the CVGCA and Zone IV

A total of 23 food species representing 17 families were captured across the CVGCA and Zone IV potential habitat sites (Appendix 4.3.2) from a total of 655 stems, 17 species in CVGCA, with a density of 0.21/m^2 and 18 species in Zone IV, with a density of 0.14/m^2. The two sites share 12 species in common (Table 6.14).

Most diet species were captured within valley plots (n= 18 species), followed closely by slope plots (n=17 species) and then ridge plots (n=12 species). Slope plots have the greatest number of food species stems (n=350 stems), followed by valleys (n=190 stems) and ridges (n=115 stems). Fifteen of the species are classified by the IUCN Red List, with 11 species classified as Vulnerable.

The NDMS applied a Wisconsin double standardisation transformation and achieved a solution after 20 runs. A stress of 1.54 was returned, indicating a fair two-dimensional representation of the plant community similarities across plots.

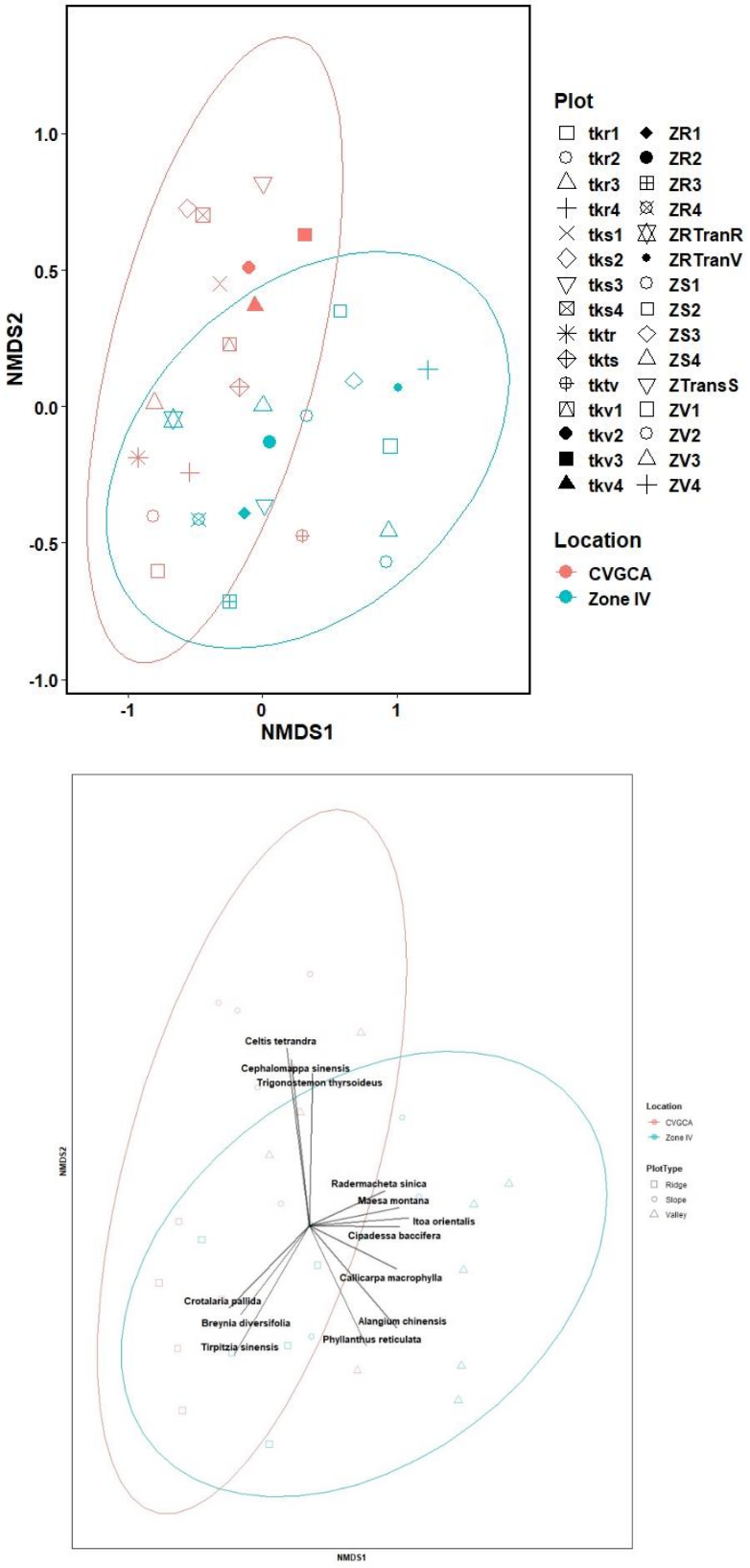


Figure 6.18 NMDS of tree species in CVGCA and Zone IV. Top: NMS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors where p<0.05

Table 6.14 Food species captured within CVGCA and Zone IV

Species	Occurrence CVGCA (n)	Occurrence Zone IV (n)	Form: parts eaten	IUCN Red List Status
Acer tonkinensis	47	32	Tree: fruits, young leaves	NT
*Alangium kurzii^*	2	1	Tree: leaves	LC
Allophylus caudatus*	20	0	Unknown: fruits	NE
Bischofia javanica	7	0	Unknown: young leaves	LC
Bridelia ovata	6	6	Unknown: fruits	NE
Broussonetia papyrifera	1	0	Tree: fruits, leaves	LC
*Burretiodendron hsienmu^*	49	4	Tree: fruits, young leaves, buds, flower	VU
*Caryota bacsonensis^*	5	1	Unknown: fruits, flowers	NE
Celtis tetrandra	10	25	Tree: fruits	LC
Cephalomappa sinensis	175	21	Tree: young leaves	VU
*Choerospondias axillaris^*	0	1	Tree: fruits, leaves	LC
Cipadessa baccifera	0	54	Tree: fruits	LC
Citrus grandis*	0	2	Tree: fruits	NE
Diospyros kaki	0	1	Tree: fruits	LC
Engelhardtia roxburghiana	2	13	Unknown: fruits, young leaves	LC
Erythropalum scandens	9	19	Unknown: young leaves	LC
Ficus cyrtophylla	0	7	Tree: fruits	LC
Mallotus barbatus^*	8	8	Vine: leaves	LC
Mallotus philippinensis^*	2	9	Vine: leaves	NE
*Pistacia weinmannifolia^*	6	0	Tree: leaves	DD
Sinosideroxylon wightianum	29	11	Unknown: fruits	NE
*Tetrastigma obtectum^*	0	49	Tree: leaves	NE
Tetrastigma planicaule	13	0	Vine: fruits	NE
Total	**391**	**264**		

*Only recorded by genus sp. in studies.
^ Not observed consumed within CVGCA, only BNNR

There is very little separation between the CVGCA and Zone IV plots based on their diet abundances (Figure 6.19), with confidence ellipses heavily overlapping. The CVGCA plots show most variation along the NMDS2 axis, while variation is more even across both axes in Zone IV. The ridge plots for both areas are closely grouped, while the CVGCA plots and the Zone IV valley plots are not closely grouped and appear to be driving most of the spread observed in the 0.95 confidence ellipses. In particular, the third valley plot (TkV3) and valley transect (TkVTran) fall outside of the confidence ellipses, suggesting they may represent outliers in terms of their food species abundances.

A PERMANOVA shows that only 10 per cent of the variation can be explained by location (R^2=0.10, F=3.07, P=0.002), however 17 per cent can be explained by plot type across the sites (R^2=0.17, F=2.8, P=0.001). These are still low levels of variation and suggest that the two sites a fairly similar based on the abundances and compositions of food species within them.

Applying the intrinsic vectors shows that five food species are significantly (p<0.05) contributing to the composition and distribution of the sites. *Tetrastigma obtectum* (p=0.05) has a positive gradient and contributes to both sites.

Cephalomappa sinensis (p=0.03) and *Caryota bacsonensis* (p=0.01) have a negative gradient and while they appear across both sites, they both contribute more to CVGCA. *Erythropalum scandens* (p=0.01) however, has a negative gradient and contributes more to Zone IV. *Sinosideroxylon wightianum* (p=0.05) has a steep positive gradient and contributes to both plots.

6.4.5 CVGCA, Corridor and Zone IV Potential habitat comparison

6.4.5.1 Vegetation of Corridor area

One hundred and forty-seven species representing 65 families were identified within the Corridor transects from a total of 2814 stems (Appendix 4.2.2). The valley transect had the greatest number of species (n=87), followed by the slope transect (n=82) and ridge transect (n=48). Although the valley and slope transect had similar numbers of species, the valley had significantly greater stems (n=1754) with over 2.5 times the number sampled in the slope (n=640) and four times the number of stems in the ridge transect (n=420).

The valley transect is highly represented by the top ten species identified across all three transects (Table 6.15). Three of the top ten species are list on the IUCN Red List: *Eragrostis unioloides*, a herb species found around the world, and *Diospyros apiculate*, a tropical tree species found in southeast Asia, are both considered Least Concern, while *Cephalomappa sinensis* – a limestone tree found in Guangxi, China and Cao Bang, Vietnam, is listed as Vulnerable due to use as cattle feed and wood harvesting (IUCN, 2022a).

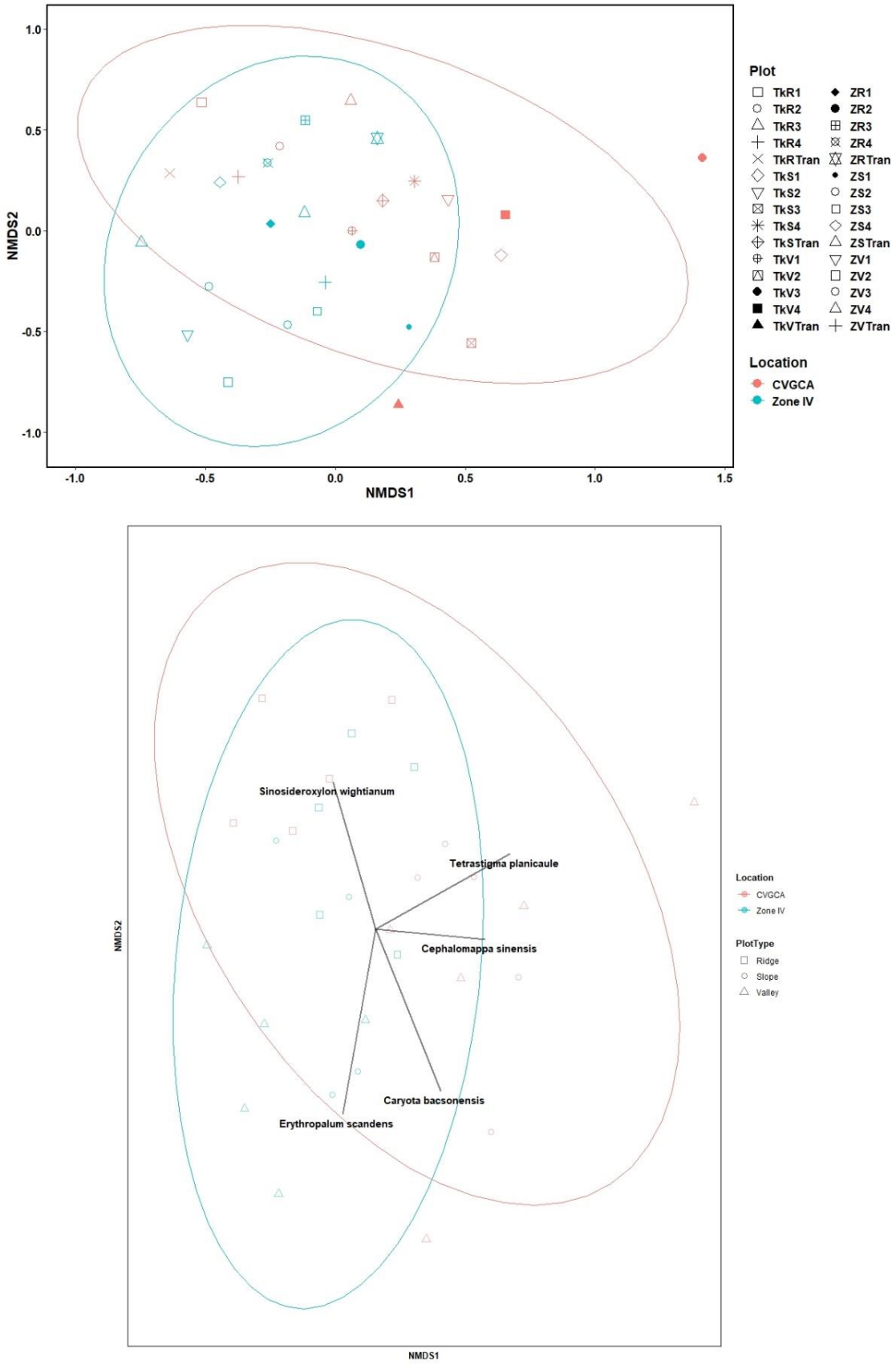


Figure 6.19 NMDS of food species in CVGCA and Zone IV. Top: NMDS with 0.95 confidence ellipses. Bottom: NMDS with intrinsic vectors

Table 6.15 Top ten species in Corridor transects

Species	Ridge (n)	Slope (n)	Valley (n)	IUCN Red List Status
Asplenium normale	34	29	398	NE
Eragrostis unioloides	0	0	198	LC
Selaginella uncinata	0	43	132	NE
Arachniodes hasseltii	0	22	134	NE
Panicum notatum	0	29	97	NE
Achyranthes aspera	0	0	118	NE
Cephalomappa sinensis	98	20	0	VU
Diospyros apiculata	22	33	25	LC
Boehmeria holosericea	7	0	66	NE
Chirita speciosa	0	1	72	NE
Total	**161**	**177**	**1240**	

6.4.5.2 Comparison of tree characteristics in the Corridor, CVGCA and Zone IV

A two-way ANOVA shows that only elevation has a significant difference across the three sites based on the linear model applied (Appendix 4.1.8).

The estimated marginal means analysis confirms only elevation has a significant difference across the sites (Appendix 4.1.9). The Corridor area has a significantly lower elevation than the CVGCA (p=0.013) and Zone IV (p=0.006). However, there is no significant difference across the tree metrics gathered from transects across the CVGCA, Corridor area or Zone IV potential habitat. In general, the mean canopy heights, tree density and basal areas are greater in both CVGCA, and Zone IV potential habitat compared to the corridor vegetation, however not significantly. In contrast, corridor vegetation had higher mean canopy cover than both other sites, however again, this was not a significant difference.

Within the Corridor, the transects captured 140 trees from 40 species and 27 families (Appendix 4.2.4). The slope transect captured 57 trees from 20 species and the valley transect had similar abundances with 53 trees from 21 species identified. The ridge transect captured the fewest number of trees (n=30) from only 13 species. In the CVGCA transects, 141 trees from 57 species were identified. The CVGCA slope transect also had the greatest number of trees (n=51) from 20 species. Like the Corridor, the ridge and valley transects in CVGCA had similar compositions. The ridge transect had 46 trees from 20 species and the valley transect had 44 trees also from 20 species.

The tree composition in Zone IV transects is slightly different across the plot types compared to both the Corridor and CVGCA. In Zone IV 144 trees were captured within the three transects. The valley transect had 83 trees from only 10 species, followed by the ridge transect, which had 41 tree from 18 species. The slope transect of Zone IV had the fewest trees (n=20) from 15 species.

6.4.5.3 Diet species in corridor

The corridor transects captured ten food species, represented by 211 stems (Table 6.16). The slope and ridge transect had the greatest number of species (n=7), followed closely by valleys (n=6). Ridges had the greatest number of food stems (n=108), followed by valleys (n=54) and slopes had the least (n=49).

Table 6.16 Food species captured in corridor transects

Species	Ridge (n)	Slope (n)	Valley (n)	Total (n)
Bridelia ovata	1	0	0	1
Burretiodendron hsienmu	2	1	1	4
Caryota bacsonensis	0	0	1	1
Celtis tetrandra	2	1	4	7
Cephalomappa sinensis	98	20	0	118
Cipadessa baccifera	0	13	21	34
Ficus cyrtophylla	1	0	0	1
Mallotus philippinensis	2	2	6	10
Sinosideroxylon wightianum	2	9	0	11
Tetrastigma obtectum	0	3	21	24
Total	**108**	**49**	**54**	**211**

6.5 Discussion

6.5.1 CVGCA habitat

6.5.1.1 Composition and historical use

The extremes of limestone karst are reflected in the habitat of the CVG. The CVGCA core zone has steep slopes and increases rapidly in elevation as you move from valleys up to the mountains and peaks. The lower topographic complexity of the valleys compared to that found on the slopes and ridges is likely a result of the flow and accumulation of soil into the deep valleys. This is further reflected by the fact that the most frequently occurring species in slopes and ridges are lithic epiphytes and small orchids and flowering herbs – species capable of surviving in environments such as rock crevices. It is this accumulation of soil that made

valleys in this area ripe for farming prior to the establishment of the CVGCA in 2007 (Anon, 2007).

Interviews suggested that most local farmers accept the fact that they can no longer graze their animals or access the CVGCA for wood, and that they considered an improvement in the CVGCA vegetation since protections began. Although no farming is legally permitted within the CVGCA, during interviews it was revealed that some farming on the border with China still remained despite protections. Barriers have been established to prevent access to Luong Si valley where farming occurs, FFI reported that these were often destroyed to allow grazing of cattle and even planting of food for livestock.

The CVGCA habitat is largely uniform across valley and slope areas, while ridges typically display distinct plant communities. It is unsurprising then that elevation is a significant contributor to plant community compositions, as the soil availability is lowest and exposure to climatic changes the highest for the limestone ridges, making it less hospitable for larger species. This is further reflected by the greater tree density found on ridges, but the smaller size and less canopy cover measured.

In contrast, the valleys and slopes are very similar in plant compositions, including trees. The accumulation of soil in valleys may also account for the greatest species richness and density recorded at these sites. Valleys, however, are characterised by greater density in the lower vegetation levels such as mat, shrub and liana coverage. While tree density is slightly greater in valleys than slopes, trees are smaller and younger. These areas tend to be more open in the canopy, either as a result of natural processes or regeneration from historical disturbance.

Historical use of the CVGCA may also account for why the largest trees and greatest canopy cover are found on the slopes of the CVGCA. Being less accessible than trees in the valley, may account for their continued growth. For example, from 1970-90, the timber from large *Burretiodendron hsienmu* was collected for furniture and fuel wood, particularly closer to the villages (Fan, Zhang, Fei et al., 2011). Today, *Burretiodendron hsienmu* is one of the most frequently identified species on slopes (n=35), suggesting that the species may have bounced back or that those specimens on slopes were too difficult to access compared to those in valleys.

Slope plots appear to have the clearest distinctions between vegetation levels, with intermediate mat, shrub, large shrub and liana coverage compared to valley and ridge plots. Their low plant density and tree density may be linked to the taller trees and higher canopy coverage as larger trees may limit the growth of denser vegetation. While species richness and density are lower in slope plots than valleys, the high species diversity suggests a more even distribution of species, potentially making them less prone to climatic impacts.

6.5.1.2 CVGCA sleeping trees and canopy

The average canopy height in CVGCA is only 5.68m, much lower than the findings of Fan et al. (2011) in BNNR where the canopy is on average 10m in height. At 10m, this is the lowest canopy height recorded for a gibbon species (Fan et al., 2011; Fan et al., 2013), indicating that the mean canopy of CVGCA is worryingly low. It is possible this is a direct result of sampling all trees within plots, rather than just well-established trees. When considering the distribution of tree heights across CVGCA, it appears that a majority of trees are 10m tall or shorter, which may provide enough suitably tall trees to accommodate the CVG.

During data collection, gibbons were often observed travelling through the canopy on slopes, down into the valleys rather than along the valleys. This may be linked to the much higher percentage of canopy cover found in slopes compared to that in valleys and ridges, creating 'arboreal highways' (David John Chivers, 1974) for the CVG to travel along. Canopy connectivity is critical for highly arboreal primate such as gibbons and can reflect suitability of habitat as suggested by Fan et al. (2013). Canopy connectivity has been demonstrated to positively influence population density of some Hylobatids such as Siamang and the lar gibbon, however the degree of connectivity required to maintain an arboreal pathway varies according to species, likely due to differences in body size and locomotion across gibbon species (Hankinson et al., 2021). It is unlikely that differences in CVG density between CVGCA and BNNR can be linked to canopy connectivity and instead, the higher density of CVG within the Vietnamese forest may then be a result of other factors such as vegetation distribution across the region or availability of diet species.

The quality of trees found on slopes is generally greater than those in valleys and ridges, as trees on slopes are on average, taller, with greater DBH and canopy cover. This may explain

why slopes are the preferred sites for CVG to sleep and call from (H. L. Fei et al., 2012) as these are where the largest trees are found. A preference for the tallest trees on ridges and slopes to be used for calling has also been observed in other gibbon species, including black-crested gibbons (*Nomascus concolor jingdongensis*) (Fan et al., 2009), and Kloss's gibbon (*Hylobates klossi*) (Whitten, 1982a). This is because taller trees are thought to offer greater sound transmission for calling bouts, improving intra- and inter-group messaging (Whitten, 1982a).

Of the five most frequently used sleeping tree species used in BNNR (Fei et al. 2012), only *Broussonetia papyrifera* and *Ficus sp*. were identified in this study as mature trees. This may indicate that other preferred species have been missed through random sampling, or that they are less common within the CVGCA region. The resident CVGCA gibbons may also possess different preferences for sleeping trees compared to those within the BNNR. This may be the case considering the difference in the average canopy height within the CVGCA compared to that of the BNNR and the CVGCA gibbons may select different species as a result. Additional study of sleeping tree choice in the CVGCA should be further investigated to further improve our understanding of this critical CVG behaviour.

6.5.1.3 Food species in CVGCA

The CVG diet has a high proportion of fruit and generally follows a diurnal pattern in food choice whereby fruit is consumed at the beginning and end of the day (Fan et al., 2011; Fan , Ni, Sun, Huang, & Jiang, 2009; Geissmann et al., 2002). Fan et al. (2009) suggests that this may be to improve blood sugar levels in the morning and store energy-rich foods overnight. While fruit represents 58 per cent of the diet of CVG in BRNP (Fan et al., 2011) - CVG are less frugivorous than many *Hylobates* and *Hoolock* species (Bartlett, 2008). CVG diets are also highly seasonal, with an increase of leaves observed when fruit availability is limited (Fan et al., 2012; C. Ma, Liao, & Fan, 2017).

The low capture of only 17 food species across the CVGCA sampling is concerning as over 118 species have been identified as being eaten by the gibbons across several studies (B. P. L. Chan & Ng, 2006; Fan et al., 2011; Insua-Cao et al., 2012; Thien & Dine, 2012; Vu Ngoc et al., 2005). However, Fan et al. (2011) noted that many of the top species consumed by the CVG are uncommon within the BNNR site. Ten of the 19 top species comprising more than one per

cent of the CVG diet, have sparse distributions across BNNR (Fan et al., 2011; C. Ma et al., 2017). This may account for a similar situation within the Vietnamese CVGCA and explain the low sampling of food species. It also means that the conservation and maintenance of the CVGCA ecology is critical to prevent the loss of important food species for the gibbons (C. Ma et al., 2017)

The high proportion of a small number of key species in the CVG diet is a common pattern across gibbon species (Asensio et al., 2014). However, of the top 19 species identified by Fan et al. (2011) consumed by the CVG in BNNR, only three were captured in my sampling: *B. papyrifera, B. hsienmu* and *C.axillaris*, along with a number of shared genera. *B. papyrifera* has been identified as the most frequently consumed species by the BNNR CVG, with all three parts, fruit, leaves and flowers consumed in high levels (C. Ma et al., 2017). *C. axillaris* was also identified as a critical food resource during autumn, and several *Ficus* species, of which my study did not capture (though several other *Ficus* species were identified), have been suggested as important winter foods, due to the year-round fig production (Fan et al., 2011; Fan et al., 2012; C. Ma et al., 2017). The presence of these species in the CVGCA suggests some continuity in preferred foods between the two sites.

Low capture of exact species but high levels of sister-species from my sampling may be a result of potential sampling errors: potentially under capture of specimens in my study and/or in other studies due to the distance at which diet records are often collected (over 50m away) (Fan et al., 2011). It may also be simply a result of low distribution frequencies of many key diet species due to previous anthropological-led degradation of the site. It is worth noting that studies of CVG within BNNR represents only two gibbon groups, as the majority of CVG inhabit the CVGCA are exclusively. Therefore, it is possible that the composition of food species consumed in the CVGCA occurs in different ratios, which could indicate different preferences for some foods.

While there was a high level of overlap between the three plot types and their food species compositions, food species were most frequently sampled within slope plots, followed by valleys. Once again, the higher levels of food species on slopes may be a direct result from historical use of valleys for farming and plantations. The influence of elevation also appears

to influence the food species communities across plots. The higher elevation of slopes may be more conducive to the growth of certain food species, however, the greater accessibility along slopes may have also impacted food selection in the CVG. Lower canopy connectivity within valleys may reduce their ability to reach certain species, leading to a greater use of available species found on slopes. Continued regeneration of valleys may lead to increased use and introduction of additional food species as they become accessible. A longitudinal study of CVG use of different areas for food may reveal more about adaptability or selectivity of CVG diets.

This low distribution of food species throughout the CVGCA may also account for the large home range of 11 to 13.3 km^2 for the CVG (Fan et al., 2010) as they require larger ranges to allow sustainable use of feeding patches. Despite being the most at risk, with some of the smallest populations, the CVG and Hainan gibbon have the largest home ranges of any gibbons (Bryant et al., 2015). Considering the high density of groups in such a small forest fragment, large home ranges may be a direct result of low resource distribution. Observations of the CVG within the BNNR suggest that they occupied larger home ranges than gibbon groups in the CVGCA, theorised to be due to the 'better habitat' available on the Vietnamese area (C. Ma et al., 2017).

Understanding the exact links between primate distribution and food availability can be difficult to determine due to the rapid changes that can occur in plant availability as a result of climatic conditions (C. Chapman, Rothman, & Lambert, 2012; Hanya & Chapman, 2013). Based on changes of primate home ranges in response to seasonal changes, it is theorised that species limited by fallback foods may increase their home range during times of low food availability (Hanya & Chapman, 2013).

If low densities of quality food are driving greater home ranges in the CVG, then it does seem at odds with the high density of CVG (1.6 groups per km^2) – one of the highest of the *Nomascus* gibbons (Dat et al., 2008a). In other primate populations, such as *Procolobus tephrosceles* (red colobus) in Kibale National Park, Uganda, increased availability of high-quality foods is linked to higher densities (Colin A. Chapman & Chapman, 1999). Gibbon species such as the *Hylobates albibarbis* (white bearded gibbon) in Borneo have had population abundances linked to the availability of the fig, identified as an important fallback food (Clink, Dillis, Feilen,

Beaudrot, & Marshall, 2017; Andrew J. Marshall & Leighton, 2006). In contrast to the CVG however, the white bearded gibbon had not experienced hunting or habitat loss in over 20 years (Andrew J. Marshall & Leighton, 2006). This is important as it is difficult to tease apart the impacts of food availability, the size of available habitat fragment in CVGCA, past hunting and habitat degradation from past use by humans (Dat et al., 2008a) when trying to explain CVG density levels. The higher levels of gibbons within the CVGCA compared to BNNR however, does suggest that there is a quality issue either in regard to the overall vegetation or specifically food species that is driving CVG abundances.

Fruit resources are often located in clumped patches, enabling the high-demand resource to be defended against other individuals, particularly other females (Z. H. Guan et al., 2018). Highly frugivorous species such as gibbons, are expected to be intolerant of other females in situations where high-value fruit resources can be defended (Bartlett, 2008). The lower levels of frugivory observed in *Nomascus* species compared to other gibbon species may then also contribute to the higher levels of polygyny reported (Bartlett, 2008; Fan et al., 2015). Where available resources are more widely dispersed as suggested by the low capture of food species in the CVGCA in this study, larger home ranges may be required in addition to greater tolerance of additional females in CVG mating groups.

Within the CVGCA, there is a small patch of forest to the southeast that is not frequently utilised by the CVG. This area is predominately valley, historically used for farming prior to the creation of the conservation area. The vegetation within this region is largely regenerating farmland, with few large trees and minimal continuous canopy. Rangers reported that CVG only venture into this area occasionally to eat in remnant banana trees, but do not remain in the area after feeding bouts. The irregular use of this patch may offer an opportunity for targeted rehabilitation to attract more regular use of the region to help support more gibbon groups within the protected zone. While this would not result in a significant increase in available space, it may buy more time for conservation groups to plan for when the area will reach carrying capacity – expected by Fan et al. (2013) to occur within 30-40 years.

6.5.2 Zone IV potential habitat

6.5.2.1 Composition and current use

The Zone IV potential habitat was identified by (Fan et al., 2013) using remote sensing, as a possible secondary priority for conservation after the CVGCA and BNNR CVG habitat. As part of this analysis, Fan et al. (2013) noted that this region may not be adequate to support gibbons due to poorer quality forests due to canopy cover, and the presence of adjacent farmlands.

Analysis of this region using in situ ecological sampling, shows that the vegetation characteristics across the valley, slopes and plots appear relatively homogenous, with the exception that slopes exhibited greater canopy cover and greater basal area than other plot types. In terms of plant community abundances, there is a high level of overlap, largely driven by slopes; valleys and ridges have little to no overlap in their plant communities. The same can be said for tree species and diet species abundances – there is a high level of homogeneity across the valleys, slopes and ridges.

The presence of a highly abundant invasive weed species *Erigeron canadense* in the valleys of Zone IV is of concern and should be considered by the National Park as a priority to eradicate. These valley characteristics are once again, likely to be a function of accessibility to humans, as valley areas have been historically and, in some cases, still are used for farmland or grazing of cattle. There is also evidence that some collection of wood is still occurring in this area despite its status as a protected area. When sampling a valley, evidence of recent tree cutting was found (Figure 6.20). National Park rangers monitoring my fieldwork in the area indicated that responsibility for monitoring and reporting these activities sat with the Forest Management Board and was beyond their responsibilities.

Figure 6.20 Evidence of tree cutting in two Zone IV valleys. Photos: K. Apthorp, 2016.

During sampling of one of the slopes, a small trap for birds or bats was also found hanging from a sapling (Figure 6.21), suggesting that some degree of hunting continues in the area. Interviews also suggested that there needed to be some increased or ongoing educational advertising regarding the importance of protecting the CVGCA as people were still entering protected areas. While Zone IV is not home to any CVG currently, it is a protected area and hunting is illegal. Due to these ongoing activities, it is not recommended that efforts to expand the CVG distribution into this area is pursued without an assessment of the ongoing human use of the area.

Figure 6.21 Small trap found in forest of Zone IV. Photos: K. Apthorp 2016.

In comparing Zone IV to the CVGCA, it appears that unexpectedly, the former has a greater species richness and density. This might be a signal of high levels of biodiversity. Alternatively, when viewed in the context of the overall composition of Zone IV plots, which have high levels mat and shrub cover, high liana coverage, and low tree density, it may signal poorer quality vegetation compared to CVGCA. The two sites have dissimilar plant community abundances, suggesting a divergence in species distribution since their historical fragmentation from one another. It is likely that this is also a function of the protection of the CVGCA area, which means it has likely undergone less habitat degradation since it was protected in 2007. For example, the valleys in Zone IV, where extensive evidence of ongoing use was observed are distinctly different in their species composition compared to the valleys in CVGCA, suggesting that considerations around potential need for rehabilitation of the Zone IV to make it suitable for CVG groups.

6.5.2.2 Tree characteristics within Zone IV

As seen in the CVGCA, slopes in Zone IV exhibit the greatest canopy cover, and canopy height but unlike the CVGCA, slopes in Zone IV also have the greatest basal area. Slopes offer the most accessibility for any potential gibbons entering Zone IV, however the composition of the overall tree community may not match CVGCA. While there is some overlap in the tree abundances for both sites, this is largely driven by similarities in ridge tree communities. The increasingly slope areas exhibit only a small amount of grouping - Zone IV slope plots group more closely to Zone IV valley plots, suggesting lower similarity between Zone IV and CVGCA tree communities.

The height, density and mean DBH of trees could also indicate whether or not this region could successfully support CVG populations due to their reliance on trees for transport, sleeping and socialising (Fan , Scott, Fei, & Ma, 2013). Based on a comparison of these measures between CVGCA and Zone IV, the latter has significantly lower tree height, mean DBH and total basal area. The region also exhibits lower tree density and lower canopy cover than those seen in the CVGCA, though notably, these were not significant differences.

Theses tree metrics are thought to play a role in sleeping tree selection for arboreal primates (S. M. Cheyne, Höing, Rinear, & Sheeran, 2013). In *Rhinopithecus bieti*, slope, aspect, tree

height and DBH are all important characteristics in sleeping tree choice (D. Li et al., 2006). While in gibbon and siamang species such as *Hylobates albibarbis* (S. M. Cheyne et al., 2013), *Hylobates pileatus* (Phoonjampa et al., 2010), *Hylobates klossi* (Whitten, 1982b) and *Symphalangus syndactylus* (N. J. Harrison et al., 2021) height and connectivity to the canopy play a role in sleeping tree selection, with a preference for tall or emergent trees. No study has been conducted to ascertain the influence of these factors on CVG sleeping tree choice, beyond a preference for taller trees without lianas, likely influenced by predator avoidance behaviours (H. L. Fei et al., 2012).

Of the five top sleeping tree species identified by H. L. Fei et al. (2012), none were captured within Zone IV plots. This suggests that the tree community does not overlap for species important in CVG behavioural ecology. While the CVG have been shown to prefer certain species of sleeping tree in BNNR, they have also been shown to only occasionally reuse sleeping sites (H. L. Fei et al., 2012), which may indicate a flexibility in the selection of sleeping trees. Without further study on the selection of sleeping trees within CVGCA, it is difficult to determine whether Zone IV could accommodate CVG sleeping requirements.

When considering the potential of Zone IV as habitat for the CVG, tree metrics suggest it is significantly poorer quality than the CVGCA. In their original analysis, Fan et al. (2013) determined that for 'canopy dwellers' canopy cover could be used to evaluate habitat quality. Contiguous canopy is essential for gibbons and is used in all aspects of their behavioural ecology (S. Cheyne et al., 2013). The current canopy height of the CVG in BNNR and CVGCA is already the lowest recorded canopy height amongst gibbons (Fan et al., 2011; H. L. Fei et al., 2012; Hanlan et al., 2015). In Zone IV, the mean canopy height is significantly lower than that in CVGCA, measuring 4.38m in Zone IV versus 5.68m in the CVGCA. This suggests that the area may not provide enough trees suitable to support the CVG.

Other gibbon species including the Bornean agile gibbon (*Hylobates albibarbis*), have been found to prefer connected canopy cover, taller canopy heights, and trees with a larger DBH, and actively avoid trees below 10m in height (S. Cheyne et al., 2013). Similarly, the Western Hoolock gibbon (*Hoolock hoolock*) in Inner-line Reserve Forest, India, was found to prefer canopy heights of 11-15m for feeding, travel, resting, calling and social activities (Islam, 2014).

The CVG has been found to utilise the mid canopy 5-10m in height for most locomotion (Fan et al., 2013) and feeding (Hanlan et al., 2015) in BNNR, however, this behaviour may be constrained by the fact that the majority of trees in BNNR, like CVGCA, are only a maximum of 5-10m high – over ten metres lower than canopies observed in other gibbon habitats (W. V. Bleisch & Chen, 1991; Fan et al., 2013).

6.5.2.3 Food species in Zone IV

A similar number of food species were captured within the Zone IV (n=18) as in CVGCA (n=17), however, CVGCA captured a greater number of total individual food stems (n=391) compared to Zone IV (n=264). Of the 23 food species identified across the two sites, 12 species are shared, and Zone IV has a greater number of unique food species compared to the CVGCA. In terms of density however, Zone IV has a lower food species density (0.14/m^2) than found in CVGCA (0.21/m^2). Fruit stems also make up less than three per cent of all stems captured within Zone IV compared to five per cent in the CVGCA.

Once again, differences between the two sites in terms of food abundances were largely found between the valley plots, and the greatest similarity occurred between the ridge plots. As observed in CVGCA, the slope plots in Zone IV had the highest frequency of food species compared to the valley and ridge plots. The general species abundances were fairly similar, and *B. hsienmu* and *C. axillaris,* two of the top five species identified by Fan et al. (2011), were captured, albeit in very low frequencies in Zone IV (n=4 and n=1 respectively). Several species of *Ficus sp.* were also identified.

As food resource availability is likely a driving factor in primate distribution (Carl, 2009), the low density of food species within Zone IV may make it less suitable for the CVG or at least reduce the likelihood of natural dispersal into the area. Of the 23 food species found across both CVGCA and Zone IV, fourteen species that produce fruit that have been observed to be consumed by the CVG in the CVGCA or BNNR. There were more fruiting food species identified in Zone IV (n= 11) representing 61 per cent of food species found there, and only 8 fruiting species were found in CVGCA representing 47 per cent of food species captured in my sampling.

Figs have also been identified as important key or fallback species for several species of gibbons due to their high availability compared to other temporal restricted fruits (Clink et al., 2017; Conklin & Wrangham, 1994; Janzen, 1979; Andrew J. Marshall, Boyko, Feilen, Boyko, & Leighton, 2009; R. W. Wrangham et al., 1993) and fourteen species of *Ficus* (fig trees) are consumed by the CVG (B. P. L. Chan & Ng, 2006; Fan et al., 2011; Insua-Cao et al., 2012; Thien & Dine, 2012). An additional 13 species of fig trees were captured within my sampling across the CVGCA and Zone IV, with the majority found exclusively in Zone IV (CVGCA n=6 and Zone IV n=9). Although these particular species have not been directly observed to be consumed by the CVG, the fig in general has been found to be an important component of frugivorous primate diets (Conklin & Wrangham, 1994), particularly gibbons where figs have been found to make up on average, a quarter of their diet

The availability of figs has been found to influence the abundance of other apes including *Hylobates albibarbis* (Bornean white-bearded gibbon) (Conklin & Wrangham, 1994) and *Pongo abelii* (Sumatran orangutan) (Wich, Buij, & Carel van, 2004). Part of their appeal has been attributed to high availability throughout the year, the production of large crops that ripen at the same time, and lack of any protective coverings (Janzen, 1979; Kinnaird & O'brien, 2005). Figs have also been found to provide strong levels of metabolizable energy, sugar, and protein for primates (Conklin & Wrangham, 1994; C. Ma et al., 2017; R. W. Wrangham et al., 1993).

Previous studies have identified figs as important to CVG diets, representing 21.9 per cent of their diet in BNNR (Fan et al., 2011), particularly in winter when many other fruits are scarce (Fan et al., 2011; Insua-Cao et al., 2012; C. Ma et al., 2017). Figs represent 3.8 per cent of all stems identified in Zone IV, compared to 0.03 per cent in CVGCA. While this is a low level for CVGCA, there is a high level of fruit production per fig tree (Janzen, 1979). The high levels of figs present in Zone IV could indicate the area could maintain a larger number of CVG groups during periods when other food species are unavailable, however, the low abundance of other food species may limit long-term utilisation of the region. Further investigation into food choice of the CVG within the CVGCA would provide greater insight into the suitability of Zone IV.

6.5.3 Corridor connection

As arboreal locomotors that predominately move via brachiating, gibbons rely on contiguous canopy in order to travel throughout their home range (Fan et al., 2013; Michilsens et al., 2009). Brachiating in gibbons has evolved as an energy saving mode of locomotion through the ongoing transformation of potential and kinetic energy as they swing through the full range of motion (Bertram, Ruina, Cannon, Chang, & Coleman, 1999). CVG have been found to predominately brachiate over other locomotion modes such as climbing and leaping via branches rather than other strata including lianas (Fan et al., 2013). Based on the low canopies and disturbed vegetation in CVGCA and BNNR, it also provides a faster and safer method for gibbons to traverse their home range when foraging and protecting against intruders Fan et al. (2013).

Without continuous canopy connecting the CVGCA to other forest fragments, it is unlikely that the CVG would cross large gaps to naturally disperse. The presence of such clearings has been found to prevent the movement of insects, amphibians, reptiles, birds and larger mammals (William F. Laurance et al., 2009). Discontinuous canopy poses a serious risk to obligate canopy dwellers such as gibbons, increasing the energy expenditure required to negotiate breaks in canopy (S. Cheyne et al., 2013). Dispersed canopies across grassland and bamboo patches have also been thought to act as barriers to the movement of gibbon species such as black crested gibbon, as no observations have been made of this species travelling on the ground through these areas (Fauna & Flora International, 2016). Travelling on the ground for extended distances opens up opportunities for predation or injury of gibbons (Umapathy & Kumar, 2003).

The trees sampled within the corridor area show no significant differences to those as the other two sites, and ten diet species were captured in the transects. As found in both CVGCA and Zone IV, food species occur on slopes at higher frequencies than valleys and ridges in the corridor. This is somewhat encouraging, as it suggests that the corridor area could be contiguous to the CVGCA based on tree structure and food species availability, making it more accessible for the CVG. It also suggests that the CVG could naturally enter the Corridor region based on tree metrics and availability of some food species. Yet despite the similar profile of

the corridor, the connection formed by the corridor area between the CVGCA and Zone IV is by no means complete.

A large gap as a result of an established path crossing the Vietnamese/Chinese international border interrupts the corridor on the Vietnamese side, resulting in several metres of scramble vegetation either side before it transitions to secondary forest. This presents a major barrier for the CVG to disperse regardless of whether the Zone IV habitat becomes a conservation area. Gibbons such as *Hylobates albibarbis* (Bornean white-bearded gibbon) have been observed to baulk at gaps greater than 12m (S. Cheyne et al., 2013) and it is likely that the CVG, which primarily travels by brachiating through the canopy (Fan et al., 2013), would have a similar response.

While the corridor may persist in a more continuous form on the Chinese side of the border (Fan et al., 2013), it does not appear that many Vietnamese-based groups cross over into the Chinese BNNR with any regularity. Instead, it is only Chinese-based CVG that travel into the Vietnamese CVGCA forest (C.-Y. Ma et al., 2020). Without the natural movement of groups into China, it seems unlikely that the majority of CVG will find the corridor in China to access it. The suitability of the corridor on the Chinese side is also uncertain as no Chinese CVG have been observed to enter it as of 2016.

Despite this, efforts to improve corridor connections between the CVG habitats and potential forest are underway. A collaboration between the People's Republic of China and the Asian Development Bank via the Greater Mekong Subregion's Core Environment Program was underway to replant and improve vegetation corridors between the CVG habitat in China and karst forest fragments (Greater Mekong Subregion, 2014). Similar efforts were being planned through collaboration with the Vietnamese government, however, it was unclear whether reforesting would use native or introduced tree species (pers comm. FFI). The use of non-native plantations to boost or improve forest fragments should be carefully considered, particularly when attempting to induce natural dispersal of mammals (Blair et al., 2011).

Regardless, the impact of replanted corridors will require decades of costly investment and monitoring before their impact can be truly known. This timeframe could be greatly exaggerated for species such as the CVG, which rely largely on canopy connectivity (Arroyo-

Rodriguez & Mandujano, 2009). Instead, in an effort to bridge the gap between the CVGCA area and any future conservation area within the Zone IV potential habitat area, the use of man-made artificial corridors could be considered.

The use of artificial corridors such as bridges, have been shown to offer a more cost effective and timely solution to connecting forest fragments (Cunneyworth, Donaldson, & Onyancha, 2022; Nekaris et al., 2020). The type of artificial corridor to employ can be species-specific depending on the target species' preferences (Birot et al., 2020; Linden et al., 2020; Narváez-Rivera & Lindshield, 2022). The construction of artificial connections as well as materials used, require experimentation to understand the needs of the target species (Birot et al., 2020; Narváez-Rivera & Lindshield, 2022; Yap et al., 2022). The introduction of artificial corridors could also allow the CVG to overcome the threats posed by the many roads, rivers, and farmland encircling the CVGCA and BNNR (Cunneyworth et al., 2022; Linden et al., 2020; Yap et al., 2022).

Artificial canopies have been successfully used by other gibbon species, providing an opportunity that they could be similarly used by the CVG. The construction of an artificial bridge was found to reduce the impact of fragmentation for lar gibbons in Thailand (Saralamba & Menpreeda, 2018), and to reduce the need for *Hoolock hoolock* gibbons in India to descend to the ground (Das et al., 2009). The use of a rope bridge to connect forest fragments was also found to be successful for wild Hainan gibbons, covering an area of over 15m (Chan et al., 2020). It also demonstrated the behavioural flexibility of the Hainan gibbons in utilising an artificial corridor: despite a preference for brachiating, the rope bridge was primarily traversed via climbing, suggesting that while the rope choice may not have been the preferred support for the gibbons, the benefit it provided to them outweighed other locomotion preferences (Chan et al., 2020)

In the case of the CVG, it is possible that a preference would be for a semi-rigid canopy bridge that offered some flexibility to mimic the branches used for brachiating (Fan et al., 2013). While the CVG uses multiple supports to traverse their home ranges, branches were found to be preferred for brachiating over firmer boughs or flexible lianas (Fan et al., 2013).

6.6 Conclusion

Overall, the vegetation in Zone IV appears to be less differentiated across valleys, slopes and ridges as the vegetation within the CVGCA. This may be somewhat influenced by the significantly lower topographic complexity of the limestone karst within Zone IV. The CVGCA region has a complex karst structure, making it difficult to traverse during sampling. In contrast, Zone IV was generally easier to access. While this is beneficial for studying the region, improved accessibility to humans is concerning when taking into account the human activity observed across the site including ongoing cattle grazing, wood collection, and hunting. All of which have likely contributed to the introduction of invasive weed species.

Yet while the general vegetation compositions of the two sites only have some overlap, the two sites appear to be more similar to one another based on tree and diet abundances. The physical characteristics of these communities, however, are markedly different in several important tree metrics: canopy height, canopy cover and DBH, all of which have important implications regarding the structural requirements of the CVG to utilise a forest fragment.

Conservation efforts for the CVGCA have ensured their ongoing survival within their current habitat fragment. However, their future survival may require expansion into other suitable forest as the CVGCA and BNNR inhabited areas reach carrying capacity in the next few decades (Fan et al., 2013; C.-Y. Ma et al., 2020). If expansion of the current CVG habitat is pursued, overall, Zone IV may be a suitable option, particularly through targeted restoration and improved protections. Any habitat restoration should focus on improving the distribution of key sleeping tree and food species within Zone IV. As noted by C. Ma et al. (2017), due to the slow growth of trees on limestone karst through natural recovery (F. Zeng et al., 2007), rehabilitation must be targeted and also seek to conserve existing key species.

FFI with the support of Vietnamese and Chinese National Parks responsible for the CVG protected areas have made strides in reducing the reliance of local communities on the local forest through initiative to upgrade to fuel efficient stoves, the establishment of fuelwood plantations, and the restriction of goat farming around the CVGCA (Fauna & Flora International, 2016; Insua-Cao et al., 2012). Efforts to rehabilitate sites around and within the

protected zones have been implemented, largely through the plantation of food species, however evaluation is required to assess their impact (C.-Y. Ma et al., 2020).

It is recommended that the macaque population within and around CVGCA should also be surveyed, with particular focus on interactions with the gibbons and their use of the CVGCA. With concerns around whether the CVGCA may reach carrying capacity in the near future (Fan et al., 2013), it is important to understand how a sympatric primate species may impact the CVG, particularly in regard to resource competition. Better understanding of the macaque population may also identify ways to redirect groups away from local farms and reduce tensions between local communities and the primates.

The corridor gap on the Vietnamese side of the border presents an ongoing obstacle to any future natural dispersal for the Vietnamese-based CVG. It is a significant gap of several metres on each side, with scramble vegetation eventually transitioning to established trees and degraded forest. In its current state, it will not be utilised by the CVG as it would require several meters of terrestrial travel to cross.

While the benefit of rehabilitation of habitat through plantations should not be ignored, its use to create natural corridors between fragments can result in costly and lengthy timeframes before animals can hope to use it to disperse. Furthermore, due to the presence of informal border crossings bisecting the Corridor area, it is unlikely that ongoing human access could be prevented without increased security or infrastructure. Instead, it may be appropriate to consider the implementation of an artificial crossing or bridge, which could easily span the gap in vegetation.

The threat presented by the roads, farmland, and border crossings also presents a problem when considering corridor creation (William F. Laurance et al., 2009). Narrow corridors can exaggerate edge effects, offering a pathway not just for the target species, but also for invasive plants and animals into the habitats of endangered species (William F. Laurance et al., 2009; Pohlman et al., 2009). Replanted corridors will also require decades of investment before their impact can be truly known, in order to establish a suitably connected canopy for the gibbons to disperse through.

As a result, it is recommended that further research into the potential for rehabilitation of the Zone IV potential habitat should be undertaken, alongside efforts to establish the region as a conservation zone similar to the CVGCA. Particular care should be made at both sites to conserve slope vegetation as a priority, as these are expected to be high-use zones due to the tree and canopy structures, and high levels of sleeping and food species. In rehabilitating valleys within Zone IV, action should be taken to control invasive food species and to increase education programs about CVG conservation and habitat protections.

To enable access and encourage natural dispersal into Zone IV, consideration of the implementation of an artificial corridor to bridge the gap between the two regions should also be undertaken. While these processes will require significant resources and time, other opportunities for CVG habitat expansion appear limited. While more study of the CVGCA gibbons is required to confirm and expand our understanding gathered from the BNNR groups, this should not come at the expense of implementing habitat restoration of Zone IV and the corridor region. By taking a landscape approach to conservation planning, the CVG population may have room to grow.

Chapter 7 MaxEnt modelling of cao vit gibbon distribution

7.1 Introduction

The CVG, one of the world's most endangered gibbons, has experienced decades of habitat loss as a result of logging, conversion of forest to farmland, and expansion of the local human population. Once thought to be extinct, the world's only known population sits at an estimated 135 (Fauna & Flora International, 2021) and inhabits a limestone karst forest fragment that straddles the China-Vietnam border (Dat et al., 2008a; Geissmann et al., 2002; Trung & Hoang, 2004).

While the habitat of the CVG extends across the Chinese-Vietnamese border, the majority of CVG groups inhabit the Vietnamese side of the border within the protected CVGCA (Fan et al., 2013; Fan et al., 2010; H. L. Fei et al., 2012). Only three groups are known to inhabit the BNNR, one of which remains exclusively within the Chinese forest (C.-Y. Ma et al., 2020). The current available habitat for the CVG is 16.56 km^2 of disturbed primary limestone karst forest within the CVGCA, and 65.3 km^2 of limestone karst forest within BNNR (Insua-Cao et al., 2012).

Core areas are often the focus of protection for conservation planning (Asensio et al., 2014). While these areas may represent where the most important activities such as feeding, sleeping and defence occur (Asensio et al., 2014), they do not necessarily represent the extent of habitat requirements for primates. For instance, not all of the available forest within the CVGCA and BNNR regions appear to be utilised by the CVG. Patches of forest within the BNNR appear unused, (Fan et al., 2013) and areas within the CVGCA undergoing regeneration following historical use as farmland are only infrequently used by the gibbons for feeding (pers. comm, Anon). Conversely, there may also be areas beyond the highly monitored core area that could be suitable for the CVG.

The CVG is expected to reach carrying capacity in the CVGCA within the next few decades (Fan et al., 2013). Based on this, Fan et al. (2013), undertook an evaluation of the habitat of the current distribution of the gibbons and applied it to the surrounding forest fragments using remote sensing techniques. Geographic Information Systems (GIS) and remote sensing applications can be useful in undertaking habitat and connectivity analyses (Hansen et al., 2001), particularly at the landscape scale. Through the use of this technology, Fan et al. (2013)

identified forest patches adjacent to the CVGCA and BNNR that may offer the potential for future habitat expansion.

The possibility of additional habitat patches for the CVG offers the opportunity for population growth as the confines of the CVGCA and BNNR start to become limiting to their survival (Fan et al., 2013; C.-Y. Ma et al., 2020). Yet further investigation of any potential habitat expansions is required to support conservation planning.

GIS and SDM analysis can support in situ surveys by assessing available habitat at a larger landscape scale in a cost-effective way while minimising disruption to potential habitats (Knowlton & Graham, 2010; Zhang et al., 2010). SDMs have a wide range of applications to support at-risk populations, including habitat suitability analyses (A. Charbonnel, P. Lambert, G. Lassalle, E. Quinton, et al., 2023; J. Spiers, M. Oatham, L. Rostant & A. Farrell, et al., 2018), modelling the impact of climate change on species distributions (J. Bellis, M. Longden, J. Styles & S. Dalrymple, 2021; W.B. Foden, B.E. Young, H.R. Akçakaya, R.A. Garcia, et al., 2019), and translocation planning (Casazza et al., 2021; A. Guisan, R. Tingley, J. B. Baumgartner, I. Naujokaitis-Lewis, et al., 2013).

Using SDMs to identify potential habitat for species such as the CVG can provide researchers with the opportunity to apply in situ habitat data obtained from behavioural studies and ecological surveys and apply it to a wider geographical range (W. J. McShea, 2014). The application of SDM to identify predict habitat suitability in primates has only recently started to gain traction (Fan et al., 2013; M.F. Hansen, V. Nawangsari, F. van Beest, N. Schmidt et al., 2020; X. Ye, Q. Wu, X. Li & X. Zhao, 2022). The use of SDM offers researchers another tool to identify opportunities to expand often constrained data sets to problems of primate habitat fragementation.

Typically, SDMs focus on macroecological scales such as climate variables (Bellis et al., 2021). Climate variables are effective when studying species over a wide geographical scale, particularly when predicting the impact of climate change (G. Casazza et al., 2021). However, other key factors on habitat suitability, including predation, dispersal, biographical history, and inter-species interactions, can be underrepresented in SDM analysis (Casazza et al., 2021; Elith & Leathwick, 2009); this is particularly the case with factors that may only act at a

microecological scale such as interspecific interactions or microclimate adaptations (Bellis et al., 2021).

For a Critically Endangered species like the CVG, which is experiencing extreme habitat fragmentation and consists of a single breeding population within a constrained distribution, the use of landscape-scale variables such as climate may diminish the accuracy of the resultant predications (Bellis et al., 2021). In order to address this issue, SDMs need to be undertaken using variables at an appropriate scale to reflect the regional interactions, however, the paucity of fine-scale data for species and sites can lead to trade-offs when building SDMs (S. J. Murphy & A. B. Smith, 2021). As a result, the applications of SDM should be considered within the broader data available to conservationists, policy-makers and communities (Guisan, et al. 2013; McShea, 2014; Murphy & Smith, 2021).

Applying maximum entropy (MaxEnt) modelling to answer questions on species' distribution has become widely used by researchers studying questions of ecology, biogeography and impacts of climate change on species (Canran Liu, White, & Newell, 2011; Merow et al., 2013; Morales, Fernández, & Baca-González, 2017; Trinh-Dinh, Nguyen, Le, Cao, & Blair, 2022). Species distribution models such as those produced using MaxEnt, enable an estimate of the relationship between the presence of species and the environmental or spatial variables at those presence locations (Elith & Leathwick, 2009; Elith et al., 2011; J. Franklin, 2010).

One of the significant benefits of MaxEnt includes the use of presence-only data (Merow et al., 2013), as the methods of identifying true absence data points are often beyond the scope of most primatological studies which focus on primate behaviour, socio-ecological interactions, diet and habitat being actively utilised by the study species. MaxEnt has also been found to be one of the best approaches to model distributions for species with low sample sizes (Fourcade et al., 2014; Kiedrzyński et al., 2017; Wisz et al., 2008), making it a useful tool to model the distribution of species such as the CVG.

Using MaxEnt modelling, this chapter will seek to build and further expand on the findings from Fan et al. (2013) and the in situ ecological sampling undertaken in Chapter 6. Using ecological variables of the CVGCA and BNNR taken from satellite imagery and GIS data sets, it

may be possible to provide further sights into the suitability of forest patches to the southwest of the CVGCA as areas of potential habitat expansion to support future growth of the CVG.

The primary aim of this chapter is to test whether a SDM approach using GIS and satellite imagery and in situ ecological sampling from CVGCA can be applied within a small site-specific analysis to assess opportunities for CVG habitat expansion. Based on in situ ecological sampling and analysis undertaken (Chapter 6), I hypothesise that an SDM analysis will demonstrate that Zone IV presents only a small amount of suitable habitat for the CVG. I also hypothesise that elevation and tree cover, as suggested by Fan (2013), will influence the suitability of areas. This is in part because higher elevation may offer greater protection from human induced habitat loss – a requirement that the CVG may have after decades of habitat loss – and greater tree cover allows greater dispersal opportunities for an arboreal species such as the CVG.

7.2 Methods

7.2.1 Study site and species

The historical distribution of the CVG likely extended east of the Red River in southern China and northern Vietnam (Fan et al., 2010), however, today their distribution is restricted to a transboundary limestone karst forest fragment that sits across the Vietnamese-Chinese border (Chang-yong et al., 2020; Insua-Cao et al., 2012; C.-Y. Ma et al., 2020). The entire wild population of the CVG inhabits two protected areas within a connected fragment totalling 81.86km^2: CVGCA in Vietnam (16.56 km^2), and the BNNR in China (65.3 km^2) (Insua-Cao et al., 2012) (Figure 7.1).

The forest forming these reserves is comprised of disturbed primary forest and secondary forest on limestone karst, with areas of regenerating scramble previously used for farming and resource collection prior to the region becoming protected on both sides of the border (Dat et al., 2008a; Insua-Cao et al., 2012; C.-Y. Ma et al., 2020). Today, there is no farming of livestock within the CVGCA, however, it continues to occur close to the border within the BNNR (C.-Y. Ma et al., 2020).

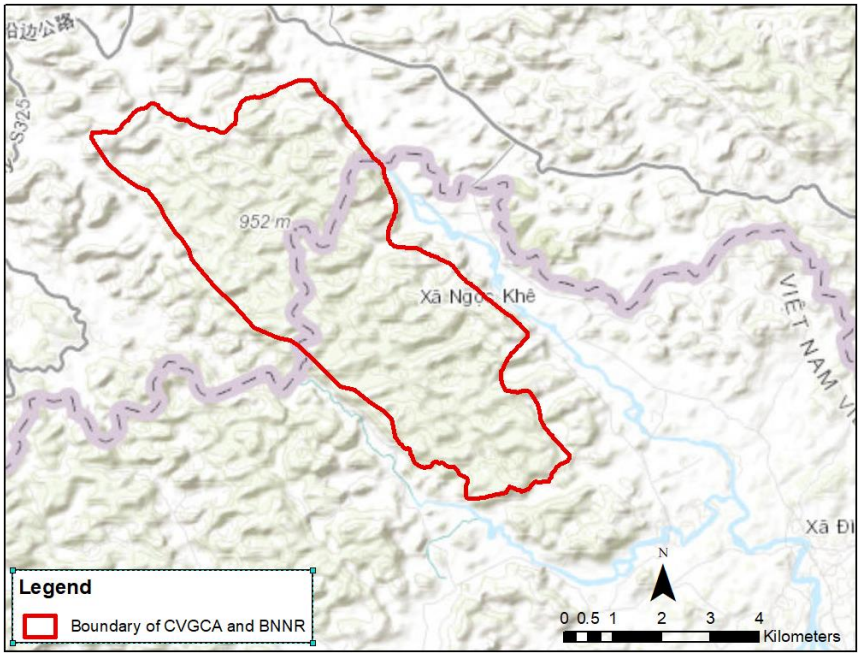


Figure 7.1 Map of the current extent of the CVG protected zones. Map shows the border of the contiguous CVGCA in Vietnam, and the BNNR in China. Basemap source: ESRI et al. (2021).

The CVGCA is bounded by rivers on two sides to the north and south, and a road to the southeast. Similarly, the BNNR is surrounded by rivers and roads, creating almost an island of forest containing the two protected zones**.** To the southwest of the CVGCA within Vietnam, there are larger forest fragments, largely restricted to the slopes and peaks of limestone karst (Figure 7.2).

Figure 7.2 River bounding CVGCA and forest fragments on limestone karst slopes and peaks to the southwest of the CVGCA. Photos by K. Apthorp 2016.

At one point on the Vietnamese side of the border, however, the river disappears underground for approximately 900m (Fan et al., 2013), and an informal border crossing bisects the adjacent forest fragments canopy. The separation is only several metres, as a result of unpaved border crossings (Figure 7.3). This gap is predominately filled by low scramble shrubs but is the closest connection between the CVGCA and largest adjacent forest fragment on the Vietnamese side of the border.

Figure 7.3 Border crossing separating the CVGCA and adjacent forest fragments. Photos by K. Apthorp 2016.

It is this adjacent region that Fan et al. (2013), identified as Zone IV, containing two areas of conservation interest (Figure 7.4). The current extent of the CVG within the CVGCA and BNNR was identified as being the first area of conservation priority (Fan et al. 2013). For the MaxEnt modelling, I included the CVG extent within both the CVGCA and BNNR, and Zone IV as identified by Fan et al. (2013). The use of MaxEnt allows me to include a larger geographic extent to analyse whether parts within Zone IV may be suitable as potential habitat for the CVG than was possible using ecological modelling in Chapter 6.

The bulk of the CVG population currently inhabits the CVGCA within Vietnam, with only three gibbon groups found to range on the Chinese side of the border, and only one group exclusively (Fan et al., 2010; C.-Y. Ma et al., 2020). Based on a 2016 survey, the current CVGCA population is comprised of 20 to 22 groups, totalling 107-136 individuals (C.-Y. Ma et al., 2020) with an average home range size of 1.3km^2 (Fan et al., 2011).

Based on Fan et al.'s 2013 study, the CVG are predicted to reach carrying capacity within the CVGCA and BNNR before 2030 unless significant habitat restoration of the current protected region, and additional zones, including Zone IV is pursued.

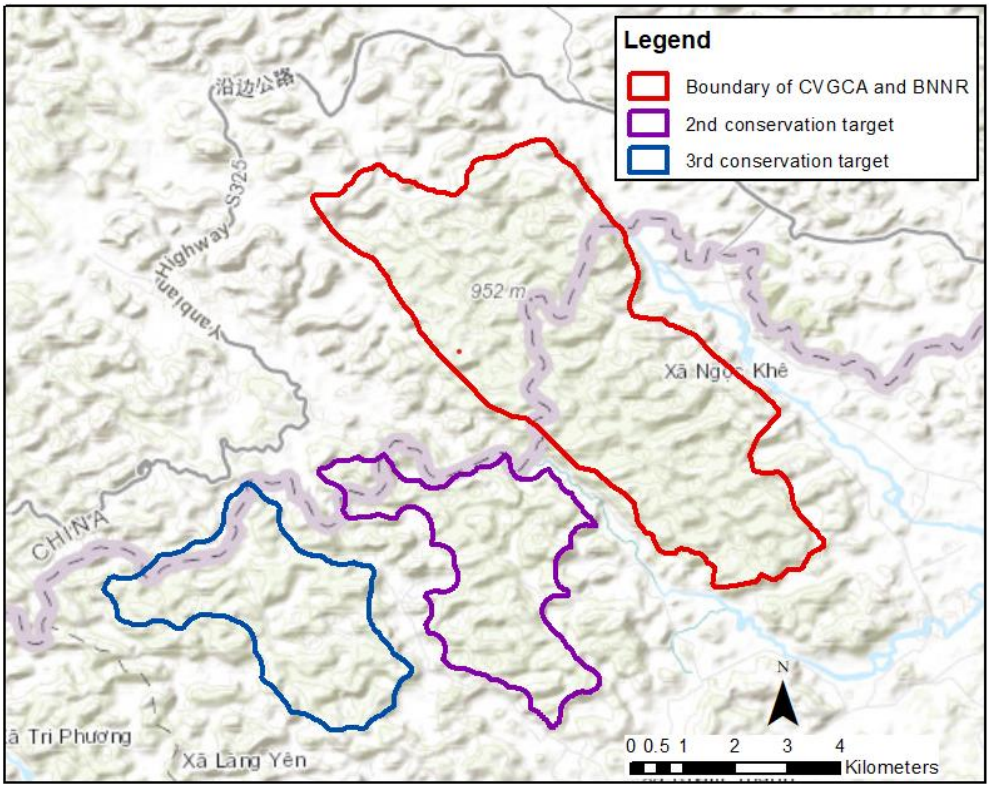


Figure 7.4 Areas of conservation priority identified by Fan et al. 2013 The second conservation target area was sampled in this study. Basemap source: ESRI et al. (2021). Conservation target polygons: Fan et al. (2013).

7.2.2 Occurrence data

Presence data is essential to undertaking species distribution modelling. In order to make estimations of the relationship between known CVG sites and environmental and spatial variables, accurate presence data is required at a minimum where absence data is not available (Elith & Leathwick, 2009; Elith et al., 2011). While absence data can also provide important insights into the habitat use and distribution of a population within a known range, collecting true absence data can be expensive due to the extensive sampling effort required to ensure an area is genuinely not utilised by a species (Elith et al., 2010). Identifying true absence data can also be difficult to determine for small populations that have undergone distribution contraction due to human pressures (Elith & Leathwick, 2009), as is the case of the CVG. For the purposes of this analysis, I only utilised presence data and generated random background points via MaxEnt.

I collected occurrence data from published and unpublished field surveys undertaken within the CVG distribution in CVGCA Vietnam and BNNR in China. Only locations where direct GPS locations were provided for the location of gibbon individuals or groups were used to ensure a high level of detail for modelling. Based on this requirement, I excluded location data in literature that provided only general location descriptions such as valley names or generalised locations of listening posts (Trinh-Dinh et al., 2022). Historical data based on historical interviews or museum specimens were also not included. As a result, a total of 41 presence data collected between 2008 and 2016 were identified, as collected by Fan et al. (2009), Dat et al. (2008a), Chan et al. (2008) and points I collected during data collection in the CVGCA.

7.2.2.1 Sampling bias

The use of presence-only data when modelling species distributions, requires the consideration of sampling bias during the collection of species occurrence records (Barber et al., 2022; Fourcade et al., 2014; Moua et al., 2020).

The number of occurrences reported in the literature for the CVG are limited, leading to a risk of overfitting distribution models where large numbers of variables are used on only a small number of occurrence points (Wisz et al., 2008). Sampling and spatial bias is also a significant issue when attempting to build a distribution model for a small population within a narrow distribution range as the requirements for such species can be very specific and difficult to extrapolate when occurrence points have inherent biases due to collection methods (Kiedrzyński et al., 2017; Merow et al., 2013).

In addition to only having a small population distributed over an equally small area, determining accurate GPS locations for the CVG can also be difficult to capture due to the somewhat inexact methods required in surveying gibbon populations. Their arboreal nature and limestone karst habitat can make it difficult to directly observe individuals. This requires the use of other methods that rely on their loud calling to assist population surveys (Kidney et al., 2016). Different techniques used to sample gibbons, including fixed point auditory surveys, line transects, and range mapping may produce varying location, density and population estimates (Höing, Quinten, Indrawati, Cheyne, & Waltert, 2013; Naher et al., 2021; Nijman & Menken, 2005; Vu, Tran, Nguyen, Van Tran, & Ta, 2018). This can be further compounded at sites where the terrain dictates the sampling method used.

In the CVGCA, auditory surveys are conducted from fixed listening posts on ridge and mountain points, however this method has been suggested to overestimate the number of individuals recorded calling and has the potential to miss any individuals that do not call during the survey periods (B. M. Rawson, 2010; Vu et al., 2018). This technique is also limited by the fact that not all individuals in a population may call, such as infants, or by calling individuals occurring outside the sampling range (Vu et al., 2018). The non-random placement of listening posts both as a factor of accessibility and maximising data points in fragmented populations can also impact the overall pattern of distribution determined from acoustic surveys (B. M. Rawson, 2010).

Efforts to improve the application and outcomes of auditory sampling are ongoing (Kidney et al., 2016) and for species such as gibbons, which are known to regularly vocalise, and which often inhabit terrain making direct follows impractical, auditory surveys continue to offer the best opportunity to track population size and density for increasingly endangered populations.

In order to address sampling bias present in occurrence data for MaxEnt modelling, studies have noted the benefit of applying methods to reduce the density of occurrence points to avoid overfitting models (Barber et al., 2022; Elith et al., 2010; Freire Filho & Palmeirim, 2020; Kiedrzyński et al., 2017; Vidal-García & Serio-Silva, 2011).

To reduce the effects of spatial bias and over sampling present in the CVG occurrence data, I filtered GPS records so that only one point per 30 x 30m was used to match the resolution of the ecological variables. Filtering the records reduced the number used in the MaxEnt analysis from 41 to 29 records captured within the CVGCA and BNNR regions.

7.2.2.2 Study limitations

Small sample sizes can limit the discrimination of distribution models due to inadequate data, however, MaxEnt has been shown to perform better with smaller sample sizes (Proosdij, Sosef, Wieringa, & Raes, 2016). Although MaxEnt is sensitive enough for small sample sizes, Grainger et al., (2019), suggests that there is a tipping point where fewer than 30 samples become less accurate.

For species at high risk of extinction such as the CVG, it is necessary to utilise whatever resources are available to improve our understanding of the species. The use of remote

sensing and GIS approaches can offer additional insights, but they can be limited by available data. In order to best serve at risk species, conservation planning must balance constraints on the money, time and manpower required to obtain perfect datasets (Grainger et al., 2019; Low et al., 2021; Warren & Seifert, 2011). The combination of distribution modelling alongside in situ ecological sampling, can provide a strong tool to support conservation planning and to provide insights into the needs of a target species (Morales et al., 2017; Palminteri et al., 2012).

7.2.3 Predictor variables

Twelve predictor variables were chosen to model the distribution of the CVG based on spatial and ecological knowledge of the species. These included: a digital elevation model, slope, aspect (Eastness and Northness), normalised difference vegetation index, normalised difference moisture index, land use data, Terrain Roughness Index, and the visible bands of the Spot6 satellite multispectral imagery (Table 7.1). Due to the restricted distribution of the CVG within CVGCA and BNNR, a spatial resolution of 1 second (approximately 30 metres) was selected as this represented the best highest resolution while enabling the use of relevant datasets.

Higher resolution datasets, typically of 30 seconds (1 km) were determined not to be fine grained enough to account for the relationships between CVG and environmental variables. Ideally in the future even greater resolution datasets will be used.

7.2.3.1 Pre-processing and datasets

I clipped all rasters to a geographical extent covering the current distribution of the CVG in Vietnam and China, and the adjacent forest patches identified by Fan et al. (2013). Spatial information was imported into ArcGIS Desktop 10.8 and calculations were undertaken using Spatial Analyst and Data Management Tools. All datasets were projected in the Universal Transverse Mercator coordinate system (datum: WGS 1984, zone: 48N).

I used a Shuttle Radar Topography Mission v3 Collection 2, tier 1SRTM v.3 (SRTMv3) digital elevation model (DEM), downloaded from the United States Geological Survey (NASA and NGIA 2015, accessed 11 November, 2022), to produce a slope raster in the spatial analyst toolbox in ArcGIS 10.8. The calculated slope raster represents the rate of change of elevation

in the direction of deepest descent (Amatulli et al., 2018) in each cell based on the elevation of the DEM.

All pre-processing calculations to generate a NDMI, NDVI, Eastness, Northness, slope and TRI were carried as per the protocol in Chapter 4, Section 4.2.3.2.1.

I also used a land use dataset for the Trung Khanh region provided by the Earth Observation Research Centre (EORC) ALOS/ALOS-2 Science Project "High-resolution land use cover map" (HRLULC) of the Japan Aerospace Exploration Agency (JAXA, 2020 [version 20.06], accessed December, 2022). The land use map identifies twelve categories: Water, Urban/Built up, Rice, Other crops, Grass/Shrub, Orchard/Crop mosaic, Barren, Evergreen Broadleaf Forest, Coniferous Forest, Deciduous Forest, Plantation Forest, and Mangrove. Categories were identified using Landsat data, Sentinel data, ALOS PRISM Digital Surface Model, ground survey data and interpretation of satellite data, and a random-forest-based algorithm (EORC, JAXA).

A commercially available Spot6 unenhanced multispectral satellite image with 6m resolution was used to prepare separated bands representing Band 1 (Blue 0.455µm – 0.525µm), Band 2 (Red 0.530µm – 0.590µm), Band 3 (Green 0.625µm – 0.695µm), Band 4 (Near Infrared 0.760µm – 0.890µm). I resampled each raster to 30m using the resample tool.

All rasters were extracted to the same column (819) and row (720) length (Appendix 4.4.1) using the spatial analyst tool in ArcGIS to allow analysis in MaxEnt.

7.2.3.2 Limitations

Due to the fine resolution selected, I did not use more frequently utilised raster data sets such as climactic data derived from the WorldClim database as the resolution of this data is provided at 1km or higher. Higher resolution climatic data may be suitable for wider landscape analysis (Trinh-Dinh et al., 2022), however, in attempting to determine the ecological factors influencing CVG distribution, higher resolution is preferred. No local high resolution climatic data were available for the CVGCA region.

The accuracy of DEMs vary in accordance with other variables such as cloud cover, angle of capture, time of day, climatic conditions, and the terrain type (Riley et al., 1999). These inaccuracies then have implications for subsequent datasets derived from the original DEM.

To limit the impact of these factors, I selected the SRTM v.3 DEM where less than 20 per cent cloud cover was captured, and orthorectification had occurred. Due to the location near the equator and the nature of limestone, other factors are more difficult to account for and due to the wide-use of SRTM DEM and data, considered reasonable as a starting point for MaxEnt modelling of a restricted species such as the CVG.

Table 7.1 Input predictor variables for CVG MaxEnt modelling

Data type	Data set origin	Final Projection	Resolution (cell size)
Digital elevation model	Shuttle Radar Topography Mission v3 Collection 2, tier 1	UTM	30m
(Aspect) Eastness	Shuttle Radar Topography Mission v3 Collection 2, tier 1	UTM	30m
(Aspect) Northness	Shuttle Radar Topography Mission v3 Collection 2, tier 1	UTM	30m
Slope	Shuttle Radar Topography Mission v3 Collection 2, tier 1	UTM	30m
Normalised Difference Vegetation Index	Landsat 8-9 Operational Land Imager (OLI) and Thermal Infrared Sensor (TIRS) Collection 2 Level-1	UTM	30m
Normalised Difference Moisture Index	Landsat 8-9 Operational Land Imager (OLI) and Thermal Infrared Sensor (TIRS) Collection 2 Level-1	UTM	30m
Land use and land cover	High-Resolution Land Use and Land Cover, 10m resolution map of Vietnam [2016] (ver.20.06), HRLULC Japan Aerospace Exploration Agency	UTM	30m (resampled from 10m)
Spot6 satellite imagery colour band 1	SPOT6 Multispectral Imagery 6m resolution, unenhanced RGBN	UTM	30m (resampled from 6m)
Spot6 satellite imagery colour band 2	SPOT6 Multispectral Imagery 6m resolution, unenhanced RGBN	UTM	30m (resampled from 6m)
Spot6 satellite imagery colour band 3	SPOT6 Multispectral Imagery 6m resolution, unenhanced RGBN	UTM	30m (resampled from 6m)
Spot6 satellite imagery colour band 4	SPOT6 Multispectral Imagery 6m resolution, unenhanced RGBN	UTM	30m (resampled from 6m)
Topographic Ruggedness Index	Shuttle Radar Topography Mission v3 Collection 2, tier 1	UTM	30m

7.2.4 MaxEnt modelling technique

7.2.4.1 Predictor variable correlation for CVG variables

Prior to commencing the MaxEnt modelling, I used ENMTools in R to conduct a Pearson's correlation to identify continuous variables that were highly correlated (Morales et al., 2017) (Appendix 4.4.2). Variables with a correlation coefficient (*r*) greater than 0.7 or less than -0.7 were considered strongly correlated.

7.2.4.2 MaxEnt distribution analysis settings for the CVG

I undertook all modelling analyses in MaxEnt version 3.4.3 (S. J. Phillips, 2017) and subsequent model evaluations using ENMTools in R.

The use of default settings for MaxEnt modelling is common throughout the literature, however, as these settings have been developed based on testing for a large number of species, they may not be optimal for species with small populations and ranges (Dorji et al., Preprint 2020; Merow et al., 2013; Morales et al., 2017). Due narrow geographic range of the CVG under consideration, I tested a combination of feature classes and regularisation multiplier values in an attempt to identify the most appropriate model for the distribution of the CVG (Dorji et al., Preprint 2020; Low et al., 2021; T. V. Nguyen et al., 2022).

I tested multiple feature class combinations including: the automatic settings which includes Linear, Quadratic, Product and Hinge (LQPH) (S. J. Phillips, 2017), Quadratic features only (Q), Hinge features only (H), and Quadratic and Hinge features together (Q+H). These feature classes were selected as quadratic and hinge features have been previously identified as suitable for small occurrence samples (Galante et al., 2018).

The regularisation multiplier setting avoids overfitting in MaxEnt by limiting model complexity (Radosavljevic & Anderson, 2014; Warren & Seifert, 2011). Lower regularisation multiplier values will produce a more localised model, incorporating a greater number of predictors and features, while larger values can produce more less complex, more generalised models (Merow et al., 2013; Warren & Seifert, 2011). To test the best outcome for the CVG, I tested the regularization at 0.25, 0.5, 1, and 2 for each of the feature class combinations as per the protocols of previous MaxEnt modelling of primates (Dorji et al., Preprint 2020; Radosavljevic & Anderson, 2014; Van Phung et al., 2023). I used smaller regularization multipliers due to the smaller geographic scale under investigation. I set the random test percentage at 50 (Vidal-

García & Serio-Silva, 2011), used cross validation as the replicated run type, and ran a jack-knife to measure variable importance for all models. All other settings were based on the predetermined settings.

The Area under the Curve (AUC) is produced for each model during the training and testing (S. J. Phillips, 2017). For each feature class, the best performing model was determined by the difference (AUC_{DIFF}) between the AUC values determined during model training (AUC_{TRAIN}) and during model testing (AUC_{TEST}) (Low et al., 2021). Higher AUC_{DIFF} values indicate model overfitting, and do not perform well when extrapolated to the testing data (Low et al., 2021). The best performing model within each feature class was then rerun with the variable contributing least to the model removed.

The top two models across the feature classes based on their $AUC_{DIFF,}$ were then rerun with replications set to 10 and evaluated against each other based on their mean AUC values. A model with no predictive ability greater than randomisation will have an AUC of <0.5, and a model with an AUC of 1 indicates a perfect model (Elith et al., 2011).

Based on the best performing model, the total area identified by the MaxEnt modelling as having 90 per cent and greater suitability for the CVG was determined for each target site. This was repeated for the total area identified as having 60 per cent or greater suitability for the CVG to determine the level of potential conservation action that may be required.

7.3 Results

7.3.1 Pearson's correlation of predictor variable results

Based on a Pearson's correlation, two variables were identified as being strongly correlated with other variables: Spot6 Band2 and Band3 (Appendix 4.4.2). I removed them from the subsequent MaxEnt analysis, which left nine continuous variables and one categorical variable for the modelling: Eastness, Northness, NDMI, NDVI, DEM, TRI, Slope, Spot6 Band1 (blue), Spot6 Band4 (near infrared), and land use.

7.3.2 MaxEnt modelling results

The feature class and regularization multiplier combinations all performed similarly in terms of AUC_{Test} and AUC_{DIFF}, suggesting the various settings have very little influence on the model

for predicting habitat suitability for the CVG (Appendix 4.4.3.1). Despite little variation, overall, 2 was the best performing regularization multiplier value.

The Quadratic-only models show little variation in AUC across the regularization multiplier variations, suggesting very little change in response to model overfitting . The best performing model was Test 4, which has the lowest AUC_{DIFF} (0.049) and has a regularization multiplier of 2, which suggests a low risk of model overfitting. Based on the AUC_{TEST} of 0.847, the model demonstrates very good performance (as AUC>0.8) (Elith et al., 2011). Land use and NDMI were the two variables to contribute the most to all the models, including in Test 4, while the NDVI and Spot6 Band 4 variables consistently contributed very little to each of the Quadratic-only models. A jack-knife of the test gain for the model shows that the Test 4 performs better without the inclusion of the NDVI and Spot Band 4 variables .

To test this, the model was rerun with the same settings as Test 4 and the removal of the Spot Band 4 and NDVI variables. This provided the highest AUC_{TEST} of 0.852 and lowest AUC_{DIFF} of 0.038 for the Quadratic-only models.

The hinge feature variables show greater variation in the AUC_{TEST} values (0.765 to 0.823), suggesting a stronger response to the regularization multiplier changes. Higher regularization multiplier values produce better performing models within the Hinge feature class models. A regularization multiplier value of two performed the best across the model combinations.

Test 8 has a highest AUC_{Test} for the Hinge models (AUC_{TEST} = 0.836, AUC_{DIFF} =0.096), however based on the AUC_{DIFF}, the best performing model is Test 9 (AUC_{TEST} = 0.823, AUC_{DIFF} = 0.079). The lower difference between the training and test AUC suggests a model with less overfitting during the training stage (Low et al., 2021). All models show very poor test gains in the jack-knife of AUC, with only a few variables contributing to the model in the test component. Land use and NDVI contributed the most to these models, however NDVI, Northness, Slope, Spot6 Band4, TRI all have a negative impact on the overall AUC. To test the impact of this variable, Test 10 includes the same parameters as Test 9, with the exclusion of those variables. This produces the best hinge feature model (AUC_{TEST} = 0.855, AUC_{DIFF} = 0.035).

The Quadratic and Hinge (Q+H) combination show more marked disparity across the regularization multiplier variations, with the 0.25 variation (Test 11) performing the worst (AUC_{DIFF} = 0.972, an AUC_{TEST} =0.771). This suggests that lower regularization multipliers produce worse performing and potentially over-fitted models under this combination of features. Once again, the best performing test does not have the highest AUC_{TEST}. Test 14 has the smallest AUC_{DIFF} = 0.066, an AUC_{TEST} = 0.836 and a regularization multiplier value of 2. The variables shown to contribute the most to the models ware once again land use and NDVI, however, under the best performing Q+H, NDVI, alongside Northness, Slope, Spot6 Band1, does not positively contribute to the best AUC. Removing the NDVI and maintaining the parameters of TEST 14, produces a better model in Test 15 (AUC_{DIFF} =0.037, an AUC_{TEST} = 0.855), which suggests that the removal of those variables improves the performance of the model and improves the transferability of the model.

Finally, the use of the automatic feature parameters shows some variation across the AUC_{TEST} values based on the regularization multiplier, with 0.25 performing the worst (Test 16: AUC_{DIFF} = 0.200, an AUC_{TEST} = 0.772) and a value of 2 performing the best (Test 19 with an AUC_{TEST} = 0.838 and AUC_{DIFF} = 0.064). As with the other tests, land-use and NDVI are the highest contributors to the models, however NDVI has a negative impact on most of the models as do the variables Northness, Slope, and Spot6 band 4. Retesting the parameters of Test 19 without the inclusion of those variables, shows a strong difference. Test 20 has an AUC_{TEST} of 0.856 and AUC_{DIFF} of 0.037, representing the best model under the automatic feature parameters.

The best performing models based on the AUC_{DIFF} are the Hinge, and the Quadratic and Hinge (Q+H) and Automatic feature classes which performed the same. The optimal regularization multiplier value is 2, which performs consistently better across the four feature classes, suggesting a more generalised model that reduces over parameterisation performs better in predicting the suitability of habitat for the CVG.

7.3.3 Top performing model comparison for the CVG

The top two performing tests are Test 10 (AUC_{TEST} = 0.890, and AUC_{DIFF} = 0.035), and Test 15 (AUC_{DIFF} = 0.855, and AUC_{TEST} = 0.037) and 20 (AUC_{DIFF} = 0.8956 and AUC_{TEST} = 0.037), with

identical results AUC_{DIFF} = 0.037. For further analysis, Test 15 was selected over Test 20 based on the higher AUC_{TEST} value (Galante et al., 2018; T. V. Nguyen et al., 2022).

The top models perform similarly, producing a very good model based on mean AUCs greater than 0.8 (Elith et al., 2011). The best performing model was Test 15 based on a mean AUC of 0.874 ±0.059, using a Quadratic and Hinge (Q+H) feature class, a regularization multiplier of 2 and six variables (Appendix 4.4.3.2). The Hinge-only model, Test 10, performed only slightly worse with a mean AUC of 0.871 ±0.058.

Based on the comparison of the top models, it appears that the Quadratic and Hinge (Q+H) feature class and regularization multiplier value of 2 produces the best model for predicting the distribution of the CVG.

7.3.4 Distribution

The mean AUC for the potential distribution of the CVG is 0.874, representing a very good performance (Elith et al., 2011). The top three variables contributing the most to the model are land use, DEM and NDMI (Appendix 4.4.3.3). Land use category 8, representing evergreen broadleaf forest, is most positively associated with predicting the CVG distribution. The probability of the CVG being distributed in any other land use type, including plantations, is close to zero. The presence of the CVG is also closely correlated to greater elevations from approximately 900m and above – the highest elevations are associated with the highest probability of CVG presence. The amount of water absorption within the canopy as measured by the NDMI also may predict CVG presence. Lower values representing low water retention appear to have a low influence on CVG presence until values above 0.05 when the probability of the presence of the CVG increases as the NDMI increases. As the NMDI reaches 0.35, the probability of the CVG presence reaches 1, indicating that even medium levels of water retention may positively impact the distribution of CVG. It also suggests that overall, there is a low water retention in the canopy in the CVGCA and BNNR, with values topping out at 0.45.

In contrast, there is a negative relationship between the probability of habitat suitability for the CVG and Eastness (Appendix 4.4.3.3). The distribution of the CVG declines as the aspect of the topography becomes more easterly. Instead, the presence of the CVG is more likely to be associated with western aspects. Based on the Spot6 Band 1 (blue) predicator variable, the

CVG is associated with areas with water. The CVG is also not well associated with high levels of terrain roughness. However, these are not important contributors to the overall distribution model.

The distribution map produced by the model aligns with the findings of the in situ ecological modelling. Compared to other forest fragments captured within the study area, the CVGCA and BNNR region is the most suitable for the CVG (Figure 7.5). The are expected to be most highly suited to the CVG is in the north, on the Chinese side of the border, while the suitability of the forest declines as the forest fragment extends south-east on the Vietnamese side.

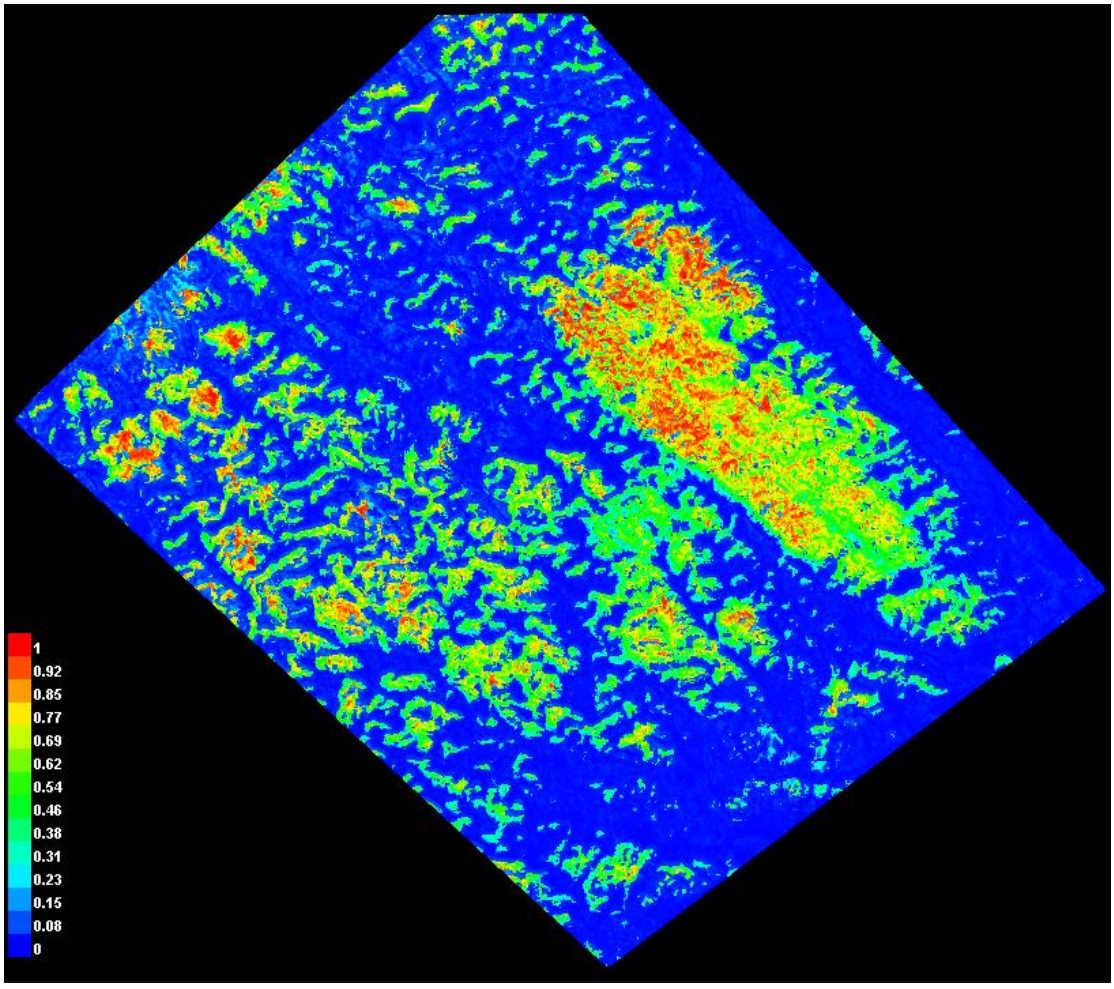


Figure 7.5 Median model summary projected onto the study area. Map of CVG habitat and surrounding region, including Zone IV with presence modelling. Blue indicates zero per cent suitability for CVG presence based on predictors and red indicates 100 per cent suitability.

The decline in the suitability of forest to the southeast supports ad hoc observations by CVGCA rangers who report low levels of interaction with this region by the CVG. A review of this area during sampling (Chapter 6), identified low topographic complexity: this end of the CVGCA area is largely a flat bowl-shaped region, with elevations increasing to the sides of the CVGCA boundary. Rangers reported that this area was regenerating vegetation, having previously been used for agricultural purposes, including fruit plantations. Gibbons reportedly enter this area only to feed on remnant banana and fruit trees but do not remain long in the area.

The distribution map produced by the model, shows that there is a secondary forest fragment connected to the CVGCA region that could be suitable for the CVG, particularly further south-east. Other fragments identified as suitable appear to be scattered unconnected across the landscape, concurring with observations made during in situ sampling.

Based on the distribution model summary produced, approximately 1.85 km^2 of land within the study area has a probability of 90 per cent or higher that it would be suitable for the CVG (Figure 7.6). When removing areas that the CVG are unlikely to be able to naturally disperse to, the amount of suitable habitat reduces to 1.47 km^2. The majority (1.36km^2) of suitable habitat falls within the boundaries of the CVGCA and BNNR.

When considering the available habitat at a suitability probability of 60 per cent or above, the model indicates that a total area of 23.91 km^2 is suitable across the study area (Figure 7.7). Of that, 17.86 km^2 falls within areas that may have some level of accessibility for the CVG to disperse into. The majority of the suitable habitat (14.05km^2) falls within the CVGCA and BNNR.

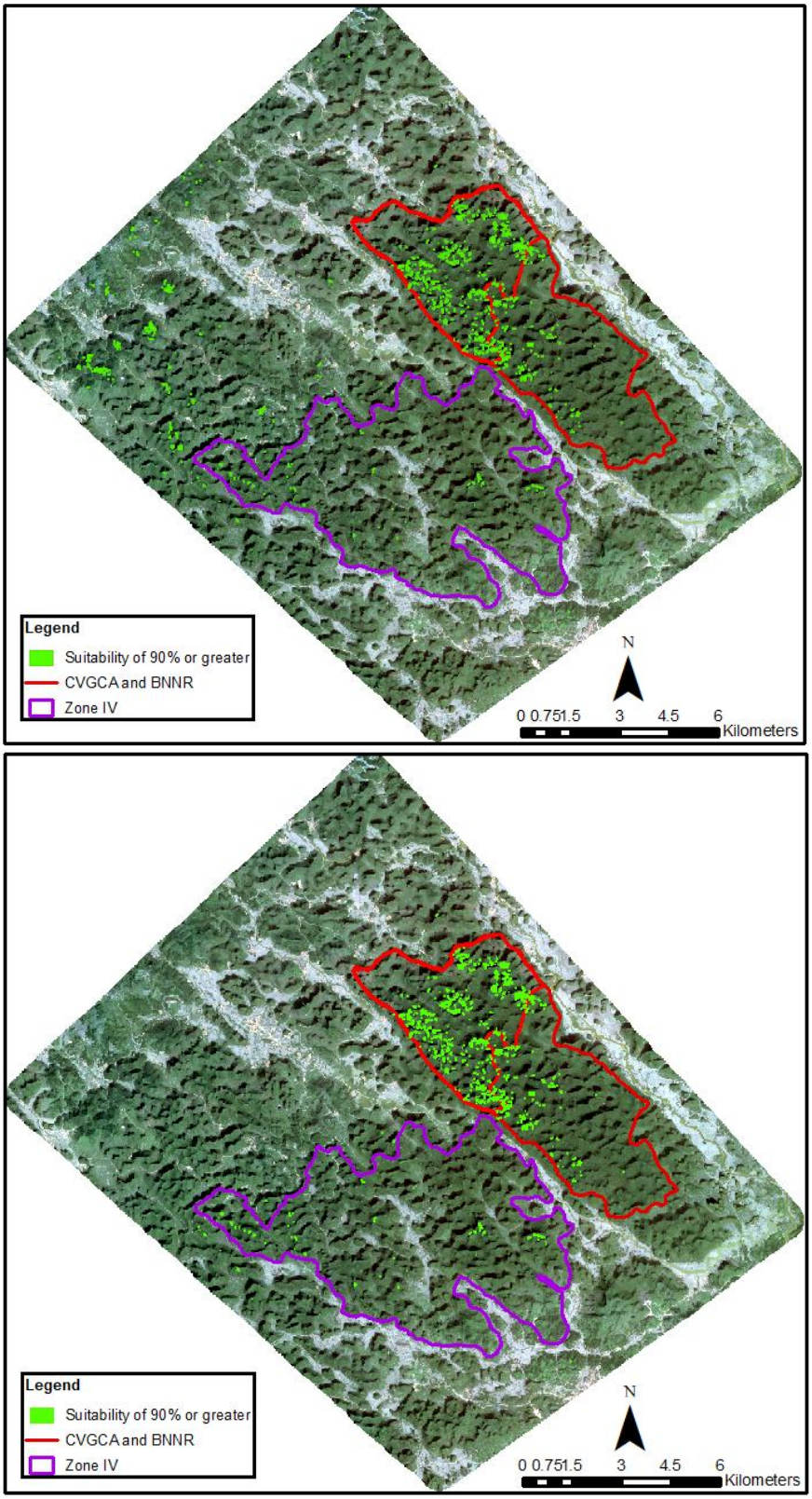


Figure 7.6 Distribution of suitable habitat with a probability of 90% or greater. Top: the total distribution of habitat with a 90 per cent or greater probability of being suitable for the CVG. Bottom: the distribution of habitat within potential dispersal range, based on forest connectivity, of the CVGCA and BNNR, with a 90 per cent or greater probability of being suitable for the CVG. Basemap source: Spot6. Zone IV polygon: Fan et al. (2013).

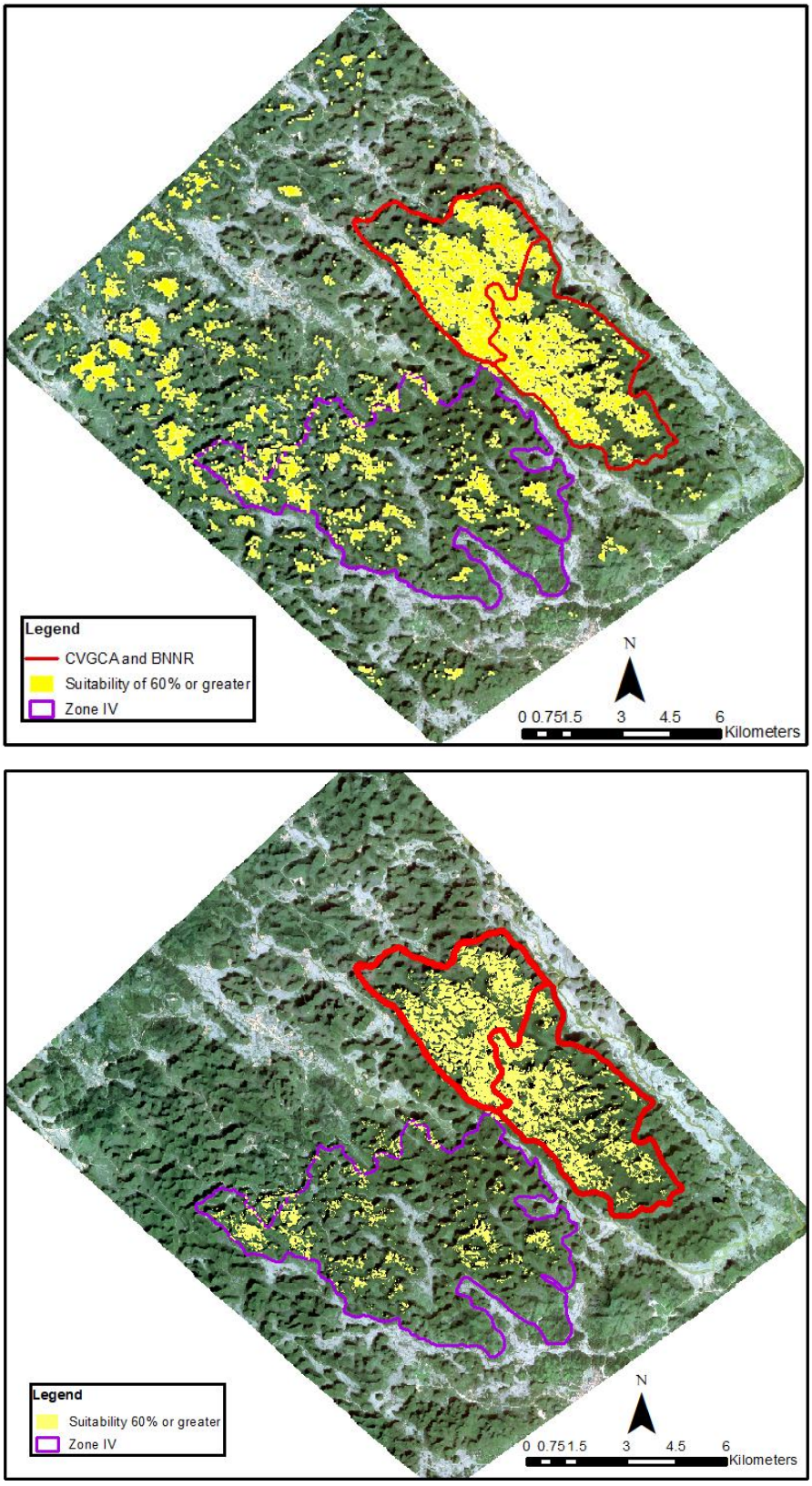


Figure 7.7 Distribution of suitable habitat with a probability of 60% or greater. Top: the total distribution of habitat with a 60 per cent or greater probability of being suitable for the CVG. Bottom: the distribution of habitat within potential dispersal range, based on forest connectivity, of the CVGCA and BNNR, with a 60 per cent or greater probability of being suitable for the CVG. Basemap source: Spot6. Zone IV polygon: Fan et al. (2013).

7.4 Discussion

7.4.1 Model design for the CVG distribution

The performance of the various models generally resulted in a high AUC_{TEST} value >0.8, which suggests that the models had a strong transferability. It may also however, be a symptom of the underlying AUC calculation on a sample with a narrow geographic range, as seen with the current CVG distribution (S. J. Phillips, 2017). The use of the AUC_{DIFF} to test the performance of the models can offset the influence of an inflated AUC_{TEST} as lower values indicate that the training model is not over fitting the training data and is performing well on the partitioned testing data (Low et al., 2021), suggesting a strong model when combined with a higher AUC_{TEST} value.

Although higher regularization multipliers performed better in modelling the CVG distribution based on a small number of samples (n=29), there is a risk that at such small scales, over generalisation of the model through increasingly greater regularization multipliers (Warren & Seifert, 2011) may result in providing very little insight to the potential distribution of the CVG. This may also be compounded by the variables used in the analysis. Typically, MaxEnt analyses utilise climatic variables from the WorldClim data sets, however the scale available was too coarse (typically>1km) for the purposes of this analysis (Nüchel et al., 2018). As the CVG has a very restricted global distribution, a smaller scale of 30m was utilised in an effort to understand if specific ecological variables were impacting their limited dispersal.

7.4.2 Potential distribution of the CVG

The final model indicates that only an area of 1.85km^2 within the study area is suitable (90 per cent or greater) for the CVG based on the ecological predictor variables. Within the CVGCA and BNNR, only 1.36km^2 of a total protected area of 81.86km^2 (1.66 per cent) is identified as suitable for the CVG. The current home range size of the CVG is 1.3km^2 (Fan et al., 2011), suggesting that the suitable habitat available for the CVG within the core protected area constitutes the home range of a single CVG group.

The highly suitable habitat is highly fragmented across the landscape, which would require the gibbons to cross several roads and gaps in the forest to reach, particularly within the China forest. When only considering suitable fragments that could be reached by the gibbons

through minimal dispersion (1.47km^2), the majority of suitable habitat is confined to the Vietnamese side of the border and largely falls within the boundaries of Zone IV. This supports the findings of Fan et al. (2013) that this region may be suitable as an area of habitat expansion pending significant regeneration efforts.

The low level of habitat considered suitable for the CVG based on a probability of 90 per cent or greater is alarmingly low. It could suggest that the CVG is currently inhabiting forest that is not entirely meeting their preferences, likely as a consequence of historical disruptions (Li & Rogers, 2005a). However, the availability of food species and other vegetation-based variables not captured within the predictor variables but sampled as part of in situ ecological data collection should be considered alongside the SDM modelling to further determine the suitability of the forest fragments. The loss of key food species due to forest degradation is suspected the be the cause of the loss of two gibbon groups between 1995 and 2005 (Fan et al., 2010). Furthermore, the distribution of key food species within the CVGCA and BNNR may explain why CVG inhabit larger home ranges than other members of the Nomascus group (Fan et al., 2010).

Based on the 90 per cent suitability mapping, there appears to be an uneven spread of suitable habitat, with the most suitable habitat identified primarily in the BNNR. This is somewhat at odds with the low number of CVG identified as residing on that side of the border (Fan et al., 2010; C.-Y. Ma et al., 2020). Only three groups of CVG have been observed to live within the BNNR (Fan et al., 2010; C.-Y. Ma et al., 2020), and only one of these appears to remain exclusively within the BNNR limits, while the other groups move back and forth across the border (S. Wei et al., 2017). In contrast, over 20 groups have been estimated to live within the CVGCA (C.-Y. Ma et al., 2020). If the CVGCA forest is less suitable as the MaxEnt modelling suggests, then it is likely that other factors such as the availability of foods, sleeping trees or general forest composition is affecting their distributions.

When considering the available habitat at a threshold of 60 per cent or above, the model indicates that 23.91 km^2 would be considered suitable across the study area. This potentially presents a model closer to the current reality of the CVG distribution based on the known use of the CVGCA by the gibbons. It also indicates there is greater potential within the forest in

Zone IV adjacent to the CVGCA. Available habitat within a dispersal range due to potential forest connectivity indicates a suitable area of 17.86 km^2. Once again, this is highly fragmented, but it does offer more opportunity for CVG groups to establish new home ranges in the adjacent habitat fragment in Zone IV (Fan et al., 2006; Fan et al., 2010).

The total area found to be suitable for the CVGCA at both the 60 and 90 per cent suitability threshold, is considerable dwarfed by the potential distributions identified for other gibbon species. Modelling of potential habitat for *Nomascus siki* (southern white-cheeked gibbon) in Vietnam and Laos, identified 9894.15km^2 of additional habitat (Van Tran et al., 2023), while 81.286 km^2 was predicted for the Javan gibbon in Central Java (Widyastuti, Perwitasari, Prasetyo, Iskandar, & Setiawan, 2020). Although the use of different variables such as the addition of climate data, and the resolution and scale of the modelling will influence the final outputs of MaxEnt modelling, it puts the challenge faced by the CVG into perspective – there is such little opportunity for habitat expansion due to the surrounding anthropogenic matrix that even an additional few kilometres of habitat should be carefully considered. With an estimated home range of 1.28-1.33km^2 (Dat et al., 2008b; Fan et al., 2006) CVG groups require access to larger tracts of forest compared to most gibbons. It is possible that larger home ranges are required as a response to the distribution of key foods (Fan et al., 2010) and to the low level of highly suitable habitat available, as indicated by the best performing model.

The distribution map generated by the model largely reflects the findings of Fan et al. (2013), who identified two areas of conservation adjacent to the CVGCA and BNNR. The distribution map shows the only closely connected fragment of forest to the CVGCA is the fragment identified by Fan et al. (2013) as the 2nd conservation priority area. This area was also sampled as part of the in situ ecological sampling undertaken in Chapter 6.

The findings of the ecological sampling suggest that there is significant rehabilitation required of the Zone IV area to better align with the ecology of the CVGCA. Based on in situ surveys, the sample sites in Zone IV were found to contain high levels of mat and shrub vegetation but low tree density, and significantly lower tree heights, mean tree DBH and total tree basal area when compared to the CVGCA (Chapter 6). Furthermore, the lack of key sleeping tree species and lower food species density within Zone IV, suggest it may not be an attractive area for

dispersal for the CVG. Further surveys, particularly targeting the areas identified through the MaxEnt modelling may provide greater insight to the realistic potential of the region to support the CVG.

Of note, is that the distribution model also identifies a patch of forest outside the bounds of the 2nd protected zone identified by Fan et al. (2013) but within the larger Zone IV area. This area was sampled as part of the in situ ecological modelling work as set out in Chapter 6. This region is selected as a patch of highly suitable forest for the CVG in comparison to the forest immediately adjacent to the CVGCA (Figure 7.8).

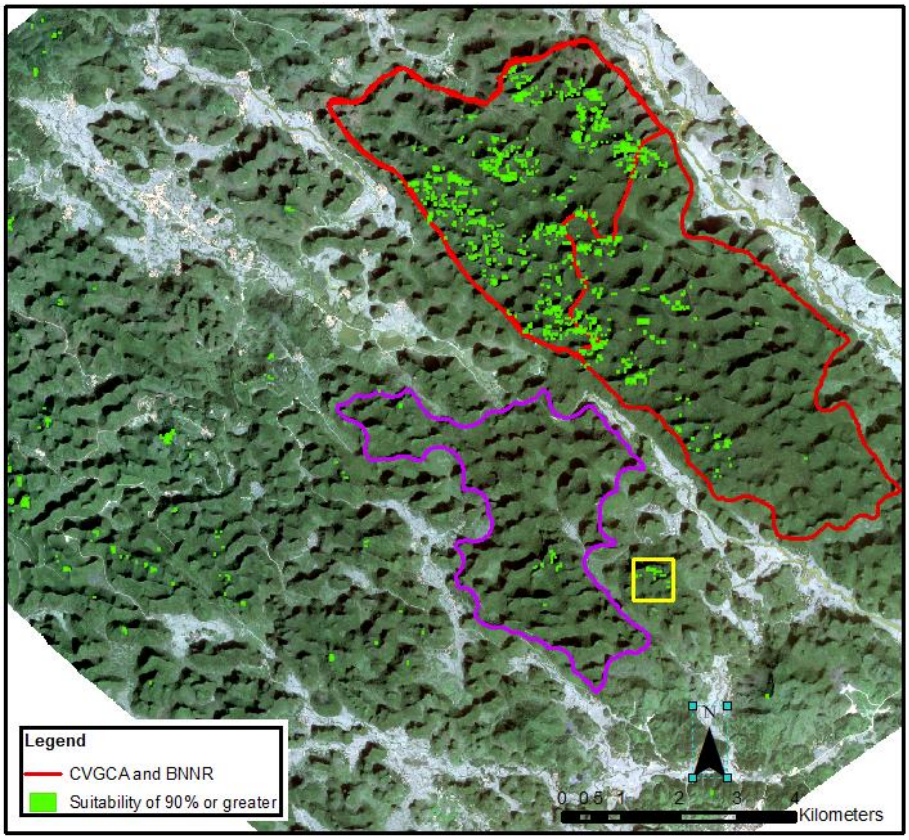


Figure 7.8 Location of additional ecological sampling within Zone IV. The yellow box indicates an area sampled as part of the ecological sampling of Zone IV in Chapter 6. This area sits outside the 2nd conservation priority area identified by Fan et al. 2013, but within the larger Zone IV region.

7.4.2.1 Contribution of predictor variables to the distribution of the CVG

It is unsurprising that the main contributing factor to the distribution map generated by the modelling was the land use variable. It clearly reflects the highly fragmented forest across the immediate landscape as a result of forest destruction and redevelopment by the surrounding communities (Fan et al., 2011). The CVG appear to be associated with broadleaf green forest,

which is to be expected for arboreal canopy dwellers (Fan et al., 2013). Similar findings have been made for distribution modelling of Javan gibbon (Widyastuti et al., 2020). Like the CVG, the Javan gibbon appears to be associated with natural forest and elevations of around 500m (Widyastuti et al., 2020).

Unlike the Javan gibbon however, the distribution of the CVG has no association with plantations (Widyastuti et al., 2020). This preference may reflect the choice of plantation species throughout Trung Khanh which is predominately deciduous or pine. The presence of deciduous forest has been previously suggested to act as a barrier to the dispersal of yellow-cheeked gibbons and Northern buffed cheeked gibbons in Cambodia (B. Rawson et al., 2011; Widyastuti et al., 2020). It is possible then that there is a lack of overlap between plantations and the CVG's dietary and behavioural preferences such as sleeping and calling locations.

The lack of association with plantations has implications regarding current replanting efforts underway throughout the Trung Khanh region adjacent to the CVGCA, and any future plans to improve the ecological profile of surrounding forests in Zone IV as recommended in Chapter 6, Section 6.6). Rehabilitation of forest within the CVGCA (Fan et al., 2013) and within adjacent fragments will have to be carefully considered and focus on native species, particularly those associated with the dietary and behavioural preferences of the CVG.

The contribution of elevation in modelling the potential habitat distribution of the CVG may indicate a preference of the CVG. Elevation has been found strongly influence primate distributions, including *Trachypithecus* species (Gray, Nguyen Quang, & Nguyen Van, 2014; Hansen, et al., 2020; Van Tran & Vu, 2020). During sampling of the CVGCA, it was found that slopes had higher levels of canopy coverage than valleys and ridges, potentially offering a preferred activity zone (Chapter 6, Section 6.5.1.3). In particular, the CVG have been found to prefer trees on slopes near ridges between elevations of 700m and 910m (H. L. Fei et al., 2012).

The sampling method used to survey the CVG population relies on listening stations positioned on mountain ridges and peaks within the CVGCA (Höing et al., 2013; B. M. Rawson, 2010; Vu, Tran, Nguyen, Van Tran, Doherty, et al., 2018; Vu, Tran, Nguyen, Van Tran, & Ta, 2018). The use of vocalisation triangulation methods may result in over representation of CVG

presence at high elevations, particularly as gibbons have been found to prefer the tallest trees for calling (Fan et al., 2009; H. L. Fei et al., 2012; Whitten, 1982a). It is possible then that the distribution model underrepresents lower elevations in modelling CVG habitat suitability. Slopes also offer greater accessibility to food species for the CVG in CVGCA based on ecological sampling (Chapter 6). These areas then may be overrepresented during sampling as higher elevations may see higher usage rates than lower elevations.

The relatively steep incline for values above 0.15 suggests that water levels may impact CVG gibbon distribution. The contribution of NMDI to the CVG distribution may reflect the limited fresh water available within the CVGCA (Fan et al., 2011). The nature of their limestone means that freshwater does not easily pool within the rocky elevations throughout the CVGCA. Limestone is particularly porous, absorbing water and making it difficult for standing pools to be created or maintained (Clements et al., 2006; M. Day & Urich, 2000; Gillieson, 2005; Gunn, 2003; Tuyet, 2001). There is potential that higher moisture content in leaves within the canopy could provide the CVG with additional water in their diets (Oktaviani, Kim, Cahyana, & Choe, 2018) or alternatively may reflect the health of diet species and provision of other nutrients. Unfortunately, the NDMI values associated with the CVG presence may also reflect the climate at the time of capture of the satellite imagery. The lack of higher values above 0.45 suggests that the region may have been going through a period of limited rain.

The inclusion of NDVI in MaxEnt modelling has been identified to be a meaningful variable in other studies (Low et al., 2021; Q. Huang et al., 2010). Yet based on the results of this model, the NDVI appears to have no positive impact on the distribution of the CVG. Given that NDVI can be linked to the presence or even density of green canopy, it is unclear why this variable does not contribute to the CVG distribution within the model.

It is possible that the NDVI values generated have been underestimated unevenly across the layer due to the influence of the underlying limestone karst (Yue et al., 2012). This unevenness could have impacted the relationship between CVG occurrence points and the NDVI environmental layer. It is also possible that the low NDVI variable reflects the high fragmentation of the forest fragments, and that forest type plays a greater role than generic canopy coverage.

As canopy specialists, the CVG should be expected to be highly influenced by the presence of higher NDVI values, particularly in light of the findings of Fan et al. (2013), who identified canopy coverage as a proxy to habitat quality and suitability for CVG. MaxEnt modelling, however, suggests that the forest type (broadleaf green forest) plays more of a role than the canopy structure itself when predicting habitat suitability for the CVG.

While canopy density may play a role in predicting habitat suitability for CVG in terms of moving through the forest fragment (Fan et al., 2013), it does not necessarily indicate suitability for the CVG in terms of forest composition, particularly in terms of food and sleeping tree preferences. This is where in situ surveys and the consideration of micro-ecological variables can contribute to the use of SDMs in conservation planning (Casazza et al., 2021; Elith & Leathwick, 2009; McShea, 2014).

7.5 Conclusion

While the distribution map generated may have distinct limitations as a result of data limitations and sampling size, it can still contribute to our increasing understanding of CVG ecology and provide further insights to support conservation planning.

As hypothesised, the potential distribution of the CVG based on suitable habitat identified through the use of MaxEnt modelling is highly fragmented. Results also indicate that CVG distributions are positively influenced by natural (evergreen broadleaf) forests and elevation. Moisture levels in the canopy also play a role in habitat suitability, however, the influence of forest density (or canopy) (NDVI) and terrain roughness has less influence.

Based on the outcomes of the MaxEnt modelling, it appears that the current CVGCA may not represent a continuous patch of high-quality forest and that the majority of CVG groups inhabit an area of lower quality compared to the groups in the BNNR. The availability of habitat highly suited to the CVG beyond the borders of the protected areas, is highly fragmented. Even when considering forest characterised as having a probability of only 60 per cent or greater of being suitable for the CVG, the areas identified are not contiguous with the CVGCA or BNNR areas but are dispersed across the Zone IV region.

Overall, the MaxEnt modelling suggests a similar outcome to that of the in situ modelling undertaken, indicating that there may be potential for Zone IV to occur additional habitat for the CVG, however, it requires significant rehabilitation and further research. Additional sampling of the CVGCA and BNNR region as a single study site, coupled with further SDM modelling, is recommended as a priority to provide a more complete dataset to understand the ecological characteristics of the CVG.

In 2013, Fan et al., suggested that the current CVG range will reach carrying capacity within 30-40 years. Remote sensing undertaken as part of Fan et al.'s (2013) work identified areas for potential conservation prioritisation to provide opportunities for the CVG to disperse as the population continued to recover from its near extinction in the early 21st century (Chan et al., 2008; Insua-Cao et al., 2012; B. Rawson et al., 2011). Based on their calculations, the current forest extent could support up to 20 gibbon groups, with potential for up to 26 through habitat restoration within the protected zones (Fan et al., 2013). Subsequent surveys by C.-Y. Ma et al. (2020) suggest that the current population comprises 20-22 groups, suggesting that carrying capacity may be reached earlier than previously estimated.

Without committed action to implementing conservation activities to support future habitat expansion for the CVG, the species may not be capable of continuing its current pattern of population growth. Actions to identify opportunities for habitat expansion should thus be prioritised to encourage ongoing growth of this Critically Endangered species.

Based on the findings of Fan et al., (2013), and in situ ecological sampling undertaken in Chapter 6 and subsequent MaxEnt modelling areas within Zone IV region have real potential to offer an area for additional dispersal, if targeted rehabilitation is implemented. Establishing additional protected areas that prevent human activities such as livestock grazing and resource collection, could support the ongoing growth and recovery of the forest within Zone IV. Rehabilitation activities should also focus on the introduction of CVG food species and sleeping tree species. The use of SDM modelling can support policy makers and conservation groups to identify key areas for protection and rehabilitation, to reduce conflict between the protection of the CVG and the loss of agricultural land for the surrounding communities. The findings of this analysis, suggest initial areas within Zone IV to consider.

The patch of forest within Zone IV, with proper protections and targeted rehabilitation, could offer an additional 17.86 km^2 of suitable habitat for additional groups of CVG. However, the highly fragmented pattern of suitable habitat across the region means that serious consideration must be given for rehabilitation efforts to maintain a natural link or establish an artificial connection between fragments.

Chapter 8 Conclusion

The limestone karst habitats of Vietnam's Critically Endangered primates are poorly understood and under studied (Clements et al., 2006; Kauppi et al., 2006). This is particularly concerning in light of the high level of fragmentation and increasing isolation these habitats are experiencing as demonstrated by the findings of this research. The CBL, TSNM and CVG are each facing their own specific challenges regarding their habitats, yet there is significant overlap in the contributing stressors present at each site. Each share extensive histories of human-led habitat destruction and degradation within their current geographic distributions and increasing habitat isolation and fragmentation with implications for the genetic health of their small populations. They are also subject to pressures from other sympatric primate macaque species, which are poorly studied in regard to their potential impact on these at-risk species. Amongst these ongoing threats, all three species are also the focus of dedicated conservation programmes with high levels of community engagement.

This study provides detailed data on the vegetation and topographic profiles of the habitats of three Critically Endangered primates. By examining these profiles and in-site differences in relation to behavioural and nutritional data for each species, it provides greater insight into their habitats and will facilitate targeted monitoring and planning for specific areas within these fragments. Furthermore, this data supports practical validation of landscape-level analyses such as SDMs, by comparing modelled habitat suitability to the results of ecological surveys and habitat comparisons.

8.1 Key findings on current habitat fragments

Regeneration of limestone karst is notoriously difficult (Fan et al., 2011; Pambudi et al., 2020) and as such, must be carefully planned. It is also highly site-specific, with no universal approach to conservation of limestone karst sites possible due to the specifics of the historical and modern interactions between each site and their local communities, and the requirement of their plant and animal compositions (Clements et al., 2008; Clements et al., 2006). Detailed analysis of strata interactions within limestone karst sites can improve our understanding of their value to each of the primate species (Schwarzkopf & Rylands, 1989).

At all sites, differences between the different site strata (coast, valley, slope, ridge) can be linked to the characteristics of the limestone topography and vegetation characteristics such as canopy height and coverage, and species densities. For instance, on Cat Ba Island, the coast plots display the greatest variation in elevation and species diversity compared to the valleys and slopes. In Khau Ca, which has typically less exposed limestone and has a bowl-like shape, valleys display the most significant differences in characteristics such as plant density, and shrub coverage compared to the steep ridges. In the CVGCA, limestone is jagged with significant variation in elevation; here, the ridges and valleys are significantly different based on characteristics such as species density, canopy height and canopy coverage. Considering the characteristics of each site in light of behavioural studies can provide further insight into the habitat usage and support targeted management of specific plot types within sites to maintain areas of value for the primates.

The severe topography of limestone karst influences the structure of the vegetation at different stratums, which in turn influences the behaviours of primates and their use of different segments of their habitats. Each species has a unique relationship with different strata within their habitat based on interactions between food availability, predation, accessibility, and socioecological interactions.

On Cat Ba Island, the vegetation composition of the Cua Dong and Sanctuary does not significantly differ, however the internal structure of vegetation and site characteristics varies across coast, slopes and valleys within each site. It is possible then that habitat within the Sanctuary is utilised by the CBL in different ways. As long-term socioecological and nutritional studies of the CBL have primarily focussed on the Cua Dong population (Hendershott, et al., 2016; Hendershott, 2017; Hendershott et al., 2018; Ruskin, unpublished) it is recommended that further study of the Sanctuary population is prioritised.

Hendershott (2017) identified the use of valleys and exposed slopes as critical for CBL foraging (Hendershott et al., 2016). Ecological surveys of slopes, valleys and coastal plots, indicate that the slopes of Cua Dong and the Sanctuary provide the greatest number of food species and greatest density of individual food stems, while valley plots in both areas were found to contain the fewest food species. These findings indicate why exposed slopes may be of high

value for foraging by CBL (Hendershott, 2017; Hendershott et al., 2018) due to the availability of food species in these areas. In contrast, the ecological survey suggests that valley plots across both sites contain low levels of food species, yet Hendershott et al. (2018) also identified valleys as key foraging sites. Based on this, it is possible that the food species available within valleys have different nutritional value to the CBL. I concur with Hendershott et al., (2018) in recommending these areas as conservation priority but additionally suggest valleys are further investigated and monitored to better account for the potential underrepresentation of valleys in the current CBL research.

In Khau Ca, ecological surveys of the valleys, slopes and ridges provided further data to build on previous tree phenological studies and further contextualise the behavioural patterns of the TSNM observed by previous studies (Hai, 2008; Thach, 2009; Quyet, 2014). The vegetation and topography of Khau Ca varies significantly across the valley, slope and ridge plots based on elevation, topographic complexity, slope, species density, and percentage of large shrub.

Based on analysis of the plant communities and food species distributions, ridges and slopes are expected to play a critical role as foraging sites for the TSNM as food genera and species are found to occur in greater frequencies in these areas compared to valleys. This is also due to the high representation of key food species identified by Hai (2008) and Quyet (2014) in these areas. As result, these areas should be monitored to ensure food species availability remain consistent to support the TSNM population. Reviewing the wide variation in food species attributed to the TSNM and the low representation of specific species captured within the ecological surveys of this study (Covert et al. 2008; Hai 2011; Le & Boonratana 2006; Quyet et al. 2007; Pham et al. 1993/4), it is recommended that a full review of the existing literature on TSNM food preferences.

While potentially less utilised for feeding, valleys in Khau Ca may be more important for the TSNM as sleeping sites based on sleeping tree metrics identified by Hai (2011). As valleys possess older growth trees compared to slopes and ridges, the trees in these areas should be monitored as a critical resource for the TSNM.

In Trung Khan, surveys of the CVGCA indicate that there are significant differences between the ridges, slopes and valleys suggesting plot-specific vegetation characteristics. Plant

communities captured along ridges vary compared to those of the valleys and slopes, however, the characteristics of trees found on the slopes, suggest that this area is critical for the CVG. Slope plots within CVGCA possess the largest trees and greatest canopy cover, potentially as a direct result of historical use of the area by humans involved in logging and agricultural practices within the valleys (Fan et al., 2011). Based on tree metrics and food species abundances recorded in through the surveys, slope plots have been identified as key areas for feeding, calling and selection of sleeping sites (Fan et al., 2011; Fan et al., 2011; Fan et al., 2012; Hanlan et al., 2015; C. Ma et al., 2017). Based on this, the protection and monitoring of slopes should be a key priority for the management of the CVGCA.

While the differences across the strata at most sites may be enhanced due to historical use and degradation, particularly amongst valley forest compositions, it further highlights the need to include strata-specific monitoring tailored for each site as part of species conservation action plans. This is the only way to ensure these limestone habitats continue to meet the utilisation needs of the primate inhabitants.

In areas targeted for regeneration, particularly in areas that have historically been used for agricultural or plantation purposes such as valleys, efforts should focus on meeting primate needs of the area through targeted monitoring to understand the best approach to regeneration. Primates at these sites are already experiencing the effects of human-altered forests (Yang et al., 2019), thus, further alteration as a result of poor planning should be avoided.

The presence of non-native plant species can have differing impacts across species. For instance, while in Cua Dong, the CBL has adapted to easting a non-native invasive plant species, in the CVGCA habitat suitability for the CVG is negatively associated with the presence of non-native plantations. However, in other regenerating parts of the CVGCA core habitat, the CVG have been observed to travel to an area of regeneration for fruit provided by fruit trees left over from historical agricultural use (pers. comm, Anon). The introduction of any species into the habitats of at-risk species, should be carefully monitored and planned to limit negative impacts (Stenke & Canh, 2004).

8.1.1 Limestone karst as a refuge or preference?

Limestone karst covers over 400,000 km^2 of Southeast Asia and act as biodiversity hotspots, supporting high levels of endemic flora and fauna (Clements et al., 2008; Clements et al., 2006; Vermeulen & Whitten, 1999). Despite this, limestone karst forests are increasingly becoming isolated pockets within an urbanised and agricultural landscape (Struebig et al., 2009). The remaining pockets continue to face ongoing degradation caused by unsustainable resource collection and destruction through quarrying and mining activities, chiefly for cement (Vermeulen & Whitten, 1999).

Ongoing demand for limestone karst resources, particularly through mining continues to pose a serious risk to the karst ecosystem (Clements et al., 2006; Pambudi et al., 2020). Demand for limestone products is expected to continue to grow, particularly as a result of a growing global demand within the construction sector (Simoes & Hidalgo, 2022). Vietnam is the second largest exporter of limestone in the world and limestone minerals for manufacturer of lime or cement from the country are worth US$90.1 million (Simoes & Hidalgo, 2022). Growth of exports is also increasing – between 2019 and 2020, limestone exports in Vietnam grew US$9.6 million, representing the fastest growth of limestone exports in the world (Simoes & Hidalgo., 2022). As a result, limestone karst ecosystems can expect to face increasing pressure from mining. For species such as the TSNM in Khau Ca, mining is already starting to encroach on their local forest; the mine at Minh Son is a key factor preventing forest linkages to the larger Du Gia forest. With the continued use of the mine and risk of expansion, the ability to regenerate the buffer zone or corridor to the larger Du Gia forest in this area is low.

Understanding the interaction of primates and their limestone karst habitats is somewhat restricted by a lack of knowledge as to whether these karst arcs present preferred habitat or a refuge due to encroaching human activity and habitat loss (Li & Rogers, 2005a; Nüchel et al., 2018). While to species such as *Trachypithecus leucocephalus* in Fusui, China (Li & Rogers, 2005a) limestone karst appears as a refuge based on their uneven use of the different elevations and lack of dependence on endemic limestone karst plants, the relationship between other primates and limestone karst are yet to be determined.

In the case of the CBL, their historical persistence on a karst island and ad hoc observation of their use of the different elevations would suggest that for this Critically Endangered species, limestone karst is essential habitat. The high levels of karst-related locomotion, limestone caves for sleeping, use of ridges and peaks for travelling and predation lookouts by males, may indicate their evolutionary adaptation for this environment (Hendershott, 2017; Hendershott et al., 2016).

The high reliance of the TSNM on limestone karst-specific food species (Anh et al., 2014) suggests that limestone may also be a preferred habitat. Yet the presence of TSNM in other non-karst fragments and records of their historical distribution (Nüchel et al., 2018), suggests that the limestone karst forest in Khau Ca represents a refuge rather than a preference. It is similarly unclear for the CVG; while their distribution is positively associated with the high elevations present in karst landscapes based on MaxEnt modelling, it is not related to topographic roughness – a potential indicator of limestone karst.

An important opportunity to understand the evolutionary preferences of these species also lies in analysis of the habitat of their closest relatives. As a member of the limestone langur group, it appears likely that the CBL is evolutionary adapted to this environment, along with its closest relatives. In contrast, both the TSNM and CVG appear to be the only members of their immediate relatives to strictly inhabit limestone karst forest, further suggesting that limestone karst is a refuge habitat rather than essential habitat. It also suggests that these species have high levels of ecological plasticity in light of their ongoing persistence and even limited growth of their populations.

8.2 Corridor connections and areas for potential habitat expansion

Based on studies of population viability of the CBL (Lees et al., 2014) and CVG (Fan et al., 2013), the current habitat fragments of each species are predicted to reach maximum carrying capacity in the next few decades. Without action now, it is possible that any hope for expansion of the current distribution of the species will be lost due to ongoing habitat degradation, human expansion, and climate change.

While the critical effective size of a population to ensure the genetic security of a population and their long term survival is considered much higher than the populations of any of the species in this study (I. R. Franklin & Frankham, 1998; Harcourt, 2002; Lynch & Lande, 1998; Pérez-Pereira, Wang, Quesada, & Caballero, 2022; Shaffer, 1981), all three are exhibiting ongoing breeding which suggests some population growth.

For the CBL, there is hope that linking the two main population fragments could improve genetic diversity. As there are no significant captive populations to support restocking to promote genetic diversity (Marsh, 2003c), careful planning is required each of the wild populations remaining. Without action to support the long-term survival of each of these three species and their habitats, any future opportunities to expand their distributions will be lost. For two of the study species, the use of corridors has the potential to expand their current distribution and promote dispersal and new group creation through accessibility to new territories.

The effectiveness of corridors is not certain (Damschen et al., 2006) and depends on the ability and awareness of the target species to utilise it (Ricketts, 2001). It also requires careful planning to structure the corridor to the needs of the target species (Li et al., 2021); in the case of primates, canopy connectivity is considered critical to support arboreal dispersal (Bennett & Davies, 1994). The ability to entice species to utilise a connectivity point such as a corridor may also impact its success if it is not passively utilised (Lima & Zollner, 1996). In such cases, the incorporation of important diet species may be useful to attract its use by the target species. Improving connectivity between habitat fragments is also not a one-way interaction. While the creation of a corridor may increase the connectivity of forest fragments across a landscape for a particular species, it can also increase the access for other animals, plants and even humans to the original fragment (Beier & Noss, 1998; Gilbert-Norton et al., 2010). Thus, conservation managers much choose the design carefully and commit to ongoing monitoring.

For the CBL, the use of a vegetation corridor could not only link the two major populations currently isolated from one another by several kilometres of coastline to support gene flow (Damschen et al., 2006) but allow them to access other protected forest within the National Park. For the CVG, an artificial corridor, coupled with targeted regeneration of an adjacent

forest fragment, could increase the available habitat for future groups. The TSNM however, has less opportunity for habitat expansion and without extensive monitoring and longer-term studies of the adjacent Du Gia NR, it is not recommended that any expansion is pursued regardless of the planned incorporation of Khau Ca into a Du Gia National Park.

8.2.1 Cat Ba langur

In the case of the CBL, the VHC is already being irregularly utilised by the langurs from the Cua Dong population (pers comm. H. Cam). Based on the outcomes of the vegetation analyses, and species distribution analysis, it appears that the current composition of the VHC has some potential as either a corridor to link the two populations, or as an area of expansion for the Cua Dong population. The overall profile of the region appears to be of better quality based on tree metrics and while it had the lowest number of food species, it was similar in levels to the Sanctuary. MaxEnt distribution modelling of the region also showed some limited suitability of the region, and while it was highly fragmented so was the suitable habitat within Cua Dong and the Sanctuary, suggesting that there is some flexibility in the ecological adaptations of the CBL.

Expanded use of the VHC as a corridor or expanded habitat will require additional protections to be provided, further habitat surveys to consider the need for restoration projects and increased surveillance by rangers. The latter is particularly important in the face of ongoing risks of poaching in the region. By increasing protections and limiting access even further than is already in place, the langurs may naturally begin to stay longer and increase travel time within the VHC. Further research into the diet and socioecology of the Sanctuary population will also be critical to better understand how this region might encourage use by the langurs with the ultimate aim of establishing connections between the two sub-populations.

8.2.2 Tonkin snub-nosed monkey

Although studies of the TSNM and surveys suggest the population has continued to grow since its discovery (N. X. Dang, Nghia, & The, 2019; Kempinski et al., 2009; Knight, 2019; Quyet, 2008; X. C. Le & Boonratana, 2006; Truong & Linh, 2017), the small size of the habitat and its isolation from any other surviving population indicates that the potential for ongoing growth of the Khau Ca population is limited. And despite the official merging of Khau Ca with the

larger Du Gia NR, there does not appear to be any meaningful forest connection that could support the TSNM safely.

Based on my results, the species composition of the general vegetation structure varies insignificantly between Khau Ca and Du Gia. The key difference between the two sites based on vegetation is the significantly lower canopy in Du Gia compared to Khau Ca. This has implications for the ability for the large-bodied TSNM to move through the forests of Du Gia. The trees in Du Gia are generally smaller and exhibit less canopy continuity. For an arboreal species such as the TSMN, this has the potential to act as a major deterrent against natural dispersal should a connection between the two sites persist. The lack of shared food species is also a potential limitation to the ability of Du Gia to support TSNM groups. While the TSNM have been suggested to be highly capable of adapting their diets to different sites, the combination of low overlap of preferred food species and poor canopy structure may not act as a motivator for the TSNM to disperse into the larger Du Gia region, particularly with the persistence of larger predators that no longer exist in Khau Ca.

In order to encourage movement into the Du Gia forest, extensive replanting and enforced protections would be needed for a significant stretch of several kilometres, which is likely to take several years if not decades. If this avenue is pursued, there must be increased efforts to reduce human degradation of Du Gia via logging and collection of forest resources, as well as additional surveys of the deeper forest. Restrictions and monitoring must also be undertaken to mitigate the risks posed by nearby mines and major infrastructure in the region.

A genetic analysis of the TSNM in Khau Ca showed no mitochondrial variability (Ang et al., 2016), suggesting that the largest population of TSNM are at risk from stochastic processes. While additional genetic analysis of the Khau Ca population and other remaining groups will help to further build our understanding of the genetic variability present within the TSNM, currently, their ongoing viability appears limited unless new populations are located. The only confirmed surviving population is 35km away in Tung Vai (James, 2016).

Based on the low population numbers - estimated at 15-37 individuals (T. D. Le, 2010; Truong, 2014; Truong, Linh, & Dat, 2016) – and ongoing threats within Tung Via, including cultivation of cardamom crops (N. X. Dang et al., 2019; James, 2016), connecting the two groups would

require major conservation intervention with potentially little to gain as neither habitat could sustain them long term. The Tung Vai region is currently classified as a watershed protection forest – which largely focusses on protecting waterways (Initiative, 2014). Reclassification as a Special Use forest is required to better protect the biodiversity of the forest and assist in conservation (N. X. Dang et al., 2019).

8.2.3 Cao vit gibbon

The CVG are expected to reach carrying capacity with the next few decades (Fan et al., 2013), signalling the need for detailed planning for their future distribution. Based on the outcomes of land cover assessments by Fan et al. (2013) and the in situ ecological analysis undertaken in this study suggests that a nearby forest patch offers some opportunity to expand the current forest available to the CVG, should major conservation action be taken to better protect the region termed 'Zone IV' in this study. MaxEnt distribution modelling further supports this finding, noting the potential for at least 17.86 km^2 of additional habitat. This however will require improving the connectivity between the two forest fragments (Sha et al., 2022) on the Vietnamese side of the border.

This can be achieved through a long- and shorter-term process. In the short term, consideration and piloting of the use of a made-made corridor to bridge the gap between the current CVGCA habitat and Zone IV potential habitat should be further studied to determine the likelihood of success. Due to the presence of CVG food species along the corridor and similar tree and canopy profiles, it is possible that the transmission of CVG group could occur naturally should they be provided with the means to do so.

In the longer term, additional resources should be sought to build on existing efforts to reforest parts of the corridor region in Vietnam and China. The Vietnamese government has been working to limit deforestation and implement reforestation programs since 1965 however the protection of primary forest has lagged behind (Sha et al., 2022). Any reforestation of the corridor and surrounding should seek to regenerate species native to the region (Meyfroidt & Lambin, 2008b, 2009), particularly those species found to be important to the gibbons.

Based on MaxEnt results, it appears that dedicated rehabilitation of native species of importance to the CVG may encourage dispersal out of the CVGCA into adjacent forest fragments (via manmade corridors). Modelling of ecological variables suggests that the adjacent forest patch in Zone IV is a potential candidate as suitable habitat for the CVG. However, this modelling also suggests that the presence of plantations is not associated with the occurrence of the CVG, requiring careful planning to ensure rehabilitation efforts are not wasted.

Due to the potential suitability of the adjacent forest fragment, it may be possible to support the continued growth of the CVG population, which may be reaching carrying capacity at a faster rate than previously estimated (Fan et al., 2013; C.-Y. Ma et al., 2020). Of particular interest, however, is that the distribution modelling suggested that there was a significant area of the BNNR that is suitable for the CVG, potentially at odds with the current low number of CVG that exclusively inhabit the BNNR. This suggests that additional factors may be deterring greater densities in this region, potentially as a result of ongoing human activity within the protected zone along the international border. Further research into the combined CVGCA and BNNR habitats should be prioritised as a joint project for conservation groups with support from the Vietnamese and Chinese governments.

8.3 Conservation Engagement

The current persistence of these Critically Endangered species is in large part a direct result of in situ conservation efforts by local government and dedicated conservation groups including FFI and the CBLCP. Their success is due to an approach that acknowledges the influence of local socio-cultural and local economic factors alongside traditional biological and ecological factors (Estrada et al., 2017). Local communities are critical to the long-term success of conservation efforts, through shifting attitudes, changes in activities regarding primates and their habitat, and engagement in the conservation process itself (Gomiero et al., 2000).

The inclusion of local rangers to support the monitoring of the CBL has produced an economic and socio-cultural incentive for the ongoing protection of the langurs. As langur guards are from the local villages, the willingness of other people from the community to disrupt or interfere with the CBL is significantly reduced (Hendershott, 2017). Locals are also willing to

provide information to guards about sightings of langurs and strangers to the area suspected of poaching. As a result, the CBL has become a point of pride for the community, particularly in Cat Ba Town where local businesses promote conservation activities via posters and t-shirts worn by staff. While hunting and unauthorised access to protected areas still occurs, the inclusion of the local community in the CBL conservation provides additional resources and support that can boost the success of small-scale conservation efforts.

The efforts in place at Khau Ca for the TSNM have seen similar successes. Through integration of conservation efforts through the national park service as seen on Cat Ba Island, government and conservation efforts have been undertaken in unison. Community patrol groups under the leadership of the Ha Giang Provincial Forestry Protection Department complement other national park activities, providing additional resources to monitor and protect the TSNM protection zone (Covert et al., 2008). Through the work of FFI, members of the local community in Tung Ba commune outside Khau Ca have transitioned from extracting timber and hunting in the TSNM habitat to actively protecting it as community offices and guards (Covert et al., 2008). This has ensured that local knowledge and experience is redirected towards the continued protection of the TSNM and that it is viewed as a benefit to the community rather than a burden.

The efforts in Trung Khanh for the protection of the CVG are similar, however, local engagement is lower based on results of interviews with local community members and National Park staff. As with the CBL, the protection CVGCA resulted in a loss of access to former agricultural land and reduced the ability of locals to access forest resources. Local National Park rangers are responsible for monitoring the CVGCA, however, knowledge of the gibbons and the habitat among the guards appears low when compared to CBL and TSNM rangers. One National Park ranger at the CVGCA explained this was due to lower wages compared to the TSNM rangers, however it was unclear if this was an actual or perceived disparity.

Many members of the community around the CBL and TSNM protected zones expressed a desire to implement ecotourism to promote the endangered primates and increase economic benefits to the local community (pers comm. Interviews). While ecotourism may appear as a

solution to profit both endangered species and local communities, the realities are often less clear cut (Marsh, 2003c; Russon & Wallis, 2014). Ecotourism comes in many forms (Leasor & Macgregor, 2014). While the economic benefits of ecotourism can lead to improved outcomes for the local community (Snyman, 2014) and to wider conservation efforts through community support, this is not always the case particularly where there is economic leakage and profits are redirected away from local communities (Russell & Russon, 2007). The impacts of political, economic and environmental instabilities can make ecotourism a volatile source of income (Maekawa, Lanjouw, Rutagarama, & Sharp, 2013).

It can also lead to negative outcomes for target species and their wider ecosystem through increasing access of poachers to protected habitat and increasing habituation of groups to human presence (Russon & Wallis, 2014). Primate ecotourism has also been linked to disease transmission between humans and primates (Afonso et al., 2021), injuries from human-primate interactions, behavioural changes, and changes to habitat use (Russell & Russon, 2007; J.L. Williams & Behie, 2020; J. L Williams, Behie, & Fan, 2021).

The relationship between rangers and primates is also critical to the success in preventing negative interactions as a result of ecotourism (Usui et al., 2014). Rangers on the ground are often responsible for policing tourist behaviour and protecting primates (Usui et al., 2014). Without effective training and commitment to enforcing rules, ecotourism can become unregulated risking both tourist and primate health.

Based on the current situations of the CBL, CVG and TSNM considering their small population numbers and relatively low data available on their socio-behavioural and ecological interactions, it is not recommended that ecotourism is pursued at these sites. All species are unhabituated and due to a history of poaching, habituation through ecotourism could have negative impacts on their safety, in addition to being difficult to reverse (Russon & Wallis, 2014). In response to community support for ecotourism, further educational programs and forums should be established to allow local communities to provide feedback into the conservation initiatives at these sites. In doing so, it may be possible to identify other opportunities to increase community participation in the protection of these species.

The sites themselves are also not conducive to tourism – both the TSNM and CVG habitats require extensive hikes to access through limestone karst, both of which would require significant infrastructure investments and disruptions to the habitat to support regular ecotourism. Prior to any consideration of ecotourism in these regions, further extensive research into each species and potential impacts on the forest is required.

8.4 Conservation recommendations

8.4.1 Cross-site recommendations

This study presented a detailed analysis of the habitat of three Critically Endangered species and areas for potential habitat expansion or connections between existing population fragments. In the case of the CBL, it represents the first ecological study of the two major populations on Cat Ba Island, encompassing both the Cua Dong population and Sanctuary population. For both the TSNM and CVG, this study expanded on the work of previous ecological surveys to consider new areas for habitat expansion.

Based on the research and engagement with conservation groups, local government and local communities at each site, the following actions are recommended to support the ongoing conservation of the CBL, CVG and TSNM.

I recommend that research into the interactions of each species with each stratum (valley, slope, and ridge) is expanded to understand spatial relationships of feeding, locomotion, social and other behavioural relationships. This may further support the ability of conservation groups to protect or improve vegetation within each stratum to benefit the target species, and further our quantitative understanding as to whether limestone karst represents an evolutionary preference for each species. The application of phylogenetic species distribution methods may also assist in supporting this work.

Based on the in situ ecological surveys, I also recommend that detailed habitat monitoring is expanded at each site to develop longitudinal data sets that allow for monitoring of vegetation changes, particularly in response to ongoing climate change. To reduce the impact this monitoring may have on the habitat each species, ecological plots should be established for long-term monitoring, thereby restricting the number of sites that may be disturbed through

this process. This may be further reduced through the adoption of newer technological methods such as LiDAR analysis, allowing for the creation of three-dimensional models of habitats to be developed through remote sensing (Palminteri et al., 2012; Simonson et al., 2014). The security sensitivities at sites, particularly on Cat Ba Island and the transboundary CVGCA in Trung Khanh, may limit its use without significant collaboration with conservation groups, and local and national-level governments led by international research groups.

I also strongly recommend the commencement of detailed studies of any other primate species living sympatrically at each site and their interactions with the CBL, CVG and TSNM. The presence of large populations of macaques at each site, and the lack of quantitative or even qualitative data on their relationships with the target species, the limestone forest is concerning. Effective conservation of these Critically Endangered species cannot be achieved without acknowledging their interactions within the wider ecosystem, allowing for the identification of additional pressures and resource competition that may impact them. An additional benefit will also be to improve datasets available for species distribution modelling to account for sampling bias and understand niche distributions across multiple primate species at sites that are heavily fragmented.

In order to understand the genetic viability of each of the species, it is also recommended that further genetic analysis is undertaken to determine the genetic diversity of each population. While analysis of the mitochondrial genome of the TSNM Khau Ca population have indicated no genetic variability, Ang et al. (2016), recommend further genetic testing on nuclear DNA and other persisting TSNM populations to provide greater clarity. Low genetic variability has been linked to greater risk of extinction (W. Miller et al., 2011) as a result of stochastic events, vulnerability to disease, and even climate change (Reed & Frankham, 2003; Spielman, Brook, Briscoe, & Frankham, 2004; W. Wang et al., 2017). Thus, understanding the current genetic diversity of each of these species will add greater strength to conservation planning for their survival (Schwartz, Luikart, & Waples, 2007).

8.4.2 Cat Ba langur

In addition to the recommendations identified in section 8.1 relating to the management of different strata within Cua Dong and the Sanctuary, there are broader landscape-level actions that should be implemented to support CBL growth.

Based on assessment of the VHC through both ecological and MaxEnt modelling, it appears that there is potential for the introduction of a corridor connection and area of potential habitat expansion. Based on these findings, I recommend that the VHC is extended additional protections as an area for potential dispersal for the CBL. This includes expanding the current CBL protected areas to include the coastal corridor from Cua Dong along to Viet Hai and the Sanctuary and implementing increased monitoring by the National Park. As part of this, a corridor linkage to overcome the potential barrier presented by Viet Hai port and road should also be considered.

Further ecological research of the corridor region is required with the potential to consider interventions increasing the presence of diet species in these areas to encourage the dispersal of Cua Dong and Sanctuary populations. This should also include long-term monitoring of the macaques inhabiting the VHC and Sanctuary to better understand interactions between the two species.

I also recommend that further research into the socioecological and dietary behaviours of the CBL in the Sanctuary are undertaken to expand our knowledge of the entire population. Limiting research to the Cua Dong region limits the ability of conservationists account for the ecological differences between the two sites demonstrated through this study. Differences in topographic, vegetation characteristics, and plant communities suggests that a one-size-fits-all approach to their ongoing conservation may not be the most effective.

8.4.3 Tonkin snub-nosed monkey

Due to the lack of forest connections between the TSNM habitat in Khau Ca and Du Gia National Park, the apparent limitations of the forest canopy and food species overlap with Khau Ca, and the extensive evidence of ongoing human activity within the protected area of Du Gia, I recommend that a buffer zone is re-established bordering Khau Ca through greater protections, monitoring and regeneration activities. It is also recommended that further

research is conducted to determine whether any additional TSNM populations persist within the Du Gia National Park.

It is not recommended at this stage that a corridor is pursued to link Khau Ca and Du Gia National Park due to the high levels of logging, human access and mining activities that persist between the two areas. Only with the opportunity to increase genetic diversity by improving dispersal pathways between the Khau Ca population and any newly discovered TSNM populations within Du Gia, should a direct linkage be considered. Furthermore, greater community engagement and monitoring of illegal logging in Du Gia should be pursued by local authorities and conservation groups to improve ecological and socio-economic outcomes for the region.

A dedicated ecological survey of the extent of Du Gia, utilising in situ surveys and remote sensing methods should also be pursued to provide a greater insight into the profile of the deeper reaches of the protected forest. The limitations of this study did not allow further surveys to be taken. Further focus on this region may have benefits for the future of the TSNM and other species within the Du Gia region.

8.4.4 Cao vit gibbon

Based on my in situ and distribution modelling of the CVG habitat, I further support the original recommendations by Fan et al. 2013, that the adjacent forest fragment (Zone IV) is provided immediate additional protections and established as conservation priority area for the CVG. Zone IV exhibits strong levels of CVG foods species, particularly fallback foods such as figs, and distribution modelling also suggests the region has a significant area of suitable habitat for the CVG.

Large scale surveys to assess the need for any rehabilitation of Zone IV should be commenced immediately. This includes assessing opportunities for regeneration of valley areas and exclusion of human activities including livestock grazing through dedicated monitoring by rangers. It is also recommended that opportunities for linking this region to the CVGCA/BPNR habitat is further investigated, including an assessment of the viability of an artificial corridor linkage between the CVGCA and Zone IV.

8.5 Significance

Today's primates predominately persist in habitats that have been impacted by anthropological interventions, resulting in some degree of habitat fragmentation. Our ability to prevent or reverse habitat fragmentation requires baseline data on the primate and their habitat to support targeted conservation action plans.

While behavioural and nutritional data for primates continues to grow, there remains a paucity of detailed habitat data for many species (Isabirye-Basuta & Lwanga, 2008; Wei Wang, Ren, He, & Zhu, 2008). This is particularly true of those inhabiting limestone karst forest potentially due to two key issues. First, that the conservation of limestone karst regions has lagged due to a lack of baseline environmental or biodiversity data prior to anthropogenic-led degradation (Clements et al., 2008; Struebig et al., 2009). Second, due to the difficulty in accessing and conducting large-scale in situ ecology assessments in what can be a dangerous environment (Tanja Haus et al., 2012).

By undertaking ecological surveys within the current habitat fragments of each species, I have analysed the vegetation and topographic characteristics of each site, including plant profiles, which can be used as foundational data to support development of targeted monitoring, rehabilitation and fragment connectivity planning for each species. If the health of their habitat declines, so too will the health of the primates (Estrada et al., 2017). By sampling the full range of vegetation contained within the survey plots, we can better track future changes in the plant composition, food species availability and sleeping site availability, provide insights into past disturbances and identify future risks (Vellend & Gerber, 2005).

This dissertation represents the first ecological study of the CBL in Cua Dong and the Sanctuary, and the first distribution model of the CBL to be undertaken. It provides key insights into the habitat of the CBL and areas for potential expansion, including an assessment and recommendation for the formal establishment of a corridor to link the Cua Dong and Sanctuary CBL populations.

It also provides the first ecological evaluation of the suitability of an area for habitat expansion for the TSNM. By comparing the TSNM habitat at Khau Ca to the recently merged Du Gia NR,

I have provided key insights into the current state of the habitat, finding that the Du Gia site is not currently suitable to for the Khau Ca TSNM, and any connection between the two sites may put the population at risk due to high levels of huma activity within the Du Gia forest. The outcomes of this work are intended to support planning for the TSNM and future study of Du Gia.

This is also the first study to evaluate the CVGCA habitat and an area of potential habitat expansion using both in situ sampling and distribution modelling. In doing so, I have provided further evidence to support the potential expansion of CVGCA and identified key opportunities to improve the natural dispersion of the CVG into new areas.

Forest health cannot be rehabilitated quickly and the high level of habitat fragmentation faced by these species means that there are no backup sites available to support populations. The results of this thesis can assist efforts to monitor and plan for the entire habitat in an effort to maintain or even improve the suitability of these areas. This can also be further extrapolated to help identify, manage and cultivate new areas of expansion to support population growth.

It is the hope that the species-specific findings of this study will contribute to our knowledge of limestone karst primates in Vietnam and assist those involved in planning for the ongoing conservation of the CBL, TSNM and CVG and their continued growth.

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Appendix

Appendix 1 Methods

1.1 Interview script and questions

These are a list of the questions I will be asking you. You are not required to answer any question that you do not want to answer and can end the interview at any time.

1. Initial introductions around name and occupation.

2. How long have you lived in the area?

3. Have you seen this monkey/ape [*show picture of primate*] before?
    a. Where?
    b. When?

4. When was the last time you saw one of these monkeys/apes in the wild?

5. Have you seen them in the past 10 to 15 years in other places?
    a. Where [*use map*]?
    b. When did they stop being found there?

6. Are people using the surrounding environment differently than in the past? If yes, how?

7. Have the forests, rivers and streams, bird life, animals, insects, and plants changed in the past fifteen years?
    a. If yes, how?

8. Has the weather changed in the last fifteen years?
    a. If yes, can you give some concrete examples?

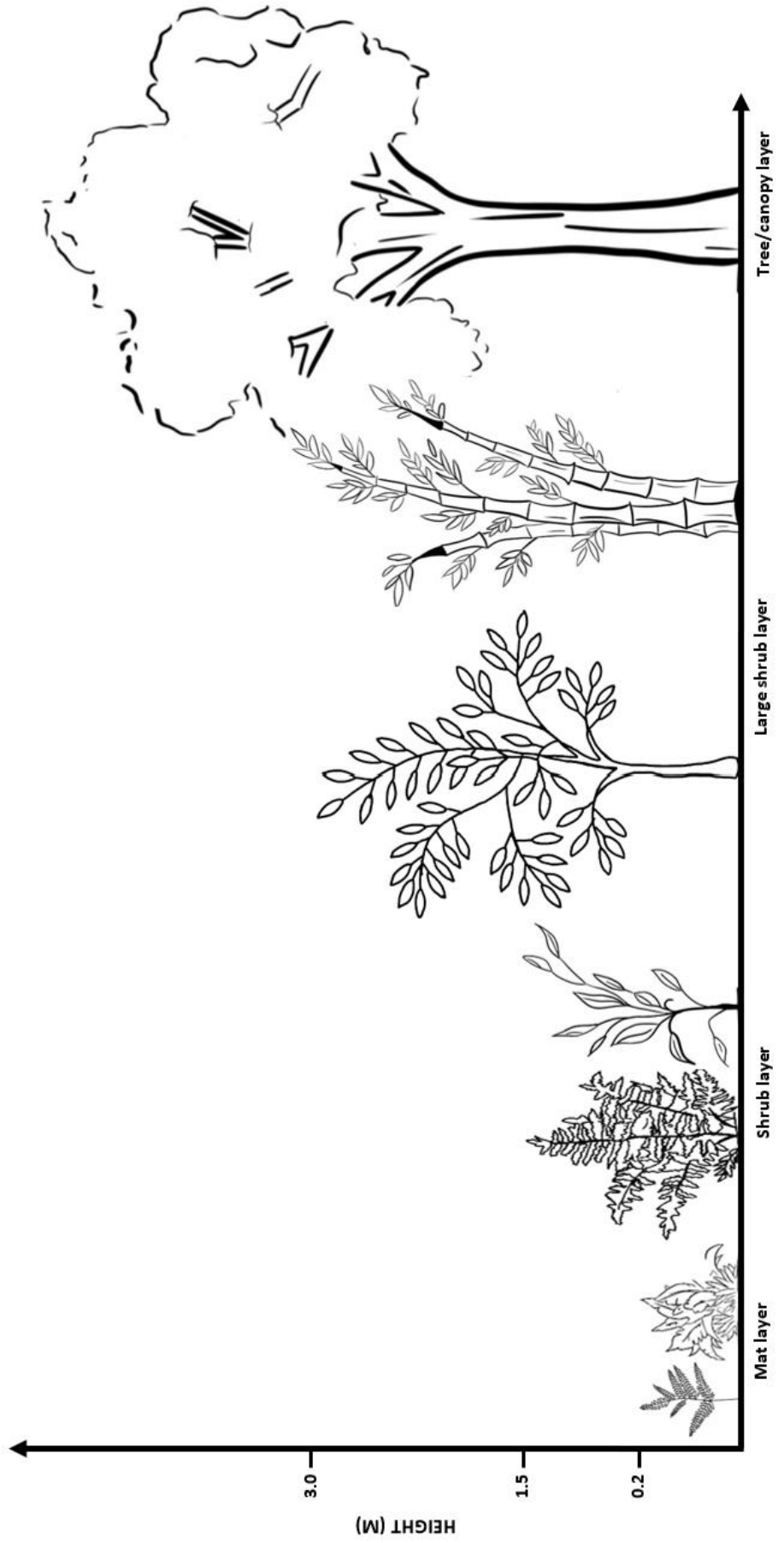
9. Do you think there will be monkeys/apes in the forest in another fifteen years?
    a. Why do you think that?

10. Do you know about conservation efforts for the [*insert species name*]?

a. Are there additional actions they should be taking?

1.2 Vegetation layer definitions and visual representation

Layer	Metrics	Composition
Mat layer	<20cm	Seedlings and grass
Shrub layer	20-150cm	Ferns, small seedlings and shrubs
Large shrubs layer	150-300cm	Large shrubs and bushes, saplings and bamboo
Canopy layer	>300cm DBH≥2cm	Trees
Lianas layer	Throughout plot	Vines and lianas



The Liana layer percentage of cover was determined by density throughout the plot.
Images courtesy of G.H. McGhee, 2023

1.3 General vegetation density scale

Score	Visual estimation of vegetation	Example
1	Vegetation within the plot is easy to navigate, with a low density of shrubs and few trees.	
2	Vegetation within the plot is navigable but with a greater density of larger shrubs and trees.	
3	Vegetation within the plot is more difficult to navigate due to the presence of more shrubs, particularly large shrub or saplings, and trees.	

4	Vegetation within the plot is hard to navigate due to high density of shrubs, large shrubs, trees and lianas.	
5	Vegetation within the plot is largely impenetrable due to high density of shrubs, large shrubs, trees and/or lianas.	

1.4 Topographic density scale

Score	Visual estimation of limestone complexity	Example
1	Plot contains only minor to no visible limestone karst.	
2	Plot contains discrete sections of limestone karst, which are easy to navigate.	
3	Plot contains limestone throughout and can be navigated easily.	

4	Plot contains limestone karst throughout, with clear layering of limestone karst segments and difficult to navigate.	
5	Plot is entirely composed of limestone karst segments, there are various levels of limestone segments which may be unstable and very difficult to navigate.	

Appendix 2 Cat Ba langur

2.1 ANOVA analysis and Estimated marginal means result tables for Cat Ba langur (CBL) habitat on Cat Ba Island

2.1.1 Summary data tables for Cua Dong, the Sanctuary and Viet Hai Corridor ANOVA analyses

Plot	Site	Plot type	Elev-ation (m)	General density	Topo-graphic complex-ity	Slope (deg)	Species richness	Species Diversity	Tree density	Species Density	Av Canopy height (m)	Mat cover (%)	Shrub cover (%)	Large Shrub cover (%)	Canopy cover (%)	Liana cover (%)	Av DBH (cm)	Total basal area (m^2)
CDC1	Cua Dong	Coast	8	4	3	27	36	3.17	0.09	1.11	3.00	10	10	70	30	5	4.90	7.66
CDC2	Cua Dong	Coast	9	3	3	20	34	2.88	0.17	0.93	3.80	2	40	40	50	5	4.20	10.09
CDC3	Cua Dong	Coast	11	4	2	26	42	3.48	0.22	1.54	3.00	40	50	30	40	40	4.86	10.31
CDC4	Cua Dong	Coast	3	4	1	1	38	2.94	0.16	1.76	4.90	2	20	5	85	80	6.59	16.15
CDV1	Cua Dong	Valley	34	3	2	16	19	2.06	0.48	2.36	4.30	5	40	60	25	5	4.53	20.67
CDV2	Cua Dong	Valley	28	3	5	32	35	2.97	0.07	1.71	2.86	10	80	2	50	5	5.31	4.73
CDV3	Cua Dong	Valley	23	2	1	5	41	3.01	0.24	1.42	5.20	2	20	40	85	2	6.49	19.59
CDV4	Cua Dong	Valley	36	2	1	12	51	3.13	0.15	2.65	4.60	10	30	60	40	5	8.93	17.66
CDS1	Cua Dong	Slope	57	1	4	15	33	2.55	0.06	1.29	3.00	5	5	20	5	5	4.03	2.05
CDS2	Cua Dong	Slope	43	3	3	25	36	2.16	0.44	3.65	4.00	20	40	40	80	20	4.46	22.16
CDS3	Cua Dong	Slope	17	2	4	30	28	2.71	0.03	1.40	3.00	5	10	30	10	40	5.33	7.89
CDS4	Cua Dong	Slope	34	3	3	15	18	2.08	0.04	1.18	3.00	2	10	2	2	95	4.25	0.87
SanC1	Sanctuary	Coast	0	3	3	36	41	2.89	0.36	2.34	3.70	5	5	25	95	5	4.1	10.91
SanC2	Sanctuary	Coast	1	4	2	36	49	2.61	0.47	4.80	3.50	15	45	10	85	40	3.44	9.57
SanC3	Sanctuary	Coast	12	3	5	46	42	2.61	0.09	3.44	3.4	30	10	5	80	30	5.99	12.46
SanC4	Sanctuary	Coast	30	4	5	44	44	3.01	0.15	3.48	4.30	20	30	10	90	20	5.88	25.00
SanV1	Sanctuary	Valley	2	2	2	2	40	2.40	0.42	5.24	5.20	10	10	5	95	10	4.94	18.12
SanV2	Sanctuary	Valley	48	3	2	7	67	2.72	0.22	8.30	5.20	70	60	50	70	2	10.49	80.89
SanV3	Sanctuary	Valley	26	2	2	10	71	3.15	0.19	9.09	5.50	70	60	10	70	5	4.40	5.62
SanV4	Sanctuary	Valley	14	2	2	5	44	2.04	0.16	10.44	4.20	80	75	5	10	5	4.42	3.67
SanS1	Sanctuary	Slope	38	2	4	40	18	2.12	0.02	1.26	0.00	2	10	60	2	5	5.00	2.02
SanS2	Sanctuary	Slope	39	3	2	20	75	3.42	0.24	5.15	5.80	70	50	10	85	40	7.53	43.53
SanS3	Sanctuary	Slope	19	3	4	41	24	2.00	0.03	2.21	3.80	15	10	15	35	85	5.95	6.43
SanS4	Sanctuary	Slope	50	2	4	43	26	2.59	0.03	2.70	2.10	10	25	5	0	5	4.18	139.34

Plot	Site	Plot type	Elev-ation (m)	General density	Topo-graphic complex-ity	Slope (deg)	Species richness	Species Diversity	Tree density	Species Density	Av Canopy height (m)	Mat cover (%)	Shrub cover (%)	Large Shrub cover (%)	Canopy cover (%)	Liana cover (%)	Av DBH (cm)	Total basal area (m^2)
VHC1	Viet Hai	Coast	1	2	2	14	44	2.64	0.12	3.65	3.50	10	5	5	50	40	5.60	10.13
VHC2	Viet Hai	Coast	14	4	3	40	56	3.55	0.23	2.14	3.70	10	5	5	95	50	5.30	12.93
VHC3	Viet Hai	Coast	1	4	3	30	54	3.06	0.22	2.78	4.50	5	10	15	85	50	4.20	12.77
VHC4	Viet Hai	Coast	17	4	4	27	45	3.08	0.04	2.35	5.50	40	30	40	20	30	6.35	3.69
VHV1	Viet Hai	Valley	8	2	1	2	45	2.68	0.07	3.69	8.60	20	10	60	90	10	7.70	7.71
VHV2	Viet Hai	Valley	10	2	1	4	45	1.61	0.15	8.68	5.00	65	20	5	65	15	9.40	36.23
VHV3	Viet Hai	Valley	12	3	2	8	28	1.92	0.17	4.12	5.60	20	10	20	80	5	8.20	20.15
VHV4	Viet Hai	Valley	37	3	1	6	57	1.93	0.12	6.92	6.40	20	95	5	60	5	9.90	29.27
VHS1	Viet Hai	Slope	51	3	2	42	48	2.99	0.26	2.17	4.20	5	10	10	80	30	5.20	13.19
VHS2	Viet Hai	Slope	43	4	3	36	34	2.79	0.23	2.23	4.60	5	20	10	90	60	5.30	12.18
VHS3	Viet Hai	Slope	44	2	4	33	31	2.55	0.07	2.64	3.30	20	5	25	5	10	4.30	4.86
VHS4	Viet Hai	Slope	33	4	4	39	46	3.02	0.22	3.50	4.40	15	10	30	80	10	4.80	27.37

2.1.2 ANOVA analysis results table for Cua Dong habitat

	Response	Degrees of Freedom	Sum of Squares	Mean Square	F-value	P-value
*Elevation (m)**	Plot	2	1950.00	975.00	8.93	0.007
	Residuals	9	982.25	109.14		
*Topographic complexity**	Plot	2	4.17	2.08	1.29	0.32
	Residuals	9	14.50	1.61		
Slope (degrees)	Plot	2	50.17	25.08	0.23	0.80
	Residuals	9	998.50	110.94		
*General density scale**	Plot	2	5.17	2.58	5.17	0.03
	Residuals	9	4.50	0.50		
Species richness	Plot	2	183.50	91.75	1.09	0.378
	Residuals	9	760.75	84.53		
Species diversity	Plot	2	1.11	0.55	4.04	0.06
	Residuals	9	1.24	0.137		
Species density (stem/m^2)	Plot	2	1.08	0.54	0.87	0.45
	Residuals	9	5.61	0.623		
Tree density (tree stem/m^2)	Plot	2	0.02	0.009	0.39	0.69
	Residuals	9	0.22	0.02		
Canopy height (m)	Plot	2	1.97	0.99	1.45	0.29
	Residuals	9	6.14	0.68		
Mat cover (%)	Plot	2	10.3.17	51.58	0.38	0.69
	Residuals	9	1223.75	135.97		
Shrub cover (%)	Plot	2	1379.2	689.58	1.62	0.25
	Residuals	9	3843.8	427.08		
Large shrub cover (%)	Plot	2	666.5	333.25	0.58	0.58
	Residuals	9	5199.8	577.75		
Canopy cover (%)	Plot	2	1858.2	929.08	1.07	0.38
	Residuals	9	7845.5	871.72		
Liana cover (%)	Plot	2	2843.2	1421.58	1.51	0.27
	Residuals	9	8481.7	942.42		
Av DBH (cm)	Plot	2	6.67	3.34	1.98	0.19
	Residuals	9	15.16	1.68		
Total basal area (m^2)	Plot	2	112.34	56.17	1.03	0.39
	Residuals	9	489.69	54.41		

* Indicates significant variables where p<0.05

2.1.3 Estimated marginal means results table for Cua Dong habitat

	Coast Plots		Slope Plots		Valley plots		SE	*P*<0.05
	Mean	Confidence levels	Mean	Confidence levels	Mean	Confidence levels		
*Elevation (m)**	7.75	-4.07,19.6	37.75	25.93,49.60	30.25	18.43,42.10	±5.22	Coast-Slope 0.007 Coast-Valley 0.034 Slope-Valley 0.586
Topographic Complexity	2.25	0.81,3.69	3.50	2.06,4.94	2.25	0.81,3.66	±0.635	Coast-Slope 0.384 Coast-Valley 1.000 Slope-Valley 0.384
Slope (degrees)	18.50	6.59,30.4	21.25	9.34,33.20	16.25	4.34,28.20	±5.27	Coast-Slope 0.928 Coast-Valley 0.951 Slope-Valley 0.785
*General density**	3.75	2.95,4.55	2.25	1.45,3.05	2.50	1.70,3.30	±0.354	Coast-Slope 0.036 Coast-Valley 0.079 Slope-Valley 0.873
Species richness	37.50	27.1,47.9	28.75	18.4,39.10	36.50	26.1,46.90	±4.60	Coast-Slope 0.407 Coast-Valley 0.987 Slope-Valley 0.487
*Species diversity**	3.12	2.70,3.54	2.37	1.96,2.79	2.79	2.37,3.21	±0.19	Coast-Slope 0.047 Coast-Valley 0.460 Slope-Valley 0.297
Species density (stem/m^2)	1.33	0.44,2.23	1.88	0.99,2.77	2.04	1.14,2.93	±0.39	Coast-Slope 0.609 Coast-Valley 0.454 Slope-Valley 0.959
Tree density (stem/m^2)	0.16	-0.02,0.34	0.14	-0.04,0.32	0.24	0.06,0.41	±0.08	Coast-Slope 0.986 Coast-Valley 0.783 Slope-Valley 0.693
Av Canopy height (m)	3.68	2.74,4.61	3.25	2.32,4.18	4.24	3.31,5.17	±0.41	Coast-Slope 0.754 Coast-Valley 0.614 Slope-Valley 0.259
Mat cover (%)	13.50	0.31,26.70	8.00	-5.19,21.20	6.75	-6.44,19.90	±8.25	Coast-Slope 0.788 Coast-Valley 0.702 Slope-Valley 0.987
Shrub cover (%)	30.0	6.63,53.40	16.25	-7.12,39.60	42.50	19.13,65.90	±10.30	Coast-Slope 0.630 Coast-Valley 0.680 Slope-Valley 0.230
Large Shrub cover (%)	36.25	9.06,63.40	23.00	-4.19,50.20	40.50	13.31,67.70	±12.00	Coast-Slope 0.724 Coast-Valley 0.966 Slope-Valley 0.578
Canopy cover (%)	51.25	17.85,84.60	24.25	-9.15,57.60	50.00	16.60,83.40	±14.80	Coast-Slope 0.433 Coast-Valley 0.998 Slope-Valley 0.465
Liana cover (%)	32.50	-2.22,67.20	40.00	5.28,74.70	4.25	-30.47,39.0	±15.30	Coast-Slope 0.937 Coast-Valley 0.429 Slope-Valley 0.277
Av DBH (cm)	5.14	3.67,6.60	4.52	3.05,5.99	6.32	4.85,7.78	±0.65	Coast-Slope 0.783 Coast-Valley 0.438 Slope-Valley 0.178
Total Basal Area (m^2)	11.05	2.71,19.40	8.24	-0.10,16.60	15.66	7.32,24.00	±3.69	Coast-Slope 0.854 Coast-Valley 0.663 Slope-Valley 0.370

*Indicates significant variables where p<0.05.

2.1.4 ANOVA analysis results table for the Sanctuary habitat

	Response	Degrees of Freedom	Sum of Squares	Mean Square	F-value	P-value
Elevation (m)	Plot	2	1329.50	664.75	2.67	0.12
	Residuals	9	2234.80	248.31		
Topographic complexity	Plot	2	7.17	3.58	3.31	0.08
	Residuals	9	9.75	1.08		
*Slope (degrees)**	Plot	2	2814	1407.00	27.35	0.0001
	Residuals	9	463	51.44		
*General density scale**	Plot	2	3.50	1.75	5.73	0.02
	Residuals	9	2.75	0.31		
Species richness	Plot	2	787.17	393.58	1.23	0.34
	Residuals	9	2871.75	319.08		
Species diversity	Plot	2	0.14	0.07	0.32	0.74
	Residuals	9	2.01	0.22		
Species density (stem/m^2)*	Plot	2	70.16	35.08	12.21	0.003
	Residuals	9	25.85	2.87		
Tree density (tree stem/m^2)	Plot	2	0.08	0.04	2.24	0.16
	Residuals	9	0.17	0.02		
Canopy height (m)	Plot	2	8.99	4.49	2.05	0.18
	Residuals	9	19.72	2.19		
Mat cover (%)	Plot	2	3668.20	1834.08	2.63	0.13
	Residuals	9	6276.80	697.42		
Shrub cover (%)	Plot	2	2112.50	1056.25	2.11	0.18
	Residuals	9	4512.50	501.39		
Large shrub cover (%)	Plot	2	200	100.00	0.25	0.78
	Residuals	9	3575	397.22		
Canopy cover (%)	Plot	2	6511.50	3255.80	3.34	0.08
	Residuals	9	8776.80	975.20		
Liana cover (%)	Plot	2	1641.50	820.75	1.47	0.28
	Residuals	9	5020.50	557.83		
Av DBH (cm)	Plot	2	6.67	3.34	1.98	0.19
	Residuals	9	15.16	1.68		
Total basal area (m^2)	Plot	2	112.34	56.17	1.032	0.39
	Residuals	9	489.69	54.41		

* Indicates significant variables where $p<0.05$

2.1.5 Estimated marginal means results table for the Sanctuary

	Valley Plots		Slope Plots		Coast Plots		SE	*P*<0.05
	Mean	Confidence levels	Mean	Confidence levels	Mean	Confidence levels		
Elevation (m)	22.5	4.68, 40.3	36.5	18.68, 54.3	10.8	-7.07, 28.6	±7.88	Coast-Slope 0.11 Coast-Valley 0.56 Slope-Valley 0.45
Topographic Complexity	2	0.82, 3.18	3.5	2.32, 4.68	3.75	2.57, 4.93	±0.52	Coast-Slope 0.94 Coast-Valley 0.10 Slope-Valley 0.16
*Slope (degrees)**	6	2.11, 14.1	36	27.89, 44.1	40.5	32.39, 48.6	±3.59	Coast-Slope 0.661 Coast-Valley .0002 Slope-Valley .0006
*General density**	2.25	1.62, 2.88	2.5	1.87, 3.13	3.5	2.87, 4.13	±0.28	Coast-Slope 0.072 Coast-Valley 0.027 Slope-Valley 0.803
Species richness	55.5	35.3, 75.7	35.8	15.5, 56.0	44	23.8, 64.2	±8.93	Coast-Slope 0.795 Coast-Valley 0.648 Slope-Valley 0.309
Species Diversity	2.58	2.04, 3.11	2.53	2.00, 3.07	2.78	2.25, 3.32	±0.24	Coast-Slope 0.745 Coast-Valley 0.816 Slope-Valley 0.991
*Species Density (stem/m2)**	8.27	6.35, 10.18	2.83	0.91, 4.75	3.52	1.60, 5.43	±0.85	Coast-Slope 0.838 Coast-Valley 0.008 Slope-Valley 0.003
Tree density tree (stem/m2)	0.25	0.09, 0.40	0.08	-0.08, 0.24	0.27	0.12, 0.42	±0.07	Coast-Slope 0.187 Coast-Valley 0.977 Slope-Valley 0.250
Av Canopy height (m)	5.03	3.35, 6.7	2.93	1.25, 4.6	3.73	2.05, 5.40	±0.74	Coast-Slope 0.733 Coast-Valley 0.460 Slope-Valley 0.166
Mat cover (%)	57.5	27.63, 87.4	24.3	-5.62, 54.1	17.5	-12.37, 47.4	±13.2	Coast-Slope 0.931 Coast-Valley 0.136 Slope-Valley 0.230
Shrub cover (%)	51.3	25.92, 76.6	23.8	-1.58, 49.1	22.5	-2.83, 47.8	±11.2	Coast-Slope 0.997 Coast-Valley 0.219 Slope-Valley 0.245
Large Shrub cover (%)	17.5	-5.04, 40	22.5	-0.04, 45	12.5	-10.04, 35	±9.97	Coast-Slope 0.764 Coast-Valley 0.934 Slope-Valley 0.934
Canopy cover (%)	61.3	25.93, 96.6	30.5	-4.82, 65.8	87.5	52.18, 122.8	±15.6	Coast-Slope 0.069 Coast-Valley 0.488 Slope-Valley 0.385
Liana cover (%)	5.5	-21.21, 32.2	33.8	7.04, 60.5	23.8	-2.96, 50.5	±11.8	Coast-Slope 0.824 Coast-Valley 0.542 Slope-Valley 0.260
Av DBH (cm)	6.32	4.85, 7.78	4.52	3.05, 5.99	5.14	3.67, 6.60	±0.65	Coast-Slope 0.783 Coast-Valley 0.438 Slope-Valley 0.178
Total Basal area (m2)	15.7	7.32, 24.0	8.24	-0.10, 16.6	11.1	2.71, 19.4	±3.69	Coast-Slope 0.854 Coast-Valley 0.663 Slope-Valley 0.370

*****Indicates significance where p<0.5

2.1.6 ANOVA analysis results table of comparison between Cua Dong and the Sanctuary

	Response	Degree of Freedom	Sum of Squares	Mean Square	F-value	P-value
*Elevation (m)**	Plot	1	24.0	24.00	0.13	0.72
	Residuals	18	3217.0	178.72		
Topographic complexity	Plot	1	1.04	1.04	0.77	0.39
	Residuals	18	24.25	1.35		
Slope (degrees)	Plot	1	468.17	468.17	5.77	0.027
	Residuals	18	1461.50	81.19		
General density scale	Plot	1	0.04	0.04	0.10	0.75
	Residuals	18	7.25	0.40		
Species richness	Plot	1	704.20	704.17	3.49	0.08
	Residuals	18	3632.50	201.81		
Species diversity	Plot	1	0.10	0.10	0.56	0.46
	Residuals	18	3.25	0.18		
Species density (stem/m^2)*	Plot	1	58.44	58.44	33.44	1.764e-05
	Residuals	18	31.46	1.75		
Tree density (tree stem/m^2)	Plot	1	0.002	0.002	0.10	0.75
	Residuals	18	0.39	0.02		
*Av Canopy height (m)**	Plot	1	0.17	0.17	0.12	0.73
	Residuals	18	25.86	1.44		
Mat cover (%)	Plot	1	3360.70	3360.70	8.07	0.01
	Residuals	18	7500.50	416.70		
Shrub cover (%)	Plot	1	51.00	51.04	0.11	0.74
	Residuals	18	8356.20	464.24		
Large shrub cover (%)	Plot	1	1488.40	1488.38	3.05	0.10
	Residuals	18	8774.70	487.49		
*Canopy cover (%)**	Plot	1	1926.00	1926.00	2.09	0.17
	Residuals	18	16622.20	923.50		
Liana cover (%)	Plot	1	126.00	126.04	0.17	0.69
	Residuals	18	13502.3	750.13		
Av DBH (cm)	Plot	1	0.25	0.25	0.08	0.77
	Residuals	18	52.59	2.92		
Total basal area (m^2)	Plot	1	1975.20	1975.24	2.11	0.16
	Residuals	18	1683.20	935.07		

* Indicates significant variables where $p<0.05$

2.1.7 Estimated marginal means results table for the comparison between Cua Dong and the Sanctuary

	Cua Dong		Sanctuary		SE	*P* <0.05
	Mean	Confidence levels	Mean	Confidence levels		
Elevation (m)	25.25	17.1, 33.4	23.25	15.1, 31.4	±3. 86	0.718
Topographic Complexity	2.67	1.96, 3.37	3.08	2.38, 3.79	±0.33	0.391
*Slope (degrees)**	18.67	13.20, 24.10	27.50	22.00, 33.0	±2.60	0.027
General density	2.83	2.45, 3.22	2.75	2.37, 3.13	±0.18	0.751
Species richness	34.25	25.60, 42.90	45.08	36.50, 53.70	±4.10	0.078
Species Diversity	2.76	2.50, 3.02	2.63	2.37, 2.89	±0.12	0.464
*Species Density (stem/m^2)**	1.75	0.95, 2.55	4.87	4.07, 5.67	±0.38	<.0001
Tree density tree (stem/m^2)	0.18	0.09, 0.27	0.20	0.11, 0.29	±0.05	0.732
Av Canopy height (m)	3.72	2.99, 4.45	3.89	3.16, 4.62	±0.35	0.732
*Mat cover (%)**	9.42	-2.96, 21.8	33.08	20.70, 45.5	±5.89	0.011
Shrub cover (%)	29.58	16.50, 42.70	32.50	9.40, 45.60	±6.22	0.744
Large Shrub cover (%)	33.25	19.86, 46.60	17.50	4.11, 30.90	±6.37	0.098
Canopy cover (%)	41.83	23.40, 60.30	59.75	41.30, 78.20	±8.77	0.754
Liana cover (%)	25.58	8.97, 42.20	21.00	4.39, 37.60	±7.91	0.686
Av DBH *(cm)*	5.32	4.29, 6.36	5.53	4.49, 6.56	±0.49	0.774
Total Basal area (m^2)	11.65	-6.89, 30.20	29.79	11.25, 48.30	±8.82	0.163

* Indicates significant variables where p<0.05

2.1.8 ANOVA analysis results table of Viet Hai corridor

	Response	Degrees of Freedom	Sum of Squares	Mean Square	F-value	P-value
*Elevation (m)**	Plot	2	2584.67	1292.33	12.45	0.003
	Residuals	9	934.25	103.81		
*Topographic complexity**	Plot	2	9.5	4.75	7.77	0.011
	Residuals	9	5.5	0.61		
*Slope (degrees)**	Plot	2	2225.17	1112.58	24.44	0.0002
	Residuals	9	409.75	45.53		
General density scale	Plot	2	2.17	1.08	1.44	0.29
	Residuals	9	6.75	0.75		
Species richness	Plot	2	202.67	101.33	1.21	0.344
	Residuals	9	756.25	84.03		
*Species diversity**	Plot	2	2.39	1.20	9.13	0.007
	Residuals	9	1.18	0.13		
Species density (stem/m^2)*	Plot	2	26.82	13.41	6.26	0.020
	Residuals	9	19.28	2.14		
Tree density (tree stem/m^2)	Plot	2	0.01	0.005	0.81	0.474
	Residuals	9	0.05	0.006		
Canopy height (m)*	Plot	2	12.82	6.41	5.29	0.030
	Residuals	9	10.91	1.21		
Mat cover (%)	Plot	2	866.67	433.33	1.59	0.26
	Residuals	9	2456.25	272.92		
Shrub cover (%)	Plot	2	1279.20	639.58	1.026	0.40
	Residuals	9	5612.50	623.61		
Large shrub cover (%)	Plot	2	79.20	39.58	0.11	0.89
	Residuals	9	3162.50	351.39		
Canopy cover (%)	Plot	2	304.20	152.08	0.16	0.86
	Residuals	9	8762.50	973.61		
Liana cover (%)*	Plot	2	2287.50	1143.75	5.10	0.033
	Residuals	9	2018.80	224.31		
Av DBH (cm)*	Plot	2	36.32	18.16	26.59	0.0002
	Residuals	9	6.15	0.68		
Total basal area (m^2)	Plot	2	3758270	1879135	2.18	0.170
	Residuals	9	7773412	863712		

* Indicates significant variables where $p<0.05$

2.1.9 Estimated marginal means results table for the Viet Hai Corridor

	Coast Plots		Slope Plots		Valley Plots		SE	*P*<0.05
	Mean	Confidence levels	Mean	Confidence levels	Mean	Confidence levels		
*Elevation (m)**	8.25	-3.27, 19.8	42.75	31.23, 54.3	16.75	5.23, 28.3	±5.09	Coast-slope 0.003 Coast-Valley 0.493 Slope-Valley 0.014
*Topographic Complexity**	3.00	2.11, 3.88	3.25	2.37, 4.13	1.25	0.37, 2.13	±0.39	Coast-Slope 0.895 Coast-Valley 0.028 Slope-Valley 0.014
*Slope (degrees)**	27.75	20.12, 35.40	37.50	29.87, 45.10	5.00	-2.63, 12.60	±3.37	Coast-Slope 0.157 Coast-Valley 0.003 Slope-Valley 0.0002
General density	3.50	2.52, 4.48	3.25	2.27, 4.23	2.50	1.52, 3.48	±0.43	Coast-Slope 0.913 Coast-Valley 0.282 Slope-Valley 0.469
Species richness	49.75	39.40, 60.10	39.75	29.40, 50.10	43.75	33.40, 54.10	±4.58	Coast-Slope 0.318 Coast-Valley 0.639 Slope-Valley 0.815
*Species Diversity**	3.08	2.67, 3.49	2.84	2.43, 3.25	2.04	1.63, 2.45	±0.18	Coast-Slope 0.623 Coast-Valley 0.007 Slope-Valley 0.030
Species Density (stem/m^2)*	2.73	0.09, 0.99	2.64	-3.02, 0.0	5.85	-3.11, 0.03	±0.73	Coast-Slope 0.995 Coast-Valley 0.035 Slope-Valley 0.031
Tree density (stems/m^2)	0.15	0.07, 0.24	0.20	0.11, 0.28	0.13	0.04, 0.21	±0.04	Coast-Slope 0.716 Coast-Valley 0.888 Slope-Valley 0.451
*Av Canopy height (m)**	4.30	3.05, 5.55	4.13	2.88, 5.37	6.40	5.15, 7.65	±0. 55	Coast-Slope 0.973 Coast-Valley 0.058 Slope-Valley 0.041
Mat cover (%)	16.25	-2.44, 34.90	11.25	-7.44, 29.90	31.25	12.56, 49.90	±8.26	Coast-Slope 0.905 Coast-Valley 0.438 Slope-Valley 0.253
Shrub cover (%)	12.50	-15.70, 40.70	11.25	-17.00, 39.50	33.75	5.50, 62.00	±12.49	Coast-Slope 0.997 Coast-Valley .481 Slope-Valley 0.443
Large Shrub cover (%)	16.25	-4.95, 37.50	18.75	-2.45, 40.00	22.50	1.30, 43.70	±9.37	Coast-Slope 0.981 Coast-Valley 0.886 Slope-Valley 0.957
Canopy coverage (%)	62.50	27.20, 97.80	63.75	28.50, 99.00	73.75	38.5, 109.00	±15.60	Coast-Slope 0.998 Coast-Valley 0.869 Slope-Valley 0.894
*Liana cover (%)**	42.50	25.56, 59.40	27.50	10.56, 44.40	8.75	-8.19, 25.70	±10.59	Coast-Slope 0.373 Coast-Valley 0.027 Slope-Valley 0.233
*Av DBH (cm)**	5.363	4.43, 6.30	4.900	3.97, 5.83	8.80	7.87, 9.73	±0.41	Coast-Slope 0.717 Coast-Valley 0.0006 Slope-Valley 0.0002
Total Basal Area (m^2)	9.88	-0.64, 20.40	14.40	3.89, 24.90	23.34	12.83, 33.90	±4.65	Coast-Slope 0.776 Coast-Valley 0.156 Slope-Valley 0.400

* Indicates significant variables where p<0.05

2.1.10 ANOVA analysis results table of comparison between Cua Dong and the Sanctuary and Viet Hai corridor

	Response	Degrees of Freedom	Sum of Squares	Mean Square	F-value	P-value
Elevation (m)	Plot	2	46.20	23.11	0.15	0.861
	Residuals	27	4151.30	153.75		
Topographic	Plot	2	0.72	0.36	0.70	0.507
complexity	Residuals	27	14.00	0.52		
*Slope (degrees)**	Plot	2	469.10	234.53	3.39	0.049
	Residuals	27	1871.30	69.31		
General density scale	Plot	2	0.72	0.36	0.70	0.507
	Residuals	27	14.00	0.52		
Species richness	Plot	2	884.70	442.33	2.72	0.084
	Residuals	27	4388.80	162.55		
*Species diversity**	Plot	2	0.11	0.06	0.35	0.705
	Residuals	27	4.43	0.16		
*Species density**	Plot	2	59.91	29.95	15.94	2.685e-05
(stem/m^2)	Residuals	27	50.74	1.88		
Tree density	Plot	2	0.010	0.005	0.29	0.749
(tree stem/m^2)	Residuals	27	0.44	0.02		
Canopy height (m)*	Plot	2	10.48	5.24	3.85	0.034
	Residuals	27	36.77	1.36		
Mat cover (%)	Plot	2	3382.90	1691.44	4.59	0.019
	Residuals	27	9956.80	368.77		
Shrub cover (%)	Plot	2	1179.20	589.58	1.14	0.335
	Residuals	27	13968.70	517.36		
Large shrub cover (%)	Plot	2	1796.70	898.36	2.03	0.151
	Residuals	27	11937.20	442.12		
Canopy cover (%)	Plot	2	3942.20	1971.08	2.10	0.142
	Residuals	27	25384.80	940.18		
Liana cover (%)*	Plot	2	196.10	98.03	0.17	0.844
	Residuals	27	15521.00	574.85		
Av DBH (cm)*	Plot	2	7.16	3.58	1.65	0.212
	Residuals	27	58.73	2.18		
Total basal area (m^2)	Plot	2	2163.50	1081.77	1.66	0.209
	Residuals	27	17608.60	652.17		

* Indicates significant variables where $p<0.05$

2.1.11 Estimated marginal means results table for the comparison between the Viet Hai Corridor, Cua Dong and the Sanctuary

	VHC		Cua Dong (CD)		Sanctuary (S)		SE	P<0.05
	Mean	Confidence levels	Mean	Confidence levels	Mean	Confidence levels		
Elevation (m)	22.58	15.20, 29.90	25.25	17.90, 32.60	23.25	15.90, 30.60	±3.58	CD-S 0.918 CD-VHC 0.859 S-VHC 0.991
Topographic Complexity	2.50	1.88, 3.12	2.67	2.04, 3.29	3.083	2.46, 3.71	±0.30	CD-S 0.600 CD-VHC 0.920 S-VHC 0.375
*Slope (degrees)**	23.42	18.5, 28.3	18.67	13.70, 23.60	27.50	22.60, 32.40	±2.40	CD-S 0.039 CD-VHC 0.356 S-VHC 0.463
General density	3.08	2.66, 3.51	2.83	2.41, 3.26	2.75	2.32, 3.18	±0.21	CD-S 0.957 CD-VHC 0.676 S-VHC 0.502
Species richness	44.42	36.90, 52.00	34.25	26.70, 41.80	45.08	37.50, 52.60	±3.68	CD-S 0.113 CD-VHC 0.143 S-VHC 0.991
Species Diversity	2.65	2.41, 2.89	2.76	2.52, 3.00	2.63	2.39, 2.87	±0.12	CD-S 0.715 CD-VHC 0.792 S-VHC 0.991
Species Density (stems/m^2)*	3.74	2.93, 4.55	1.75	0.94, 2.56	4.87	4.06, 5.68	±0.40	CD-S <.0001 CD-VHC 0.004 S-VHC 0.126
Tree density (stems/m^2)	0.16	0.08, 0.23	0.18	0.10, 0.26	0.19	0.12, 0.27	±0.04	CD-S 0.917 CD-VHC 0.929 S-VHC 0.728
*Av Canopy height (m)**	4.94	4.25, 5.63	3.72	3.03, 4.41	3.89	3.20, 4.58	±0.34	CD-S 0.932 CD-VHC 0.042 S-VHC 0.089
*Mat cover (%)**	19.58	8.21, 31.00	9.42	-1.96, 20.80	33.08	21.71, 44.50	±5.54	CD-S 0.015 CD-VHC 0.042 S-VHC 0.216
Shrub cover (%)	19.17	5.69, 32.60	29.58	16.11, 43.10	32.5	19.03, 46.00	±6.57	CD-S 0.947 CD-VHC 0.509 S-VHC 0.337
Lg Shrub cover (%)	19.17	6.71, 31.60	33.25	20.80, 45.70	17.5	5.05, 30.00	±6.07	CD-S 0.178 CD-VHC 0.246 S-VHC 0.979
Canopy coverage (%)	66.67	48.5, 84.80	41.83	23.70, 60.00	59.75	41.60, 77.90	±8.85	CD-S 940.18 CD-VHC 0.136 S-VHC 0.846
Liana cover (%)	26.25	12.0, 40.50	25.6	11.40, 39.80	21.0	6.80, 35.20	±6.92	CD-S 0.887 CD-VHC 0.997 S-VHC 0.854
Av DBH (cm)	6.35	5.48, 7.23	5.32	4.45, 6.20	5.53	4.65, 6.40	±0.43	CD-S 0.939 CD-VHC 0.2190 S-VHC 0.368
Total Basal Area (m^2)	15.87	0.75, 31.00	11.65	-3.47, 26.80	29.79	14.67, 44.90	±7.37	CD-S 0.209 CD-VHC 0.914 S-VHC 0.388

2.2 Plant species captured in Cat Ba langur analysis

2.2.1 All species captured in both Cua Dong and the Sanctuary

Family	Species	Cua Dong				The Sanctuary			
		Coast (n)	Slope (n)	Valley (n)	**Total**	Coast (n)	Slope (n)	Valley (n)	**Total**
Amaranthaceae	*Achyranthes aspera*	0	0	0	**0**	0	91	1	**92**
Amaranthaceae	*Achyranthes bidentata*	0	0	0	**0**	0	0	20	**20**
Phyllanthaceae	*Actephila sp.*	0	0	1	**1**	0	0	0	**0**
Pteridaceae	*Adiantum caudatum*	7	16	1	**24**	42	44	133	**219**
Asteraceae	*Ageratum conyzoides*	0	0	1	**1**	1	0	0	**1**
Asteraceae	*Ageratum houstonianum*	2	0	0	**2**	0	0	0	**0**
Meliaceae	*Aglaia elaeagnoidea*	5	0	8	**13**	0	1	4	**5**
Moraceae	*Alchornea scandens*	5	6	55	**66**	5	12	4	**21**
Moraceae	*Alchornea tiliifolia*	0	0	81	**81**	0	0	0	**0**
Athyriaceae	*Allantodia hirtipes*	0	0	0	**0**	0	0	5	**5**
Athyriaceae	*Allantodia megaphylla*	0	0	13	**13**	0	0	86	**86**
Sapindaceae	*Allophylus livescens*	0	0	0	**0**	0	1	4	**5**
Araceae	*Alocasia hainanica*	0	0	15	**15**	0	0	0	**0**
Araceae	*Alocasia lecomtei*	0	3	4	**7**	3	1	2	**6**
Araceae	*Alocasia macrorrhizos*	0	0	0	**0**	4	0	2	**6**
Zingiberaceae	*Alpinia calcicola*	1	4	6	**11**	12	2	0	**14**
Zingiberaceae	*Alpinia chinensis*	2	0	7	**9**	2	13	43	**58**
Apocynaceae	*Alyxia reinwardtii*	0	0	0	**0**	13	6	1	**20**
Commelinaceae	*Amischotolype hispida*	0	0	0	**0**	1	0	9	**10**
Araceae	*Amorphophallus interruptus*	11	14	4	**29**	18	1	7	**26**
Araceae	*Amorphophallus paeoniifolius*	0	0	0	**0**	3	1	0	**4**
Vitaceae	*Ampelopsis annamensis*	3	2	0	**5**	1	0	0	**1**
Vitaceae	*Ampelopsis glandulosa*	0	0	1	**1**	0	0	0	**0**

Phyllanthaceae	*Antidesma eberhardtii*	0	0	0	**0**	1	3	25	**29**
Meliaceae	*Aphanamixis polystachya*	0	0	3	**3**	0	0	3	**3**
Mimosoideae	*Archidendron clypearia*	0	1	0	**1**	0	0	0	**0**
Primulaceae	*Ardisia gigantifolia*	0	0	0	**0**	0	0	1	**1**
Primulaceae	*Ardisia lecomtei*	0	0	0	**0**	0	0	19	**19**
Primulaceae	*Ardisia pseudocrispa*	0	0	2	**2**	5	0	1	**6**
Convolvulaceae	*Argyreia acuta*	0	0	0	**0**	1	0	4	**5**
Araceae	*Arisaema balansae*	0	0	2	**2**	0	0	0	**0**
Aristolochiaceae	*Aristolochia indica*	0	8	0	**8**	0	16	0	**16**
Tectariaceae	*Arthropteris palisotii*	0	0	0	**0**	9	0	0	**9**
Poaceae	*Arundinella bengalensis*	1	0	0	**1**	0	0	0	**0**
Liliaceae	*Asparagus cochinchinensis*	2	6	0	**8**	0	0	0	**0**
Aspleniaceae	*Asplenium nidus*	0	0	0	**0**	23	0	0	**23**
Aspleniaceae	*Asplenium sampsoni*	0	0	0	**0**	6	4	0	**10**
Aspleniaceae	*Asplenium saxicola*	0	4	2	**6**	1	22	0	**23**
Rutaceae	*Atalantia stenocarpa*	0	0	0	**0**	0	62	23	**85**
Auriculariaceae	*Auricularia polytricha*	1	0	0	**1**	0	0	1	**1**
Phyllanthaceae	*Baccaurea ramiflora*	0	0	32	**32**	0	0	0	**0**
Fabaceae	*Bauhinia cardinalis*	0	3	5	**8**	3	0	1	**4**
Fabaceae	*Bauhinia ornata*	0	0	1	**1**	1	24	46	**71**
Fabaceae	*Bauhinia oxysepala*	1	0	0	**1**	0	3	1	**4**
Begoniaceae	*Begonia boisiana*	0	0	0	**0**	36	0	0	**36**
Annonaceae	*Beilschmiedia tsangii*	0	0	0	**0**	0	0	36	**36**
Rubiaceae	*Benkara depauperata*	0	2	1	**3**	1	0	0	**1**
Rhamnaceae	*Berchemia loureiriana*	1	0	0	**1**	1	0	0	**1**
Asteraceae	*Bidens pilosa*	0	8	7	**15**	0	0	0	**0**
Moraceae	*Bleekrodea tonkinensis*	0	0	44	**44**	0	0	0	**0**

Asteraceae	*Blumea megacephala*	3	0	2	**5**	0	1	0	**1**
Asteraceae	*Blumea membranacea*	0	1	0	**1**	0	3	0	**3**
Urticaceae	*Boehmeria nivea*	0	0	0	**0**	0	1	0	**1**
Phyllanthaceae	*Breynia fruticosa*	7	0	7	**14**	21	0	0	**21**
Phyllanthaceae	*Bridelia balansae*	9	2	6	**17**	7	0	0	**7**
Simaroubaceae	*Brucea javanica*	3	1	6	**10**	0	0	3	**3**
Crassulaceae	*Bryophyllum pinnatum*	0	0	0	**0**	1	0	0	**1**
Arecaceae	*Calamus tenuis*	0	0	0	**0**	0	4	3	**7**
Acanthaceae	*Campylotropis bonii*	0	0	0	**0**	0	0	5	**5**
Leguminosae	*Canavalia lineata*	0	0	0	**0**	3	3	7	**13**
Capparaceae	*Capparis annamensis*	2	1	4	**7**	3	0	0	**3**
Capparaceae	*Capparis cantoniensis*	0	0	1	**1**	0	0	0	**0**
Capparaceae	*Capparis pubifolia*	1	0	0	**1**	0	0	0	**0**
Capparaceae	*Capparis pyrifolia*	0	0	0	**0**	0	0	13	**13**
Rhizophoraceae	*Carallia brachiata*	0	0	0	**0**	0	0	1	**1**
Cyperaceae	*Carex cruciata*	0	0	0	**0**	0	30	107	**137**
Arecaceae	*Caryota maxima*	0	0	0	**0**	0	1	0	**1**
Fagaceae	*Castanopsis indica*	1	0	0	**1**	0	0	1	**1**
Vitaceae	*Cayratia tenuifolia*	0	0	2	**2**	1	0	2	**3**
Celastraceae	*Celastrus hindsii*	0	0	0	**0**	0	0	10	**10**
Ulmaceae	*Celtis philippensis*	0	1	26	**27**	0	0	0	**0**
Apocynaceae	*Cerbera odollam*	6	0	0	**6**	0	0	0	**0**
Poaceae	*Chimonocalamus griffithianus*	40	67	1	**108**	52	36	0	**88**
Anacardiaceae	*Choreospondias axilaris*	1	0	0	**1**	0	0	0	**0**
Compositae	*Chromolaena odorata*	0	0	0	**0**	2	0	0	**2**
Menispermaceae	*Cissampelos pareira*	0	0	5	**5**	0	0	0	**0**
Vitaceae	*Cissus adnata*	0	0	0	**0**	1	0	0	**1**

Vitaceae	*Cissus annamicus*	3	3	2	**8**	1	4	0	**5**
Vitaceae	*Cissus subtetragona*	0	1	1	**2**	1	0	0	**1**
Euphorbiaceae	*Claoxylon hainanense*	0	0	0	**0**	0	0	490	**490**
Rutaceae	*Clausena anisata*	10	1	1	**12**	0	0	0	**0**
Rutaceae	*Clausena excavata*	0	0	0	**0**	0	2	0	**2**
Rutaceae	*Clausena indica*	47	1	4	**52**	0	1	1	**2**
Phyllanthaceae	*Cleistanthus tonkinensis*	1	34	17	**52**	73	0	3	**76**
Ranunculaceae	*Clematis loureiroana*	0	0	0	**0**	2	0	7	**9**
Euphorbiaceae	*Cnesmone javanica*	1	0	1	**2**	3	1	7	**11**
Menispermaceae	*Cocculus laurifolius*	0	0	0	**0**	0	1	0	**1**
Combretaceae	*Combretum indicum*	0	0	1	**1**	0	0	0	**0**
Combretaceae	*Combretum sundaicum*	0	0	4	**4**	0	0	4	**4**
Commelinaceae	*Commelina communis*	0	1	0	**1**	3	0	0	**3**
Commelinaceae	*Commelina paludosa*	0	0	0	**0**	6	0	0	**6**
Cantharellaceae	*Craterellus sp.*	0	0	1	**1**	0	0	0	**0**
Hypericaceae	*Cratoxylum formosum*	0	1	1	**2**	0	0	0	**0**
Hymenophyllaceae	*Crepidomanes kurzii*	0	0	0	**0**	36	0	0	**36**
Euphorbiaceae	*Croton argyratus*	0	3	0	**3**	0	0	3	**3**
Euphorbiaceae	*Croton lachnocarpus*	0	1	0	**1**	1	0	0	**1**
Euphorbiaceae	*Croton tiglium*	1	1	0	**2**	0	0	0	**0**
Moraceae	*Cudrania tricuspidata*	0	0	0	**0**	0	1	1	**2**
Cycadaceae	*Cycas tropophylla*	0	1	0	**1**	0	7	0	**7**
Menispermaceae	*Cyclea tonkinensis*	2	0	2	**4**	0	0	1	**1**
Orchidaceae	*Cymbidium aloifolium*	0	0	0	**0**	2	3	0	**5**
Fabaceae	*Dalbergia assamica*	7	0	0	**7**	0	0	0	**0**
Fabaceae	*Dalbergia pierreana*	6	0	0	**6**	0	0	0	**0**
Fabaceae	*Dalbergia rimosa*	0	0	0	**0**	2	4	1	**7**
Athyriaceae	*Deparia formosana*	0	0	0	**0**	0	1	27	**28**

Fabaceae	*Derris tonkinensis*	0	2	0	**2**	0	0	12	**12**
Fabaceae	*Derris trifoliata*	13	17	6	**36**	15	27	1	**43**
Annonaceae	*Desmos chinensis*	0	6	4	**10**	0	3	8	**11**
Euphorbiaceae	*Deutzianthus tonkinensis*	0	0	0	**0**	0	4	0	**4**
Sapindaceae	*Dimocarpus longan*	0	0	1	**1**	0	0	12	**12**
Dioscoreaceae	*Dioscorea collettii*	0	0	0	**0**	0	7	0	**7**
Dioscoreaceae	*Dioscorea deltoidea*	0	0	0	**0**	0	0	7	**7**
Dioscoreaceae	*Dioscorea poilanei*	0	0	0	**0**	1	2	2	**5**
Ebenaceae	*Diospyros apiculata*	0	0	0	**0**	1	0	1	**2**
Ebenaceae	*Diospyros mollis*	0	18	0	**18**	2	18	32	**52**
Apocynaceae	*Dischidia acuminata*	0	0	0	**0**	4	0	0	**4**
Asparagaceae	*Dracaena cambodiana*	15	10	6	**31**	20	38	1	**59**
Polypodiaceae	*Drynaria bonii*	12	1	9	**22**	216	0	0	**216**
Boraginaceae	*Ehretia longiflora*	0	0	0	**0**	0	1	0	**1**
Urticaceae	*Elatostema monandrum*	0	0	1	**1**	0	0	0	**0**
Primulaceae	*Embelia laeta*	0	0	0	**0**	0	3	0	**3**
Rosaceae	*Eriobotrya cavaleriei*	2	0	0	**2**	0	0	0	**0**
Celastraceae	*Euonymus tonkinensis*	0	0	0	**0**	0	4	8	**12**
Euphorbiaceae	*Euphorbia antiquorum*	6	0	1	**7**	0	0	0	**0**
Moraceae	*Ficus alongensis*	2	2	0	**4**	0	1	0	**1**
Moraceae	*Ficus benjamina*	1	1	0	**2**	3	0	0	**3**
Moraceae	*Ficus hispida*	0	0	0	**0**	0	0	11	**11**
Moraceae	*Ficus lacor*	0	0	0	**0**	0	1	0	**1**
Moraceae	*Ficus pumila*	0	0	0	**0**	0	18	0	**18**
Moraceae	*Ficus superba*	0	0	0	**0**	1	0	0	**1**
Moraceae	*Ficus capensis*	0	0	1	**1**	0	0	3	**3**
Moraceae	*Ficus virens*	0	3	0	**3**	0	0	0	**0**
Malvaceae	*Firmiana simplex*	9	1	0	**10**	0	0	0	**0**
Salicaceae	*Flacourtia rukam*	0	0	0	**0**	7	0	0	**7**
Fabaceae	*Galactia longipes*	0	0	2	**2**	0	0	0	**0**

Clusiaceae	*Garcinia oligantha*	0	0	3	**3**	0	0	0	**0**
Euphorbiaceae	*Geophila repens*	0	0	0	**0**	0	0	39	**39**
Ulmaceae	*Gironniera subaequalis*	1	0	0	**1**	0	0	0	**0**
Phyllanthaceae	*Glochidion zeylanicum*	0	0	7	**7**	0	17	0	**17**
Phyllanthaceae	*Glochidion zeylanicum*	0	0	0	**0**	0	0	3	**3**
Rutaceae	*Glycosmis lucida*	0	0	0	**0**	3	0	5	**8**
Rutaceae	*Glycosmis ovoidea*	0	0	0	**0**	0	3	3	**6**
Gnetaceae	*Gnetum montanum*	0	0	0	**0**	0	0	1	**1**
Cucurbitaceae	*Gynostemma laxum*	0	0	0	**0**	0	5	2	**7**
Cucurbitaceae	*Gynostemma pentaphyllum*	3	2	1	**6**	5	0	1	**6**
Apocynaceae	*Habenaria malintana*	0	0	0	**0**	1	0	0	**1**
Flacourtiaceae	*Hemidesmus indicus*	1	0	0	**1**	3	1	0	**4**
Smilacaceae	*Hemiscolopia trimera*	1	0	0	**1**	0	0	0	**0**
Smilacaceae	*Heterosmilax gaudichaudiana*	0	0	0	**0**	0	2	0	**2**
Flacourtiaceae	*Hibiscus tilliaceus*	2	0	0	**2**	0	0	0	**0**
Dipterocarpaceae	*Homalium cochinchinensis*	2	1	0	**3**	0	0	0	**0**
Apocynaceae	*Hopea chinensis*	0	0	0	**0**	3	0	2	**5**
Apocynaceae	*Hoya balansae*	0	0	1	**1**	3	0	0	**3**
Apocynaceae	*Hoya bonii*	0	0	0	**0**	1	0	0	**1**
Apocynaceae	*Hoya fungii*	3	0	0	**3**	0	0	0	**0**
Styracaceae	*Huodendron parvifolium*	0	0	0	**0**	0	0	1	**1**
Poaceae	*Ichnanthus pallens*	13	0	5	**18**	0	4	13	**17**
Apocynaceae	*Ichnocarpus frutescens*	0	0	0	**0**	0	1	4	**5**
Aquifoliaceae	*Ilex kaushue*	0	0	0	**0**	0	0	3	**3**
Balsaminaceae	*Impatiens halongensis*	4	4	9	**17**	137	1	25	**163**
Balsaminaceae	*Impatiens verrucifer*	0	0	0	**0**	11	91	0	**102**
Poaceae	*Imperata conferta*	0	0	3	**3**	0	0	0	**0**
Icacinaceae	*Iodes cirrhosa*	0	0	0	**0**	2	0	1	**3**

Convolvulaceae	*Ipomoea mauritiana*	3	0	2	**5**	0	0	2	**2**
Rubiaceae	*Ixora chinensis*	0	0	0	**0**	0	0	1	**1**
Rubiaceae	*Ixora henryi*	1	0	0	**1**	10	3	3	**16**
Oleaceae	*Jasminum alongense*	1	0	0	**1**	0	0	0	**0**
Oleaceae	*Jasminum coffeinum*	0	0	0	**0**	3	0	0	**3**
Oleaceae	*Jasminum elongatum*	9	0	0	**9**	7	12	0	**19**
Oleaceae	*Jasminum nervosum*	0	1	0	**1**	0	0	0	**0**
Lythraceae	*Lagerstroemia crispa*	0	0	1	**1**	0	0	0	**0**
Urticaceae	*Laportea interrupta*	0	0	5	**5**	0	0	0	**0**
Rubiaceae	*Lasianthus chinensis*	0	0	5	**5**	0	0	0	**0**
Opiliaceae	*Lepionurus sylvestris*	9	0	0	**9**	0	0	0	**0**
Sapindaceae	*Lepisanthes senegalensis*	0	0	1	**1**	0	0	0	**0**
Acanthaceae	*Leptostachya wallichii*	0	0	1	**1**	0	3	712	**715**
Fagaceae	*Lithocarpus corneus*	0	0	0	**0**	1	0	0	**1**
Lauraceae	*Litsea glutinosa*	7	1	8	**16**	2	0	0	**2**
Orchidaceae	*Ludisia discolor*	0	0	2	**2**	0	0	0	**0**
Lygodiaceae	*Lygodium conforme*	0	0	0	**0**	0	3	3	**6**
Lygodiaceae	*Lygodium japonicum*	0	0	4	**4**	0	8	23	**31**
Lauraceae	*Machilus bonii*	0	0	0	**0**	0	12	74	**86**
Lauraceae	*Machilus thunbergii*	0	1	0	**1**	9	3	1	**13**
Moraceae	*Maclura cochinchinensis*	0	1	0	**1**	0	0	0	**0**
Primulaceae	*Maesa balansae*	1	0	10	**11**	1	1	1	**3**
Primulaceae	*Maesa balansae*	0	1	0	**1**	1	4	4	**9**
Magnoliaceae	*Magnolia coco*	0	0	0	**0**	0	1	21	**22**
Euphorbiaceae	*Mallotus apelta*	0	0	0	**0**	0	0	1	**1**
Euphorbiaceae	*Mallotus paniculatus*	0	0	0	**0**	0	0	8	**8**
Euphorbiaceae	*Mallotus repandus*	0	0	0	**0**	2	0	0	**2**
Apocynaceae	*Marsdenia tonkinensis*	0	0	0	**0**	2	0	0	**2**

Sapindaceae	*Melicoccus bijugatus*	0	0	0	**0**	0	3	1	**4**
Apocynaceae	*Melodinus cochinchinensis*	3	1	3	**7**	0	0	0	**0**
Melastomataceae	*Memecylon edule*	16	1	1	**18**	5	0	0	**5**
Gesneriaceae	*Microchirita hamosa*	0	0	0	**0**	4	0	16	**20**
Malvaceae	*Microcos tomentosa*	4	1	2	**7**	1	3	1	**5**
Celastraceae	*Microtropis osmanthoides*	0	1	26	**27**	32	0	29	**61**
Annonaceae	*Miliusa balansae*	0	0	0	**0**	0	2	7	**9**
Annonaceae	*Miliusa sinensis*	23	0	7	**30**	0	6	25	**31**
Fabaceae	*Mucuna hainanensis*	2	6	2	**10**	1	0	1	**2**
Fabaceae	*Musa acuminata*	0	0	5	**5**	0	0	0	**0**
Rubiaceae	*Mussaenda densiflora*	1	0	0	**1**	0	0	0	**0**
Rubiaceae	*Mussaenda glabra*	1	0	1	**2**	0	1	0	**1**
Mycenaceae	*Mycena sp.*	0	0	2	**2**	0	0	0	**0**
Rubiaceae	*Oldenlandia biflora*	2	3	1	**6**	3	24	0	**27**
Pteridaceae	*Onychium siliculosum*	0	5	0	**5**	0	4	0	**4**
Asparagaceae	*Ophiopogon dracaenoides*	0	0	0	**0**	0	0	10	**10**
Asparagaceae	*Ophiopogon latifolius*	15	11	19	**45**	36	3	249	**288**
Fabaceae	*Ormosia tsangii*	0	0	0	**0**	0	0	18	**18**
Rubiaceae	*Paederia foetida*	0	0	3	**3**	6	0	2	**8**
Pandanaceae	*Pandanus odorifer*	1	0	0	**1**	0	0	0	**0**
Gesneriaceae	*Paraboea halongensis*	11	12	1	**24**	0	2	0	**2**
Arecaceae	*Phoenix paludosa*	0	0	6	**6**	0	0	0	**0**
Phyllanthaceae	*Phyllanthus ruber*	0	0	6	**6**	0	0	0	**0**
Urticaceae	*Pilea hookeriana*	0	2	16	**18**	33	16	8	**57**
Urticaceae	*Pilea peltata*	10	40	31	**81**	43	130	0	**173**
Urticaceae	*Pilea peploides*	10	77	11	**98**	128	36	0	**164**
Piperaceae	*Piper bonii*	0	0	0	**0**	0	0	1	**1**
Piperaceae	*Piper laetispicum*	0	0	1	**1**	0	20	21	**41**

Piperaceae	*Piper saxicola*	0	0	2	**2**	0	4	11	**15**
Asteraceae	*Piptocarpha riedelii*	0	0	0	**0**	1	0	0	**1**
Anacardiaceae	*Pistacia weinmannifolia*	8	1	0	**9**	0	0	0	**0**
Annonaceae	*Polyalthia cerasoides*	0	0	0	**0**	0	1	2	**3**
Porellaceae	*Porella sp*	0	0	0	**0**	0	1	2	**3**
Araceae	*Pothos chinensis*	0	0	1	**1**	0	0	0	**0**
Araceae	*Pothos grandis*	0	0	0	**0**	0	0	24	**24**
Araceae	*Pothos scandens*	0	0	0	**0**	0	0	10	**10**
Lamiaceae	*Premna fulva*	0	0	0	**0**	4	0	0	**4**
Gesneriaceae	*Primulina drakei*	0	15	3	**18**	1	40	0	**41**
Gesneriaceae	*Primulina halongensis*	0	0	0	**0**	1	0	8	**9**
Gesneriaceae	*Primulina modesta*	0	0	0	**0**	9	2	0	**11**
Rosaceae	*Prunus javanica*	0	0	0	**0**	0	0	4	**4**
Rubiaceae	*Psychotria elliptica*	0	1	1	**2**	0	0	0	**0**
Rubiaceae	*Psychotria fleuryi*	1	0	8	**9**	0	15	67	**82**
Rubiaceae	*Psydrax dicoccos*	2	0	1	**3**	0	0	0	**0**
Pteridaceae	*Pteris grevilleana*	0	0	0	**0**	0	0	178	**178**
Pteridaceae	*Pteris insignis*	0	0	1	**1**	1	2	41	**44**
Malvaceae	*Pterospermum truncatolobatum*	2	0	12	**14**	11	0	5	**16**
Polypodiaceae	*Pyrrosia lanceolata*	1	1	1	**3**	108	2	0	**110**
Araceae	*Rhaphidophora tonkinensis*	0	0	0	**0**	0	1	53	**54**
Anacardiaceae	*Rhus chinensis*	1	0	0	**1**	0	0	0	**0**
Connaraceae	*Rourea nimor*	2	0	0	**2**	0	0	0	**0**
Euphorbiaceae	*Sapium rotundifolium*	0	0	0	**0**	1	3	0	**4**
Apocynaceae	*Sarcostemma acidum*	4	1	0	**5**	1	4	0	**5**
Phyllanthaceae	*Sauropus garrettii*	1	0	0	**1**	0	0	0	**0**
Phyllanthaceae	*Sauropus racemosus*	1	0	23	**24**	1	0	0	**1**
Rubiaceae	*Schizomussaenda henryi*	0	1	0	**1**	2	0	0	**2**

Poaceae	*Schizostachyum dullooa*	0	0	4	**4**	0	0	0	**0**
Salicaceae	*Scolopia chinensis*	0	0	0	**0**	3	0	0	**3**
Apocynaceae	*Secamone elliptica*	9	6	1	**16**	5	4	1	**10**
Selaginellaceae	*Selaginella frondosa*	8	1	0	**9**	0	0	0	**0**
Anacardiaceae	*Semecarpus tonkinensis*	0	0	1	**1**	0	0	0	**0**
Poaceae	*Setaria viridis*	3	5	1	**9**	0	0	0	**0**
Rutaceae	*Severinia monophylla*	11	6	1	**18**	0	2	2	**4**
Smilacaceae	*Smilax glabra*	0	0	0	**0**	0	0	2	**2**
Smilacaceae	*Smilax lanceifolia*	0	0	0	**0**	0	0	13	**13**
Smilacaceae	*Smilax perfoliata*	0	1	3	**4**	0	4	1	**5**
Fabaceae	*Sophora tonkinensis*	0	0	0	**0**	0	5	0	**5**
Rubiaceae	*Spiradiclis caespitosa*	0	0	0	**0**	3	3	0	**6**
Stemonaceae	*Stemona tuberosa*	9	0	4	**13**	1	0	4	**5**
Menispermaceae	*Stephania rotunda*	0	10	0	**10**	2	4	0	**6**
Malvaceae	*Sterculia cochinchinensis*	1	0	0	**1**	0	0	0	**0**
Malvaceae	*Sterculia hymenocalyx*	0	0	0	**0**	0	1	1	**2**
Malvaceae	*Sterculia lanceolata*	6	1	42	**49**	0	0	2	**2**
Moraceae	*Streblus asper*	0	0	0	**0**	0	0	4	**4**
Moraceae	*Streblus ilicifolius*	9	142	42	**193**	11	0	0	**11**
Apocynaceae	*Strophanthus divaricatus*	0	0	0	**0**	0	1	0	**1**
Loganiaceae	*Strychnos umbellata*	0	2	0	**2**	9	3	1	**13**
Styracaceae	*Styrax agrestis*	0	0	0	**0**	0	0	1	**1**
Myrtaceae	*Syzygium bullockii*	0	0	0	**0**	0	2	6	**8**
Myrtaceae	*Syzygium levinei*	0	0	1	**1**	0	0	0	**0**
Myrtaceae	*Syzygium myrsinifolium*	0	0	0	**0**	0	0	2	**2**
Rubiaceae	*Tarenna attenuata*	7	0	1	**8**	9	2	0	**11**
Rubiaceae	*Tarenna collinsae*	2	2	0	**4**	2	0	0	**2**
Moraceae	*Taxotrophis macrophylla*	0	84	0	**84**	0	0	10	**10**

Tectariaceae	*Tectaria sagenioides*	0	0	0	**0**	0	3	0	**3**
Tectariaceae	*Tectaria subpedata*	0	0	0	**0**	0	0	8	**8**
Tectariaceae	*Tectaria subtriphylla*	0	0	0	**0**	0	0	1	**1**
Dilleniaceae	*Tetracera sarmentosa*	0	0	0	**0**	0	0	1	**1**
Vitaceae	*Tetrastigma beauvaisii*	0	0	1	**1**	0	0	2	**2**
Vitaceae	*Tetrastigma erubescens*	1	2	0	**3**	1	3	26	**30**
Vitaceae	*Tetrastigma rupestre*	4	12	7	**23**	13	11	1	**25**
Orchidaceae	*Thrixspermum annamense*	0	0	0	**0**	0	0	1	**1**
Poaceae	*Thysanolaena latifolia*	0	0	0	**0**	2	0	0	**2**
Menispermaceae	*Tinospora sinensis*	1	5	1	**7**	0	0	0	**0**
Anacardiaceae	*Toxicodendron succedaneum*	1	0	0	**1**	0	2	0	**2**
Polyporaceae	*Trametes gibbosa*	0	0	0	**0**	0	1	0	**1**
Polyporaceae	*Trametes versicolor*	0	0	0	**0**	0	2	3	**5**
Cannabaceae	*Trema politoria*	2	0	0	**2**	0	0	0	**0**
Convolvulaceae	*Tridynamia sinensis*	0	0	0	**0**	0	0	2	**2**
Orchidaceae	*Tropidia angulosa*	0	0	0	**0**	0	0	28	**28**
Orthotrichaceae	*Ulota sp.*	0	0	0	**0**	0	6	1	**7**
Rubiaceae	*Uncaria cordata*	0	0	0	**0**	0	0	3	**3**
Rubiaceae	*Uncaria homomalla*	0	0	0	**0**	0	2	0	**2**
Rubiaceae	*Uncaria macrophylla*	1	0	4	**5**	0	1	1	**2**
Malvaceae	*Urena lobata*	0	0	4	**4**	0	0	0	**0**
Annonaceae	*Uvaria tonkinensis*	2	5	4	**11**	4	19	15	**38**
Lamiaceae	*Vitex stylosa*	7	1	0	**8**	0	1	0	**1**
Lamiaceae	*Vitex trifolia*	0	1	0	**1**	12	6	17	**35**
Vitaceae	*Vitis balansaeana*	0	0	2	**2**	0	0	0	**0**
Meliaceae	*Walsura pinnata*	3	2	0	**5**	0	0	0	**0**
Rubiaceae	*Wendlandia formosana*	0	0	1	**1**	0	0	0	**0**
Thymelaeaceae	*Wikstroemia indica*	1	0	0	**1**	0	2	0	**2**
Apocynaceae	*Wrightia sikkimensis*	0	1	0	**1**	0	0	0	**0**

Rubiaceae	*Xanthophytum balansae*	0	0	0	**0**	0	0	109	**109**
Sapindaceae	*Xerospermum noronhianum*	5	8	0	**13**	0	0	0	**0**
Sapindaceae	*Xerospermum tonkinensis*	0	0	0	**0**	0	0	3	**3**
Flacourtiaceae	*Xylosma longifolia*	0	0	0	**0**	0	3	0	**3**
Rutaceae	*Zanthoxylum nitida*	0	0	1	**1**	0	0	0	**0**
Rutaceae	*Zanthoxylum nitidum*	0	0	0	**0**	0	1	2	**3**
Rutaceae	*Zanthoxylum scandens*	0	0	0	**0**	3	0	3	**6**
Cucurbitaceae	*Zehneria maysorensis*	0	4	0	**4**	1	0	2	**3**
Total		**529**	**752**	**828**	**2094**	**1405**	**1132**	**3307**	**5844**

2.2.2 Tree species captured in Cua Dong and the Sanctuary

Family	Species	Cua Dong				The Sanctuary			
		Coast (n)	Slope (n)	Valley (n)	**Total**	Coast (n)	Slope (n)	Valley (n)	**Total**
Meliaceae	*Aglaia elaeagnoidea*	0	0	7	**7**	0	0	1	**1**
Phyllanthaceae	*Antidesma eberhardtii*	0	0	0	**0**	0	0	1	**1**
Meliaceae	*Aphanamixis polystachya*	0	0	1	**1**	0	0	0	**0**
Mimosoideae	*Archidendron clypearia*	0	1	0	**1**	0	0	0	**0**
Primulaceae	*Ardisia lecomtei*	0	0	0	**0**	0	0	13	**13**
Primulaceae	*Ardisia pseudocrispa*	0	0	2	**2**	0	0	0	**0**
Annonaceae	*Beilschmiedia tsangii*	0	0	0	**0**	0	0	13	**13**
Moraceae	*Bleekrodea tonkinensis*	0	0	20	**20**	0	0	0	**0**
Phyllanthaceae	*Breynia fruticosa*	0	0	0	**0**	1	0	0	**1**
Phyllanthaceae	*Bridelia balansae*	4	2	5	**11**	6	0	0	**6**
Capparaceae	*Capparis pyrifolia*	0	0	0	**0**	0	0	2	**2**
Fagaceae	*Castanopsis indica*	1	0	0	**1**	0	0	1	**1**
Ulmaceae	*Celtis philippensis*	0	0	1	**1**	0	0	0	**0**
Apocynaceae	*Cerbera odollam*	5	0	0	**5**	0	0	0	**0**
Anacardiaceae	*Choreospondias axilaris*	1	0	0	**1**	0	0	0	**0**
Rutaceae	*Clausena anisata*	2	1	0	**3**	0	0	0	**0**
Rutaceae	*Clausena indica*	2	0	0	**2**	0	0	0	**0**
Phyllanthaceae	*Cleistanthus tonkinensis*	0	2	10	**12**	43	0	1	**44**
Euphorbiaceae	*Croton argyratus*	0	1	0	**1**	0	0	0	**0**
Euphorbiaceae	*Croton tiglium*	1	0	0	**1**	0	0	0	**0**
Euphorbiaceae	*Deutzianthus tonkinensis*	0	0	0	**0**	0	2	0	**2**
Sapindaceae	*Dimocarpus longan*	0	0	0	**0**	0	0	1	**1**
Ebenaceae	*Diospyros apiculata*	0	0	0	**0**	1	0	0	**1**
Ebenaceae	*Diospyros mollis*	0	1	0	**1**	1	3	6	**10**
Asparagaceae	*Dracaena cambodiana*	6	1	4	**11**	12	3	0	**15**
Moraceae	*Ficus alongensis*	0	1	0	**1**	0	1	0	**1**
Moraceae	*Ficus benjamina*	0	1	0	**1**	2	0	0	**2**
Moraceae	*Ficus hispida*	0	0	0	**0**	0	0	11	**11**
Moraceae	*Ficus lacor*	0	0	0	**0**	0	1	0	**1**
Moraceae	*Ficus superba*	0	0	0	**0**	1	0	0	**1**
Moraceae	*Ficus tuphapensis*	0	0	1	**1**	0	0	0	**0**

Moraceae	*Ficus virens*	0	1	0	**1**	0	0	0	**0**
Malvaceae	*Firmiana simplex*	9	1	0	**10**	0	0	0	**0**
Clusiaceae	*Garcinia oligantha*	0	0	1	**1**	0	0	0	**0**
Phyllanthaceae	*Glochidion zeylanicum*	0	0	2	**2**	0	0	0	**0**
Rutaceae	*Glycosmis lucida*	0	0	0	**0**	1	0	0	**1**
Phyllanthaceae	*Hemiscolopia trimera*	1	0	0	**1**	0	0	0	**0**
Malvaceae	*Hibiscus tilliaceus*	1	0	0	**1**	0	0	0	**0**
Salicaceae	*Homalium cochinchinensis*	2	0	0	**2**	0	0	0	**0**
Dipterocarpaceae	*Hopea chinensis*	0	0	0	**0**	2	0	0	**2**
Styracaceae	*Huodendron parvifolium*	0	0	0	**0**	0	0	1	**1**
Aquifoliaceae	*Ilex kaushue*	0	0	0	**0**	0	0	1	**1**
Rubiaceae	*Ixora henryi*	0	0	0	**0**	3	0	2	**5**
Lythraceae	*Lagerstroemia crispa*	0	0	1	**1**	0	0	0	**0**
Sapindaceae	*Lepisanthes senegalensis*	0	0	1	**1**	0	0	0	**0**
Fagaceae	*Lithocarpus corneus*	0	0	0	**0**	1	0	0	**1**
Lauraceae	*Litsea glutinosa*	2	0	1	**3**	1	0	0	**1**
Lauraceae	*Machilus bonii*	0	0	0	**0**	0	10	30	**40**
Lauraceae	*Machilus thunbergii*	0	1	0	**1**	3	1	1	**5**
Magnoliaceae	*Magnolia coco*	0	0	0	**0**	0	1	3	**4**
Sapindaceae	*Melicoccus bijugatus*	0	0	0	**0**	0	0	1	**1**
Melastomataceae	*Memecylon edule*	1	0	0	**1**	2	0	0	**2**
Malvaceae	*Microcos tomentosa*	3	0	2	**5**	1	3	0	**4**
Celastraceae	*Microtropis osmanthoides*	0	0	3	**3**	0	0	0	**0**
Annonaceae	*Miliusa sinensis*	3	0	1	**6**	0	0	0	**0**
Rubiaceae	*Mussaenda densiflora*	0	0	2	**1**	0	0	0	**0**
Fabaceae	*Ormosia tsangii*	1	0	0	**0**	0	0	0	**1**
Arecaceae	*Phoenix paludosa*	0	0	0	**3**	0	0	1	**0**
Anacardiaceae	*Pistacia weinmanniifolia*	0	0	3	**5**	0	0	0	**0**
Annonaceae	*Polyalthia cerasoides*	4	1	0	**0**	0	0	0	**1**
Rubiaceae	*Psychotria fleuryi*	0	0	0	**2**	0	1	0	**4**
Rubiaceae	*Psydrax dicoccos*	0	0	2	**1**	0	1	3	**0**
Malvaceae	*Pterospermum truncatolobatum*	1	0	0	**5**	0	0	0	**9**
Euphorbiaceae	*Sapium rotundifolium*	0	0	5	**0**	8	0	1	**3**

Phyllanthaceae	*Sauropus racemosus*	0	0	0	**2**	1	2	0	**0**
Rubiaceae	*Schizomussaenda henryi*	0	0	2	**1**	0	0	0	**1**
Salicaceae	*Scolopia chinensis*	0	1	0	**0**	1	0	0	**3**
Rutaceae	*Severinia monophylla*	0	0	0	**4**	3	0	0	**0**
Stemonaceae	*Stemona tuberosa*	2	2	0	**1**	0	0	0	**0**
Malvaceae	*Sterculia lanceolata*	1	0	0	**11**	0	0	0	**0**
Moraceae	*Streblus ilicifolius*	3	0	8	**32**	0	0	0	**6**
Myrtaceae	*Syzygium bullockii*	2	22	8	**0**	6	0	0	**4**
Myrtaceae	*Syzygium levinei*	0	0	0	**1**	0	2	2	**0**
Rubiaceae	*Tarenna attenuata*	0	0	1	**2**	0	0	0	**5**
Rubiaceae	*Tarenna collinsae*	2	0	0	**3**	5	0	0	**2**
Moraceae	*Taxotrophis macrophylla*	1	2	0	**7**	2	0	0	**1**
Anacardiaceae	*Toxicodendron succedanea*	0	7	0	**1**	0	0	1	**1**
Lamiaceae	*Vitex stylosa*	1	0	0	**1**	0	1	0	**0**
Apocynaceae	*Wrightia sikkimensis*	0	1	0	**1**	0	0	0	**0**
Sapindaceae	*Xerospermum noronhianum*	0	1	0	**5**	0	0	0	**0**
Sapindaceae	*Xerospermum tonkinense*	2	3	0	0	0	0	0	2
Total		**64**	**54**	**94**	**212**	**107**	**32**	**97**	**238**

2.2.3 All species captured in the Viet Hai corridor

Family	Species	Viet Hai			
		Coastal (n)	Slope (n)	Valley (n)	Total
Pteridaceae	*Acrostichum aureum*	0	0	14	**14**
Pteridaceae	*Adiantum caudatum*	8	25	0	**33**
Pentaphylacaceae	*Adinandra caudata*	0	0	6	**6**
Asteraceae	*Ageratum conyzoides*	3	0	0	**3**
Asteraceae	*Ageratum houstonianum*	3	0	0	**3**
Meliaceae	*Aglaia elaeagnoidea*	1	1	1	**3**
Fabaceae	*Albizia kalkora*	0	4	0	**4**
Moraceae	*Alchornea scandens*	3	3	7	**13**
Moraceae	*Alchornea tiliifolia*	0	0	3	**3**
Sapindaceae	*Allophylus livescens*	1	7	13	**21**
Sapindaceae	*Allophylus macrodontus*	2	2	8	**12**
Sapindaceae	*Allophylus petelotii*	0	0	1	**1**
Araceae	*Alocasia hainanica*	12	1	2	**15**
Araceae	*Alocasia macrorrhizos*	0	0	98	**98**
Zingiberaceae	*Alpinia calcicola*	11	6	0	**17**
Zingiberaceae	*Alpinia chinensis*	0	0	14	**14**
Apocynaceae	*Alyxia hainanensis*	0	31	0	**31**
Apocynaceae	*Alyxia reinwardtii*	6	11	0	**17**
Araceae	*Amorphophallus interruptus*	60	38	13	**111**
Araceae	*Amorphophallus paeoniifolius*	2	3	0	**5**
Vitaceae	*Ampelopsis annamensis*	1	0	1	**2**
Phyllanthaceae	*Antidesma eberhardtii*	3	5	6	**14**
Phyllanthaceae	*Antidesma fordii*	4	0	0	**4**
Phyllanthaceae	*Aporosa yunnanensis*	0	0	4	**4**
Primulaceae	*Ardisia mamillata*	0	0	1	**1**
Primulaceae	*Ardisia pseudocrispa*	0	0	1	**1**
Convolvulaceae	*Argyreia acuta*	0	0	5	**5**
Aristolochiaceae	*Aristolochia indica*	0	5	0	**5**
Asparagaceae	*Aspidistra tonkinensis*	0	0	2	**2**
Aspleniaceae	*Asplenium nidus*	5	0	0	**5**
Aspleniaceae	*Asplenium sampsoni*	11	0	0	**11**
Aspleniaceae	*Asplenium saxicola*	11	5	0	**16**
Rutaceae	*Atalantia stenocarpa*	1	0	2	**3**
Fabaceae	*Bauhinia carcinophylla*	0	2	0	**2**
Fabaceae	*Bauhinia cardinalis*	4	2	0	**6**
Fabaceae	*Bauhinia ornata*	6	2	3	**11**

Fabaceae	*Bauhinia oxysepala*	0	1	0	**1**
Begoniaceae	*Begonia boisiana*	13	2	0	**15**
Lauraceae	*Beilschmiedia tsangii*	0	0	3	**3**
Rubiaceae	*Benkara depauperata*	0	1	0	**1**
Rhamnaceae	*Berchemia loureiriana*	2	0	0	**2**
Phyllanthaceae	*Bischofia javanica*	0	0	4	**4**
Asteraceae	*Blumea membranacea*	2	0	0	**2**
Urticaceae	*Boehmeria nivea*	16	0	0	**16**
Phyllanthaceae	*Bridelia balansae*	17	1	3	**21**
Simaroubaceae	*Brucea javanica*	1	0	0	**1**
Leguminosae	*Caesalpinia sinensis*	8	0	0	**8**
Arecaceae	*Calamus tenuis*	0	0	4	**4**
Lamiaceae	*Callicarpa formosana*	3	1	0	**4**
Lamiaceae	*Callicarpa longifolia*	1	0	0	**1**
Leguminosae	*Campylotropis bonii*	34	0	2	**36**
Rubiaceae	*Canthium parvifolium*	0	0	1	**1**
Capparaceae	*Capparis annamensis*	2	2	0	**4**
Capparaceae	*Capparis cantoniensis*	1	0	0	**1**
Capparaceae	*Capparis trinervia*	0	1	0	**1**
Arecaceae	*Carallia brachiata*	0	0	3	**3**
Cyperaceae	*Carex cruciata*	1	0	0	**1**
Arecaceae	*Caryota maxima*	0	0	9	**9**
Rubiaceae	*Catunaregam tomentosa*	1	0	0	**1**
Vitaceae	*Cayratia tenuifolia*	1	0	0	**1**
Celastraceae	*Celastrus hindsii*	0	0	3	**3**
Ulmaceae	*Celtis philippensis*	2	1	0	**3**
Opiliaceae	*Champereia manillana*	0	0	2	**2**
Menispermaceae	*Cissampelos pareira*	0	0	3	**3**
Vitaceae	*Cissus annamicus*	5	0	1	**6**
Rutaceae	*Clausena anisata*	0	0	1	**1**
Rutaceae	*Clausena indica*	1	5	1	**7**
Phyllanthaceae	*Cleistanthus tonkinensis*	4	133	12	**149**
Lamiaceae	*Clerodendrum canescens*	0	0	1	**1**
Lamiaceae	*Clerodendrum chinense*	1	0	0	**1**
Lamiaceae	*Clerodendrum japonicum*	0	0	2	**2**
Euphorbiaceae	*Cnesmone javanica*	3	4	4	**11**
Combretaceae	*Combretum indicum*	1	0	0	**1**
Combretaceae	*Combretum sundaicum*	1	1	7	**9**
Commelinaceae	*Commelina communis*	1	1	0	**2**
Hypericaceae	*Cratoxylum formosum*	0	1	0	**1**
Cryphaeaceae	*Cryphaea sp*	0	1	0	**1**

Menispermaceae	*Cyclea tonkinensis*	0	0	4	**4**
Orchidaceae	*Cymbidium aloifolium*	1	0	0	**1**
Fabaceae	*Dalbergia rimosa*	4	2	1	**7**
Fabaceae	*Dalbergia tonkinensis*	0	0	1	**1**
Compositae	*Decaneuropsis vagans*	0	0	9	**9**
Fabaceae	*Derris elliptica*	1	0	0	**1**
Fabaceae	*Derris tonkinensis*	0	6	0	**6**
Fabaceae	*Derris trifoliata*	25	86	3	**114**
Annonaceae	*Desmos chinensis*	13	21	15	**49**
Sapindaceae	*Dimocarpus longan*	0	2	0	**2**
Dioscoreaceae	*Dioscorea collettii*	0	0	4	**4**
Dioscoreaceae	*Dioscorea deltoidea*	39	0	5	**44**
Dioscoreaceae	*Dioscorea poilanei*	0	0	20	**20**
Ebenaceae	*Diospyros apiculata*	0	3	3	**6**
Ebenaceae	*Diospyros mollis*	0	2	2	**4**
Apocynaceae	*Dischidia acuminata*	0	12	0	**12**
Asparagaceae	*Dracaena cambodiana*	9	14	0	**23**
Polypodiaceae	*Drynaria bonii*	107	61	1	**169**
Elaeagnaceae	*Elaeagnus bonii*	0	0	4	**4**
Rutaceae	*Euodia lepta*	0	0	9	**9**
Celastraceae	*Euonymus tonkinensis*	0	0	1	**1**
Moraceae	*Ficus alongensis*	1	1	1	**3**
Moraceae	*Ficus benjamina*	1	1	0	**2**
Moraceae	*Ficus lacor*	1	0	0	**1**
Moraceae	*Ficus superba*	1	1	0	**2**
Moraceae	*Ficus tuphapensis*	0	0	1	**1**
Annonaceae	*Fissistigma bracteolatum*	0	0	4	**4**
Salicaceae	*Flacourtia rukam*	1	0	0	**1**
Clusiaceae	*Garcinia oligantha*	0	0	1	**1**
Euphorbiaceae	*Geophila repens*	0	0	5	**5**
Cannabaceae	*Gironniera subaequalis*	0	6	71	**77**
Phyllanthaceae	*Glochidion zeylanicum*	1	0	0	**1**
Rutaceae	*Glycosmis cymosa*	0	1	1	**2**
Rutaceae	*Glycosmis lucida*	0	4	1	**5**
Rutaceae	*Glycosmis ovoidea*	2	5	0	**7**
Rutaceae	*Glycosmis pseudoracemosa*	0	1	0	**1**
Lamiaceae	*Gmelina racemosa*	0	0	1	**1**
Gnetaceae	*Gnetum montanum*	0	0	59	**59**
Cucurbitaceae	*Gynostemma laxum*	3	4	0	**7**
Apocynaceae	*Hemidesmus indicus*	2	8	0	**10**
Malpighiaceae	*Hiptage bengalensis*	1	0	1	**2**

Salicaceae	*Homalium cochinchinensis*	1	1	1	**3**
Apocynaceae	*Hoya balansae*	0	5	0	**5**
Apocynaceae	*Hoya bonii*	7	0	0	**7**
Apocynaceae	*Hoya fungii*	4	2	0	**6**
Achariaceae	*Hydnocarpus ilicifolia*	0	0	1	**1**
Poaceae	*Ichnanthus pallens*	0	0	96	**96**
Balsaminaceae	*Impatiens halongensis*	108	0	0	**108**
Balsaminaceae	*Impatiens verrucifer*	30	34	0	**64**
Icacinaceae	*Iodes cirrhosa*	1	5	1	**7**
Rubiaceae	*Ixora chinensis*	4	0	0	**4**
Oleaceae	*Jasminum alongense*	2	0	1	**3**
Oleaceae	*Jasminum elongatum*	2	10	2	**14**
Oleaceae	*Jasminum nervosum*	0	1	0	**1**
Sapindaceae	*Lepisanthes senegalensis*	4	0	0	**4**
Acanthaceae	*Leptostachya wallichii*	0	0	128	**128**
Lauraceae	*Litsea glutinosa*	0	1	1	**2**
Lauraceae	*Litsea rotundifolia*	0	0	1	**1**
Celastraceae	*Loeseneriella pauciflora*	0	9	0	**9**
Orchidaceae	*Ludisia discolor*	2	9	0	**11**
Lygodiaceae	*Lygodium conforme*	0	0	1	**1**
Lygodiaceae	*Lygodium japonicum*	0	0	3	**3**
Lauraceae	*Machilus bonii*	0	0	1	**1**
Lauraceae	*Machilus thunbergii*	6	31	0	**37**
Primulaceae	*Maesa balansae*	2	0	0	**2**
Primulaceae	*Maesa perlaria*	0	1	1	**2**
Magnoliaceae	*Magnolia coco*	0	0	1	**1**
Euphorbiaceae	*Mallotus philippensis*	1	0	0	**1**
Euphorbiaceae	*Mallotus repandus*	0	1	1	**2**
Marasmiaceae	*Marasmiellus sp.*	1	0	0	**1**
Apocynaceae	*Marsdenia tenacissima*	4	0	0	**4**
Apocynaceae	*Marsdenia tonkinensis*	24	7	4	**35**
Opiliaceae	*Melientha suavis*	0	1	0	**1**
Apocynaceae	*Melodinus cochinchinensis*	0	8	10	**18**
Melastomataceae	*Memecylon edule*	3	1	150	**154**
Gesneriaceae	*Microchirita hamosa*	15	5	0	**20**
Malvaceae	*Microcos tomentosa*	4	5	4	**13**
Celastraceae	*Microtropis osmanthoides*	12	0	0	**12**
Annonaceae	*Miliusa balansae*	0	4	0	**4**
Annonaceae	*Miliusa campanulata*	0	0	1	**1**
Annonaceae	*Miliusa sinensis*	17	12	1	**30**
Sapindaceae	*Mischocarpus sundaicus*	0	0	2	**2**

Fabaceae	*Mucuna hainanensis*	0	1	3	**4**
Rubiaceae	*Mussaenda glabra*	1	0	0	**1**
Rubiaceae	*Oldenlandia biflora*	0	3	0	**3**
Asparagaceae	*Ophiopogon dracaenoides*	0	0	3	**3**
Asparagaceae	*Ophiopogon latifolius*	9	3	534	**546**
Urticaceae	*Oreocnide integrifolia*	0	0	7	**7**
Rubiaceae	*Paederia foetida*	2	0	0	**2**
Gesneriaceae	*Paraboea halongensis*	0	52	0	**52**
Passifloraceae	*Passiflora edulis*	1	0	0	**1**
Piperaceae	*Peperomia blanda*	37	0	0	**37**
Urticaceae	*Pilea hookeriana*	39	2	0	**41**
Urticaceae	*Pilea peltata*	92	54	0	**146**
Urticaceae	*Pilea peploides*	24	78	0	**102**
Piperaceae	*Piper saxicola*	0	0	2	**2**
Asteraceae	*Piptocarpha riedelii*	0	3	0	**3**
Annonaceae	*Polyalthia cerasoides*	1	0	0	**1**
Polygonaceae	*Polygonum chinense*	0	0	35	**35**
Polypodiaceae	*Polypodium bonii*	0	0	30	**30**
Porellaceae	*Porella sp*	2	3	0	**5**
Araceae	*Pothos chinensis*	0	0	10	**10**
Araceae	*Pothos grandis*	0	0	1	**1**
Lamiaceae	*Premna chevalieri*	0	3	0	**3**
Lamiaceae	*Premna fulva*	1	2	0	**3**
Gesneriaceae	*Primulina drakei*	1	24	0	**25**
Gesneriaceae	*Primulina halongensis*	0	2	0	**2**
Rosaceae	*Prunus javanica*	0	0	14	**14**
Rubiaceae	*Psychotria fleuryi*	0	0	1	**1**
Rubiaceae	*Psydrax dicoccos*	2	0	0	**2**
Pteridaceae	*Pteris grevilleana*	0	0	3	**3**
Pteridaceae	*Pteris insignis*	4	6	0	**10**
Malvaceae	*Pterospermum truncatolobatum*	10	10	55	**75**
Fabaceae	*Pueraria phaseoloides*	0	0	2	**2**
Polypodiaceae	*Pyrrosia lanceolata*	1	12	0	**13**
Araceae	*Rhaphidophora tonkinensis*	12	0	0	**12**
Arecaceae	*Rhapis micrantha*	0	0	188	**188**
Connaraceae	*Rourea minor*	1	1	0	**2**
Polyporaceae	*Sarcodontia sp.*	0	0	1	**1**
Apocynaceae	*Sarcostemma acidum*	0	6	0	**6**
Actinidiaceae	*Saurauia roxburghii*	0	0	10	**10**
Phyllanthaceae	*Sauropus racemosus*	0	2	0	**2**

Araliaceae	*Schefflera alongensis*	7	0	0	**7**
Rubiaceae	*Schizomussaenda henryi*	1	0	1	**2**
Salicaceae	*Scolopia chinensis*	0	1	0	**1**
Apocynaceae	*Secamone elliptica*	3	3	2	**8**
Poaceae	*Setaria viridis*	0	0	3	**3**
Rutaceae	*Severinia monophylla*	0	1	0	**1**
Smilacaceae	*Smilax lanceifolia*	0	4	44	**48**
Smilacaceae	*Smilax perfoliata*	1	0	7	**8**
Rubiaceae	*Spiradiclis caespitosa*	5	0	0	**5**
Stemonaceae	*Stemona tuberosa*	0	2	1	**3**
Menispermaceae	*Stephania rotunda*	0	2	0	**2**
Malvaceae	*Sterculia cochinchinensis*	0	1	0	**1**
Malvaceae	*Sterculia hymenocalyx*	1	0	0	**1**
Malvaceae	*Sterculia lanceolata*	1	3	6	**10**
Moraceae	*Streblus ilicifolius*	10	0	0	**10**
Acanthaceae	*Strobilanthes sulfurea*	0	0	22	**22**
Loganiaceae	*Strychnos cathayensis*	3	1	0	**4**
Loganiaceae	*Strychnos umbellata*	4	1	2	**7**
Myrtaceae	*Syzygium bullockii*	0	0	2	**2**
Myrtaceae	*Syzygium odoratum*	0	2	0	**2**
Myrtaceae	*Syzygium zeylanicum*	2	0	6	**8**
Rubiaceae	*Tarenna attenuata*	1	3	0	**4**
Rubiaceae	*Tarenna collinsae*	1	0	0	**1**
Moraceae	*Taxotrophis macrophylla*	0	1	0	**1**
Tectariaceae	*Tectaria decurrens*	0	0	1	**1**
Vitaceae	*Tetrastigma erubescens*	8	2	2	**12**
Vitaceae	*Tetrastigma rupestre*	11	11	2	**24**
Thelypteridaceae	*Thelypteris tonkinensis*	0	0	396	**396**
Menispermaceae	*Tinospora crispa*	0	0	8	**8**
Menispermaceae	*Tinospora sinensis*	0	1	5	**6**
Anacardiaceae	*Toxicodendron succedanea*	2	2	1	**5**
Polyporaceae	*Trametes versicolor*	0	1	0	**1**
Staphyleaceae	*Turpinia cochinchinensis*	0	2	0	**2**
Orthotrichaceae	*Ulota sp.*	1	0	0	**1**
Rubiaceae	*Uncaria cordata*	0	0	1	**1**
Rubiaceae	*Uncaria macrophylla*	0	0	1	**1**
Annonaceae	*Uvaria tonkinensis*	17	11	11	**39**
Lamiaceae	*Vitex trifolia*	14	11	0	**25**
Vitaceae	*Vitis balansaeana*	2	0	0	**2**
Meliaceae	*Walsura pinnata*	0	7	0	**7**
Rubiaceae	*Wendlandia formosana*	0	0	1	**1**

Compositae	*Wollastonia biflora*	1	0	0	**1**
Rutaceae	*Zanthoxylum nitida*	0	1	0	**1**
Rutaceae	*Zanthoxylum scandens*	1	0	0	**1**
Cucurbitaceae	*Zehneria maysorensis*	8	0	0	**8**
Total		1092	1044	2335	**4471**

2.2.4 Tree species captured in the Viet Hai corridor

Family	Species	Viet Hai Trees			
		Coast (n)	Slope (n)	Valley (n)	Total
Pentaphylacaceae	*Adinandra caudata*	0	0	2	**2**
Meliaceae	*Aglaia elaeagnoidea*	0	1	0	**1**
Sapindaceae	*Allophylus livescens*	0	1	0	**1**
Sapindaceae	*Allophylus macrodontus*	1	0	0	**1**
Phyllanthaceae	*Antidesma fordii*	1	0	0	**2**
Phyllanthaceae	*Aporosa yunnanensis*	0	0	1	**1**
Convolvulaceae	*Argyreia acuta*	0	0	1	**1**
Lauraceae	*Beilschmiedia tsangii*	0	0	1	**1**
Phyllanthaceae	*Bischofia javanica*	0	0	4	**4**
Urticaceae	*Boehmeria nivea*	3	0	0	**3**
Phyllanthaceae	*Bridelia balansae*	8	1	2	**11**
Ulmaceae	*Celtis philippensis*	1	0	0	**1**
Opiliaceae	*Champereia manillana*	0	0	1	**1**
Rutaceae	*Clausena indica*	0	1	0	**1**
Phyllanthaceae	*Cleistanthus tonkinensis*	1	16	1	**18**
Hypericaceae	*Cratoxylum formosum*	0	1	0	**1**
Fabaceae	*Dalbergia tonkinensis*	0	0	1	**1**
Fabaceae	*Derris trifoliata*	0	0	1	**1**
Annonaceae	*Desmos chinensis*	0	1	0	**1**
Sapindaceae	*Dimocarpus longan*	0	1	0	**1**
Ebenaceae	*Diospyros apiculata*	0	2	1	**3**
Ebenaceae	*Diospyros mollis*	0	1	1	**2**
Asparagaceae	*Dracaena cambodiana*	8	7	0	**15**
Celastraceae	*Euonymus tonkinensis*	0	0	1	**1**
Moraceae	*Ficus alongensis*	1	1	0	**2**
Moraceae	*Ficus benjamina*	1	1	0	**2**
Moraceae	*Ficus lacor*	1	0	0	**1**
Moraceae	*Ficus superba*	1	1	0	**2**
Cannabaceae	*Gironniera subaequalis*	0	0	10	**10**
Phyllanthaceae	*Glochidion zeylanicum*	1	0	0	**1**
Rutaceae	*Glycosmis cymosa*	0	1	0	**1**
Rutaceae	*Glycosmis ovoidea*	2	1	0	**3**
Salicaceae	*Homalium cochinchinensis*	1	0	0	**1**
Achariaceae	*Hydnocarpus ilicifolia*	0	0	1	**1**
Rubiaceae	*Ixora chinensis*	3	0	0	**3**
Lauraceae	*Litsea glutinosa*	0	1	1	**2**
Lauraceae	*Litsea rotundifolia*	0	0	1	**1**
Lauraceae	*Machilus thunbergii*	2	11	0	**13**
Primulaceae	*Maesa balansae*	1	0	0	**1**
Opiliaceae	*Melientha suavis*	0	1	0	**1**
Melastomataceae	*Memecylon edule*	1	0	0	**1**
Malvaceae	*Microcos tomentosa*	2	5	2	**9**
Annonaceae	*Miliusa sinensis*	2	2	0	**4**
Urticaceae	*Oreocnide integrifolia*	0	0	1	**1**
Annonaceae	*Polyalthia cerasoides*	1	0	0	**1**
Rubiaceae	*Psychotria fleuryi*	0	1	0	**1**

Pteridaceae	*Pteris grevilleana*	0	0	1	**1**
Malvaceae	*Pterospermum truncatolobatum*	7	5	6	**18**
Actinidiaceae	*Saurauia roxburghii*	0	0	3	**3**
Phyllanthaceae	*Sauropus racemosus*	0	1	0	**1**
Araliaceae	*Schefflera alongensis*	1	0	0	**1**
Rubiaceae	*Schizomussaenda henryi*	1	0	1	**2**
Malvaceae	*Sterculia hymenocalyx*	1	0	0	**1**
Malvaceae	*Sterculia lanceolata*	1	3	2	**6**
Moraceae	*Streblus ilicifolius*	4	0	0	**4**
Myrtaceae	*Syzygium bullockii*	0	0	1	**1**
Myrtaceae	*Syzygium odoratum*	0	2	0	**2**
Myrtaceae	*Syzygium zeylanicum*	1	0	2	**3**
Rubiaceae	*Tarenna attenuata*	0	1	0	**1**
Anacardiaceae	*Toxicodendron succedanea*	2	2	1	**5**
Staphyleaceae	*Turpinia cochinchinensis*	0	2	0	**2**
Meliaceae	*Walsura pinnata*	0	3	0	**3**
Total		**61**	**78**	**51**	**191**

2.2.5 Food species identified in Cua Dong, the Sanctuary and Viet Hai

This list represents food species captured within the ecological survey of this study. A full list of diet species can be found in K. Ruskin (unpublished, 2016).

Family	Species	Cua Dong				The Sanctuary				Viet Hai Corridor (VHC)			
		C (n)	V (n)	S (n)	Total	C (n)	V (n)	S (n)	Total	C (n)	V (n)	S (n)	Total
Zingiberaceae	*Alpinia calcicola*	1	6	4	**11**	12	0	2	**14**	11	0	6	**17**
Aristolochiaceae	*Aristolochia indica*	0	0	8	**8**	0	0	16	**16**	0	0	5	**5**
Fabaceae	*Bauhinia cardinalis*	0	5	3	**8**	3	1	0	**4**	4	0	2	**6**
Phyllanthaceae	*Breynia fruticosa*	7	7	0	**14**	21	0	0	**21**	0	0	0	**0**
Vitaceae	*Cissus annamicus*	3	2	3	**8**	1	0	4	**5**	5	1	0	**6**
Rutaceae	*Clausena anisata*	10	1	1	**12**	0	0	0	**0**	0	1	0	**1**
Fabaceae	*Derris trifoliata*	13	6	17	**36**	15	1	27	**43**	25	3	86	**114**
Annonaceae	*Desmos chinensis*	0	4	6	**10**	0	8	3	**11**	13	15	21	**49**
Asparagaceae	*Dracaena cambodiana*	15	6	10	**31**	20	1	38	**59**	9	0	14	**23**
Boraginaceae	*Ehretia longiflora*	0	0	0	**0**	0	0	1	**1**	0	0	0	**0**
Rosaceae	*Eriobotrya cavaleriei*	2	0	0	**2**	0	0	0	**0**	0	0	0	**0**
Moraceae	*Ficus alongensis*	2	0	2	**4**	0	0	1	**1**	1	1	1	**3**
Moraceae	*Ficus lacor*	0	0	0	**0**	0	0	1	**1**	1	0	0	**1**
Malvaceae	*Firmiana simplex*	9	0	1	**10**	0	0	0	**0**	0	0	0	**0**
Phyllanthaceae	*Glochidion zeylanicum*	0	7	0	**7**	0	0	17	**17**	0	0	0	**0**
Salicaceae	*Homalium cochinchinensis*	2	0	1	**3**	0	0	0	**0**	1	1	1	**3**
Icacinaceae	*Iodes cirrhosa*	0	0	0	**0**	2	1	0	**3**	1	1	5	**7**
Convolvulaceae	*Ipomoea mauritiana*	3	2	0	**5**	0	2	0	**2**	0	0	0	**0**
Lauraceae	*Litsea glutinosa*	7	8	1	**16**	2	0	0	**2**	0	1	1	**2**
Euphorbiaceae	*Mallotus repandus*	0	0	0	**0**	2	0	0	**2**	0	1	1	**2**
Fabaceae	*Mucuna hainanensis*	2	2	6	**10**	1	1	0	**2**	0	3	1	**4**
Urticaceae	*Pilea hookeriana*	0	16	2	**18**	33	8	16	**57**	39	0	2	**41**
Anacardiaceae	*Pistacia weinmannifolia*	8	0	1	**9**	0	0	0	**0**	0	0	0	**0**
Lamiaceae	*Premna chevalieri*	0	0	0	**0**	0	0	0	**0**	0	0	3	**3**
Gesneriaceae	*Primulina drakei*	0	3	15	**18**	1	0	40	**41**	1	0	24	**25**
Araliaceae	*Schefflera alongensis*	0	0	0	**0**	0	0	0	**0**	7	0	0	**7**

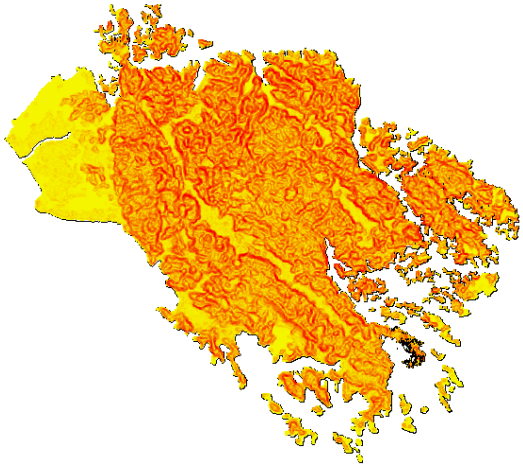
Apocynaceae	*Secamone elliptica*	9	1	6	**16**	5	1	4	**10**	3	2	3	**8**
Rutaceae	*Severinia monophylla*	11	1	6	**18**	0	2	2	**4**	0	0	1	**1**
Menispermaceae	*Stephania rotunda*	0	0	10	**10**	2	0	4	**6**	0	0	2	**2**
Malvaceae	*Sterculia cochinchinensis*	1	0	0	**1**	0	0	0	**0**	0	0	1	**1**
Malvaceae	*Sterculia lanceolata*	6	42	1	**49**	0	2	0	**2**	1	6	3	**10**
Loganiaceae	*Strychnos umbellata*	0	0	2	**2**	9	1	3	**13**	4	2	1	**7**
Vitaceae	*Tetrastigma beauvaisii*	0	1	0	**1**	0	2	0	**2**	0	0	0	**0**
Vitaceae	*Tetrastigma rupestre*	4	7	12	**23**	13	1	11	**25**	11	2	11	**24**
Menispermaceae	*Tinospora sinensis*	1	1	5	**7**	0	0	0	**0**	0	5	1	**6**
Anacardiaceae	*Toxicodendron succedanea*	1	0	0	**1**	0	0	2	**2**	2	1	2	**5**
Lamiaceae	*Vitex trifolia*	0	0	1	**1**	12	17	6	**35**	14	0	11	**25**
Thymelaeaceae	*Wikstroemia indica*	1	0	0	**1**	0	0	2	**2**	0	0	0	**0**
Apocynaceae	*Wrightia sikkimensis*	0	0	1	**1**	0	0	0	**0**	0	0	0	**0**
Sapindaceae	*Xerospermum noronhianum*	5	0	8	**13**	0	0	0	**0**	0	0	0	**0**
Flacourtiaceae	*Xylosma longifolia*	0	0	0	**0**	0	0	3	**3**	0	0	0	**0**
Total		**123**	**128**	**133**	**384**	**154**	**49**	**203**	**406**	**153**	**46**	**209**	**408**

C= coast, V= valley, S= slope

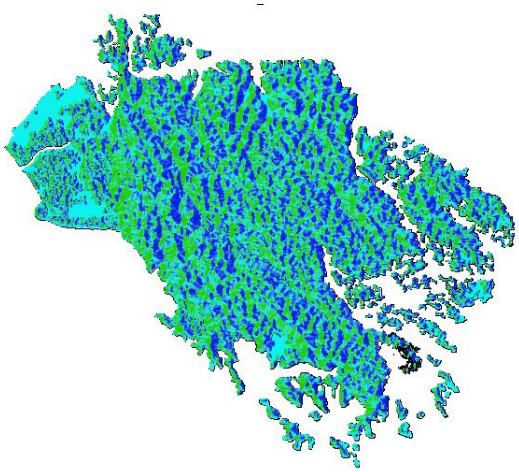
2.3 Results for MaxEnt analysis for the Cat Ba langur

2.3.1 Predictor variables for Cat Ba langur distribution

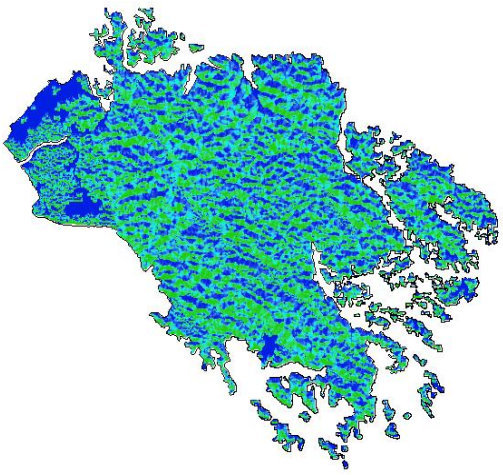
Digital Elevation Model



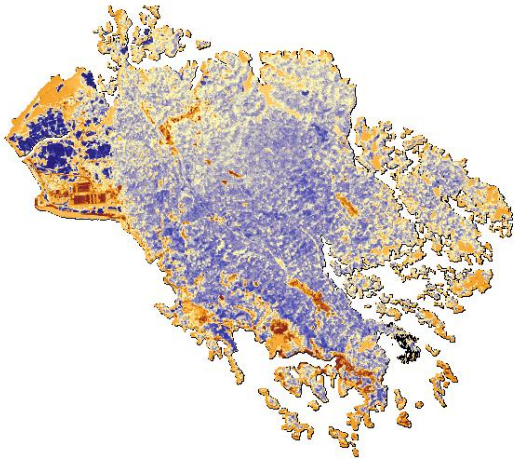
Slope



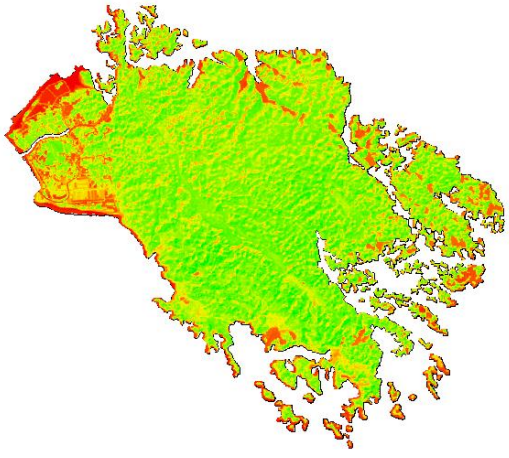
Eastness



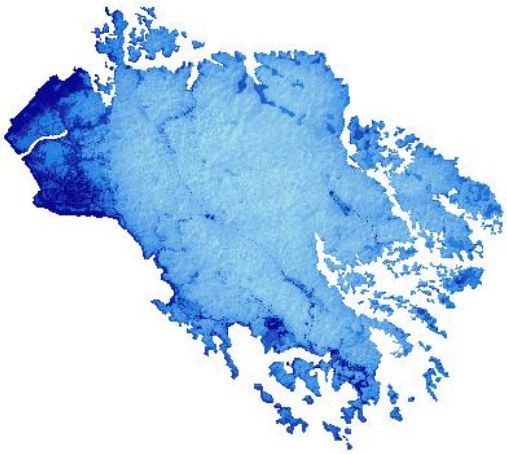
Northness



Normalised Difference Moisture Index



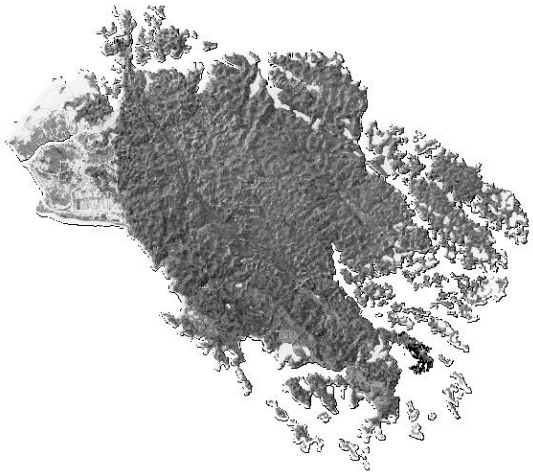
Normalised Difference Vegetation Index



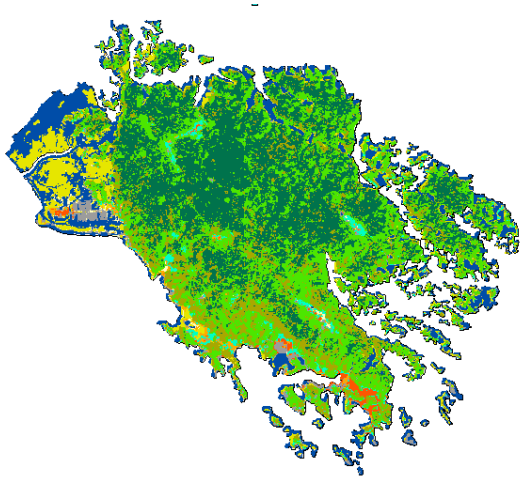
Spot6 Band 1

Spot6 Band 2

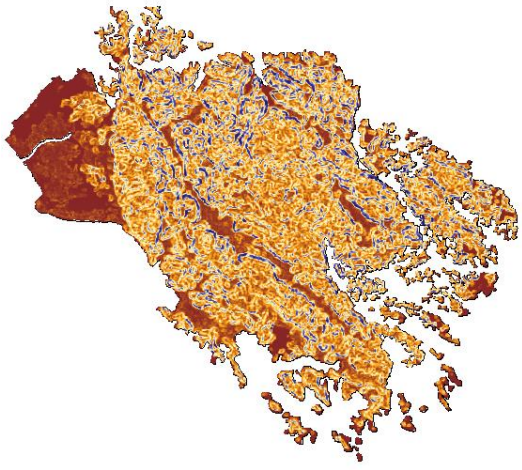
Spot6 Band 3



Spot6 Band 4



Land use (12 categories)



Topographic Roughness Index

2.3.2 Pearson's correlation of variables for Cat Ba langur MaxEnt analysis

	Eastness	NDMI	NDVI	Northness	Spot6 band1 (Blue)	Spot6 band2 (Green)	Spot6 band3 (Red)	Spot6 band4 (NIR)	DEM	Slope	TRI
Eastness	1.000										
NDMI	0.147	1.000									
NDVI	0.291	0.677	1.000								
Northness	0.058	-0.154	-0.367	1.000							
Spot6 band1 (Blue)	-0.015	-0.538	-0.564	0.093	1.000						
Spot6 band2 (Green)	0.088	-0.425	-0.307	0.003	0.914*	1.000					
Spot6 band3 (Red)	0.271	0.554	0.886*	-0.252	-0.567	-0.260	1.000				
Spot6 band4 (NIR)	0.028	-0.456	-0.338	0.038	0.897*	0.938*	-0.310	1.000			
DEM	0.017	0.365	0.443	-0.105	-0.606	-0.473	0.447	-0.433	1.000		
Slope	0.018	0.229	0.326	-0.115	-0.447	-0.365	0.361	-0.372	0.367	1.000	
TRI	0.018	0.217	0.320	-0.115	-0.441	-0.363	0.348	-0.370	0.358	0.977*	1.000

*Strong correlation -0.7<r>0.7

2.3.3 MaxEnt model results

2.3.3.1 *Results of models with feature class and regularisation multiplier variations*

Feature type	Test #	Regularisation multiplier	Number of variables	Training AUC	Test AUC	AUC Difference	Highest contributing variables	Lowest contributing variables (<1.0%)	Negative test gain
Linear-only	1	0.5	8	0.816	0.801	0.015	Spot 6 Band 4, DEM, land use	Eastness	Eastness
	2	1	8	0.816	0.801	0.015	Spot 6 Band 4, DEM, land use	Eastness	Eastness
	3	2	8	0.815	0.8	0.015	Spot 6 Band 4, DEM, land use	Eastness	Eastness
	4	4	8	0.813	0.799	0.014	Spot 6 Band 4, DEM, land use	Eastness	Eastness
Best performing test rerun	5	4	7	0.813	0.8	0.013	Spot 6 Band 4, DEM, land use	-	-
Quadratic - only	6	0.5	8	0.81	0.792	0.018	DEM, Spot6 Band 4, land use	TRI, Eastness	Eastness, Northness
	7	1	8	0.81	0.792	0.018	DEM, Spot6 Band 4, land use	TRI, Eastness	Eastness, Northness
	8	2	8	0.81	0.792	0.018	DEM, Spot6 Band 4, land use	TRI, Eastness	Eastness, Northness
	9	4	8	0.808	0.791	0.017	DEM, Spot6 Band 4, land use	TRI, Eastness	Eastness, Northness, TRI
Best performing test rerun	10	4	5	0.807	0.792	0.015	DEM, Spot6 Band 4, land use	NDVI	-
Linear and Quadratic	11	0.5	8	0.861	0.841	0.02	DEM, Spot6 Band 4, NDVI, land use	Eastness	Eastness, Spot6 Band 4
	12	1	8	0.86	0.838	0.022	DEM, Spot6 Band 4	Eastness	Eastness, Spot6 Band 4
	13	2	8	0.857	0.832	0.025	DEM, Spot6 Band 4	Eastness, TRI	Eastness, Spot6 Band 4
	14	4	8	0.853	0.823	0.03	DEM	Eastness, TRI	Eastness, Spot6 Band 4

Table 2.3.3.1 continued

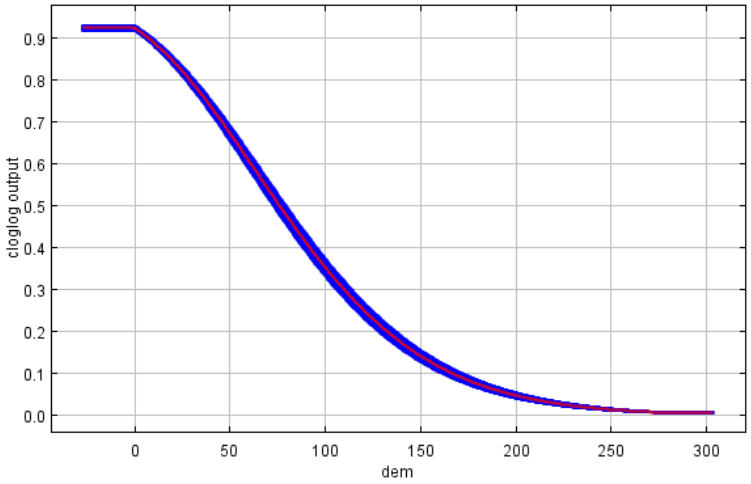
Best performing test rerun	**15**	**0.5**	**6**	**0.842**	**0.842**	**0**	**DEM, land use**		
Hinge	16	0.5	8	0.905	0.847	0.058	DEM	-	Eastness, Spot6 Band 4, Northness
	17	1	8	0.894	0.849	0.045	DEM	-	Eastness, Spot6 Band 4
	18	2	8	0.883	0.846	0.037	DEM	-	Eastness, Spot6 Band 4
	19	4	8	0.863	0.842	0.021	DEM	Eastness	Eastness, Spot6 Band 4
Best performing test rerun	20	4	6	0.846	0.844	0.002	DEM, land use	-	Northness
Linear + Quadratic + Hinge	21	0.5	8	0.905	0.847	0.058	DEM	-	Eastness, Spot6 Band 4
	22	1	8	0.894	0.85	0.044	DEM	-	Eastness, Spot6 Band 4
	23	2	8	0.881	0.848	0.033	DEM	-	Eastness, Spot6 Band 4
	24	4	8	0.862	0.84	0.022	DEM	Eastness	Eastness, Spot6 Band 4
Best performing test rerun	25	4	6	0.845	0.844	0.001	DEM	-	
Automatic	26	0.5	8	0.913	0.851	0.062	DEM	-	Eastness, Spot6 Band 4
	27	1	8	0.904	0.855	0.049	DEM	-	Eastness, Spot6 Band 4
	28	2	8	0.888	0.851	0.037	DEM	Eastness	Eastness, Spot6 Band 4
	29	4	8	0.866	0.845	0.021	DEM	Eastness	Eastness
Best performing test rerun	30	4	7	0.864	0.843	0.021	DEM	-	-

2.3.3.2 *Top performing model comparison for Cat Ba langur distribution modelling*

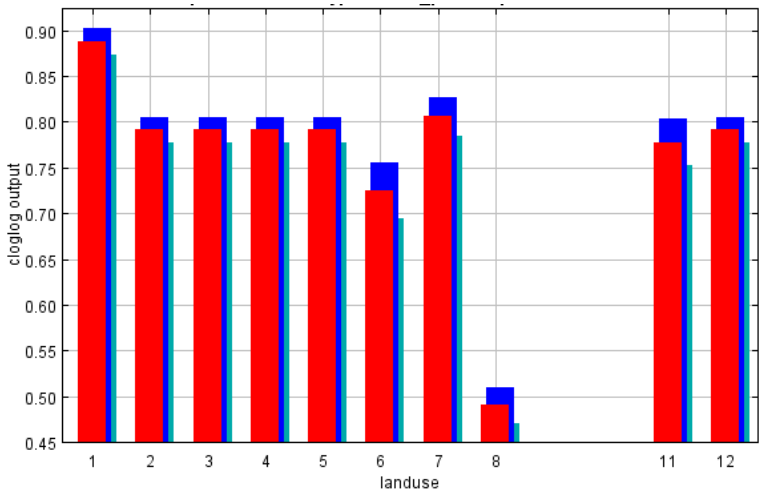
Feature Type	Test #	Number of variables	Number of replications	Regularisation multiplier	Mean AUC	Standard deviation
Linear-only	5	7	10	4	0.8	±0.052
Quadratic-only	10	5	10	4	0.791	±0.042
Linear and Quadratic	15	6	10	0.5	0.835	±0.03
Hinge	20	6	10	4	0.84	±0.026
Linear + Quadratic + Hinge	25	6	10	4	0.841	±0.028
Automatic	30	7	10	4	0.85	±0.033

2.3.3.3 *Response curves of predictor variables for top performing model for Cat Ba langur distribution*

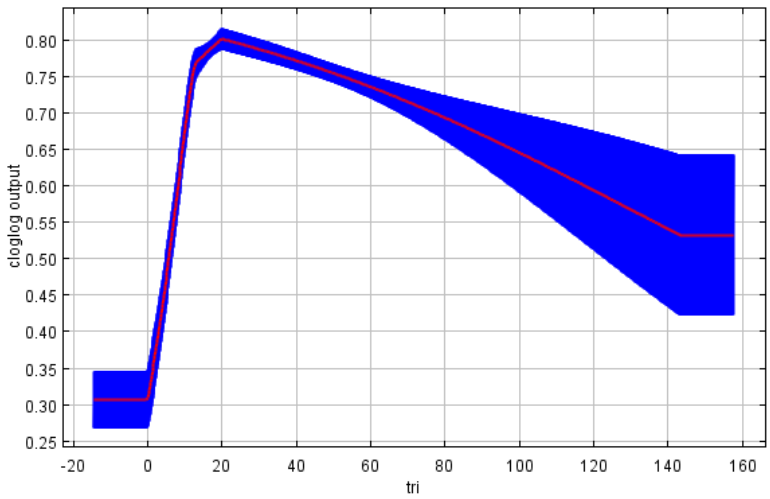
Response curves in order of highest to lowest per cent contribution to model



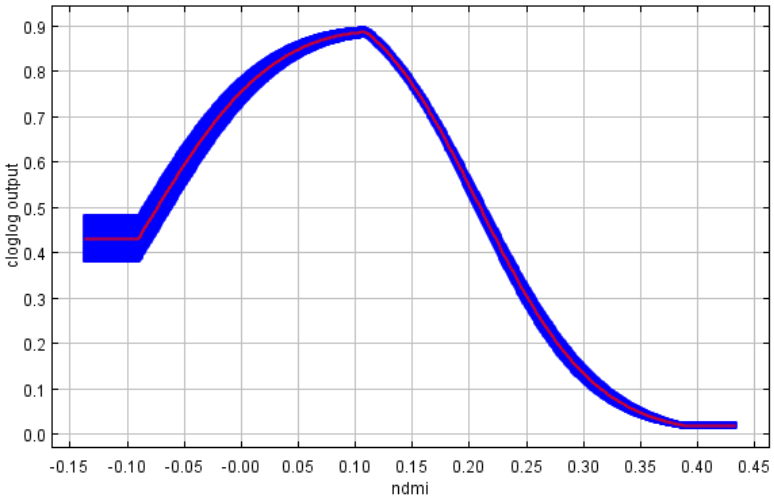
A Digital Elevation Model 36% contribution



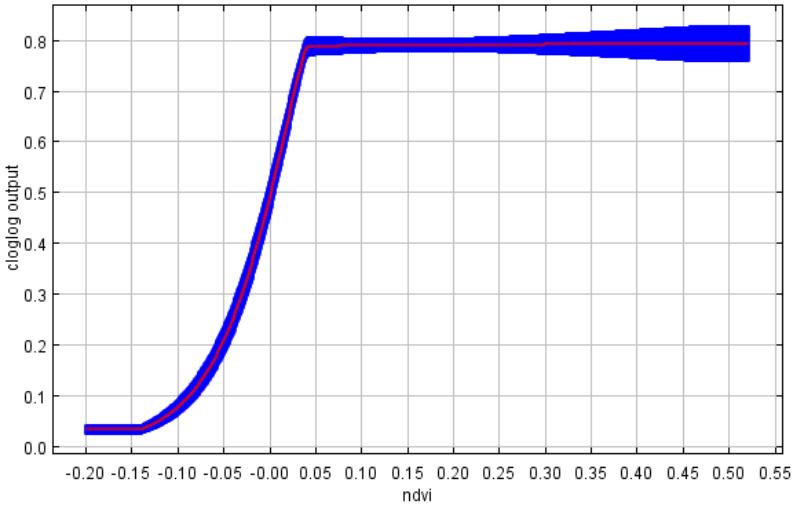
B Land use 19.3% contribution. Categories: 1- water, 2- urban, 3- rice field, 4- crops, 5- grass and shrubs, 6- orchards, 7- barren (limestone), 8- evergreen broadleaf forest, 9- coniferous Forest, 10- deciduous forest, 11- plantation forest, 12 – mangroves.



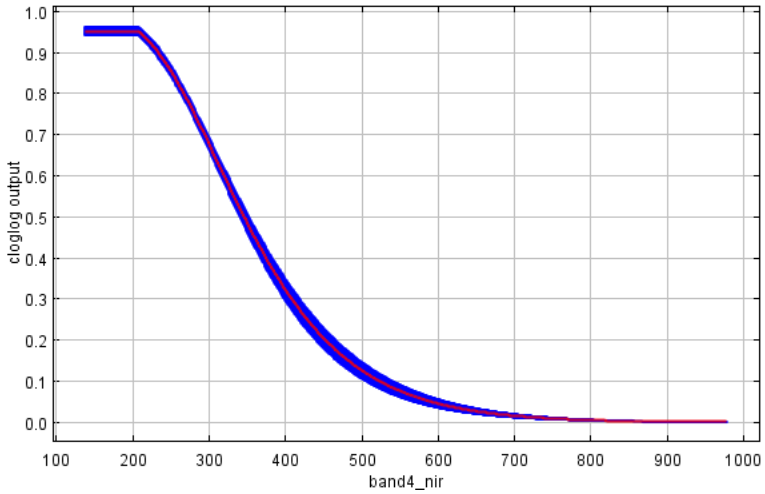
C Terrain Roughness Index 16.7% contribution



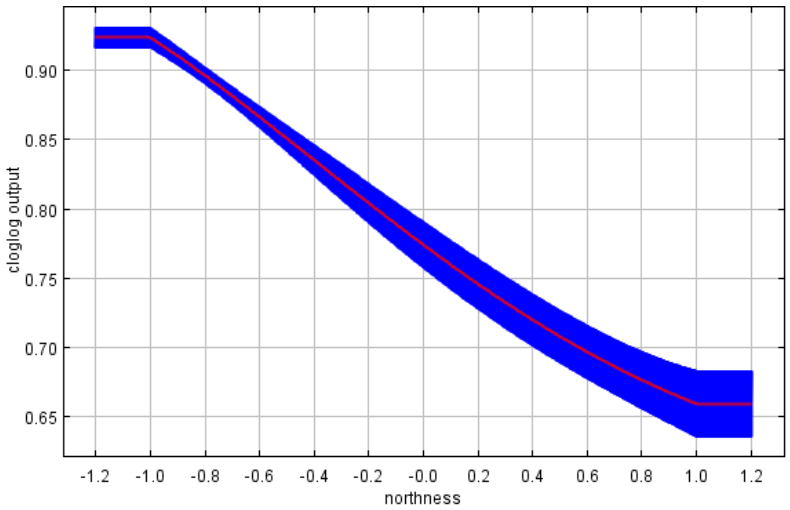
D Normalized Difference Moisture Index 10.7% contribution



E Normalised Difference Vegetation Index 7.9% contribution



F Spot6 Band 4 (Near Infra-red) 5.5% contribution



G Northness 3.9% contribution

Appendix 3 Tonkin snub-nosed monkey

3.1 ANOVA analysis tables for Tonkin snub-nosed monkey (TSNM) habitat

3.1.1 Summary data tables for Khau Ca and Du Gia ANOVA analyses

Plot	Site	Plot type	Elev-ation (m)	General density	Topo-graphic Complex-ity	Slope (deg)	Species richness	Species Diversity	Tree density	Species Density	Canopy height (m)	Mat cover (%)	Shrub cover (%)	Large Shrub cover (%)	Canopy cover (%)	Liana cover (%)	DBH (cm)	Total Basal area (m^2)
KCR 1	Khau ca	Ridge	879	3	3	1	33	2.76	0.11	5.03	9.47	5	90	10	60	2	11.68	20.50
KCR 2	Khau ca	Ridge	1062	4	3	40	56	3.51	0.56	2.94	4.99	20	40	30	60	1	6.38	32.77
KCR 3	Khau ca	Ridge	1029	2	2	30	50	3.35	0.42	3.11	5.17	15	40	30	80	1	6.60	43.07
KCR 4	Khau ca	Ridge	925	2	4	37	46	2.81	0.34	4.04	6.17	10	20	5	50	2	8.28	24.93
KCV 1	Khau ca	Valley	756	4	3	7	48	3.28	0.25	3.31	8.02	5	50	20	80	1	18.63	502.01
KCV 2	Khau ca	Valley	750	2	1	2.4	33	1.98	0.10	6.08	4.30	70	85	20	20	1	6.60	5.97
KCV 3	Khau ca	Valley	825	3	1	8.8	42	2.79	0.12	4.88	12.84	50	70	60	60	1	22.93	105.98
KCV 4	Khau ca	Valley	450	4	1	5	33	2.65	0.20	3.76	4.50	40	85	40	50	1	5.23	8.14
KCS 1	Khau ca	Slope	897	2	4	35	37	3.10	0.16	2.56	7.54	20	60	10	80	5	9.72	21.03
KCS 2	Khau ca	Slope	849	2	4	40	40	3.21	0.21	2.35	8.84	10	30	5	50	1	11.07	83.58
KCS 3	Khau ca	Slope	727	3	2	30	45	3.43	0.21	2.22	5.71	50	90	5	70	5	9.02	17.64
KCS 4	Khau ca	Slope	766	2	4	30	56	3.71	0.31	3.01	5.43	30	40	5	50	5	6.43	27.13

Plot	Site	Plot type	Elev-ation (m)	General density	Topo-graphic Complex-ity	Slope (deg)	Species richness	Species Diversity	Tree density	Species Density	Canopy height (m)	Mat cover (%)	Shrub cover (%)	Large Shrub cover (%)	Canopy cover (%)	Liana cover (%)	Av DBH (cm)	Total Basal area (m^2)
DR 1	Du Gia	Ridge	1196	3	1	5	43	2.56	0.68	5.87	5.39	40	85	30	50	5	5.93	28.87
DR 2	Du Gia	Ridge	1236	2	1	3	30	2.67	0.24	2.02	7.97	10	20	10	35	5	11.44	53.83
DR 3	Du Gia	Ridge	1213	3	1	8	40	3.06	0.3	2.29	7.03	5	45	2	50	5	8.22	25.07
DR 4	Du Gia	Ridge	1153	4	1	2	48	3.30	0.51	3.59	5.53	5	60	60	45	10	5.93	26.79
DS 1	Du Gia	Slope	1114	3	1	22	49	3.15	0.62	2.93	5.48	10	80	20	60	5	5.24	24.40
DS 2	Du Gia	Slope	1058	2	1	38	40	2.19	0.38	3.45	5.00	5	30	30	55	5	7.47	42.31
DS 3	Du Gia	Slope	973	2	1	23	33	2.06	0.33	3.21	6.52	5	30	5	30	10	5.51	11.59
DS 4	Du Gia	Slope	957	4	1	34	45	2.65	0.27	3.14	6.98	10	60	30	40	10	8.43	35.95
DV 1	Du Gia	Valley	901	4	1	40	50	2.44	0.35	4.68	5.58	60	70	45	60	20	8.68	83.96
DV 2	Du Gia	Valley	903	4	3	17	50	2.59	0.31	3.81	3.92	10	70	50	45	20	5.40	16.01
DV 3	Du Gia	Valley	926	2	2	24	45	3.13	0.13	2.3	8.94	10	50	10	30	5	11.65	33.39
DV 4	Du Gia	Valley	855	3	1	30	52	2.97	0.07	3.79	10.77	50	100	2	50	5	17.97	24.11

3.1.2 ANOVA analysis results table for Khau Ca habitat

	Response	Degrees of Freedom	Sum of Squares	Mean Square	F-value	P-value
*Elevation (m)**	Plot	2	156758	78379	5.70	0.025
	Residuals	9	123780	13753		
*Topographic complexity**	Plot	2	8.67	4.33	4.88	0.036
	Residuals	9	8.00	0.89		
*Slope (degrees)**	Plot	2	1701.60	850.80	7.32	0.013
	Residuals	9	1045.40	116.15		
General density scale	Plot	2	2.00	1.00	1.44	0.287
	Residuals	9	6.25	0.69		
Species richness	Plot	2	114.50	57.25	0.79	0.485
	Residuals	9	655.75	72.86		
Species diversity	Plot	2	0.97	0.48	2.86	0.109
	Residuals	9	1.52	0.17		
Species density (stem/m2)*	Plot	2	7.96	3.98	4.62	0.042
	Residuals	9	7.75	0.86		
Tree density (tree stem/m2)	Plot	2	0.08	0.04	2.59	0.129
	Residuals	9	0.13	0.01		
Canopy height (m)	Plot	2	1.86	0.93	0.12	0.887
	Residuals	9	68.75	7.64		
Mat cover (%)	Plot	2	1654.20	827.08	2.31	0.1547
	Residuals	9	3218.80	357.64		
Shrub cover (%)	Plot	2	1316.70	658.33	1.06	0.387
	Residuals	9	5600.00	622.22		
*Large shrub cover (%)**	Plot	2	1662.50	831.25	4.57	0.043
	Residuals	9	1637.50	181.94		
Canopy cover (%)	Plot	2	266.67	133.33	0.39	0.684
	Residuals	9	3025.00	336.11		
*Liana cover (%)**	Plot	2	20.67	10.33	7.15	0.014
	Residuals	9	13.00	1.44		
Av DBH (cm)	Plot	2	60.24	30.12	1.04	0.392
	Residuals	9	260.49	28.94		
Total basal area (m2)	Plot	2	39590	19795	1.05	0.389
	Residuals	9	169785	18865		

* Indicates significant variables where $p<0.05$

3.1.3 Estimated marginal means results table for Khau Ca

	Valley Plots		Slope Plots		Ridge Plots		SE	P<0.05
	Mean	Confidence levels	Mean	Confidence levels	Mean	Confidence levels		
*Elevation (m)**	695	563,828	810	677,942	974	841,1106	±58.60	Ridge-Slope 0.173 Ridge-Valley 0.021 Slope-Valley 0.390
Slope (degrees)*	5.80	6.39,18	33.80	21.56,45.9	27.00	14.81,39.2	±5.39	Ridge-Slope 0.662 Ridge-Valley 0.051 Slope-Valley 0.013
*Topographic Complexity**	1.50	0.434,2.57	3.50	2.43,4.57	3.00	1.934,4,07	±0.67	Ridge-Slope 0.741 Ridge-Valley 0.116 Slope-Valley 0.036
General density	3.25	2.31,4.19	2.25	1.31,3.19	2.75	1.81,3.69	±0.42	Ridge-Slope 0.684 Ridge-Valley 0.684 Slope-Valley 0.258
Species richness	39	29.3,48.7	44.50	34.8,54.2	46.20	36.6,55.9	±4.27	Ridge-Slope 0.955 Ridge-Valley 0.482 Slope-Valley 0.647
Species Diversity	2.68	2.21,3.14	3.36	2.9,3.83	3.11	2.64,3.57	±0.21	Ridge-Slope 0.662 Ridge-Valley 0.344 Slope-Valley 0.097
Species density (stem/m2)*	4.51	3.46,5.56	2.54	1.49,3.58	3.78	2.73,4.83	±0.66	Ridge-Slope 0.195 Ridge-Valley 0.533 Slope-Valley 0.036
Tree density (stem/m2)	0.17	0.03,0.305	0.22	0.09,0.36	0.36	0.22,0.495	±0.06	Ridge-Slope 0.306 Ridge-Valley 0.123 Slope-Valley 0.803
Canopy height (m)	7.42	4.29,10.54	6.88	3.75,10.01	6.45	3.33,9.58	±1.38	Ridge-Slope 0.974 Ridge-Valley 0.876 Slope-Valley 0.959
Mat cover (%)	41.20	19.86,62.6	27.50	6.11,48.9	12.50	-8.89,33.9	± 9.46	Ridge-Slope 0.525 Ridge-Valley 0.134 Slope-Valley 0.579
Shrub cover (%)	72.50	44.3,100.7	55	26.8,83.2	47.50	19.3,75.7	±17.60	Ridge-Slope 0.906 Ridge-Valley 0.373 Slope-Valley 0.599
Large shrub cover (%)*	35.00	19.74,50.3	6.25	9.01,21.5	18.80	3.49,34	±9.54	Ridge-Slope 0.425 Ridge-Valley 0.256 Slope-Valley 0.035
Canopy cover (%)	52.50	31.80,73.20	62.50	41.80,83.20	62.50	41.80,83.20	±9.17	Ridge-Slope 1.00 Ridge-Valley 0.729 Slope-Valley 0.729
Mean Liana cover(%)*	1.00	-0.36,2.36	4.00	2.641,5.36	1.50	0.141,2.86	± 0.60	Ridge-Slope 0.039 Ridge-Valley 0.829 Slope-Valley 0.016
Av DBH (cm)	13.40	7.26,19.40	9.06	0.97,15.10	8.24	2.15,14.30	±2.69	Ridge-Slope 0.975 Ridge-Valley 0.408 Slope-Valley 0.523
Total Basal Area (m2)	156	0.172,311	37.30	-118,193	30.30	-125,186	±68.70	Ridge-Slope 0.997 Ridge-Valley 0.435 Slope-Valley .4733

3.1.4 ANOVA analysis results table for Du Gia forest

	Response	Degrees of Freedom	Sum of Squares	Mean Square	F-value	P-value
*Elevation (m)**	Plot	2	185256	92628	36.76	4.675e-05
	Residuals	9	22681	2520		
Topographic	Plot	2	1.50	0.75	2.45	0.141
complexity	Residuals	9	2.75	0.31		
*Slope (degrees)**	Plot	2	1540.50	770.25	13.96	0.002
	Residuals	9	496.50	55.17		
General density scale	Plot	2	0.50	0.25	0.3	0.748
	Residuals	9	7.50	0.83		
Species richness	Plot	2	186.00	93.00	2.45	0.142
	Residuals	9	342.25	38.03		
Species diversity	Plot	2	0.31	0.16	1.01	0.404
	Residuals	9	1.39	0.16		
Species density	Plot	2	0.43	0.22	0.16	0.857
(stem/m^2)	Residuals	9	12.33	1.37		
Tree density	Plot	2	0.11	0.06	1.99	0.191
(tree stem/m^2)	Residuals	9	0.25	0.03		
Canopy height (m)	Plot	2	3.49	1.75	0.43	0.660
	Residuals	9	36.23	4.025		
Mat cover (%)	Plot	2	1316.70	658.33	2.01	0.190
	Residuals	9	2950.00	327.78		
Shrub cover (%)	Plot	2	1216.70	608.33	1.03	0.395
	Residuals	9	5300.00	588.89		
Large shrub cover (%)	Plot	2	66.50	33.25	0.07	0.931
	Residuals	9	4188.50	465.39		
Canopy cover (%)	Plot	2	4.17	2.08	0.02	0.984
	Residuals	9	1187.50	131.94		
Liana cover (%)	Plot	2	87.50	43.75	1.47	0.281
	Residuals	9	268.75	29.86		
Av DBH (cm)	Plot	2	38.60	19.30	1.53	0.267
	Residuals	9	113.27	12.59		
Total basal area (m^2)	Plot	2	233.90	116.94	0.27	0.769
	Residuals	9	3902.80	433.64		

*Indicates significance where $p<0.05$

3.1.5 Estimated marginal means results table for Du Gia

	Valley Plots		Slope Plots		Ridge Plots		SE	*P*<0.05
	Mean	Confidence levels	Mean	Confidence levels	Mean	Confidence levels		
*Elevation (m)**	896	839, 953	1026	969, 1082	1200	1143, 1256	±25.10	Ridge-Slope 0.002 Ridge-Valley 0.0001 Slope-Valley 0.013
*Slope (degrees)**	27.80	19.3, 36.2	29.2	20.80, 37.70	4.5	-3.90, 12.90	±3.71	Ridge-Slope 0.003 Ridge-Valley 0.004 Slope-Valley 0.956
Topographic Complexity	1.75	1.12, 2.38	1	0.38, 1.63	1	0.38, 1.63	±0.28	Ridge-Slope 1.00 Ridge-Valley 0.189 Slope-Valley 0.189
General density	3.25	2.22, 4.28	2.75	1.72, 3.78	3	1.97, 4.03	±0.46	Ridge-Slope 0.921 Ridge-Valley 0.921 Slope-Valley 0.727
Species richness	49.2	42.30, 56.20	41.80	34.80, 48.70	40.20	33.30, 47.20	±3.08	Ridge-Slope 0.937 Ridge-Valley 0.153 Slope-Valley 0.250
Species diversity	2.78	2.34, 3.23	2.51	2.07, 2.96	2.90	2.45, 3.34	±0.19	Ridge-Slope 0.389 Ridge-Valley 0.911 Slope-Valley 0.613
Species density (stem/m^2)	3.64	2.32, 4.97	3.18	1.86, 4.51	3.44	2.12, 4.77	±0.59	Ridge-Slope 0.947 Ridge-Valley 0.968 Slope-Valley 0.845
Tree density (stem/m^2)	0.22	0.03, 0.40	0.40	0.21, 0.59	0.43	0.25, 0.62	±0.08	Ridge-Slope 0.958 Ridge-Valley 0.208 Slope-Valley 0.304
Mat cover (%)	7.30	5.03, 9.57	6	3.73, 8.26	6.48	4.21, 8.75	±1.00	Ridge-Slope 0.938 Ridge-Valley 0.834 Slope-Valley 0.641
Shrub cover (%)	32.50	12.02, 53.00	7.50	-12.98, 28.00	15	-5.48, 35.50	±9.05	Ridge-Slope 0.831 Ridge-Valley 0.397 Slope-Valley 0.179
Large Shrub cover (%)	72.50	45.10, 99.90	50	22.60, 77.40	52.50	25.10, 79.90	±12.10	Ridge-Slope 0.988 Ridge-Valley 0.501 Slope-Valley 0.424
Canopy cover (%)	26.80	2.35, 51.20	21.20	-3.15,45.70	25.50	1.10, 49.90	±10.80	Ridge-Slope 0.958 Ridge-Valley 0.996 Slope-Valley 0.931
Liana cover (%)	46.20	33.30, 59.20	46.20	33.30, 59.20	45	32.00, 58.00	±5.74	Ridge-Slope 0.987 Ridge-Valley 0.987 Slope-Valley 1.00
Mat cover (%)	12.5	6.32, 18.7	7.5	1.32, 13.7	6.25	0.069, 12.4	±2.73	Ridge-Slope 0.944 Ridge-Valley 0.288 Slope-Valley 0.433
Av DBH (cm)	10.90	6.91, 14.90	6.66	2.65, 10.70	7.88	3.87, 11.9	±1.77	Ridge-Slope 0.879 Ridge-Valley 0.475 Slope-Valley 0.257
Total Basal Area (m^2)	39.40	15.82, 62.92	28.60	5.01, 52.12	33.60	0.09, 57.20	±10.40	Ridge-Slope 0.937 Ridge-Valley 0.921 Slope-Valley 0.750

3.1.6 ANOVA analysis results table of comparison between Khau Ca and Du Gia

	Response	Degree of Freedom	Sum of Squares	Mean Square	F-value	P-value
*Elevation (m)**	Plot	1	275204	275204	33.82	1.647e-05
	Residuals	18	146461	8137		
Topographic complexity	Plot	1	12.04	12.04	20.16	0.0003
	Residuals	18	10.75	0.59		
Slope (degrees)	Plot	1	17.00	17.00	0.20	0.661
	Residuals	18	1541.90	85.66		
General density scale	Plot	1	0.38	0.38	0.49	0.493
	Residuals	18	13.75	0.76		
Species richness	Plot	1	1.50	1.50	0.03	0.871
	Residuals	18	998.00	55.44		
Species diversity	Plot	1	0.61	0.61	3.73	0.07
	Residuals	18	2.92	0.16		
Species density (stem/m^2)*	Plot	1	0.20	0.20	0.18	0.674
	Residuals	18	20.08	1.12		
Tree density (tree stem/m^2)	Plot	1	0.06	0.06	2.84	0.110
	Residuals	18	0.38	0.02		
*Av Canopy height (m)**	Plot	1	0.63	0.63	0.11	0.747
	Residuals	18	104.98	5.83		
Mat cover (%)	Plot	1	459.40	459.38	1.34	0.262
	Residuals	18	6168.80	342.71		
Shrub cover (%)	Plot	1	0.00	0.00	0.00	1.000
	Residuals	18	10900.00	605.56		
Large shrub cover (%)	Plot	1	121.50	121.50	0.38	0.548
	Residuals	18	5826.00	323.67		
*Canopy cover (%)**	Plot	1	1066.7	1066.67	4.56	0.047
	Residuals	18	4212.5	234.03		
Liana cover (%)	Plot	1	260.042	260.042	16.61	0.0007
	Residuals	18	281.750	15.653		
Av DBH (cm)	Plot	1	17.84	17.839	0.86	0.366
	Residuals	18	373.76	20.765		
Total basal area (m^2)	Plot	1	9860	9860.3	1.02	1.022
	Residuals	18	173688	9649.3		

*Indicates significance where $p<0.05$

3.1.7 Estimated marginal means results table for comparison of Khau Ca and Du Gia

	Khau Ca		Du Gia		SE	*P*<0.05
	Mean	Confidence levels	Mean	Confidence levels		
*Elevation (m)**	826	772, 881	1040	986, 1095	±26.00	0.0001
Slope (degrees)	22.2	16.6, 27.8	20.50	14.9, 26.1	±2.67	0.661
*Topographic Complexity**	2.67	2.20, 3.14	1.25	0.78, 1.72	±0.22	0.0003
General density	2.75	2.22, 3.28	3	2.47, 3.53	±0.25	0.490
Species richness	43.20	38.70, 47.80	43.80	39.20, 48.30	±2.15	0.870
Species diversity	3.05	2.80, 3.29	2.73	2.49, 2.98	±0.12	0.069
Species density (stem/m^2)	3.61	2.97, 4.25	3.42	2.78, 4.06	±0.31	0.674
Tree density (stem/m^2)	0.25	0.16, 0.34	0.35	0.26, 0.44	± 0.04	0.109
Mean canopy height (m)	6.92	5.45, 8.38	6.59	5.13, 8.06	±0.69	0.750
Mat cover (%)	27.10	15.86, 38.30	18.30	7.11, 29.60	±5.34	0.260
Shrub cover (%)	58.3	43.40, 73.30	58.30	43.40, 73.30	±7.10	1
Large Shrub cover (%)	20	9.09, 30.90	24.50	13.59, 35.40	±5.19	0.550
Canopy cove (%)	59.20	49.90, 68.40	45.80	36.60, 55.10	±4.42	0.040
*Liana cover (%)**	2.17	0.23, 4.57	8.75	6.35, 11.15	±1.14	0.0007
Av DBH (cm)	10.20	7.45, 13.00	8.49	5.73, 11.30	±1.32	0.367
Total Basal Area (m^2)	74.40	14.82, 133.97	33.9	25.72, 93.43	±28.36	0.326

*Indicates significant variables where p<0.05.

3.2 Plant species captured in Tonkin snub-nosed monkey analysis

3.2.1 All species captured in Du Gia and Khau Ca

Family	Species	Du Gia				Khau Ca			
		Ridge (n)	Slope (n)	Valley (n)	**Total**	Ridge (n)	Slope (n)	Valley (n)	**Total**
Orchidaceae	*Acampe ochracea*	0	0	2	**2**	0	0	0	**0**
Sapindaceae	*Acer cambelii*	0	0	0	**0**	6	0	0	**6**
Sapindaceae	*Acer erythranthum*	0	0	0	**0**	20	0	0	**20**
Sapindaceae	*Acer laurinum*	0	0	0	**0**	2	0	0	**2**
Sapindaceae	*Acer tonkinensis*	1	0	0	**1**	12	0	0	**12**
Acoraceae	*Acorus gramineus*	0	0	3	**3**	0	0	0	**0**
Lauraceae	*Actinodaphne elliptibacca*	0	0	2	**2**	4	0	0	**4**
Lauraceae	*Actinodaphne obovata*	0	0	1	**1**	0	0	0	**0**
Pteridaceae	*Adiantum caudatum*	0	0	0	**0**	0	0	172	**172**
Pteridaceae	*Adiantum philippense*	94	0	86	**180**	0	21	13	**34**
Theaceae	*Adinandra integerrima*	15	0	0	**15**	0	0	0	**0**
Gesneriaceae	*Aeschynanthus evrardii*	0	0	1	**1**	6	0	0	**6**
Gesneriaceae	*Aeschynanthus poilanei*	0	0	0	**0**	1	0	2	**3**
Connaraceae	*Agelaea trinervis*	4	0	0	**4**	0	0	0	**0**
Meliaceae	*Aglaia odoratissima*	0	0	0	**0**	0	0	11	**11**
Meliaceae	*Aglaia spectablis*	0	3	7	**10**	1	3	0	**4**
Meliaceae	*Aglaia viridis*	0	0	0	**0**	0	0	1	**1**
Araceae	*Aglaonema siamense*	0	0	13	**13**	0	51	19	**70**
Araceae	*Aglaonema simplex*	0	0	0	**0**	0	3	0	**3**
Rubiaceae	*Aidia pycnantha*	0	4	0	**4**	23	0	0	**23**
Cornaceae	*Alangium barbatum*	0	1	0	**1**	0	0	0	**0**
Sapindaceae	*Allophylus caudatus*	0	0	0	**0**	57	0	0	**57**
Anacardiaceae	*Allospondias lakhoensis*	0	0	0	**0**	0	1	0	**1**
Styracaceae	*Alniphyllum eberhardtii*	0	1	0	**1**	0	2	2	**4**
Zingiberaceae	*Alpinia chinensis*	0	9	8	**17**	0	0	0	**0**
Zingiberaceae	*Alpinia globosa*	119	0	0	**119**	0	0	0	**0**

Zingiberaceae	*Alpinia tonkinensis*	0	17	0	**17**	0	0	76	**76**
Apocynaceae	*Alyxia sinensis*	7	0	0	**7**	21	8	0	**29**
Araceae	*Amorphophallus sp.*	0	0	11	**11**	0	11	23	**34**
Marattiaceae	*Angiopteris confertinervia*	0	0	0	**0**	0	0	2	**2**
Phyllanthaceae	*Antidesma hainanensis*	3	7	2	**12**	0	4	7	**11**
Phyllanthaceae	*Antidesma montanum*	0	0	0	**0**	0	0	4	**4**
Pteridaceae	*Antrophyum callifolium*	0	202	4	**206**	11	39	0	**50**
Meliaceae	*Aphanamixis polystachya*	0	0	0	**0**	2	6	7	**15**
Araliaceae	*Aralia armata*	1	0	3	**4**	0	0	0	**0**
Mimosaceae	*Archidendron ellipticum*	9	4	0	**13**	0	0	0	**0**
Mimosaceae	*Archidendron tonkinensis*	0	0	24	**24**	0	0	0	**0**
Primulaceae	*Ardisia filiformis*	0	0	0	**0**	0	0	1	**1**
Primulaceae	*Ardisia sylvestris*	0	0	0	**0**	0	0	2	**2**
Primulaceae	*Ardisia villosa*	9	0	0	**9**	5	0	0	**5**
Araceae	*Arisaema petelotii*	0	0	0	**0**	1	9	0	**10**
Moraceae	*Artocarpus styracifolius*	1	0	0	**1**	0	0	0	**0**
Poaceae	*Arundinaria amabilis*	2	0	0	**2**	0	0	0	**0**
Poaceae	*Arundinaria sat*	0	0	0	**0**	103	0	0	**103**
Aristolochiaceae	*Asarum caudigerum*	0	0	0	**0**	0	0	55	**55**
Asparagaceae	*Aspidistra typica*	0	2	9	**11**	43	5	134	**182**
Aspleniaceae	*Asplenium antrophyoides*	0	0	0	**0**	8	0	0	**8**
Aspleniaceae	*Asplenium confusum*	0	0	0	**0**	3	28	83	**114**
Aspleniaceae	*Asplenium falcatum*	0	5	0	**5**	0	0	0	**0**
Aspleniaceae	*Asplenium griffithianum*	0	0	2	**2**	31	0	0	**31**
Aspleniaceae	*Asplenium nitidus*	0	0	14	**14**	19	39	23	**81**
Aspleniaceae	*Asplenium normale*	14	355	6	**375**	48	12	63	**123**
Aspleniaceae	*Asplenium saxicola*	0	0	0	**0**	0	0	14	**14**
Balanophoraceae	*Balanophora latisepala*	0	0	0	**0**	1	0	0	**1**
Poaceae	*Bambusa sesquiflora*	0	3	0	**3**	0	0	0	**0**
Fabaceae	*Bauhinia bracteata*	0	0	0	**0**	0	3	0	**3**

Begoniaceae	*Begonia caobangensis*	0	0	3	**3**	25	37	35	**97**
Begoniaceae	*Begonia guixiensis*	0	0	0	**0**	16	0	8	**24**
Begoniaceae	*Begonia specicola*	0	0	13	**13**	0	0	0	**0**
Phyllanthaceae	*Bischofia javanica*	0	0	2	**2**	0	0	0	**0**
Phyllanthaceae	*Bridelia ovata*	0	0	3	**3**	0	1	0	**1**
Simaroubaceae	*Brucea tonkinensis*	0	0	0	**0**	1	0	0	**1**
Orchidaceae	*Bulbophyllum hymenanthum*	0	0	0	**0**	0	0	1	**1**
Malvaceae	*Burretiodendron hsienmu*	0	0	0	**0**	7	13	5	**25**
Arecaceae	*Calamus petreus*	1	13	1	**15**	0	2	0	**2**
Orchidaceae	*Calanthe triplicataa*	0	0	0	**0**	3	10	4	**17**
Lamiaceae	*Callicarpa macrophylla*	0	1	0	**1**	0	12	2	**14**
Theaceae	*Camellia caudata*	0	0	1	**1**	0	0	5	**5**
Theaceae	*Camellia kissi*	0	0	3	**3**	0	0	0	**0**
Theaceae	*Camellia tsai*	0	0	30	**30**	0	0	0	**0**
Burseraceae	*Canarium album*	0	2	0	**2**	0	0	0	**0**
Burseraceae	*Canarium tramdenanum*	0	1	0	**1**	1	1	0	**2**
Cyperaceae	*Carex baccans*	9	28	0	**37**	0	0	0	**0**
Rhizophoraceae	*Carrallia eugenioidea*	4	8	0	**12**	0	0	0	**0**
Arecaceae	*Caryota bacsonensis*	0	0	3	**3**	0	0	0	**0**
Fagaceae	*Castanopsis echinophora*	0	2	0	**2**	0	0	0	**0**
Fagaceae	*Castanopsis fabrei*	3	0	0	**3**	0	0	0	**0**
Fagaceae	*Castanopsis sp.*	0	0	0	**0**	3	0	1	**4**
Vitaceae	*Cayratia japonica*	10	0	0	**10**	0	3	0	**3**
Ulmaceae	*Celtis japonica*	0	0	0	**0**	6	5	4	**15**
Gesneriaceae	*Chirita drakei*	0	0	0	**0**	0	0	3	**3**
Lauraceae	*Cinnamomum loureirii*	33	13	7	**53**	2	1	0	**3**
Euphorbiaceae	*Claoxylon hainanensis*	0	0	1	**1**	0	0	0	**0**
Rutaceae	*Clausena heptaphylla*	0	0	0	**0**	0	1	2	**3**
Lamiaceae	*Clerodendrum canescens*	0	0	0	**0**	0	4	6	**10**
Araceae	*Colocasia gigantea*	0	0	43	**43**	28	28	12	**68**
Thelypteridaceae	*Coryphopteris falciloba*	0	0	0	**0**	0	18	0	**18**

Costaceae	*Costus tonkinensis*	0	0	7	**7**	0	0	0	**0**
Clusiaceae	*Cratoxylum formosum*	5	0	0	**5**	0	0	0	**0**
Grammitidaceae	*Ctenopteris repandula*	0	0	0	**0**	0	0	5	**5**
Hypoxidaceae	*Curculigo latifolia*	0	0	1	**1**	0	0	0	**0**
Cyatheaceae	*Cyathea gigantea*	4	10	161	**175**	0	8	0	**8**
Thelypteridaceae	*Cyclosorus angustipinnata*	35	75	376	**486**	0	0	0	**0**
Orchidaceae	*Cymbidium finlaysonianum*	0	0	1	**1**	0	0	0	**0**
Dryopteridaceae	*Cyrtomium fraxinellum*	0	0	13	**13**	0	0	0	**0**
Podocarpaceae	*Dacrydium elatum*	1	0	0	**1**	0	0	0	**0**
Myrtaceae	*Decaspermum parviflorum*	7	10	0	**17**	0	0	0	**0**
Orchidaceae	*Dendrobium acinaciforme*	0	0	3	**3**	2	0	1	**3**
Urticaceae	*Dendrocnide urentissima*	0	0	0	**0**	1	8	0	**9**
Annonaceae	*Desmos chinensis*	4	16	1	**21**	3	5	0	**8**
Dryopteridaceae	*Didymochlaena truncatula*	0	0	0	**0**	0	0	22	**22**
Dioscoreaceae	*Dioscorea glabra*	0	0	2	**2**	0	2	0	**2**
Ebenaceae	*Diospyros buxifolia*	0	0	0	**0**	2	8	10	**20**
Ebenaceae	*Diospyros quaesita*	0	55	18	**73**	8	38	2	**48**
Ebenaceae	*Diospyros vaccinoides*	0	2	0	**2**	9	0	0	**9**
Aspleniaceae	*Diplazium esculentum*	0	0	12	**12**	0	0	0	**0**
Aspleniaceae	*Diplazium maximum*	0	0	0	**0**	56	22	38	**116**
Polypodiaceae	*Dipteris chinensis*	0	0	0	**0**	9	29	0	**38**
Asparagaceae	*Disporopsis longifolia*	0	0	0	**0**	2	6	3	**11**
Sapotaceae	*Donella lanceolata*	44	36	1	**81**	0	6	0	**6**
Polypodiaceae	*Drynaria bonii*	0	0	1	**1**	0	0	0	**0**
Dryopteridaceae	*Dryopteris fuscipes*	0	0	0	**0**	0	0	25	**25**
Elaeagnaceae	*Elaeagnus sarmentosus*	0	2	0	**2**	0	0	0	**0**
Elaeocarpaceae	*Elaeocarpus balansae*	2	0	0	**2**	3	3	7	**13**
Elaeocarpaceae	*Elaeocarpus japonicus*	13	1	0	**14**	0	0	0	**0**

Elaeocarpaceae	*Elaeocarpus lanceifolius*	0	0	0	**0**	1	0	0	**1**
Elaeocarpaceae	*Elaeocarpus petiolatus*	204	1	0	**205**	0	0	0	**0**
Urticaceae	*Elatostema cuneatum*	0	0	0	**0**	3	0	0	**3**
Urticaceae	*Elatostema cuneatum*	0	0	14	**14**	0	23	18	**41**
Urticaceae	*Elatostema dissectum*	0	0	0	**0**	23	0	0	**23**
Urticaceae	*Elatostema eurhynchum*	0	0	76	**76**	0	3	0	**3**
Urticaceae	*Elatostema monandrum*	0	0	0	**0**	152	22	27	**201**
Primulaceae	*Embelia polypodioides*	6	2	0	**8**	0	0	0	**0**
Juglandaceae	*Engelhardtia roxburghiana*	7	5	0	**12**	5	0	0	**5**
Araceae	*Epipremnum pinnatum*	0	4	8	**12**	8	5	6	**19**
Rosaceae	*Eriobotrya cavaleriei*	1	0	0	**1**	1	0	0	**1**
Olacacea	*Erythropalum scandens*	0	0	0	**0**	0	3	0	**3**
Rutaceae	*Euodia lepta*	7	0	0	**7**	0	0	0	**0**
Celastraceae	*Euonymus balansae*	3	12	0	**15**	3	0	0	**3**
Pentaphylacaceae	*Eurya japonica*	0	0	0	**0**	0	0	1	**1**
Potaliaceae	*Fagraea fragrans*	0	2	0	**2**	0	0	0	**0**
Moraceae	*Ficus cyrtophylla*	0	0	0	**0**	2	2	0	**4**
Moraceae	*Ficus henryi*	0	0	0	**0**	0	0	1	**1**
Moraceae	*Ficus hirta*	0	0	0	**0**	0	2	0	**2**
Moraceae	*Ficus oligodon*	3	0	0	**3**	0	0	0	**0**
Moraceae	*Ficus sarmentosa*	0	0	2	**2**	0	5	0	**5**
Moraceae	*Ficus sumatra*	0	0	5	**5**	0	0	0	**0**
Moraceae	*Ficus villosa*	0	0	0	**0**	10	4	0	**14**
Annonaceae	*Fissistigma sp.*	4	3	1	**8**	0	16	2	**18**
Oleaceae	*Fraxinus rhynchophyllus*	0	0	3	**3**	10	0	0	**10**
Clusiaceae	*Garcinia bracteata*	0	0	1	**1**	0	0	0	**0**
Clusiaceae	*Garcinia fagraeoides*	1	7	0	**8**	56	5	0	**61**
Rubiaceae	*Geophila repens*	0	0	0	**0**	2	0	0	**2**
Zingiberaceae	*Globba sp.*	1	0	0	**1**	0	0	0	**0**
Celastraceae	*Glyptopetalum poilanei*	0	0	7	**7**	4	0	0	**4**
Gnetaceae	*Gnetum latifolium*	0	0	3	**3**	0	0	0	**0**

Gnetaceae	*Gnetum montanum*	0	12	0	**12**	0	0	0	**0**
Icacinaceae	*Gomphandra tetrandra*	5	5	0	**10**	0	1	1	**2**
Theaceae	*Hartia yunnanensis*	0	0	0	**0**	1	0	0	**1**
Rubiaceae	*Hedyotis scandens*	0	0	4	**4**	0	0	0	**0**
Araceae	*Homalomena tonkinensis*	0	0	42	**42**	0	0	0	**0**
Rhamnaceae	*Hovenia dulcis*	0	0	0	**0**	2	2	0	**4**
Apocynaceae	*Hoya balansae*	2	1	3	**6**	7	0	0	**7**
Aquifoliaceae	*Ilex latifolia*	8	1	0	**9**	0	7	1	**8**
Schisandraceae	*Illicium parvifolium*	4	0	0	**4**	13	0	0	**13**
Hernandiaceae	*Illigera rhodantha*	0	3	0	**3**	0	0	0	**0**
Balsaminaceae	*Impatiens balsamina*	0	0	0	**0**	13	1	0	**14**
Icacinaceae	*Iodes cirrhoa*	3	2	2	**7**	0	1	0	**1**
Icacinaceae	*Iodes seguini*	0	0	0	**0**	0	0	1	**1**
Iridaceae	*Iris grandis*	2	0	0	**2**	0	0	0	**0**
Rubiaceae	*Ixora balansae*	0	0	1	**1**	0	3	0	**3**
Oleaceae	*Jasminum pedunculatum*	0	0	0	**0**	0	4	0	**4**
Rubiaceae	*Lasianthus cyanocarpus*	0	0	1	**1**	0	0	0	**0**
Rubiaceae	*Lasianthus hookeri*	42	16	0	**58**	10	33	5	**48**
Rubiaceae	*Lasianthus japonicus*	0	6	0	**6**	0	0	0	**0**
Rubiaceae	*Lasianthus tonkinensis*	0	16	8	**24**	0	0	0	**0**
Vitaceae	*Leea indica*	0	0	0	**0**	0	2	3	**5**
Orchidaceae	*Liparis macrantha*	4	0	1	**5**	58	0	0	**58**
Fagaceae	*Lithocarpus fenestratus*	0	0	2	**2**	3	0	0	**3**
Fagaceae	*Lithocarpus sp.*	2	6	3	**11**	1	0	6	**7**
Lauraceae	*Litsea balansae*	0	8	5	**13**	0	0	0	**0**
Lauraceae	*Litsea brevipes*	0	0	1	**1**	3	7	2	**12**
Lauraceae	*Litsea cubeba*	1	0	1	**2**	0	0	0	**0**
Lauraceae	*Litsea glutinosa*	1	0	1	**2**	0	0	0	**0**
Lauraceae	*Litsea griffithii*	19	6	0	**25**	0	0	0	**0**
Lauraceae	*Litsea helferi*	3	0	0	**3**	2	0	0	**2**
Lauraceae	*Litsea laevifolia*	0	0	0	**0**	3	0	0	**3**
Lauraceae	*Litsea monopetala*	0	1	0	**1**	0	0	0	**0**
Lauraceae	*Litsea variabilis*	7	4	0	**11**	0	0	0	**0**
Lauraceae	*Litsea verticillata*	10	4	0	**14**	0	0	0	**0**

Lauraceae	*Litsea viridis*	0	3	0	**3**	0	0	0	**0**
Arecaceae	*Livistona tonkinensis*	0	2	3	**5**	0	0	0	**0**
Euphorbiaceae	*Macaranga henryi*	133	51	1	**185**	0	0	0	**0**
Lauraceae	*Machilus macrophylla*	1	0	0	**1**	0	0	0	**0**
Lauraceae	*Machilus oreophila*	8	6	0	**14**	0	0	0	**0**
Lauraceae	*Machilus platycarpa*	2	0	0	**2**	3	3	0	**6**
Sapotaceae	*Madhuca hainnanensis*	0	0	0	**0**	0	0	2	**2**
Primulaceae	*Maesa balansae*	0	0	4	**4**	0	0	0	**0**
Primulaceae	*Maesa membranacae*	0	2	0	**2**	0	0	0	**0**
Euphorbiaceae	*Mallotus barbatus*	0	0	2	**2**	0	0	0	**0**
Anacardiaceae	*Mangifera longipes*	0	0	0	**0**	1	0	0	**1**
Marantaceae	*Maranta arundinacea*	0	0	9	**9**	0	0	0	**0**
Melastomataceae	*Melastoma normale*	1	3	0	**4**	0	0	0	**0**
Opiliaceae	*Meliantha suavis*	0	0	0	**0**	0	5	0	**5**
Melastomataceae	*Memecylon scutellatum*	0	0	1	**1**	0	0	0	**0**
Pandaceae	*Microdesmis caseariaefolia*	0	0	0	**0**	1	0	0	**1**
Rutaceae	*Micromelum intergimum*	0	0	0	**0**	0	3	0	**3**
Rutaceae	*Micromelum minutum*	0	3	3	**6**	4	0	0	**4**
Annonaceae	*Miliusa sinensis*	0	0	0	**0**	0	4	0	**4**
Annonaceae	*Miliusa sinensis*	0	8	0	**8**	0	0	0	**0**
Musaceae	*Musa acuminata*	0	0	1	**1**	0	0	0	**0**
Rubiaceae	*Mussaenda chevalieri*	0	0	0	**0**	1	0	0	**1**
Rubiaceae	*Myrioneuron tonkinensis*	0	0	1	**1**	2	9	0	**11**
Podocarpaceae	*Nageia fleuryi*	0	0	0	**0**	4	1	1	**6**
Ranunculaceae	*Naravelia laurifolia*	0	0	0	**0**	0	0	1	**1**
Polypodiaceae	*Neocheiropteris sapaensis*	0	0	0	**0**	70	0	17	**87**
Lauraceae	*Neolitsea alongensis*	0	0	0	**0**	0	1	0	**1**
Fabaceae	*Nogra grahamii*	0	0	0	**0**	0	1	0	**1**
Oleaceae	*Olea rosea*	7	0	0	**7**	2	6	4	**12**
Asparagaceae	*Ophiopogon reptans*	23	7	0	**30**	13	5	0	**18**

Rubiaceae	*Ophiorrhiza japonica*	0	0	11	**11**	0	0	96	**96**
Melastomataceae	*Oxyspora balansae*	0	0	8	**8**	0	0	0	**0**
Melastomataceae	*Oxyspora paniculata*	0	10	0	**10**	12	0	0	**12**
Pandanaceae	*Pandanus humilis*	32	1	2	**35**	6	0	0	**6**
Orchidaceae	*Paphiopedilum henryanum*	0	0	0	**0**	1	0	0	**1**
Gesneriaceae	*Paraboea multiflora*	0	0	15	**15**	18	0	0	**18**
Sapindaceae	*Paranephelium spirei*	0	0	0	**0**	1	0	3	**4**
Trilliaceae	*Paris polyphylla*	0	0	0	**0**	0	0	7	**7**
Rubiaceae	*Pavetta translucens*	3	0	0	**3**	6	0	21	**27**
Urticaceae	*Pellionia griffithiana*	0	0	3	**3**	0	0	0	**0**
Caesalpiniaceae	*Peltophorum dassyrachis*	0	1	0	**1**	0	0	0	**0**
Campanulaceae	*Pentaphragma sinense*	0	0	6	**6**	0	0	0	**0**
Orchidaceae	*Phaius indochinensis*	0	0	2	**2**	0	3	0	**3**
Acanthaceae	*Phlogacanthus annamensis*	0	1	15	**16**	15	30	46	**91**
Acanthaceae	*Phlogacanthus colainae*	0	0	11	**11**	0	0	98	**98**
Lauraceae	*Phoebe kunstleri*	4	2	1	**7**	8	5	5	**18**
Phyllanthaceae	*Phyllanthus ruber*	0	2	1	**3**	4	7	4	**15**
Urticaceae	*Pilea melastomoides*	0	0	26	**26**	0	0	0	**0**
Urticaceae	*Pilea notata*	0	0	0	**0**	16	0	3	**19**
Piperaceae	*Piper brevicaule*	0	3	23	**26**	1	0	0	**1**
Piperaceae	*Piper cubeba*	0	0	8	**8**	5	15	0	**20**
Piperaceae	*Piper saxicola*	0	0	0	**0**	7	20	10	**37**
Podocarpaceae	*Podocarpus neriifolius*	6	0	0	**6**	0	2	0	**2**
Commelinaceae	*Pollia japonica*	20	0	30	**50**	0	0	12	**12**
Annonaceae	*Polyalthia lauii*	0	13	4	**17**	24	18	31	**73**
Polygalaceae	*Polygala luteo-alba*	6	0	0	**6**	0	0	0	**0**
Convallariaceae	*Polygonatum kingianum*	0	0	0	**0**	0	1	0	**1**
Sapindaceae	*Pometia pinnata*	0	0	0	**0**	0	3	2	**5**
Araceae	*Pothos repens*	0	0	19	**19**	0	8	0	**8**
Araceae	*Pothos scandens*	0	19	0	**19**	0	4	2	**6**
Lamiaceae	*Premna flavescens*	0	0	0	**0**	1	0	0	**1**
Rosaceae	*Prunus arborea*	24	8	0	**32**	0	0	0	**0**

Rosaceae	*Prunus mume*	0	0	0	**0**	4	0	0	**4**
Rosaceae	*Prunus wallichii*	106	0	0	**106**	5	2	0	**7**
Rubiaceae	*Psychotria balansae*	0	0	0	**0**	0	0	17	**17**
Rubiaceae	*Psychotria montana*	40	20	8	**68**	52	8	7	**67**
Rubiaceae	*Psychotria rubra*	9	25	3	**37**	30	16	31	**77**
Rubiaceae	*Psychotria tonkinensis*	13	0	8	**21**	11	15	227	**253**
Pteridaceae	*Pteris vittata*	0	0	0	**0**	0	0	31	**31**
Fabaceae	*Pterolobium microphyllum*	0	0	1	**1**	0	3	0	**3**
Acanthaceae	*Pteroptychia dalzielli*	0	0	0	**0**	20	0	0	**20**
Polypodiaceae	*Pyrrosia lanceolata*	0	0	2	**2**	0	0	0	**0**
Fagaceae	*Quercus bambusaefolia*	0	6	0	**6**	0	0	0	**0**
Fagaceae	*Quercus sp.*	1	2	0	**3**	4	0	0	**4**
Bignoniaceae	*Radermachera stellata*	0	0	0	**0**	0	1	0	**1**
Ericaceae	*Rhododendron saxicolum*	0	0	0	**0**	4	0	0	**4**
Ericaceae	*Rhododendron simsii*	1	0	0	**1**	6	0	0	**6**
Hamamelidaceae	*Rhodoleia champinonii*	0	0	0	**0**	1	0	0	**1**
Gesneriaceae	*Rhynchothecum parviflorum*	0	0	0	**0**	0	0	21	**21**
Connaraceae	*Rourea minor*	4	7	0	**11**	9	4	0	**13**
Sapindaceae	*Sapindus mukorossi*	0	2	1	**3**	0	6	3	**9**
Sapindaceae	*Sapindus oocarpus*	3	9	0	**12**	1	19	0	**20**
Euphorbiaceae	*Sapium discolor*	0	0	0	**0**	1	0	0	**1**
Caesalpiniaceae	*Saraca dives*	0	0	1	**1**	0	0	0	**0**
Melastomataceae	*Sarcopyramis nepalensis*	27	0	0	**27**	0	3	28	**31**
Sargentodoxaceae	*Sargentodoxa cuneata*	0	0	0	**0**	0	3	0	**3**
Actinidiaceae	*Saurauia fasciculata*	0	0	0	**0**	2	0	16	**18**
Actinidiaceae	*Saurauia roxburghii*	0	0	51	**51**	0	0	0	**0**
Araliaceae	*Schefflera heptaphylla*	0	0	3	**3**	0	4	0	**4**
Araliaceae	*Schefflera macrophylla*	4	1	1	**6**	0	0	0	**0**
Araliaceae	*Schefflera pes-avis*	0	1	0	**1**	0	6	0	**6**
Salicaceae	*Scolopia spinosa*	0	1	1	**2**	0	0	0	**0**
Selaginellaceae	*Selaginella delicatula*	0	5	15	**20**	23	0	0	**23**

Sapotaceae	*Sinosideroxylon racemosum*	0	0	0	**0**	2	6	4	**12**
Sapotaceae	*Sinosideroxylon wightianum*	0	0	0	**0**	8	0	0	**8**
Smilacaceae	*Smilax bracteata*	29	9	5	**43**	0	2	2	**4**
Smilacaceae	*Smilax corbularia*	19	0	0	**19**	0	0	0	**0**
Menispermaceae	*Stephania rotunda*	0	0	0	**0**	7	1	0	**8**
Malvaceae	*Sterculia lanceolata*	0	1	2	**3**	0	9	4	**13**
Loganiaceae	*Strychnos axillaris*	0	0	0	**0**	4	3	0	**7**
Symplocaceae	*Symplocos cambodiana*	6	0	0	**6**	0	0	0	**0**
Myrtaceae	*Syzygium cumini*	0	0	0	**0**	0	0	2	**2**
Myrtaceae	*Syzygium formosum*	0	6	12	**18**	0	2	3	**5**
Myrtaceae	*Syzygium zeylanicum*	13	0	0	**13**	6	3	0	**9**
Apocynaceae	*Tabernaemontana bovina*	0	0	0	**0**	0	3	3	**6**
Apocynaceae	*Tabernaemontana bufalina*	0	0	5	**5**	0	0	0	**0**
Taxaceae	*Taxus chinensis*	0	0	0	**0**	1	0	0	**1**
Vitaceae	*Tetrastigma backanense*	0	0	0	**0**	8	0	0	**8**
Vitaceae	*Tetrastigma beauvaisii*	3	2	7	**12**	18	11	29	**58**
Vitaceae	*Tetrastigma cauliflorum*	0	0	0	**0**	15	12	8	**35**
Vitaceae	*Tetrastigma obtectum*	5	0	11	**16**	0	0	2	**2**
Cucurbitaceae	*Thladiantha siamensis*	1	0	0	**1**	1	0	0	**1**
Menispermaceae	*Tinomiscium petiolare*	0	0	0	**0**	0	3	2	**5**
Araliaceae	*Trevesia palmata*	0	0	0	**0**	0	4	1	**5**
Euphorbiaceae	*Trigonostemon thyrsoideus*	0	0	0	**0**	0	15	1	**16**
Asparagaceae	*Tupistra tonkinensis*	18	13	0	**31**	0	7	5	**12**
Rubiaceae	*Uncaria laevigata*	0	0	1	**1**	0	0	0	**0**
Hymenophyllaceae	*Vandenboschia radicans*	1	0	3	**4**	0	0	0	**0**
Rhamnaceae	*Ventilago calyculata*	0	0	3	**3**	0	0	0	**0**
Euphorbiaceae	*Vernicia montana*	0	0	0	**0**	9	0	0	**9**
Urticaceae	*Villebrunea integrifolia*	0	0	1	**1**	10	8	0	**18**

Lamiaceae	*Vitex quinata*	0	0	0	**0**	2	0	0	**2**
Rubiaceae	*Wendlandia laotica*	0	2	3	**5**	9	14	1	**24**
Blechnaceae	*Woodwardia japonica*	0	1	0	**1**	0	0	0	**0**
Total		**1377**	**1273**	**1458**	**4108**	**1510**	**1014**	**1803**	**4326**

3.2.2 Tree species captured in Du Gia and Khau Ca

Family	Scientific name	Khau Ca				Du Gia			
		Ridge (n)	Slope (n)	Valley (n)	Total	Ridge (n)	Slope (n)	Valley (n)	Total
Sapindaceae	*Acer cambelii*	6	0	0	6	0	0	0	0
Sapindaceae	*Acer erythranthum*	4	0	0	4	0	0	0	0
Sapindaceae	*Acer laurinum*	1	0	0	1	0	0	0	0
Lauraceae	*Actinodaphne elliptibacca*	4	0	0	4	0	0	2	2
Lauraceae	*Actinodaphne obovata*	0	0	0	0	0	0	1	1
Meliaceae	*Aglaia odoratissima*	0	0	2	2	0	0	0	0
Meliaceae	*Aglaia spectablis*	1	1	0	2	0	1	2	3
Rubiaceae	*Aidia pycnantha*	7	0	0	7	0	4	0	4
Cornaceae	*Alangium barbatum*	0	0	0	0	0	1	0	1
Anacardiaceae	*Allospondias lakhoensis*	0	1	0	1	0	0	0	0
Styracaceae	*Alniphyllum eberhardtii*	0	2	2	4	0	1	0	1
Phyllanthaceae	*Antidesma hainanensis*	0	0	1	1	1	5	2	8
Meliaceae	*Aphanamixis polystachya*	2	4	2	8	0	0	0	0
Mimosaceae	*Archidendron ellipticum*	0	0	0	0	6	2	0	8
Mimosaceae	*Archidendron tonkinensis*	0	0	0	0	0	0	7	7
Primulaceae	*Ardisia filiformis*	0	0	1	1	0	0	0	0
Moraceae	*Artocarpus styracifolius*	0	0	0	0	1	0	0	1
Simaroubaceae	*Brucea tonkinensis*	1	0	0	1	0	0	0	0
Malvaceae	*Burretiodendron hsienmu*	1	2	1	4	0	0	0	0
Lamiaceae	*Callicarpa macrophylla*	0	5	0	5	0	0	0	0
Theaceae	*Camellia caudata*	0	0	1	1	0	0	0	0
Theaceae	*Camellia kissi*	0	0	0	0	0	0	3	3
Theaceae	*Camellia tsai*	0	0	0	0	0	0	11	11
Burseraceae	*Canarium album*	0	0	0	0	0	2	0	2
Burseraceae	*Canarium tramdenanum*	1	1	0	2	0	0	0	0
Rhizophoraceae	*Carrallia eugenioidea*	0	0	0	0	0	1	0	1
Arecaceae	*Caryota bacsonensis*	0	0	0	0	0	0	1	1
Fagaceae	*Castanopsis echinophora*	0	0	0	0	0	1	0	1

Fagaceae	*Castanopsis fabrei*	0	0	0	0	3	0	0	3
Fagaceae	*Castanopsis sp.*	0	0	1	1	0	0	0	0
Ulmaceae	*Celtis japonica*	2	1	0	3	0	0	0	0
Lauraceae	*Cinnamomum loureirii*	1	1	0	2	13	3	2	18
Euphorbiaceae	*Claoxylon hainanensis*	0	0	0	0	0	0	1	1
Rutaceae	*Clausena heptaphylla*	0	1	0	1	0	0	0	0
Clusiaceae	*Cratoxylum formosum*	0	0	0	0	1	0	0	1
Myrtaceae	*Decaspermum parviflorum*	0	0	0	0	2	7	0	9
Urticaceae	*Dendrocnide urentissima*	1	0	0	1	0	0	0	0
Ebenaceae	*Diospyros buxifolia*	2	5	5	12	0	0	0	0
Ebenaceae	*Diospyros quaesita*	2	4	0	6	0	17	4	21
Ebenaceae	*Diospyros vaccinoides*	3	0	0	3	0	0	0	0
Sapotaceae	*Donella lanceolata*	0	0	0	0	33	15	1	49
Elaeocarpaceae	*Elaeocarpus balansae*	1	1	1	3	2	0	0	2
Elaeocarpaceae	*Elaeocarpus japonicus*	0	0	0	0	4	1	0	5
Elaeocarpaceae	*Elaeocarpus lanceifolius*	1	0	0	1	0	0	0	0
Elaeocarpaceae	*Elaeocarpus petiolatus*	0	0	0	0	19	1	0	20
Juglandaceae	*Engelhardtia roxburghiana*	2	0	0	2	3	3	0	6
Rosaceae	*Eriobotrya cavaleriei*	1	0	0	1	1	0	0	1
Olacacea	*Erythropalum scandens*	0	1	0	1	0	0	0	0
Rutaceae	*Euodia lepta*	0	0	0	0	3	0	0	3
Celastraceae	*Euonymus balansae*	1	0	0	1	2	3	0	5
Pentaphylacaceae	*Eurya japonica*	0	0	1	1	0	0	0	0
Potaliaceae	*Fagraea fragrans*	0	0	0	0	0	2	0	2
Moraceae	*Ficus cyrtophylla*	2	0	0	2	0	0	0	0
Moraceae	*Ficus henryi*	0	0	1	1	0	0	0	0
Moraceae	*Ficus hirta*	0	1	0	1	0	0	0	0
Moraceae	*Ficus sumatra*	0	0	0	0	0	0	2	2
Oleaceae	*Fraxinus rhynchophyllus*	0	0	0	0	0	0	1	1
Clusiaceae	*Garcinia bracteata*	0	0	0	0	0	0	1	1

Clusiaceae	*Garcinia fagraeoides*	7	3	0	10	0	5	0	5
Celastraceae	*Glyptopetalum poilanei*	4	0	0	4	0	0	5	5
Gnetaceae	*Gnetum montanum*	0	0	0	0	0	1	0	1
Icacinaceae	*Gomphandra tetrandra*	0	1	1	2	0	0	0	0
Theaceae	*Hartia yunnanensis*	1	0	0	1	0	0	0	0
Aquifoliaceae	*Ilex latifolia*	0	5	1	6	3	1	0	4
Schisandraceae	*Illicium parvifolium*	7	0	0	7	2	0	0	2
Rubiaceae	*Ixora balansae*	0	3	0	3	0	0	1	1
Rubiaceae	*Lasianthus cyanocarpus*	0	0	0	0	0	0	1	1
Rubiaceae	*Lasianthus japonicus*	0	0	0	0	0	2	0	2
Vitaceae	*Leea indica*	0	0	1	1	0	0	0	0
Fagaceae	*Lithocarpus fenestratus*	0	0	0	0	0	0	2	2
Fagaceae	*Lithocarpus sp.*	0	0	0	0	2	6	1	9
Lauraceae	*Litsea balansae*	0	0	0	0	0	8	1	9
Lauraceae	*Litsea brevipes*	3	1	1	5	0	0	1	1
Lauraceae	*Litsea glutinosa*	0	0	0	0	0	0	1	1
Lauraceae	*Litsea griffithii*	0	0	0	0	1	3	0	4
Lauraceae	*Litsea helferi*	2	0	0	2	3	0	0	3
Lauraceae	*Litsea monopetala*	0	0	0	0	0	1	0	1
Lauraceae	*Litsea variabilis*	0	0	0	0	4	0	0	4
Lauraceae	*Litsea verticillata*	0	0	0	0	4	4	0	8
Lauraceae	*Litsea viridis*	0	0	0	0	0	1	0	1
Euphorbiaceae	*Macaranga henryi*	0	0	0	0	11	13	0	24
Lauraceae	*Machilus macrophylla*	0	0	0	0	1	0	0	1
Lauraceae	*Machilus oreophila*	0	0	0	0	7	3	0	10
Lauraceae	*Machilus platycarpa*	0	1	0	1	1	0	0	1
Sapotaceae	*Madhuca hainnanensis*	0	0	2	2	0	0	0	0
Euphorbiaceae	*Mallotus barbatus*	0	0	0	0	0	0	1	1
Anacardiaceae	*Mangifera longipes*	1	0	0	1	0	0	0	0
Pandaceae	*Microdesmis casearíaefolia*	1	0	0	1	0	0	0	0
Rutaceae	*Micromelum minutum*	0	0	0	0	0	0	1	1
Annonaceae	*Miliusa sinensis*	0	0	0	0	0	8	0	8

Rubiaceae	*Mussaenda chevalieri*	1	0	0	1	0	0	0	0
Rubiaceae	*Myrioneuron tonkinensis*	1	0	0	1	0	0	0	0
Podocarpaceae	*Nageia fleuryi*	2	0	0	2	0	0	0	0
Oleaceae	*Olea rosea*	2	3	3	8	7	0	0	7
Melastomataceae	*Oxyspora paniculata*	0	0	0	0	0	7	0	7
Sapindaceae	*Paranephelium spirei*	1	0	2	3	0	0	0	0
Caesalpiniaceae	*Peltophorum dassyrachis*	0	0	0	0	0	1	0	1
Acanthaceae	*Phlogacanthus annamensis*	2	0	9	11	0	1	4	5
Lauraceae	*Phoebe kunstleri*	3	1	2	6	1	0	1	2
Phyllanthaceae	*Phyllanthus ruber*	1	5	2	8	0	1	0	1
Annonaceae	*Polyalthia lauii*	14	6	1	21	0	6	2	8
Sapindaceae	*Pometia pinnata*	0	2	0	2	0	0	0	0
Rosaceae	*Prunus arborea*	0	0	0	0	11	5	0	16
Rosaceae	*Prunus wallichii*	2	2	0	4	0	0	0	0
Rubiaceae	*Psychotria rubra*	5	0	4	9	0	7	1	8
Rubiaceae	*Psychotria tonkinesis*	0	0	0	0	0	0	2	2
Fagaceae	*Quercus sp.*	2	0	0	2	1	2	0	3
Ericaceae	*Rhododendron saxicolum*	1	0	0	1	0	0	0	0
Sapindaceae	*Sapindus mukorossi*	0	2	2	4	0	2	1	3
Sapindaceae	*Sapindus oocarpus*	1	1	0	2	0	0	0	0
Caesalpiniaceae	*Saraca dives*	0	0	0	0	0	0	1	1
Actinidiaceae	*Saurauia fasciculata*	0	0	7	7	0	0	0	0
Actinidiaceae	*Saurauia roxburghii*	0	0	0	0	0	0	7	7
Araliaceae	*Schefflera heptaphylla*	0	1	0	1	0	0	2	2
Araliaceae	*Schefflera macrophylla*	0	0	0	0	1	1	1	3
Sapotaceae	*Sinosideroxylon racemosum*	2	4	1	7	0	0	0	0
Sapotaceae	*Sinosideroxylon wightianum*	6	0	0	6	0	0	0	0
Malvaceae	*Sterculia lanceolata*	0	1	1	2	0	0	0	0
Symplocaceae	*Symplocos cambodiana*	0	0	0	0	5	0	0	5
Myrtaceae	*Syzygium cumini*	0	0	2	2	0	0	0	0
Myrtaceae	*Syzygium formosum*	0	0	2	2	0	0	2	2

Myrtaceae	*Syzygium zeylanicum*	4	3	0	7	13	0	0	13
Apocynaceae	*Tabernaemontana bovina*	0	3	2	5	0	0	0	0
Apocynaceae	*Tabernaemontana bufalina*	0	0	0	0	0	0	3	3
Araliaceae	*Trevesia palmata*	0	1	0	1	0	0	0	0
Euphorbiaceae	*Trigonostemon thyrsoideus*	0	0	1	1	0	0	0	0
Euphorbiaceae	*Vernicia montana*	1	0	0	1	0	0	0	0
Urticaceae	*Villebrunea integrifolia*	10	5	0	15	0	0	0	0
Lamiaceae	*Vitex quinata*	2	0	0	2	0	0	0	0
Rubiaceae	*Wendlandia laotica*	7	1	1	9	0	2	3	5
Total		**143**	**86**	**67**	**296**	**172**	**161**	**86**	**419**

3.3 Food species for the Tonkin snub-nosed monkey

3.3.1 Food species identified in previous studies

Species taken from Quyet et al. (2007); Covert et al. (2008); Hai (2011); Pham et al. (1993/4); Le & Boonratana (2006).

Family	Species
Sapindaceae	*Acer chapaense*
Sapindaceae	*Acer tonkinensis**
Rutaceae	*Acronychia pedunculata*
Mimosaceae	*Adenanthera microsperma*
Anacardiaceae	*Allospondias lakonensis*
Annonaceae	*Alphonsea tonkinensis*
Meliaceae	*Amoora giganta*
Meliaceae	*Ananamixis grandifolia*
Gesneriaceae	*Anna submontana*
Phyllanthaceae	*Antidesma montanum**
Phyllanthaceae	*Antidesma sp.*
Apocynaceae	*Apocynaceae sp*
Mimosaceae	*Archidendron sp.*
Primulaceae	*Ardisia crispa*
Primulaceae	*Ardisia quinquegona*
Primulaceae	*Ardisia ramondiaeformis*
Meliaceae	*Averrhoa carambola*
Euphorbiaceae	*Bacaurea sapida*
Poaceae	*Bambusa spinosa*
Rhamnaceae	*Berchemia floribunda*
Phyllanthaceae	*Bischofia trifoliata*
Moraceae	*Bleekrodea tonkinensis*
Fabaceae	*Bowringia callicarpa*
Araliaceae	*Brassaiopsis sp.*
Araliaceae	*Brassaiopsis stellata*
Phyllanthaceae	*Bridelia monoica*
Phyllanthaceae	*Bridelia retusa*
Moraceae	*Broussonetia papyrifera*
Orchidaceae	*Bulbophyllum affine*
Orchidaceae	*Bulbophyllum pectinatum*
Malvaceae	*Burretiodendron hsienmu*
Theaceae	*Camellia sasanqua*
Burceraceae	*Canarium album*
Burceraceae	*Canarium nigrum*

Burceraceae	*Canarium nigrum*
Burceraceae	*Canarium tonkinense*
Burceraceae	*Canarium tonkinensis*
Arecaceae	*Caryota lancium*
Arecaceae	*Caryota mitis*
Fagaceae	*Castanea mollisma*
Fagaceae	*Castanopsis boissi*
Fagaceae	*Castanopsis chinensis*
Fagaceae	*Castanopsis tonkinensis*
Ulmaceae	*Celtis sinensis*
Meliaceae	*Chisochenton paniculatus*
Anacardiaceae	*Choerospondias axillaris*
Rutaceae	*Clausena excavata*
Rutaceae	*Clausena laevis*
Rutaceae	*Clausena lansium*
Myrtaceae	*Cleistocalyx operculatus*
Verbenaceae	*Congea sp*
Lauraceae	*Cryptocarya sp*
Fabaceae	*Dalbergia tonkinensis*
Urticaceae	*Debregeasia squamata aff. etuberculata*
Poaceae	*Dendrocalamus dulloca*
Arecaceae	*Dendrocalamus flagellifer*
Poaceae	*Dendrocalamus flagellifer*
Poaceae	*Dendrocalamus patellaris*
Dilleniaceae	*Dillenia heterosepada*
Ebenaceae	*Diospyros choboensis*
Ebenaceae	*Diospyros pilosula*
Ebenaceae	*Diospyros sp.**
Ebenaceae	*Diospyros syvatica*
Ebenaceae	*Diospyros tonkinensis*
Menispermaceae	*Diplospora viridiflora*
Anacardiaceae	*Dracontomellum duperreanum*
Anacardiaceae	*Dubanga sonneratioides*
Sapotaceae	*Eberhardtia tonkinensis*
Elaeocarpaceae	*Elaeocarpus petiolatus*
Euphorbiaceae	*Endospermum chinense*
Moraceae	*Ercussonetia papyrifera*
Myrtaceae	*Eugenia brachiata*
Sapindaceae	*Euphoria longana*
Pentaphylacaceae	*Eurya ciliata*
Tiliaceae	*Excentrodendron tonkinensis*
Moraceae	*Ficus auriculata*
Moraceae	*Ficus championii*

Moraceae	*Ficus chrysocarpa*
Moraceae	*Ficus glomerata*
Moraceae	*Ficus hispida*
Moraceae	*Ficus religiosa*
Moraceae	*Ficus retusa*
Moraceae	*Ficus sp.*
Moraceae	*Ficus variegata*
Moraceae	*Ficus vasculosa*
Clusiaceae	*Garcinia ablongiflora*
Clusiaceae	*Garcinia bracteata*
Clusiaceae	*Garcinia cowa*
Clusiaceae	*Garcinia fagraeoides**
Clusiaceae	*Garcinia sp.*
Clusiaceae	*Garcinia tinctoria*
Rubiaceae	*Gardenia sootepensis*
Gnetaceae	*Gnetum montanum*
Asclepiadaceae	*Goniostemma punctatum*
Malvaceae	*Grewia paniculata*
Aquifoliaceae	*Ilex macrocarpa*
Aquifoliaceae	*Ilex purpurea*
Aquifoliaceae	*Ilex sp*
Icacinaceae	*Iodes seguini**
Lauraceae	*Lauraceae sp.*
Annonaceae	*Limacia sp*
Sapindaceae	*Litchi chinensis*
Lauraceae	*Litsea baviensis*
Lauraceae	*Litsea sp*
Arecaceae	*Livistona saribus*
Lauraceae	*Machilus bonii*
Sapotaceae	*Madhuca pasquieri*
Sapotaceae	*Manilkara sapota*
Sabiaceae	*Meliosma fordi*
Apocynaceae	*Melodinus tourneri*
Musaceae	*Musa coccinea*
Sapindaceae	*Nephelium bassacense*
Sapindaceae	*Nephelium chryseum*
Oleaceae	*Olea sp*
Fabaceae	*Ormosia pinnata*
Oxalidaceae	*Overrhoa carambola*
Fagaceae	*Pasania ducampi*
Rubiaceae	*Pavetta tonkinensis*
Fabaceae	*Peltophorum tonkinense*
Marantaceae	*Phrynum parvifolium*

Phyllanthaceae	*Phyllanthus emblica*
Poaceae	*Phyllostachys bambusoides*
Annonaceae	*Polyalthia memosalic*
Annonaceae	*Polyalthia sp*
Annonaceae	*Polyalthia suberosa*
Sapindaceae	*Pometia pinnata**
Lamiaceae	*Premna balansae*
Lamiaceae	*Premna chevalieri*
Lamiaceae	*Premna flavescens**
Fagaceae	*Quercus acutissima*
Fagaceae	*Quercus platycalyx*
Bignoniaceae	*Rhadermachera sp*
Rosaceae	*Rubus moluccana*
Meliaceae	*Sandoricum kontape*
Sapindaceae	*Sapindus mukorossi*
Euphorbiaceae	*Sapium rotundifolium*
Meliaceae	*Sapondias pinnata*
Fabaceae	*Saraca dives*
Sapotaceae	*Sarcosperma laurinum*
Araliaceae	*Schefflera aff. velunosa*
Araliaceae	*Schefflera delavayi*
Araliaceae	*Schefflera palmiformis*
Poaceae	*Silocalamus giganteus*
Poaceae	*Silocalamus latiflorus*
Sapotaceae	*Sinosideroxylon wightianum**
Anacardiaceae	*Spondias pinnata*
Moraceae	*Strebus asper*
Myrtaceae	*Syzygium cinereum*
Myrtaceae	*Syzygium sp*
Myrtaceae	*Syzygium wighticmum*
Myrtaceae	*Syzygium zeylanicum**
Caesalpiniaceae	*Tamarindus indica*
Vitaceae	*Tetrastigma gaudichaudianum*
Vitaceae	*Tetrastigma oliviforme*
Vitaceae	*Tetrastigma sp.*
Meliaceae	*Toona sinensis*
Araliaceae	*Trevesia palmate**
Orchidaceae	*Tropidia curculigoides*

*species captured in sampling for this study

3.3.2 Food genera identified in Khau Ca and Du Gia

Family	Genus	Khau Ca				Du Gia			
		Ridge (n)	Slope (n)	Valley (n)	**Total**	Ridge (n)	Slope (n)	Valley (n)	**Total**
Sapindaceae	*Acer*	40	0	0	**40**	1	0	0	**1**
Anacardiaceae	*Allospondias*	0	1	0	**1**	0	0	0	**0**
Euphorbiaceae	*Antidesma*	0	4	11	**15**	3	7	2	**12**
Mimosaceae	*Archidendron*	0	0	0	**0**	9	4	24	**37**
Primulaceae	*Ardisia*	5	0	3	**8**	9	0	0	**9**
Poaceae	*Bambusa*	0	0	0	**0**	0	3	0	**3**
Phyllanthaceae	*Bischofia*	0	0	0	**0**	0	0	2	**2**
Phyllanthaceae	*Bridelia*	0	1	0	**1**	0	0	3	**3**
Orchidaceae	*Bulbophyllum*	0	0	1	**1**	0	0	0	**0**
Malvaceae	*Burretiodendron*	7	13	5	**25**	0	0	0	**0**
Theaceae	*Camellia*	0	0	5	**5**	0	0	34	**34**
Burceraceae	*Canarium*	1	1	0	**2**	0	3	0	**3**
Arecaceae	*Caryota*	0	0	0	**0**	0	0	3	**3**
Fagaceae	*Castanopsis*	3	0	1	**4**	3	2	0	**5**
Ulmaceae	*Celtis*	6	5	4	**15**	0	0	0	**0**
Ebenaceae	*Diospyros*	19	46	12	**77**	0	57	18	**75**
Elaeocarpaceae	*Elaeocarpus*	4	3	7	**14**	219	2	0	**221**
Pentaphylacaceae	*Eurya*	0	0	1	**1**	0	0	0	**0**
Moraceae	*Ficus*	12	13	1	**26**	3	0	7	**10**
Clusiaceae	*Garcinia*	56	5	0	**61**	1	7	1	**9**
Gnetaceae	*Gnetum*	0	0	0	**0**	0	12	3	**15**
Aquifoliaceae	*Ilex*	0	7	1	**8**	8	1	0	**9**
Icacinaceae	*Iodes*	0	1	1	**2**	3	2	2	**7**
Lauraceae	*Litsea*	8	7	2	**17**	41	26	8	**75**
Arecaceae	*Livistona*	0	0	0	**0**	0	2	3	**5**
Lauraceae	*Machilus*	3	3	0	**6**	11	6	0	**17**
Sapotaceae	*Madhuca*	0	0	2	**2**	0	0	0	**0**
Musaceae	*Musa*	0	0	0	**0**	0	0	1	**1**
Oleaceae	*Olea*	2	6	4	**12**	7	0	0	**7**
Rubiaceae	*Pavetta*	6	0	21	**27**	3	0	0	**3**
Fabaceae	*Peltophorum*	0	0	0	**0**	0	1	0	**1**
Euphorbiaceae	*Phyllanthus*	4	7	4	**15**	0	2	1	**3**
Annonaceae	*Polyalthia*	24	18	31	**73**	0	13	4	**17**
Sapindaceae	*Pometia*	0	3	2	**5**	0	0	0	**0**
Lamiaceae	*Premna*	1	0	0	**1**	0	0	0	**0**
Fagaceae	*Quercus*	4	0	0	**4**	1	8	0	**9**
Sapindaceae	*Sapindus*	1	25	3	**29**	3	11	1	**15**
Euphorbiaceae	*Sapium*	1	0	0	**1**	0	0	0	**0**
Fabaceae	*Saraca*	0	0	0	**0**	0	0	1	**1**

Araliaceae	*Schefflera*	0	10	0	**10**	4	2	4	**10**
Sapotaceae	*Sinosideroxylon*	10	6	4	**20**	0	0	0	**0**
Myrtaceae	*Syzygium*	6	5	5	**16**	13	6	12	**31**
Vitaceae	*Tetrastigma*	41	23	39	**103**	8	2	18	**28**
Araliaceae	*Trevesia*	0	4	1	**5**	0	0	0	**0**
Total		**264**	**217**	**171**	**652**	**350**	**179**	**152**	**681**

Appendix 4 Cao vit gibbon

4.1 ANOVA Analysis tables for cao vit gibbon (CVG) habitat

4.1.1 Summary data tables for CVGCA and Zone IV ANOVA analyses

4.1.1.1 *CVGCA and Zone IV analyses*

Plot	Site	Plot Type	Elev-ation (m)	General density	Topo-graphic Complex-ity	Slope (deg)	Species richness	Species Diversity	Tree Density	Species density	Canopy Height (m)	Mat cover (%)	Shrub cover (%)	Large Shrub cover (%)	Canopy cover (%)	Liana cover (%)	Av DBH (cm)	Total Basal area (m^2)
TKV1	CVGCA	valley	738	3	3	29	54	2.80	0.27	4.84	5.68	10	80	5	40	25	6.05	14.00
TKV2	CVGCA	valley	726	2	3	5	45	2.43	0.21	5.35	8.91	20	50	20	60	5	12.16	48.30
TKV3	CVGCA	valley	654	2	4	6	32	1.93	0.19	7.82	6.70	40	10	5	40	30	9.48	19.72
TKV4	CVGCA	valley	647	3	2	16	42	2.63	0.46	3.53	4.73	50	70	20	50	30	5.60	25.72
TKS1	CVGCA	slope	726	2	4	25	36	2.89	0.27	2.14	7.57	15	60	20	60	10	8.84	26.13
TKS2	CVGCA	slope	759	1	4	18	30	3.64	0.15	1.43	8.11	20	10	5	65	10	13.34	40.59
TKS3	CVGCA	slope	781	3	3	28	33	2.73	0.38	2.35	6.59	30	35	5	70	20	7.44	19.88
TKS4	CVGCA	slope	747	2	3	27	31	2.52	0.12	2.04	7.00	30	40	20	60	0	8.45	12.61
TKR1	CVGCA	ridge	808	1	5	30	29	2.96	0.2	1.99	2.57	20	5	30	0	2	5.87	6.50
TKR2	CVGCA	ridge	804	1	4	60	34	2.81	0.31	2.73	3.15	30	10	10	30	5	6.01	14.98
TKR3	CVGCA	ridge	810	2	4	35	42	2.94	0.21	3.72	4.10	15	10	40	20	5	4.95	6.19
TKR4	CVGCA	ridge	801	4	2	17	32	2.50	0.26	3.67	3.02	10	40	20	20	20	5.76	13.78
ZV1	Zone IV	valley	521	3	1	10	46	3.26	0.2	4.78	3.55	70	90	50	10	40	4.51	3.94
ZV2	Zone IV	valley	630	1	1	4	38	2.59	0.1	2.17	3.47	5	100	2	5	20	5.76	3.81
ZV3	Zone IV	valley	767	1	2	4	42	2.15	0.18	5.55	5.53	40	80	20	30	40	5.73	8.98
ZV4	Zone IV	valley	763	2	1	18	39	1.00	0.31	6.4	5.35	60	60	20	50	10	6.27	14.62
ZS1	Zone IV	slope	606	3	3	35	55	2.04	0.32	8.09	4.43	20	80	10	65	30	6.65	18.68
ZS2	Zone IV	slope	598	3	3	36	59	3.32	0.24	3.83	4.62	20	90	40	80	50	7.72	16.39
ZS3	Zone IV	slope	718	2	1	26	51	3.02	0.36	6.06	4.47	50	60	10	60	40	5.15	28.49
ZS4	Zone IV	slope	822	3	4	41	44	2.71	0.21	4.51	5.28	20	70	10	50	40	7.59	13.76
ZR1	Zone IV	ridge	820	1	4	27	38	2.78	0.32	6.18	3.37	30	90	30	20	5	5.29	9.14
ZR2	Zone IV	ridge	828	3	3	25	61	3.15	0.36	4.68	4.84	40	70	10	60	60	6.36	15.57
ZR3	Zone IV	ridge	871	2	3	38	33	2.64	0.19	3.15	4.34	5	80	2	40	10	8.23	16.76
ZR4	Zone IV	ridge	910	3	4	35	44	2.45	0.16	4.33	3.26	2	60	20	10	5	7.52	8.77

4.1.1.2 *CVGCA, Zone IV and the Corridor transects for tree analysis*

Location	Plot	Elevation (m)	Topographic Complexity	Slope (degrees)	Tree density	Ave tree height (m)	Canopy cover (%)	Average DBH (cm)	Total Basal area (m^2)
Corridor	Ridge Transect	653	3	4	2.11	4.56	60	7.52	13.15
	Valley Transect	592	1	18	8.77	4.52	35	5.72	21.73
	Slope Transect	594	3	30	3.20	3.86	45	4.77	12.03
CVGCA	Ridge Transect	751	3	28	2.01	5.78	50	9.35	64.41
	Valley Transect	819	4	15	12.18	3.37	10	0.76	19.45
	Slope Transect	707	3	24	4.01	5.37	40	6.34	23.26
Zone IV	Ridge Transect	764	5	40	1.56	4.03	35	7.94	33.50
	Valley Transect	776	1	2.5	14.81	4.06	25	4.32	16.22
	Slope Transect	823	2	31	3.62	6.79	30	8.70	21.12

4.1.2 ANOVA analysis results table for CVGCA area

	Response	Degrees of Freedom	Sum of Squares	Mean Square	F-value	P-value
*Elevation (m)**	Plot	2	26280.7	131140.3	14.13	0.002
	Residuals	9	8372.3	930.3		
Topographic complexity	Plot	2	1.17	0.58	0.68	0.053
	Residuals	9	7.75	0.86		
Slope (degrees)	Plot	2	924.67	462.33	2.96	0.103
	Residuals	9	1408.00	156.44		
General density scale	Plot	2	0.67	0.33	0.33	0.73
	Residuals	9	9.00	1.00		
Species richness	Plot	2	266.17	133.08	3.32	0.08
	Residuals	9	360.50	40.06		
Species diversity	Plot	2	0.525	0.26	1.84	0.21
	Residuals	9	1.29	0.14		
Species density (stem/m^2)*	Plot	2	24.21	12.1	8.94	0.007
	Residuals	9	12.19	1.35		
Tree density (tree stem/m^2)	Plot	2	0.91	0.45	0.99	0.407
	Residuals	9	4.10	0.46		
*Canopy height (m)**	Plot	2	37.85	18.93	13.94	0.002
	Residuals	9	12.22	1.35		
Mat cover (%)	Plot	2	254.17	127.08	0.83	0.47
	Residuals	9	1387.50	154.17		
Shrub cover (%)	Plot	2	2637.5	1318.75	2.42	0.14
	Residuals	9	4912.5	545.83		
Large shrub cover (%)	Plot	2	416.67	208.33	1.97	0.19
	Residuals	9	950.00	105.56		
*Canopy cover (%)**	Plot	2	4404.2	2202.08	24.21	0.0002
	Residuals	9	818.7	90.97		
Liana cover (%)	Plot	2	494	247.00	2.70	0.121
	Residuals	9	823	91.44		
Av DBH *(cm)*	Plot	2	31.36	15.68	2.83	0.11
	Residuals	9	49.87	5.54		
Total basal area (m^2)	Plot	2	650.28	325.14	2.51	0.14
	Residuals	9	1166.53	129.61		

* Indicates significant variables where $p<0.05$

Only plots were included in this analysis

4.1.3 Estimated marginal means results table for CVGCA

	Valley Plots		Slope Plots		Ridge Plots		SE	*P*<0.05
	Mean	Confidence levels	Mean	Confidence levels	Mean	Confidence levels		
*Elevation (m)**	691	657,726	753	719,788	806	771,840	±15.2	Ridge-Valley: 0.001 Ridge-Slope:0.087 Slope-Valley: 0.044
Topographic Complexity	14	-0.15,28.1	24.5	10.35,38.6	35.5	21.35,49.6	±6.25	Ridge-Slope: 0.459 Ridge-Valley: 0.876 Slope-Valley: 0.489
Slope (degrees)	3	1.95,4.05	3.5	2.45,4.55	3.75	2.7,4.8	±0.46	Ridge-Valley:0.514 Ridge-Slope:0.924 Slope-Valley:0.734
General density	2.5	1.37,3.63	2	0.87,3.13	2	0.87,3.13	±0.87	Ridge-Slope: 1.00 Ridge-Valley: 0.765 Slope-Valley:0.765
Species richness	43.25	36.1,50.4	32.5	25.3, 39.7	34.25	27.1,41.4	±3.16	Ridge-Slope:0.910 Ridge-Valley:0.165 Slope-Valley:0.092
Species Diversity	2.45	2.02,2.87	2.94	2.52,3.37	2.8	2.37,3.23	±0.19	Ridge-Slope:0.850 Ridge-Valley:0.418 Slope-Valley:0.205
Species Density (stem/m2)*	5.385	4.07,6.7	1.99	0.673,3.31	3.03	1.71,4.34	±0.58	Ridge-Valley 0.044 Ridge-Slope 0.450 Slope-Valley 0.007
Tree density (stems/m^2)	0.282	-0.48,1.045	0.23	-0.53,0.99	0.84	0.0745, 1.6	±0.34	Ridge-Slope 0.440 Ridge-Slope 0.502 Slope-Valley 0.993
Av Canopy height (m)*	6.51	5.16, 7.82	7.32	6, 8.64	3.21	1.89, 4.53	±0.58	Ridge-Slope 0.002 Ridge-Valley 0.008 Slope-Valley 0.603
Mat cover (%)	30	15.96,44.0	23.75	9.71,37.8	18.75	4.71,32.8	±6.21	Ridge-Slope 0.839 Ridge-Valley 0.439 Slope-Valley 0.762
Shrub cover (%)	52.5	26.07,78.9	36.25	9.82,62.7	16.25	-10.18,42.7	±11.68	Ridge-Slope 0.476 Ridge-Valley 0.126 Slope-Valley 0.605
Large Shrub cover (%)	12.5	0.879,24.1	12.5	0.879,24.1	25	13.379,36.6	±5.14	Ridge-Slope 0.250 Ridge-Valley 0.250 Slope-valley 1.000
Canopy coverage (%)*	47.5	36.71,58.3	63.75	52.96,74.5	17.5	6.71,28.3	±4.77	Ridge-Slope 0.0002 ridge-Valley 0.004 Slope-Valley 0.091
Liana cover (%)	22.5	11.68,33.3	10	-0.816,20.8	8	-2.82,18.8	±6.76	Ridge-Slope 0.953 Ridge-Valley 0.136 Slope-Valley 0.209
Av DBH (cm)	8.32	5.66,10.99	9.52	6.85, 12.18	5.65	2.99,8.31	±1.18	Ridge-Slope 0.103 Ridge-Valley 0.291 Slope-Valley 0.760
Total Basal Area (m^2)	26.93	14.06, 39.81	24.80	11.93, 37.68	10.36	-2.51,23.24	±5.69	Ridge-Slope 0.226 Ridge-Valley 0.153 Slope-Valley 0.962

*Indicates significant variables where p<0.05.

4.1.4 ANOVA analysis results table for Zone IV Potential Habitat

	Response	Degrees of Freedom	Sum of Squares	Mean Square	F-value	P-value
*Elevation (m)**	Plot	2	86058	43029	4.80	0.04
	Residuals	9	80737	8971		
*Topographic complexity**	Plot	2	10.5	5.25	7.27	0.01
	Residuals	9	6.5	0.72		
*Slope (degrees)**	Plot	2	1541.17	770.58	18.96	0.0006
	Residuals	9	365.75	40.64		
General density scale	Plot	2	2.00	1.00	1.44	0.29
	Residuals	9	6.25	0.69		
Species richness	Plot	2	262.17	131.08	1.94	0.199
	Residuals	9	607.5	67.50		
Species diversity	Plot	2	0.13	0.06	0.297	0.75
	Residuals	9	1.96	0.22		
Species density (stem/m^2)	Plot	2	2.53	1.27	0.44	0.65
	Residuals	9	25.42	2.82		
Tree density (tree stem/m^2)	Plot	2	0.02	0.008	1.05	0.39
	Residuals	9	0.07	0.007		
Canopy height (m)	Plot	2	1.16	0.58	0.87	0.45
	Residuals	9	5.97	0.66		
Mat cover (%)	Plot	2	1243.20	621.58	1.34	0.31
	Residuals	9	4190.50	465.61		
Shrub cover (%)	Plot	2	150	75.00	0.36	0.71
	Residuals	9	1875	208.33		
Large shrub cover (%)	Plot	2	120.67	60.33	0.24	0.79
	Residuals	9	2306.00	256.22		
*Canopy cover (%)**	Plot	2	3537.50	1768.75	4.96	0.035
	Residuals	9	3212.50	356.94		
Liana cover (%)	Plot	2	816.67	408.33	1.21	0.34
	Residuals	9	3025.00	336.11		
Av DBH *(cm)*	Plot	2	4.15	2.08	1.71	0.23
	Residuals	9	10.91	1.21		
*Total basal area (m^2)**	Plot	2	2669945	1334973	4.70	0.04
	Residuals	9	2554355	283817		

* Indicates significant variables where p<0.05
Only plots were included in this analysis

4.1.5 Estimated marginal means results table for Zone IV

	Valley Plots		Slope Plots		Ridge Plots		SE	*P<0.05*
	Mean	Confidence levels	Mean	Confidence levels	Mean	Confidence levels		
*Elevation (m)**	670.25	563, 777	686	579,793	857.25	750,964	±47.40	Ridge-Slope 0.07 Ridge-Valley 0.05 Slope-Valley 0.97
*Topographic Complexity**	1.25	0.29,2.21	2.75	1.79,3.71	3.5	2.53,4.46	±0.42	Ridge-Slope 0.46 Ridge-Valley 0.01 Slope-Valley 0.079
*Slope (degrees)**	9	1.79,16.20	34.5	27.29,41.70	31.25	24.02,38.5	±3.19	Ridge-Slope 0.76 Ridge-Valley 0.002 Slope-Valley 0.0008
General density	1.75	0.81,2.69	2.75	1.81,3.69	2.25	1.31,3.19	±0.42	Ridge-Slope 0.68 Ridge-Valley 0.68 Slope-Valley 0.26
Species richness	41.25	32.00,50.50	52.25	43.00,61.50	44	34.70,53.30	±4.11	Ridge-Slope 0.37 Ridge-Valley 0.89 Slope-Valley 0.19
Species Diversity	2.25	2.02,3.07	2.78	2.25,3.30	2.75	2.23,3.28	±0.32	Ridge-Slope 0.99 Ridge-Valley 0.81 Slope-Valley 0.77
Species Density (stems/m^2)	4.73	2.82,6.63	5.62	3.72,7.52	4.585	2.68,6.49	±0.84	Ridge-Slope 0.67 Ridge-Valley 0.99 Slope-Valley 0.73
Tree density (stems/m^2)	0.20	0.10,0.29	0.28	0.19,0.38	0.26	0.16,0.35	±0.04	Ridge-Slope 0.091 Slope-Valley 0.37 Ridge-Valley 0.60
Av Canopy height (m)	4.47	3.55,5.39	4.7	3.78,5.62	3.95	3.03,4.88	±0.407	Ridge-Slope 0.43 Ridge-Valley 0.65 Slope-Valley 0.93
Mat cover (%)	43.75	19.34,68.20	27.5	3.09,51.90	19.25	-5.16,43.70	±10.79	Ridge-Slope 0.85 Ridge-Valley 0.29 Slope-Valley0.56
Shrub cover (%)	82.50	66.20,98.80	75	58.70,91.30	75	58.70,91.30	±7.22	Ridge-Slope 1.00 Ridge-Valley 0.75 Slope-Valley 0.75
Lg Shrub cover (%)	23.00	4.89,41.10	17.50	-0.61,35.60	15.50	-2.61,33.60	±8.00	Ridge-Slope 0.98 Ridge-Valley 0.79 Slope-Valley 0.88
*Canopy coverage (%)**	23.75	2.38,45.10	63.75	42.38,85.10	32.50	11.13,53.90	±9.45	Ridge-Slope 0.10 Ridge-Valley 0.79 Slope-Valley 0.04
Liana cover (%)	27.50	6.76,48.20	40	19.26,60.70	20	-0.74,40.70	±9.17	Ridge-Slope 0.32 Ridge-Valley 0.83 Slope-Valley 0.62
Av DBH (cm)	5.57	4.32,6.81	6.78	5.53,8.02	6.85	5.60,8.09	±0.55	Ridge-Slope 0.99 Ridge-Valley 0.28 Slope-Valley 0.31
Total Basal Area (m^2)	7.84	1.81,13.86	19.33	13.3,25.36	12.56	6.54,18.59	±2.66	Ridge-Slope 0.22 Ridge-Valley 0.45 Slope-Valley 0.03

*Indicates significant variables where p<0.05

4.1.6 ANOVA analysis results table for comparison between CVGCA and Zone IV Potential habitat

	Response	Degrees of Freedom	Sum of Squares	Mean Square	F-value	P-value
Elevation (m)	Plot	1	900	900	0.1819	0.67
	Residuals	18	89110	4951		
*Topographic complexity**	Plot	1	5.04	5.04	6.37	0.02
	Residuals	18	14.25	0.79		
Slope (degrees)	Plot	1	0.37	0.37	0.0038	0.95
	Residuals	18	1773.75	98.54		
General density scale	Plot	1	0.042	0.042	0.049	0.827
	Residuals	18	15.25	0.847		
*Species richness**	Plot	1	504.17	504.17	9.38	0.007
	Residuals	18	968.00	53.78		
Species diversity	Plot	1	0.11	0.11	0.39	0.537
	Residuals	18	5.15	0.29		
Species density (stem/m^2)*	Plot	1	13.681	13.68	6.55	0.02
	Residuals	18	37.62	2.09		
Tree density (tree stem/m^2)	Plot	1	0.0003	0.0003	0.029	0.865
	Residuals	18	0.161	0.009		
*Canopy height (m)**	Plot	1	10.18	10.18	10.07	0.005
	Residuals	18	18.19	1.01		
Mat cover (%)	Plot	1	216.0	216.0	0.69	0.415
	Residuals	18	5578.0	309.89		
*Shrub cover (%)**	Plot	1	10837.5	10837.5	28.74	0.00004
	Residuals	18	6787.5	377.1		
Large shrub cover (%)	Plot	1	24.0	24.0	0.133	0.72
	Residuals	18	3256.0	180.889		
Canopy cover (%)	Plot	1	51.0	51.0	0.23	0.639
	Residuals	18	4031.2	224.0		
*Liana cover (%)**	Plot	1	1472.7	1472.67	6.89	0.017
	Residuals	18	3848.0	213.78		
Av DBH *(cm)**	Plot	1	12.32	12.32	3.65	0.072
	Residuals	18	60.78	3.38		
*Total basal area (m^2)**	Plot	1	333.71	333.71	4.22	0.05
	Residuals	18	1421.76	78.99		

* Indicates significant variables where $p<0.05$

Only plots were included in this analysis

4.1.7 Estimated marginal means results table for comparison of CVGCA and Zone IV

	CVGCA		Zone IV		SE	*P*<0.05
	Mean	Confidence levels	Mean	Confidence levels		
Elevation (m)	750	707,793	738	695,781	±20.3	0.67
*Topographic Complexity**	3.42	2.88,3.96	2.50	1.96,3.04	±0.26	0.02
Slope (degrees)	24.7	18.60,30.70	24.90	18.90,30.90	±2.87	0.95
General density	2.17	1.61,2.72	2.25	1.69, 2.81	±0.27	0.83
*Species richness**	36.7	32.20,41.10	45.80	41.40,50.30	±2.12	0.007
Species Diversity	2.73	2.41,3.05	2.59	2.27,2.92	±0.15	0.54
*Species Density (stems/m^2)**	3.47	2.59,4.34	4.98	4.10,5.85	±0.42	0.019
Tree Density (stems/m^2)	0.252	0.19,0.31	0.25	0.19,0.30	±0.03	0.87
*Av canopy height (m)**	5.68	5.07,6.29	4.38	3.77,4.98	±0.29	0.005
Mat cover (%)	24.2	13.50,34.80	30.20	19.50,40.80	±5.08	0.42
*Shrub cover (%)**	35.0	23.20,46.80	77.50	65.70,89.30	±5.61	<0.0001
Large shrub cover (%)	16.7	8.51,24.80	18.70	10.51,26.80	±3.88	0.72
Canopy cover (%)	42.9	33.8,52.00	40.00	30.9,49.10	±4.32	0.64
*Liana cover (%)**	13.5	4.63,22.40	29.20	20.30,38.00	±4.22	0.017
Av DBH(cm)*	7.83	6.71,8.94	6.40	5.28,7.51	±0.53	0.007
Total Basal Area (m^2)*	20.70	15.31,26.10	13.24	7.85,18.60	±2.57	0.06

* Indicates significant variables where p<0.05

4.1.8 ANOVA analysis results table for comparison between CVGCA, Zone IV and Corridor habitat

	Response	Deg of Freedom	Sum of Squares	Mean Square	F-value	P-value
*Elevation (m)**	Plot	2	52646	26323.1	14.74	0.004
	Residuals	6	10715	1785.8		
Topographic complexity	Plot	2	1.56	0.778	0.389	0.69
	Residuals	6	12.00	2.00		
Slope (degrees)	Plot	2	81.06	40.528	0.204	0.821
	Residuals	6	1193,83	198.97		
Tree density (tree stem/m^2)	Plot	6	6.123	3.06	0.099	0.907
	Residuals	2	185.256	30.876		
Canopy height (m)	Plot	6	0.71	0.35	0.246	0.789
	Residuals	2	8.66	1.44		
Canopy cover (%)	Plot	6	466.67	233.33	1.14	0.382
	Residuals	2	1233.33	205.56		
Av DBH *(cm)*	Plot	6	3.49	1.74	0.199	0.825
	Residuals	2	52.85	8.81		
Total basal area (m^2)	Plot	6	610.97	305.49	1.25	0.351
	Residuals	2	1462.22	243.70		

* Indicates significant variables where $p<0.05$

Only transects were included in this analysis

4.1.9 Estimated marginal means results table for comparison between CVGCA, Zone IV and the Corridor

	CVGCA		Zone IV		Corridor		SE	*P*<0.05
	Mean	Confidence Levels	Mean	Confidence Levels	Mean	Confidence Levels		
*Elevation (m)**	759	699,819	788	728,847	613	553,673	±24.4	C-CVGCA 0.013 C-ZIV 0.006 CVGCA-ZIV 0.69
Topographic complexity	3.33	1.34,5.33	2.67	0.67,4.66	2.33	0.34,4.33	±0.82	C-CVGCA 0.679 C-ZIV 0.955 CVGCA-ZIV 0.837
Slope (degrees)	22.3	2.41,42.30	24.50	4.57,44.40	17.3	-2.59,37.30	±8.14	C-CVGCA 0.90 C-ZIV 0.81 CVGCA-ZIV 0.98
Canopy height (m)	4.84	3.14, 6.54	4.96	3.26,6.66	4.31	2.62,6.01	±0.69	C-CVGCA 0.86 C-ZIV 0.79 CVGCA-ZIV 0.99
Av DBH (cm)	5.48	1.29,9.68	6.99	2.79,11.18	6.0	1.81,10.20	±1.71	C-CVGCA 0.975 C-ZIV 0.915 CVGCA-ZIV 0.815
Canopy cover (%)	33.3	13.08,66.90	30.00	9.75,50.30	46.70	26.41,66.90	±8.28	C-CVGCA 0.527 C-ZIV 0.388 CVGCA-ZIV 0.957
Tree density (stems/m^2)	6.07	-1.78,13.9	6.66	-1.19,14.50	4.69	-1.19,14.50	±3.21	C-CVGCA 0.951 C-ZIV 0.903 CVGCA-ZIV 0.991
Basal area (m^2)	35.71	13.65,57.78	23.62	1.56,45.70	15.64	-6.39,37.70	±9.01	C-CVGCA 0.327 C-ZIV 0.81 CVGCA-ZIV 0.633

* Indicates significant variables where p<0.05

4.2 Plant species captured in cao vit habitat

4.2.1 All species captured in both CVGCA and Zone IV potential habitat across both plots and transects

Family	Species	CVGCA				Zone IV			
		Ridge (n)	Slope (n)	Valley (n)	Total	Ridge (n)	Slope (n)	Valley (n)	Total
Orchidaceae	*Acampe carinata*	0	0	0	**0**	1	0	0	**1**
Orchidaceae	*Acampe ochracea*	0	1	0	**1**	0	0	0	**0**
Orchidaceae	*Acampe rigida*	17	7	0	**24**	2	0	0	**2**
Sapindaceae	*Acer tonkinensis*	17	23	7	**47**	23	6	3	**32**
Amaranthaceae	*Achyranthes aspera*	0	0	0	**0**	0	0	43	**43**
Actinidiaceae	*Actinidia callosa*	0	0	1	**1**	0	0	0	**0**
Lauraceae	*Actinodaphne elliptibacca*	0	0	0	**0**	0	1	0	**1**
Lauraceae	*Actinodaphne sp.*	0	0	0	**0**	0	1	0	**1**
Fabaceae	*Adenathera microsperma*	0	0	6	**6**	0	5	8	**13**
Passifloraceae	*Adenia heterophylla*	0	0	0	**0**	0	1	0	**1**
Pteridaceae	*Adiantum falcatum*	0	0	0	**0**	7	5	0	**12**
Pteridaceae	*Adiantum philippense*	0	1	11	**12**	2	3	5	**10**
Orchidaceae	*Aerides rosea*	0	2	26	**28**	0	0	0	**0**
Gesneriaceae	*Aeschynanthus evrardii*	0	0	4	**4**	17	1	0	**18**
Gesneriaceae	*Aeschynanthus poilanei*	0	8	0	**8**	0	0	0	**0**
Connaraceae	*Agelaea trinervis*	0	0	26	**26**	0	0	1	**1**
Meliaceae	*Aglaia poilanei*	12	0	1	**13**	0	0	0	**0**
Meliaceae	*Aglaia tomentosa*	0	0	4	**4**	0	5	0	**5**
Meliaceae	*Aglaia viridis*	0	0	0	**0**	0	3	0	**3**
Araceae	*Aglaonema siamense*	0	21	215	**236**	1	35	3	**39**
Araceae	*Aglaonema simplex*	0	0	0	**0**	0	4	0	**4**
Cornaceae	*Alangium chinensis*	0	0	0	**0**	0	0	63	**63**
Cornaceae	*Alangium kurzii*	0	2	0	**2**	0	1	0	**1**
Moraceae	*Alchornea tiliaefolia*	0	9	7	**16**	6	4	0	**10**
Moraceae	*Alchornea trewIodes*	0	0	0	**0**	3	5	8	**16**
Sapindaceae	*Allophylus caudatus*	0	6	14	**20**	0	0	0	**0**
Zingiberaceae	*Alpinia bracetata*	0	0	0	**0**	0	0	41	**41**
Zingiberaceae	*Alpinia chinensis*	0	23	2	**25**	0	0	2	**2**
Zingiberaceae	*Alpinia malaccensis*	0	0	172	**172**	0	0	0	**0**
Apocynaceae	*Alstonia angustifolia*	5	0	0	**5**	0	0	0	**0**
Apocynaceae	*Alyxia sinensis*	29	9	4	**42**	1	0	7	**8**
Sapindaceae	*Amesiodendron chinense*	0	2	1	**3**	0	0	0	**0**
Araceae	*Amorphophallus tonkinensis*	0	4	8	**12**	0	2	0	**2**

Marattiaceae	*Angiopteris yunnanensis*	0	0	81	**81**	0	0	0	**0**
Combretaceae	*Anogeisus acuminata*	0	2	0	**2**	0	0	0	**0**
Phyllanthaceae	*Antidesma bunius*	0	0	7	**7**	0	0	0	**0**
Phyllanthaceae	*Antidesma fruticosum*	0	0	1	**1**	1	9	8	**18**
Pteridaceae	*Antrophyum callifolium*	4	0	0	**4**	1	0	27	**28**
Dryopteridaceae	*Arachniodes hasseltii*	0	0	0	**0**	0	87	79	**166**
Araliaceae	*Aralia chinensis*	0	0	0	**0**	0	0	2	**2**
Mimosoideae	*Archidendron tonkinensis*	0	0	1	**1**	0	2	0	**2**
Primulaceae	*Ardisia crenata*	17	4	0	**21**	8	7	0	**15**
Primulaceae	*Ardisia tinctoria*	5	4	0	**9**	21	0	0	**21**
Primulaceae	*Ardisia virens*	8	1	11	**20**	0	2	0	**2**
Convolvulaceae	*Argyreia atro-purpurea*	0	0	2	**2**	0	3	0	**3**
Araceae	*Arisaema petelotii*	0	0	20	**20**	0	0	0	**0**
Annonaceae	*Artabotrys hongkongensis*	0	0	0	**0**	2	0	0	**2**
Asteraceae	*Artemisia vulgaris*	0	0	0	**0**	0	0	49	**49**
Moraceae	*Artocarpus rigidus*	0	0	0	**0**	0	1	0	**1**
Poaceae	*Arundinaria amabilis*	0	0	168	**168**	0	5	0	**5**
Aristolochiaceae	*Asarum caudigerum*	0	0	1	**1**	0	0	0	**0**
Asparagaceae	*Asparagus filicinus*	0	0	2	**2**	0	0	0	**0**
Asparagaceae	*Aspidistra typica*	0	3	284	**287**	0	3	0	**3**
Aspleniaceae	*Asplenium falcatum*	19	18	1	**38**	12	15	8	**35**
Aspleniaceae	*Asplenium griffithianum*	0	10	0	**10**	0	18	0	**18**
Aspleniaceae	*Asplenium nitidus*	0	22	55	**77**	8	20	13	**41**
Aspleniaceae	*Asplenium normale*	13	4	77	**94**	295	57	69	**421**
Aspleniaceae	*Asplenium saxicola*	0	0	3	**3**	9	0	0	**9**
Rutaceae	*Atalantia guillauminii*	0	0	0	**0**	0	2	0	**2**
Poaceae	*Bambusa sesquiflora*	0	0	0	**0**	0	26	0	**26**
Fabaceae	*Bauhinia corymbosa*	0	5	4	**9**	0	0	0	**0**
Fabaceae	*Bauhinia ornata*	0	3	0	**3**	4	19	1	**24**
Begoniaceae	*Begonia portei*	0	0	1	**1**	0	0	0	**0**
Begoniaceae	*Begonia sonlaensis*	0	0	13	**13**	0	0	0	**0**
Rhamnaceae	*Berchemia loureiriana*	0	0	0	**0**	0	0	4	**4**
Phyllanthaceae	*Bischofia javanica*	0	0	7	**7**	0	0	0	**0**
Asteraceae	*Blumea procera*	0	0	0	**0**	35	4	72	**111**
Urticaceae	*Boehmeria holosericea*	0	0	0	**0**	25	32	44	**101**
Gesneriaceae	*Boeica porosa*	66	0	2	**68**	0	0	0	**0**

Araliaceae	*Brassaiopsis membranifolia*	0	0	21	**21**	0	3	5	**8**
Phyllanthaceae	*Breynia diversifolia*	55	0	0	**55**	6	0	0	**6**
Phyllanthaceae	*Bridelia ovata*	0	5	1	**6**	0	6	0	**6**
Moraceae	*Broussonetia papyrifera*	0	0	1	**1**	0	0	0	**0**
Orchidaceae	*Bulbophyllum ambrosia*	0	229	0	**229**	0	0	0	**0**
Orchidaceae	*Bulbophyllum hymenanthum*	0	0	0	**0**	18	0	0	**18**
Orchidaceae	*Bulbophyllum monanthum*	0	5	0	**5**	0	0	0	**0**
Malvaceae	*Burretiodendron hsienmu*	0	36	13	**49**	3	1	0	**4**
Fabaceae	*Cajanus scarabeoides*	0	0	0	**0**	0	0	1	**1**
Arecaceae	*Calamus tenui*	0	0	19	**19**	0	0	0	**0**
Orchidaceae	*Calanthe argenteo-striata*	0	0	2	**2**	0	0	0	**0**
Orchidaceae	*Calanthe triplicate*	0	0	0	**0**	4	0	0	**4**
Lamiaceae	*Callicarpa brevipes*	0	0	4	**4**	0	0	0	**0**
Lamiaceae	*Callicarpa macrophylla*	0	0	0	**0**	1	28	11	**40**
Calophyllaceae	*Calophyllum formosum*	0	0	0	**0**	0	0	2	**2**
Theaceae	*Camellia caudata*	0	0	3	**3**	0	0	0	**0**
Capparaceae	*Capparis eurycibe*	0	10	5	**15**	0	0	0	**0**
Brassicaceae	*Cardamine hirsuta*	0	0	0	**0**	0	0	41	**41**
Cyperaceae	*Carex baccans*	1	0	0	**1**	0	0	0	**0**
Rhizophoraceae	*Carrallia eugenioidea*	0	0	0	**0**	8	0	0	**8**
Juglandaceae	*Carya tonkinensis*	3	0	0	**3**	0	0	0	**0**
Arecaceae	*Caryota bacsonensis*	0	3	2	**5**	0	1	0	**1**
Fabaceae	*Cassia javanica*	0	0	0	**0**	0	1	0	**1**
Lauraceae	*Cassytha filiformis*	0	1	0	**1**	2	6	11	**19**
Fagaceae	*Castanopsis*	0	0	0	**0**	1	0	0	**1**
Fagaceae	*Castanopsis acuminatissima*	4	0	0	**4**	0	0	0	**0**
Fagaceae	*Castanopsis boisii*	4	0	0	**4**	0	0	0	**0**
Fagaceae	*Castanopsis sp.*	8	0	0	**8**	7	0	0	**7**
Vitaceae	*Cayratia japonica*	0	18	23	**41**	0	12	0	**12**
Ulmaceae	*Celtis tetrandra*	0	5	5	**10**	5	14	6	**25**
Apiaceae	*Centella asiatica*	0	0	0	**0**	0	0	161	**161**
Euphorbiaceae	*Cephalomappa sinensis*	0	123	52	**175**	0	21	0	**21**
Gesneriaceae	*Chirita drakei*	0	0	0	**0**	80	4	0	**84**
Gesneriaceae	*Chirita macrophylla*	0	0	0	**0**	8	0	0	**8**
Gesneriaceae	*Chirita speciosa*	236	0	0	**236**	71	5	138	**214**

Anacardiaceae	*Choerospondias axillaris*	0	0	0	**0**	1	0	0	**1**
Lauraceae	*Cinnamomum tonkinensis*	4	0	0	**4**	0	0	0	**0**
Meliacea	*Cipadessa baccifera*	0	0	0	**0**	0	35	19	**54**
Orchidaceae	*Cirrhopetalum taeniophyllum*	15	0	0	**15**	0	0	0	**0**
Rutaceae	*Citrus grandis*	0	0	0	**0**	0	0	2	**2**
Rutaceae	*Clausena lansium*	3	1	1	**5**	10	41	4	**55**
Orchidaceae	*Cleisostoma rostratum*	0	1	0	**1**	0	0	0	**0**
Ranunculaceae	*Clematis loureiriana*	15	0	0	**15**	3	0	4	**7**
Lamiaceae	*Clerodendrum chinense*	0	0	0	**0**	0	0	58	**58**
Lamiaceae	*Clerodendrum nutans*	0	0	2	**2**	0	0	0	**0**
Lamiaceae	*Clerodendrum serratum*	0	0	0	**0**	0	0	24	**24**
Orchidaceae	*Coelogyne lactea*	132	6	8	**146**	11	2	0	**13**
Orchidaceae	*Coelogyne pallens*	18	0	0	**18**	0	0	0	**0**
Araceae	*Colocasia gigantea*	0	1	0	**1**	0	4	8	**12**
Commelinaceae	*Commelina communis*	0	0	0	**0**	0	1	32	**33**
Connaraceae	*Connarus paniculatus*	3	5	4	**12**	25	0	0	**25**
Thelypteridaceae	*Coryphopteris falciloba*	0	8	0	**8**	0	6	0	**6**
Costaceae	*Costus tonkinensis*	0	0	27	**27**	0	2	0	**2**
Gentianaceae	*Crawfurdia sp.*	0	0	1	**1**	0	0	4	**4**
Fabaceae	*Crotalaria acicularis*	0	0	0	**0**	0	0	56	**56**
Fabaceae	*Crotalaria pallida*	69	0	0	**69**	20	0	12	**32**
Hypoxidaceae	*Curculigo latifolia*	0	0	8	**8**	0	2	0	**2**
Thelypteridaceae	*Cyclosorus philippinarum*	0	1	0	**1**	0	3	0	**3**
Orchidaceae	*Cymbidium aloifolium*	30	0	0	**30**	0	0	0	**0**
Orchidaceae	*Cymbidium lancifolium*	0	1	0	**1**	1	0	0	**1**
Poaceae	*Cymbopogon pendulus*	0	0	0	**0**	3	0	0	**3**
Cyperaceae	*Cyperus sp.*	0	0	0	**0**	2	0	2	**4**
Dryopteridaceae	*Cyrtomium fraxinellum*	0	0	2	**2**	0	0	0	**0**
Fabaceae	*Dalbergia rimosa*	1	0	0	**1**	0	0	0	**0**
Fabaceae	*Dalbergia volubilis*	0	1	0	**1**	0	0	0	**0**
Amaranthaceae	*Deeringia amaranthoides*	0	0	0	**0**	0	0	12	**12**
Orchidaceae	*Dendrobium faulhaberianum*	7	0	0	**7**	1	0	0	**1**
Urticaceae	*Dendrocnide urentissima*	0	0	5	**5**	0	1	0	**1**
Fabaceae	*Derris microphylla*	0	0	0	**0**	0	2	0	**2**

Fabaceae	*Desmodium adscendens*	0	0	0	**0**	0	1	0	**1**
Annonaceae	*Desmos chinensis*	0	1	2	**3**	2	9	1	**12**
Dichapetalaceae	*Dichapetalum hainanensis*	0	0	0	**0**	0	0	2	**2**
Gleicheniaceae	*Dicranopteris linearis*	0	0	0	**0**	0	4	0	**4**
Dioscoreaceae	*Dioscorea glabra*	0	6	1	**7**	1	15	12	**28**
Dioscoreaceae	*Dioscorea nummularia*	0	0	0	**0**	0	0	1	**1**
Ebenaceae	*Diospyros apiculata*	0	0	0	**0**	0	10	0	**10**
Ebenaceae	*Diospyros buxifolia*	0	0	0	**0**	0	1	0	**1**
Ebenaceae	*Diospyros kaki*	0	0	0	**0**	0	0	1	**1**
Ebenaceae	*Diospyros rufogemmata*	0	4	9	**13**	2	0	0	**2**
Aspleniaceae	*Diplazium maximum*	0	4	71	**75**	0	62	866	**928**
	Dipteris chinensis	0	18	0	**18**	0	28	4	**32**
Polypodiaceae	*Drynaria bonii*	0	32	5	**37**	0	0	0	**0**
Rosaceae	*Duchesnea indica*	0	0	0	**0**	0	0	17	**17**
Elaeagnaceae	*Elaeagnus conferta*	6	0	0	**6**	0	0	0	**0**
Elaeocarpaceae	*Elaeocarpus balansae*	7	0	1	**8**	6	1	0	**7**
Elaeocarpaceae	*Elaeocarpus petiolatus*	0	0	0	**0**	1	0	0	**1**
Urticaceae	*Elatostema cuneatum*	1	87	16	**104**	0	0	12	**12**
Urticaceae	*Elatostema dissectum*	0	0	9	**9**	0	57	0	**57**
Urticaceae	*Elatostema eurhynchum*	0	19	35	**54**	0	4	0	**4**
Urticaceae	*Elatostema ficoides*	0	0	0	**0**	0	0	3	**3**
Urticaceae	*Elatostema monandrum*	48	0	0	**48**	66	65	0	**131**
Primulaceae	*Embelia subcoriacea*	0	1	3	**4**	0	1	0	**1**
Juglandaceae	*Engelhardtia roxburghiana*	2	0	0	**2**	12	1	0	**13**
Araceae	*Epipremnum pinnatum*	0	38	274	**312**	49	53	2	**104**
Poaceae	*Eragrostis unioloides*	0	0	0	**0**	0	76	333	**409**
Orchidaceae	*Eria pusilla*	9	6	0	**15**	0	0	0	**0**
Asteraceae	*Erigeron canadense*	0	0	0	**0**	0	0	828	**828**
Olacaceae	*Erythropalum scandens*	0	0	9	**9**	2	3	14	**19**
Celastraceae	*Euonymus balansae*	6	0	0	**6**	5	0	0	**5**
Euphorbiaceae	*Euphorbia thyrmifolia*	0	0	0	**0**	0	0	3	**3**
Pentaphylacaceae	*Eurya cerasifolia*	19	0	0	**19**	22	1	0	**23**
Moraceae	*Ficus cyrtophylla*	0	0	0	**0**	1	2	4	**7**
Moraceae	*Ficus fulva*	0	0	0	**0**	0	4	0	**4**
Moraceae	*Ficus hirta*	0	0	12	**12**	0	2	340	**342**

Moraceae	*Ficus hispida*	0	0	0	**0**	2	0	0	**2**
Moraceae	*Ficus leavis*	0	0	1	**1**	0	0	0	**0**
Moraceae	*Ficus nervosa*	2	0	0	**2**	0	0	0	**0**
Moraceae	*Ficus obscura*	0	0	0	**0**	0	1	1	**2**
Moraceae	*Ficus sarmentosa*	0	3	8	**11**	0	0	0	**0**
Moraceae	*Ficus simplicissima*	0	0	2	**2**	0	0	0	**0**
Moraceae	*Ficus spathulifolia*	0	0	0	**0**	6	4	0	**10**
Moraceae	*Ficus sumatra*	0	0	2	**2**	0	0	0	**0**
Moraceae	*Ficus variolosa*	0	0	0	**0**	0	0	1	**1**
Moraceae	*Ficus vasculosa*	0	0	0	**0**	2	8	0	**10**
Moraceae	*Ficus villosa*	0	0	0	**0**	0	0	3	**3**
Annonaceae	*Fissistigma bracteatum*	0	5	1	**6**	1	6	2	**9**
Salicaceae	*Flacourtia rukkam*	0	0	0	**0**	3	2	3	**8**
Oleaceae	*Fraxinus rhynchophyllus*	0	0	0	**0**	3	0	0	**3**
Clusiaceae	*Garcinia fagraeoides*	1	3	0	**4**	2	2	0	**4**
Clusiaceae	*Garcinia multiflora*	0	3	8	**11**	0	3	0	**3**
Ericaceae	*Gaultheria leucocarpa*	2	0	0	**2**	0	0	0	**0**
Gleicheniaceae	*Gleichenia macrophylla*	0	0	0	**0**	34	12	0	**46**
Phyllanthaceae	*Glochidion zeylanicum*	1	0	0	**1**	0	0	0	**0**
Gnetaceae	*Gnetum latifolium*	0	4	0	**4**	0	3	0	**3**
Gnetaceae	*Gnetum montanum*	0	0	4	**4**	0	0	0	**0**
Icacinaceae	*Gomphandra tetrandra*	0	0	1	**1**	0	0	0	**0**
Malvaceae	*Grewia sessifolia*	0	0	0	**0**	1	0	0	**1**
Asteraceae	*Gynura colainie*	0	0	0	**0**	0	58	0	**58**
Rutaceae	*Harrisonia perforata*	0	0	0	**0**	0	0	5	**5**
Theaceae	*Hartia yunnanensis*	0	0	1	**1**	0	0	0	**0**
Rubiaceae	*Hedyotis capitellata*	0	0	0	**0**	0	0	1	**1**
Smilacaceae	*Heterosmilax paniculata*	0	1	0	**1**	0	0	0	**0**
Apocynaceae	*Heterostemma lutea*	4	0	0	**4**	0	0	0	**0**
Apocynaceae	*Hoya balansae*	5	57	1	**63**	29	25	6	**60**
Apocynaceae	*Hoya nummularoides*	6	0	0	**6**	0	0	0	**0**
Apocynaceae	*Hoya parasitica*	0	10	8	**18**	0	0	0	**0**
Styracaceae	*Huodendron tibeticum*	0	1	5	**6**	4	2	0	**6**
Hydrangeaceae	*Hydrangea aspera*	0	0	5	**5**	0	0	0	**0**
Acanthaceae	*Hygrophila polysperma*	6	0	0	**6**	0	0	0	**0**
Hypericaceae	*Hypericum nepaulense*	0	0	0	**0**	0	0	12	**12**
Hypericaceae	*Hypericum samsonii*	2	0	0	**2**	0	0	0	**0**

Lamiaceae	*Hyptis suaveolens*	0	0	0	**0**	0	0	2	**2**
Aquifoliaceae	*Ilex latifolia*	0	2	1	**3**	0	0	0	**0**
Schisandraceae	*Illicium parvifolium*	0	0	0	**0**	1	0	0	**1**
Balsaminaceae	*Impatiens arrensii*	0	0	946	**946**	0	0	0	**0**
Balsaminaceae	*Impatiens balansae*	0	17	30	**47**	0	0	0	**0**
Icacinaceae	*Iodes cirrhoa*	0	3	7	**10**	9	29	3	**41**
Salicaceae	*Itoa orientalis*	0	0	0	**0**	0	6	150	**156**
Rubiaceae	*Ixora balansae*	0	0	0	**0**	0	1	0	**1**
Oleaceae	*Jasminum pedunculatum*	0	10	7	**17**	0	12	1	**13**
Acanthaceae	*Justicia brandegeana*	0	0	0	**0**	0	0	3	**3**
Asteraceae	*Kalimeris indica*	0	0	0	**0**	0	0	14	**14**
Sapindaceae	*Koelreuteria paniculata*	8	0	0	**8**	0	0	0	**0**
Cyperaceae	*Kyllinga nemoralis*	0	0	0	**0**	0	0	3	**3**
Fabaceae	*Lablab purpureas*	0	0	0	**0**	0	0	2	**2**
Urticaceae	*Laportea violacea*	4	59	28	**91**	138	89	18	**245**
Rubiaceae	*Lasianthus chinensis*	0	0	3	**3**	0	0	0	**0**
Rubiaceae	*Lasianthus tonkinensis*	0	0	0	**0**	0	0	2	**2**
Vitaceae	*Leea indica*	0	0	13	**13**	0	0	0	**0**
Linderniaceae	*Legazpia polygonoides*	0	0	0	**0**	0	0	68	**68**
Orchidaceae	*Liparis balansae*	246	9	7	**262**	13	0	0	**13**
Orchidaceae	*Liparis cordifolia*	2	0	0	**2**	0	0	0	**0**
Orchidaceae	*Liparis macrantha*	0	18	0	**18**	0	0	0	**0**
Altingiaceae	*Liquidambar formosana*	0	0	0	**0**	0	3	0	**3**
Fagaceae	*Lithocarpus*	0	0	1	**1**	0	0	0	**0**
Fagaceae	*Lithocarpus sp.*	0	0	1	**1**	0	0	0	**0**
Lauraceae	*Litsea balansae*	0	0	2	**2**	3	5	0	**8**
Lauraceae	*Litsea brevipes*	0	0	3	**3**	2	0	0	**2**
Lauraceae	*Litsea chartacea*	1	0	0	**1**	0	0	0	**0**
Lauraceae	*Litsea glunitosa*	0	0	0	**0**	0	1	0	**1**
Lauraceae	*Litsea laevifolia*	4	0	0	**4**	0	0	0	**0**
Lauraceae	*Litsea verticilata*	0	0	0	**0**	0	1	0	**1**
Lauraceae	*Litsea viridis*	0	0	0	**0**	0	2	0	**2**
Lygodiaceae	*Lygodium japonicum*	0	0	0	**0**	0	3	19	**22**
Gesneriaceae	*Lysionotus serratus*	0	7	0	**7**	0	25	0	**25**
Euphorbiaceae	*Macaranga denticulata*	0	0	0	**0**	0	0	2	**2**
Euphorbiaceae	*Macaranga indica*	0	0	0	**0**	0	1	0	**1**
Lauraceae	*Machilus macrophylla*	0	0	0	**0**	0	1	0	**1**
Lauraceae	*Machilus platycarpa*	0	0	0	**0**	0	1	0	**1**

Sapotaceae	*Madhuca pasquierii*	0	9	0	**9**	0	0	0	**0**
Primulaceae	*Maesa balansae*	0	0	1	**1**	0	0	0	**0**
Primulaceae	*Maesa membranacae*	0	0	0	**0**	0	0	15	**15**
Primulaceae	*Maesa montana*	0	0	0	**0**	7	38	74	**119**
Euphorbiaceae	*Mallotus barbatus*	8	0	0	**8**	1	4	3	**8**
Euphorbiaceae	*Mallotus philippinensis*	1	1	0	**2**	4	4	1	**9**
Melastomataceae	*Melastoma septemnervium*	0	0	0	**0**	0	0	3	**3**
Apocynaceae	*Melodinus monogynus*	0	0	7	**7**	0	0	0	**0**
Rubiaceae	*Metadina trichotoma*	0	0	0	**0**	0	0	2	**2**
Rutaceae	*Micromelum integerrimum*	0	0	0	**0**	3	1	0	**4**
Annonaceae	*Miliusa balansae*	0	0	0	**0**	19	0	0	**19**
Meliaceae	*Munronia heterophylla*	0	1	0	**1**	0	0	0	**0**
Rubiaceae	*Mussaenda chevalieri*	2	0	0	**2**	0	1	2	**3**
Polypodiaceae	*Neocheiropteris sapaensis*	2	0	0	**2**	96	11	25	**132**
Orchidaceae	*Nervilia fordii*	0	0	1	**1**	0	0	0	**0**
Lamiaceae	*Ocimum gratissimum*	0	0	0	**0**	0	0	9	**9**
Asparagaceae	*Ophiopogon reptans*	0	6	119	**125**	0	12	0	**12**
Rubiaceae	*Ophiorrhiza japonica*	0	0	5	**5**	0	0	0	**0**
Oxalidaceae	*Oxalis corniculata*	0	0	0	**0**	0	0	1	**1**
Melastomataceae	*Oxyspora paniculata*	0	0	0	**0**	0	6	143	**149**
Rubiaceae	*Paederia foetida*	0	0	0	**0**	0	0	1	**1**
Poaceae	*Panicum notanum*	0	0	8	**8**	0	0	0	**0**
Poaceae	*Panicum notatum*	0	0	0	**0**	6	56	31	**93**
Poaceae	*Panicum palmifolium*	0	0	0	**0**	0	12	0	**12**
Poaceae	*Panicum repens*	0	0	2	**2**	0	0	0	**0**
Gesneriaceae	*Paraboea multiflora*	4	10	18	**32**	21	8	0	**29**
Poaceae	*Paspalum conjugatum*	0	0	0	**0**	0	1	0	**1**
Poaceae	*Paspalum notatum*	0	0	0	**0**	0	0	3	**3**
Rubiaceae	*Pavetta graciliflora*	0	0	5	**5**	0	0	0	**0**
Urticaceae	*Pellionia griffithiana*	0	26	0	**26**	0	0	0	**0**
Urticaceae	*Pellionia radicans*	0	0	0	**0**	0	23	0	**23**
Piperaceae	*Peperomia tetraphylla*	3	5	7	**15**	3	0	0	**3**
Orchidaceae	*Phaius flavus*	0	0	0	**0**	2	5	0	**7**
Orchidaceae	*Phaius indochinensis*	0	1	13	**14**	0	0	0	**0**
Acanthaceae	*Phlogacanthus annamensis*	0	3	2	**5**	0	8	0	**8**
Acanthaceae	*Phlogacanthus colainae*	0	0	0	**0**	0	2	0	**2**
Marantaceae	*Phrynium tonkinense*	0	0	21	**21**	0	0	0	**0**

Phyllanthaceae	*Phyllanthus annamensis*	0	0	0	**0**	0	0	43	**43**
Phyllanthaceae	*Phyllanthus reticulata*	0	0	0	**0**	0	0	11	**11**
Phyllanthaceae	*Phyllanthus ruber*	0	1	7	**8**	0	0	0	**0**
Gesneriaceae	*Phylloboea sinensis*	17	0	6	**23**	0	0	0	**0**
Polypodiaceae	*Phymatosorus lucidus*	0	0	8	**8**	0	0	0	**0**
Urticaceae	*Pilea melastomoides*	0	3	293	**296**	0	4	0	**4**
Urticaceae	*Pilea notata*	58	203	661	**922**	38	617	21	**676**
Urticaceae	*Pilea plantifolia*	13	0	0	**13**	0	0	0	**0**
Urticaceae	*Pilea stipulosa*	18	0	0	**18**	0	0	0	**0**
Piperaceae	*Piper carnibracteum*	0	0	0	**0**	19	9	16	**44**
Piperaceae	*Piper saxicola*	0	1	23	**24**	0	0	0	**0**
Anacardiaceae	*Pistacia cucphuongensis*	2	0	0	**2**	1	0	0	**1**
Anacardiaceae	*Pistacia weinmannifolia*	9	0	0	**9**	12	3	0	**15**
Commelinaceae	*Pollia japonica*	0	2	15	**17**	0	2	2	**4**
Annonaceae	*Polyalthia lauii*	0	11	1	**12**	1	2	0	**3**
Annonaceae	*Polyalthia nemoralis*	0	0	1	**1**	0	0	0	**0**
Polygonaceae	*Polygonum chinensis*	0	0	3	**3**	0	5	66	**71**
Polygonaceae	*Polygonum posumbu*	0	0	0	**0**	0	0	113	**113**
Sapindaceae	*Pometia pinnata*	0	0	1	**1**	0	0	0	**0**
Rosaceae	*Potentilla sundaica*	0	0	0	**0**	0	0	19	**19**
Araceae	*Pothos repens*	0	8	49	**57**	0	8	0	**8**
Araceae	*Pothos scandens*	0	0	0	**0**	0	7	11	**18**
Lamiaceae	*Premna balansae*	2	0	0	**2**	0	0	0	**0**
Rosaceae	*Prunus arborea*	10	1	0	**11**	4	2	0	**6**
Rosaceae	*Prunus zippeliana*	2	0	0	**2**	0	0	0	**0**
Rosaceae	*Pseuderanthemum poilanei*	0	0	2	**2**	0	0	0	**0**
Rubiaceae	*Psychotria montana*	0	4	14	**18**	22	18	6	**46**
Rubiaceae	*Psychotria rubra*	0	0	12	**12**	0	1	0	**1**
Rubiaceae	*Psychotria siamica*	0	0	3	**3**	0	0	0	**0**
Pteridaceae	*Pteris ensiformis*	0	0	0	**0**	0	3	0	**3**
Fabaceae	*Pterolobium microphyllum*	10	3	14	**27**	12	3	0	**15**
Fabaceae	*Pueraria montana*	0	0	0	**0**	0	2	8	**10**
Polypodiaceae	*Pyrrosia bonii*	0	13	0	**13**	322	234	0	**556**
Polypodiaceae	*Pyrrosia lanceolata*	5	21	0	**26**	8	24	7	**39**
Fagaceae	*Quercus acutissima*	3	0	0	**3**	16	0	0	**16**
Fagaceae	*Quercus bambusifolia*	0	0	0	**0**	3	0	0	**3**
Bignoniaceae	*Radermacheta sinica*	0	0	4	**4**	0	6	10	**16**
Rubiaceae	*Randia spinosa*	0	0	1	**1**	0	22	11	**33**
Arecaceae	*Rhapis grossefibrosa*	0	1	0	**1**	0	0	0	**0**

Anacardiaceae	*Rhus javanica*	0	0	0	**0**	0	5	4	**9**
Rubiaceae	*Rubia cordifolia*	0	0	0	**0**	0	3	0	**3**
Rosaceae	*Rubus chaetophorus*	0	0	0	**0**	11	5	13	**29**
Rosaceae	*Rubus rugosus*	6	2	4	**12**	0	5	7	**12**
Acanthaceae	*Ruellia patula*	0	0	9	**9**	0	0	0	**0**
Sapindaceae	*Sapindus mukorossi*	0	5	5	**10**	0	8	0	**8**
Sapindaceae	*Sapindus oocarpus*	0	6	23	**29**	3	1	0	**4**
Lamiaceae	*Satureja confinis*	0	0	0	**0**	89	4	0	**93**
Actinidiaceae	*Saurauia roxburghii*	0	0	2	**2**	0	4	0	**4**
Actinidiaceae	*Saurauia tristyla*	0	0	7	**7**	0	0	0	**0**
Araliaceae	*Schefflera macrophylla*	0	2	0	**2**	0	0	0	**0**
Araliaceae	*Schefflera pes-avis*	14	13	29	**56**	5	0	0	**5**
Cyperaceae	*Scleria terrestris*	0	0	0	**0**	4	0	0	**4**
Selaginellaceae	*Selaginella delicatula*	32	0	0	**32**	0	0	0	**0**
Selaginellaceae	*Selaginella uncinata*	0	0	0	**0**	4	53	4	**61**
Asteraceae	*Senecio scandens*	0	0	2	**2**	0	11	0	**11**
Malvaceae	*Sida rhombifolia*	0	0	0	**0**	0	0	2	**2**
Poaceae	*Sinarundinaria floribunda*	66	0	0	**66**	35	6	0	**41**
Sapotaceae	*Sinosideroxylon wightianum*	19	10	0	**29**	4	7	0	**11**
Smilacaceae	*Smilax lanceifolia*	1	1	22	**24**	7	16	7	**30**
Solanaceae	*Solanum eryanthum*	0	0	0	**0**	0	0	1	**1**
Rosaceae	*Sorbus epidendron*	2	0	0	**2**	0	0	0	**0**
Acanthaceae	*Staurogyne brachystachys*	0	1	0	**1**	0	95	0	**95**
Menispermaceae	*Stephania rotunda*	0	1	4	**5**	14	0	10	**24**
Malvaceae	*Sterculia lanceolata*	0	4	0	**4**	0	1	0	**1**
Moraceae	*Streblus tonkinensis*	0	0	0	**0**	0	0	3	**3**
Apocynaceae	*Streptocaulon griffithii*	0	0	0	**0**	2	9	0	**11**
Vitaceae	*Tetrastigma beauvaisii*	6	66	7	**79**	25	14	6	**45**
Vitaceae	*Tetrastigma chapaense*	22	0	0	**22**	0	16	12	**28**
Vitaceae	*Tetrastigma obtectum*	0	0	2	**2**	6	27	16	**49**
Vitaceae	*Tetrastigma planicaule*	0	3	10	**13**	0	0	0	**0**
Cucurbitaceae	*Thladiantha siamensis*	0	8	1	**9**	8	12	0	**20**
Orchidaceae	*Thrixspermum centipeda*	6	0	0	**6**	0	0	0	**0**
Acanthaceae	*Thunbergia eberhardtii*	0	0	1	**1**	0	0	0	**0**

Poaceae	*Thysanolaena maxima*	0	0	0	**0**	0	2	0	**2**
Menispermaceae	*Tinomiscium petiolare*	0	0	6	**6**	0	0	0	**0**
Linaceae	*Tirpitzia sinensis*	31	0	0	**31**	29	0	0	**29**
Araliaceae	*Trevesia palmata*	0	0	0	**0**	0	0	1	**1**
Euphorbiaceae	*Triadica rotundifolia*	7	0	0	**7**	3	1	0	**4**
Fabaceae	*Trifolium repens*	0	0	0	**0**	0	2	23	**25**
Euphorbiaceae	*Trigonostemon thyrsoideus*	0	45	45	**90**	0	1	0	**1**
Asparagaceae	*Tupistra albiflora*	0	0	4	**4**	0	0	0	**0**
Asparagaceae	*Tupistra tonkinensis*	0	0	54	**54**	0	0	0	**0**
Malvaceae	*Urena lobata*	0	0	0	**0**	0	0	135	**135**
Ericaceae	*Vaccinium bullatum*	4	0	0	**4**	0	0	0	**0**
Ericaceae	*Vaccinium tonkinense*	4	0	0	**4**	0	0	0	**0**
Hymenophyllaceae	*Vandenboschia radicans*	3	0	17	**20**	6	0	0	**6**
Dipterocarpaceae	*Vatica chevalieri*	0	0	0	**0**	1	0	0	**1**
Rhamnaceae	*Ventilago calyculata*	0	2	0	**2**	0	0	0	**0**
Urticaceae	*Villebrunea frutescens*	2	1	0	**3**	7	5	9	**21**
Urticaceae	*Villebrunea integrifolia*	0	1	1	**2**	7	15	0	**22**
Santalaceae	*Viscum ovalifolium*	3	0	0	**3**	8	0	0	**8**
Meliaceae	*Walsura elata*	0	5	0	**5**	0	3	0	**3**
Rubiaceae	*Wendlandia acuminata*	1	0	0	**1**	0	0	0	**0**
Rubiaceae	*Wendlandia glabrata*	0	2	1	**3**	0	0	0	**0**
Rubiaceae	*Wendlandia laotica*	0	0	0	**0**	1	2	0	**3**
Apocynaceae	*Wrightia stellata*	0	0	0	**0**	0	5	0	**5**
Rutaceae	*Zanthoxylum armatum*	0	0	1	**1**	0	0	0	**0**
Rutaceae	*Zanthoxylum avicennae*	1	3	0	**4**	26	0	0	**26**
Rutaceae	*Zanthoxylum laetum*	0	0	0	**0**	11	84	1	**96**
Cucurbitaceae	*Zehneria marginata*	0	0	0	**0**	0	1	2	**3**
Rhamnaceae	*Ziziphus incurva*	0	1	0	**1**	12	2	1	**15**
Total		**1611**	**1598**	**4586**	**7795**	**2145**	**2890**	**4851**	**9886**

4.2.2 All species captured in the corridor area transects

Family	Species	Corridor			
		Ridge (n)	Slope (n)	Valley (n)	**Total**
Amaranthaceae	*Achyranthes aspera*	0	0	118	118
Fabaceae	*Adenathera microsperma*	0	1	1	2
Gesneriaceae	*Aeschynanthus evrardii*	0	4	0	4
Araceae	*Aglaonema siamense*	0	1	0	1
Cornaceae	*Alangium chinensis*	0	1	0	1
Cornaceae	*Alangium kurzii*	0	0	2	2
Moraceae	*Alchornea tiliaefolia*	0	40	0	40
Moraceae	*Alchornea trewlodes*	0	0	11	11
Zingiberaceae	*Alpinia chinensis*	0	0	4	4
Apocynaceae	*Alyxia sinensis*	0	5	0	5
Sapindaceae	*Amesiodendron chinense*	0	1	0	1
Araceae	*Amorphophallus tonkinensis*	0	0	1	1
Phyllanthaceae	*Antidesma fruticosum*	0	1	1	2
Pteridaceae	*Antrophyum callifolium*	2	0	4	6
Dryopteridaceae	*Arachniodes hasseltii*	0	22	134	156
Primulaceae	*Ardisia tinctoria*	6	0	0	6
Poaceae	*Arundinaria amabilis*	44	0	0	44
Asparagaceae	*Aspidistra typica*	0	42	0	42
Aspleniaceae	*Asplenium falcatum*	2	1	13	16
Aspleniaceae	*Asplenium nitidus*	0	2	4	6
Aspleniaceae	*Asplenium normale*	34	29	398	461
Aspleniaceae	*Asplenium saxicola*	0	12	11	23
Rutaceae	*Atalantia guillauminii*	31	0	0	31
Fabaceae	*Bauhinia ornata*	14	1	0	15
Asteraceae	*Blumea procera*	0	5	0	5
Urticaceae	*Boehmeria holosericea*	7	0	66	73
Phyllanthaceae	*Bridelia ovata*	1	0	0	1
Malvaceae	*Burretiodendron hsienmu*	2	1	1	4
Arecaceae	*Calamus tenui*	1	2	5	8
Lamiaceae	*Callicarpa macrophylla*	0	9	1	10
Lamiaceae	*Callicarpa nudiflora*	1	0	11	12
Theaceae	*Camellia caudata*	0	0	3	3
Cyperaceae	*Carex baccans*	0	1	2	3
Rhizophoraceae	*Carrallia eugenioidea*	1	0	0	1
Arecaceae	*Caryota bacsonensis*	0	0	1	1
Fagaceae	*Castanopsis*	0	1	0	1
Vitaceae	*Cayratia japonica*	0	5	0	5
Ulmaceae	*Celtis tetrandra*	2	1	4	7
Euphorbiaceae	*Cephalomappa sinensis*	98	20	0	118
Gesneriaceae	*Chirita speciosa*	0	1	72	73
Chloranthaceae	*Chloranthus erectus*	0	0	1	1

Lauraceae	*Cinnamomum tonkinensis*	1	1	0	2
Meliaceae	*Cipadessa baccifera*	0	13	21	34
Rutaceae	*Clausena lansium*	7	3	3	13
Commelinaceae	*Commelina communis*	0	0	18	18
Connaraceae	*Connarus paniculatus*	4	6	0	10
Thelypteridaceae	*Coryphopteris falciloba*	0	0	13	13
Clusiaceae	*Cratoxylum formosum*	0	1	0	1
Gentianaceae	*Crawfurdia sp.*	0	4	0	4
Fabaceae	*Derris microphylla*	0	2	1	3
Annonaceae	*Desmos chinensis*	0	5	10	15
Gleicheniaceae	*Dicranopteris linearis*	0	2	4	6
Dioscoreaceae	*Dioscorea glabra*	1	3	2	6
Ebenaceae	*Diospyros apiculata*	22	33	25	80
Ebenaceae	*Diospyros buxifolia*	1	0	0	1
Aspleniaceae	*Diplazium maximum*	0	12	0	12
Polypodiaceae	*Dipteris chinensis*	0	43	0	43
Polypodiaceae	*Drynaria bonii*	7	0	0	7
Fabaceae	*Dunbaria podocarpa*	0	0	2	2
Elaeocarpaceae	*Elaeocarpus balansae*	1	0	0	1
Urticaceae	*Elatostema cuneatum*	0	0	2	2
Primulaceae	*Embelia subcoriacea*	14	1	3	18
Araceae	*Epipremnum pinnatum*	20	9	1	30
Poaceae	*Eragrostis unioloides*	0	0	198	198
Rutaceae	*Euodia lepta*	0	1	0	1
Moraceae	*Ficus cyrtophylla*	1	0	0	1
Moraceae	*Ficus hirta*	0	0	1	1
Moraceae	*Ficus hispida*	0	0	3	3
Moraceae	*Ficus nervosa*	0	2	0	2
Moraceae	*Ficus sarmentosa*	2	1	0	3
Annonaceae	*Fissistigma bracteatum*	0	2	13	15
Salicaceae	*Flacourtia rukkam*	0	1	13	14
Clusiaceae	*Garcinia fagraeoides*	1	0	0	1
Clusiaceae	*Garcinia multiflora*	6	0	0	6
Gnetaceae	*Gnetum latifolium*	2	1	0	3
Rutaceae	*Harrisonia perforata*	0	0	1	1
Apocynaceae	*Heterostemma lutea*	0	0	7	7
Apocynaceae	*Hoya balansae*	0	0	10	10
Styracaceae	*Huodendron tibeticum*	0	0	1	1
Icacinaceae	*Iodes cirrhoa*	0	7	0	7
Rubiaceae	*Ixora balansae*	0	0	5	5
Oleaceae	*Jasminum pedunculatum*	14	0	19	33
Acanthaceae	*Justicia brandegeana*	0	0	2	2
Urticaceae	*Laportea violacea*	0	7	23	30
Rubiaceae	*Lasianthus tonkinensis*	0	0	7	7
Lamiaceae	*Leucas mollissima*	0	0	18	18

Lauraceae	*Litsea balansae*	1	6	10	17
Lygodiaceae	*Lygodium japonicum*	0	0	1	1
Primulaceae	*Maesa montana*	4	4	10	18
Euphorbiaceae	*Mallotus philippinensis*	2	2	6	10
Dennstaedtiaceae	*Microlepia pilosula*	1	0	0	1
Rubiaceae	*Mussaenda chevalieri*	0	0	1	1
Polypodiaceae	*Neocheiropteris sapaensis*	11	0	0	11
Asparagaceae	*Ophiopogon reptans*	0	6	1	7
Poaceae	*Panicum notatum*	0	29	97	126
Poaceae	*Panicum repens*	1	0	0	1
Poaceae	*Paspalum conjugatum*	0	0	6	6
Anacardiaceae	*Pegia sarmentosa*	0	3	0	3
Caesalpiniaceae	*Peltophorum dassyrachis*	1	0	0	1
Lauraceae	*Phoebe faberi*	0	1	0	1
Phyllanthaceae	*Phyllanthus ruber*	1	0	0	1
Solanaceae	*Physalis minima*	0	0	5	5
Urticaceae	*Pilea notata*	0	32	0	32
Piperaceae	*Piper carnibracteum*	0	0	7	7
Piperaceae	*Piper saxicola*	0	9	0	9
Commelinaceae	*Pollia japonica*	0	0	2	2
Annonaceae	*Polyalthia lauii*	0	11	6	17
Polygonaceae	*Polygonum chinensis*	0	0	2	2
Dryopteridaceae	*Polystichum indochinense*	0	0	2	2
Araceae	*Pothos repens*	0	13	0	13
Rubiaceae	*Psychotria montana*	0	9	3	12
Rubiaceae	*Psychotria tonkinensis*	0	1	0	1
Pteridaceae	*Pteris ensiformis*	0	19	22	41
Fabaceae	*Pterolobium microphyllum*	5	5	0	10
Polypodiaceae	*Pyrrosia bonii*	0	10	0	10
Polypodiaceae	*Pyrrosia lanceolata*	20	18	11	49
Bignoniaceae	*Radermacheta sinica*	0	0	1	1
Rubiaceae	*Randia spinosa*	0	0	14	14
Anacardiaceae	*Rhus javanica*	0	1	10	11
Rubiaceae	*Rubia cordifolia*	0	5	8	13
Rosaceae	*Rubus chaetophorus*	0	3	0	3
Rosaceae	*Rubus rugosus*	0	1	8	9
Sapindaceae	*Sapindus oocarpus*	2	2	2	6
Actinidiaceae	*Saurauia roxburghii*	0	0	13	13
Lamiaceae	*Scutellaria indica*	0	0	10	10
Selaginellaceae	*Selaginella uncinata*	0	43	132	175
Asteraceae	*Senecio saluensis*	0	0	1	1
Asteraceae	*Senecio scandens*	0	0	3	3
Sapotaceae	*Sinosideroxylon wightianum*	2	9	0	11
Smilacaceae	*Smilax lanceifolia*	0	4	0	4
Smilacaceae	*Smilax perfoliata*	2	0	0	2

Solanaceae	*Solanum torvum*	0	2	0	2
Menispermaceae	*Stephania rotunda*	0	1	0	1
Malvaceae	*Sterculia lanceolata*	0	0	1	1
Moraceae	*Streblus tonkinensis*	0	0	2	2
Apocynaceae	*Streptocaulon griffithii*	0	0	4	4
Vitaceae	*Tetrastigma beauvaisii*	0	1	0	1
Vitaceae	*Tetrastigma chapaense*	0	1	0	1
Vitaceae	*Tetrastigma obtectum*	0	3	21	24
Euphorbiaceae	*Triadica rotundifolia*	3	0	0	3
Malvaceae	*Urena lobata*	0	0	14	14
Rhamnaceae	*Ventilago calyculata*	3	0	0	3
Urticaceae	*Villebrunea frutescens*	0	6	22	28
Urticaceae	*Villebrunea integrifolia*	0	4	0	4
Meliaceae	*Walsura elata*	0	3	0	3
Rutaceae	*Zanthoxylum laetum*	3	4	1	8
Rhamnaceae	*Ziziphus incurva*	8	0	0	8
	Total	**420**	**640**	**1754**	**2814**

4.2.3 Tree species captured in both CVGCA and Zone IV potential habitat across both plots and transects

Family	Species	CVGCA				Zone IV			
		Ridge (n)	Slope (n)	Valley (n)	Total	Ridge (n)	Slope (n)	Valley (n)	Total
Sapindaceae	*Acer tonkinensis*	4	5	2	**11**	12	2	0	**14**
Lauraceae	*Actinodaphne elliptibacca*	0	0	0	**0**	0	1	0	**1**
Lauraceae	*Actinodaphne sp.*	0	0	0	**0**	0	1	0	**1**
Meliaceae	*Aglaia poilanei*	2	0	1	**3**	0	0	0	**0**
Meliaceae	*Aglaia poilanei*	5	0	0	**5**	0	0	0	**0**
Meliaceae	*Aglaia tomentosa*	0	0	2	**2**	0	2	0	**2**
Meliaceae	*Aglaia viridis*	0	0	0	**0**	0	2	0	**2**
Cornaceae	*Alangium chinensis*	0	0	0	**0**	0	0	8	**8**
Cornaceae	*Alangium kurzii*	0	2	0	**2**	0	1	0	**1**
Moraceae	*Alchornea tiliaefolia*	0	1	0	**1**	0	0	0	**0**
Moraceae	*Alchornea trewIodes*	0	0	0	**0**	1	1	0	**2**
Sapindaceae	*Allophylus caudatus*	0	0	3	**3**	0	0	0	**0**
Sapindaceae	*Amesiodendron chinense*	0	2	1	**3**	0	0	0	**0**
Combretaceae	*Anogeisus acuminata*	0	2	0	**2**	0	0	0	**0**
Phyllanthaceae	*Antidesma bunius*	0	0	5	**5**	0	0	0	**0**
Phyllanthaceae	*Antidesma fruticosum*	0	0	1	**1**	1	4	1	**6**
Araliaceae	*Aralia chinensis*	0	0	0	**0**	0	0	1	**1**
Mimosoideae	*Archidendron tonkinensis*	0	0	1	**1**	0	2	0	**2**
Primulaceae	*Ardisia crenata*	2	1	0	**3**	0	0	0	**0**
Primulaceae	*Ardisia tinctoria*	2	2	0	**4**	10	0	0	**10**
Primulaceae	*Ardisia virens*	0	0	0	**0**	0	1	0	**1**
Moraceae	*Artocarpus rigidus*	0	0	0	**0**	0	1	0	**1**
Rutaceae	*Atalantia guillauminii*	0	0	0	**0**	0	1	0	**1**

Phyllanthaceae	*Bischofia javanica*	0	0	2	**2**	0	0	0	**0**
Urticaceae	*Boehmeria holosericea*	0	0	0	**0**	1	2	0	**3**
Araliaceae	*Brassaiopsis membranifolia*	0	0	0	**0**	0	1	0	**1**
Phyllanthaceae	*Breynia diversifolia*	11	0	0	**11**	1	0	0	**1**
Phyllanthaceae	*Bridelia ovata*	0	5	1	**6**	0	0	0	**0**
Moraceae	*Broussonetia papyrifera*	0	0	1	**1**	0	0	0	**0**
Malvaceae	*Burretiodendron hsienmu*	0	8	9	**17**	1	0	0	**1**
Lamiaceae	*Callicarpa brevipes*	0	0	1	**1**	0	0	0	**0**
Lamiaceae	*Callicarpa macrophylla*	0	0	0	**0**	0	3	7	**10**
Calophyllaceae	*Calophyllum formosum*	0	0	0	**0**	0	0	2	**2**
Theaceae	*Camellia caudata*	0	0	1	**1**	0	0	0	**0**
Juglandaceae	*Carya tonkinensis*	1	0	0	**1**	0	0	0	**0**
Arecaceae	*Caryota bacsonensis*	0	0	0	**0**	0	1	0	**1**
Fabaceae	*Cassia javanica*	0	0	0	**0**	0	1	0	**1**
Fagaceae	*Castanopsis acuminatissima*	4	0	0	**4**	0	0	0	**0**
Fagaceae	*Castanopsis boisii*	3	0	0	**3**	0	0	0	**0**
Fagaceae	*Castanopsis sp.*	7	0	0	**7**	4	0	0	**4**
Ulmaceae	*Celtis tetrandra*	0	4	4	**8**	1	0	0	**1**
Euphorbiaceae	*Cephalomappa sinensis*	0	45	28	**73**	0	10	0	**10**
Anacardiaceae	*Choerospondias axillaris*	0	0	0	**0**	1	0	0	**1**
Meliaceae	*Cipadessa baccifera*	0	0	0	**0**	0	5	6	**11**
Rutaceae	*Clausena lansium*	2	0	0	**2**	2	0	0	**2**
Lamiaceae	*Clerodendrum chinense*	0	0	0	**0**	0	0	1	**1**
Connaraceae	*Connarus paniculatus*	0	0	0	**0**	1	0	0	**1**
Costaceae	*Costus tonkinensis*	0	0	1	**1**	0	0	0	**0**
Fabaceae	*Crotalaria pallida*	19	0	0	**19**	3	0	0	**3**
Urticaceae	*Dendrocnide urentissima*	0	0	5	**5**	0	1	0	**1**

Ebenaceae	*Diospyros buxifolia*	0	0	0	**0**	0	1	0	**1**
Ebenaceae	*Diospyros kaki*	0	0	0	**0**	0	0	1	**1**
Ebenaceae	*Diospyros rufogemmata*	0	0	5	**5**	2	0	0	**2**
Elaeocarpaceae	*Elaeocarpus balansae*	4	0	1	**5**	5	1	0	**6**
Elaeocarpaceae	*Elaeocarpus petiolatus*	0	0	0	**0**	1	0	0	**1**
Juglandaceae	*Engelhardtia roxburghiana*	1	0	0	**1**	5	1	0	**6**
Celastraceae	*Euonymus balansae*	3	0	0	**3**	2	0	0	**2**
Pentaphylacaceae	*Eurya cerasifolia*	6	0	0	**6**	5	1	0	**6**
Moraceae	*Ficus cyrtophylla*	0	0	0	**0**	0	2	0	**2**
Moraceae	*Ficus hirta*	0	0	2	**2**	0	2	0	**2**
Moraceae	*Ficus leavis*	0	0	1	**1**	0	0	0	**0**
Moraceae	*Ficus obscura*	0	0	0	**0**	0	1	1	**2**
Moraceae	*Ficus spathulifolia*	0	0	0	**0**	5	2	0	**7**
Moraceae	*Ficus sumatra*	0	0	2	**2**	0	0	0	**0**
Moraceae	*Ficus vasculosa*	0	0	0	**0**	0	1	0	**1**
Annonaceae	*Fissistigma bracteatum*	0	0	0	**0**	0	0	1	**1**
Salicaceae	*Flacourtia rukam*	0	0	0	**0**	0	1	2	**3**
Oleaceae	*Fraxinus rhynchophyllus*	0	0	0	**0**	2	0	0	**2**
Clusiaceae	*Garcinia fagraeoides*	0	3	0	**3**	2	0	0	**2**
Clusiaceae	*Garcinia multiflora*	0	2	6	**8**	0	3	0	**3**
Phyllanthaceae	*Glochidion zeylanicum*	1	0	0	**1**	0	0	0	**0**
Icacinaceae	*Gomphandra tetrandra*	0	0	1	**1**	0	0	0	**0**
Malvaceae	*Grewia sessifolia*	0	0	0	**0**	1	0	0	**1**
Theaceae	*Hartia yunnanensis*	0	0	1	**1**	0	0	0	**0**
Styracaceae	*Huodendron tibeticum*	0	1	5	**6**	4	2	0	**6**
Hydrangeaceae	*Hydrangea aspera*	0	0	1	**1**	0	0	0	**0**
Aquifoliaceae	*Ilex latifolia*	0	1	1	**2**	0	0	0	**0**
Schisandraceae	*Illicium parvifolium*	0	0	0	**0**	1	0	0	**1**
Salicaceae	*Itoa orientalis*	0	0	0	**0**	0	5	28	**34**
Rubiaceae	*Ixora balansae*	0	0	0	**0**	0	1	0	**1**

Sapindaceae	*Koelreuteria paniculata*	4	0	0	**4**	0	0	0	**0**
Vitaceae	*Leea indica*	0	0	4	**4**	0	0	0	**0**
Altingiaceae	*Liquidambar formosana*	0	0	0	**0**	0	3	0	**3**
Fagaceae	*Lithocarpus sp.*	0	0	1	**1**	0	0	0	**0**
Lauraceae	*Litsea balansae*	0	0	2	**2**	3	2	0	**5**
Lauraceae	*Litsea brevipes*	0	0	2	**2**	2	0	0	**2**
Lauraceae	*Litsea chartacea*	1	0	0	**1**	0	0	0	**0**
Lauraceae	*Litsea glutinosa*	0	0	0	**0**	0	1	0	**1**
Lauraceae	*Litsea laevifolia*	3	0	0	**3**	0	0	0	**0**
Lauraceae	*Litsea verticillata*	0	0	0	**0**	0	1	0	**1**
Lauraceae	*Litsea viridis*	0	0	0	**0**	0	2	0	**2**
Macaranga	*Macaranga denticulata*	0	0	0	**0**	0	0	2	**2**
Euphorbiaceae	*Macaranga indica*	0	0	0	**0**	0	1	0	**1**
Lauraceae	*Machilus macrophylla*	0	0	0	**0**	0	1	0	**1**
Lauraceae	*Machilus platycarpa*	0	0	0	**0**	0	1	0	**1**
Sapotaceae	*Madhuca pasquierii*	0	2	0	**2**	0	0	0	**0**
Primulaceae	*Maesa balansae*	0	0	1	**1**	0	0	0	**0**
Primulaceae	*Maesa montana*	0	0	0	**0**	0	6	33	**40**
Euphorbiaceae	*Mallotus barbatus*	5	0	0	**5**	0	3	1	**4**
Euphorbiaceae	*Mallotus philippinensis*	0	1	0	**1**	4	3	1	**8**
Rutaceae	*Micromelum integerrimum*	0	0	0	**0**	1	0	0	**1**
Annonaceae	*Miliusa balansae*	0	0	0	**0**	8	0	0	**8**
Meliaceae	*Munronia heterophylla*	0	1	0	**1**	0	0	0	**0**
Rubiaceae	*Mussaenda chevalieri*	0	0	0	**0**	0	1	0	**1**
Melastomataceae	*Oxyspora paniculata*	0	0	0	**0**	0	0	28	**28**
Phyllanthaceae	*Phyllanthus annamensis*	0	0	0	**0**	0	0	19	**19**
Phyllanthaceae	*Phyllanthus reticulata*	0	0	0	**0**	0	0	2	**2**
Phyllanthaceae	*Phyllanthus ruber*	0	0	7	**7**	0	0	0	**0**

Anacardiaceae	*Pistacia cucphuongensis*	2	0	0	**2**	1	0	0	**1**
Anacardiaceae	*Pistacia weinmannifolia*	3	0	0	**3**	4	0	0	**4**
Anacardiaceae	*Pistacia weinmannifolia*	5	0	0	**5**	0	0	0	**0**
Annonaceae	*Polyalthia lauii*	0	6	1	**7**	0	2	0	**2**
Annonaceae	*Polyalthia nemoralis*	0	0	1	**1**	0	0	0	**0**
Sapindaceae	*Pometia pinnata*	0	0	1	**1**	0	0	0	**0**
Lamiaceae	*Premna balansae*	1	0	0	**1**	0	0	0	**0**
Rosaceae	*Prunus arborea*	5	1	0	**6**	2	2	0	**4**
Rubiaceae	*Psychotria rubra*	0	0	0	**0**	0	1	0	**1**
Rubiaceae	*Psychotria siamica*	0	0	1	**1**	0	0	0	**0**
Fagaceae	*Quercus acutissima*	2	0	0	**2**	11	0	0	**11**
Fagaceae	*Quercus bambusifolia*	0	0	0	**0**	1	0	0	**1**
Bignoniaceae	*Radermacheta sinica*	0	0	4	**4**	0	4	10	**14**
Rubiaceae	*Randia spinosa*	0	0	0	**0**	0	3	3	**6**
Anacardiaceae	*Rhus javanica*	0	0	0	**0**	0	3	1	**4**
Sapindaceae	*Sapindus mukorossi*	0	3	3	**6**	0	3	0	**3**
Sapindaceae	*Sapindus oocarpus*	0	2	0	**2**	0	0	0	**0**
Actinidiaceae	*Saurauia roxburghii*	0	0	2	**2**	0	4	0	**4**
Actinidiaceae	*Saurauia tristyla*	0	0	4	**4**	0	0	0	**0**
Araliaceae	*Schefflera macrophylla*	0	2	0	**2**	0	0	0	**0**
Araliaceae	*Schefflera pes-avis*	5	1	5	**11**	5	0	0	**5**
Sapotaceae	*Sinosideroxylon wightianum*	6	5	0	**11**	2	1	0	**3**
Rosaceae	*Sorbus epidendron*	2	0	0	**2**	0	0	0	**0**
Malvaceae	*Sterculia lanceolata*	0	3	0	**3**	0	0	0	**0**
Linaceae	*Tirpitzia sinensis*	17	0	0	**17**	13	0	0	**13**
Araliaceae	*Trevesia palmata*	0	0	0	**0**	0	0	1	**1**

Euphorbiaceae	*Triadica rotundifolia*	1	0	0	**1**	2	1	0	**3**
Euphorbiaceae	*Trigonostemon thyrsoideus*	0	29	23	**52**	0	0	0	**0**
Ericaceae	*Vaccinium bullatum*	3	0	0	**3**	0	0	0	**0**
Urticaceae	*Villebrunea frutescens*	1	0	0	**1**	0	0	0	**0**
Urticaceae	*Villebrunea integrifolia*	0	1	1	**2**	6	7	0	**13**
Meliaceae	*Walsura elata*	0	1	0	**1**	0	2	0	**2**
Rubiaceae	*Wendlandia acuminata*	1	0	0	**1**	0	0	0	**0**
Rubiaceae	*Wendlandia glabrata*	0	0	1	**1**	0	0	0	**0**
Rubiaceae	*Wendlandia laotica*	0	0	0	**0**	1	2	0	**3**
Apocynaceae	*Wrightia stellata*	0	0	0	**0**	0	2	0	**2**
Rhamnaceae	*Ziziphus incurva*	0	1	0	**1**	4	2	1	**7**
Total		**144**	**143**	**159**	**446**	**144**	**131**	**161**	**438**

4.2.4 Tree species captured in the Corridor, CVGCA and Zone IV transects only

Family	Species	Corridor			CVGCA			Zone IV		
		R (n)	S (n)	V (n)	R (n)	S (n)	V (n)	R (n)	S (n)	V (n)
Sapindaceae	*Acer tonkinensis*	0	0	0	0	5	0	0	1	0
Meliaceae	*Aglaia tomentosa*	0	0	0	0	0	2	0	1	0
Cornaceae	*Alangium chinensis*	0	0	0	0	0	0	0	0	2
Cornaceae	*Alangium kurzii*	0	0	2	0	1	0	0	0	0
Moraceae	*Alchornea tiliaefolia*	0	3	0	0	1	0	0	0	0
Moraceae	*Alchornea trewIodes*	0	0	0	0	0	0	1	0	0
Sapindaceae	*Allophylus caudatus*	0	0	0	0	0	3	0	0	0
Sapindaceae	*Amesiodendron chinense*	0	1	0	0	0	0	0	0	0
Phyllanthaceae	*Antidesma bunius*	0	0	0	0	0	5	0	0	0
Phyllanthaceae	*Antidesma fruticosum*	0	1	1	0	0	0	0	0	1
Mimosoideae	*Archidendron tonkinensis*	0	0	0	0	0	1	0	2	0
Primulaceae	*Ardisia crenata*	0	0	0	1	0	0	0	0	0
Primulaceae	*Ardisia tinctoria*	0	0	0	1	2	0	0	0	0
Rutaceae	*Atalantia guillauminii*	0	0	0	0	0	0	0	1	0
Phyllanthaceae	*Bischofia javanica*	0	0	0	0	0	2	0	0	0
Urticaceae	*Boehmeria holosericea*	0	0	0	0	0	0	0	1	0
Araliaceae	*Brassaiopsis membranifolia*	0	0	0	0	0	0	0	1	0
Phyllanthaceae	*Breynia diversifolia*	0	0	0	4	0	0	1	0	0
Phyllanthaceae	*Bridelia ovata*	1	0	0	0	1	0	0	0	0
Moraceae	*Broussonetia papyrifera*	0	0	0	0	0	1	0	0	0
Malvaceae	*Burretiodendron hsienmu*	1	1	0	0	2	0	1	0	0
Lamiaceae	*Callicarpa brevipes*	0	0	0	0	0	1	0	0	0
Lamiaceae	*Callicarpa macrophylla*	0	4	1	0	0	0	0	0	1
Lamiaceae	*Callicarpa nudiflora*	1	0	5	0	0	0	0	0	0
Theaceae	*Camellia caudata*	0	0	1	0	0	1	0	0	0
Fagaceae	*Castanopsis acuminatissima*	0	0	0	4	0	0	0	0	0
Fagaceae	*Castanopsis boisii*	0	0	0	3	0	0	0	0	0
Fagaceae	*Castanopsis sp.*	0	1	0	0	0	0	4	0	0
Euphorbiaceae	*Cephalomappa sinensis*	14	15	0	0	13	0	0	0	0
Lauraceae	*Cinnamomum tonkinensis*	1	0	0	0	0	0	0	0	0
Meliaceae	*Cipadessa baccifera*	0	1	7	0	0	0	0	0	3
Rutaceae	*Clausena lansium*	0	2	1	0	0	0	2	0	0
Clusiaceae	*Cratoxylum formosum*	0	1	0	0	0	0	0	0	0
Fabaceae	*Crotalaria pallida*	0	0	0	9	0	0	3	0	0
Dendrocnide	*Dendrocnide urentissima*	0	0	0	0	0	2	0	0	0
Annonaceae	*Desmos chinensis*	0	0	1	0	0	0	0	0	0
Ebenaceae	*Diospyros apiculata*	2	5	3	0	0	0	0	0	0
Ebenaceae	*Diospyros buxifolia*	1	0	0	0	0	0	0	0	0

Ebenaceae	*Diospyros rufogemmata*	0	0	0	0	0	0	2	0	0
Elaeocarpaceae	*Elaeocarpus balansae*	1	0	0	0	0	0	2	1	0
Juglandaceae	*Engelhardtia roxburghiana*	0	0	0	0	0	0	0	1	0
Rutaceae	*Euodia lepta*	0	1	0	0	0	0	0	0	0
Celastraceae	*Euonymus balansae*	0	0	0	2	0	0	1	0	0
Pentaphylacaceae	*Eurya cerasifolia*	0	0	0	2	0	0	0	1	0
Moraceae	*Ficus hirta*	0	0	1	0	0	2	0	0	0
Moraceae	*Ficus nervosa*	0	1	0	0	0	0	0	0	0
Moraceae	*Ficus sumatra*	0	0	0	0	0	1	0	0	0
Salicaceae	*Flacourtia rukam*	0	0	0	0	0	0	0	0	1
Clusiaceae	*Garcinia fagraeoides*	0	0	0	0	1	0	2	0	0
Clusiaceae	*Garcinia multiflora*	4	0	0	0	2	0	0	2	0
Phyllanthaceae	*Glochidion zeylanicum*	0	0	0	1	0	0	0	0	0
Rutaceae	*Harrisonia perforata*	0	0	1	0	0	0	0	0	0
Styracaceae	*Huodendron tibeticum*	0	0	1	0	1	0	0	0	0
Hydrangeaceae	*Hydrangea aspera*	0	0	0	0	0	1	0	0	0
Aquifoliaceae	*Ilex latifolia*	0	0	0	0	1	0	0	0	0
Schisandraceae	*Illicium parviforum*	0	0	0	0	0	0	1	0	0
Salicaceae	*Itoa orientalis*	0	0	0	0	0	0	0	0	13
Vitaceae	*Leea indica*	0	0	0	0	0	4	0	0	0
Lauraceae	*Litsea balansae*	1	5	3	0	0	2	0	0	0
Lauraceae	*Litsea brevipes*	0	0	0	0	0	0	1	0	0
Lauraceae	*Litsea chartacea*	0	0	0	1	0	0	0	0	0
Lauraceae	*Litsea laevifolia*	0	0	0	1	0	0	0	0	0
Lauraceae	*Litsea verticilata*	0	0	0	0	0	0	0	1	0
Primulaceae	*Maesa balansae*	0	0	0	0	0	1	0	0	0
Primulaceae	*Maesa montana*	0	3	1	0	0	0	0	0	20
Euphorbiaceae	*Mallotus philippinensis*	0	0	3	0	1	0	0	3	0
Melastomataceae	*Oxyspora paniculata*	0	0	0	0	0	0	0	0	27
Caesalpiniaceae	*Peltophorum dassyrachis*	1	0	0	0	0	0	0	0	0
Phyllanthaceae	*Phyllanthus annamensis*	0	0	0	0	0	0	0	0	14
Phyllanthaceae	*Phyllanthus ruber*	1	0	0	0	0	5	0	0	0
Anacardiaceae	*Pistacia cucphuongensis*	0	0	0	1	0	0	1	0	0
Anacardiaceae	*Pistacia weinmannifolia*	0	0	0	2	0	0	1	0	0
Annonaceae	*Polyalthia lauii*	0	5	5	0	2	0	0	0	0
Lamiaceae	*Premna balansae*	0	0	0	1	0	0	0	0	0
Rosaceae	*Prunus arborea*	0	0	0	3	0	0	2	0	0
Rubiaceae	*Psychotria siamica*	0	0	0	0	0	1	0	0	0
Rubiaceae	*Psychotria tonkinensis*	0	1	0	0	0	0	0	0	0
Fagaceae	*Quercus acutissima*	0	0	0	0	0	0	11	0	0
Bignoniaceae	*Radermacheta sinica*	0	0	1	0	0	0	0	0	1
Bignoniaceae	*Radermacheta sinica*	0	0	0	0	0	2	0	0	0
Anacardiaceae	*Rhus javanica*	0	1	3	0	0	0	0	0	0

Sapindaceae	*Sapindus mukorossi*	0	0	0	0	0	0	0	1	0
Actinidiaceae	*Saurauia roxburghii*	0	0	10	0	0	0	0	0	0
Actinidiaceae	*Saurauia tristyla*	0	0	0	0	0	4	0	0	0
Araliaceae	*Schefflera macrophylla*	0	0	0	0	2	0	0	0	0
Araliaceae	*Schefflera pes-avis*	0	0	0	1	1	3	0	0	0
Sapotaceae	*Sinosideroxylon wightianum*	0	0	0	2	5	0	0	1	0
Rosaceae	*Sorbus epidendron*	0	0	0	2	0	0	0	0	0
Malvaceae	*Sterculia lanceolata*	0	0	1	0	3	0	0	0	0
Moraceae	*Streblus tonkinensis*	0	0	1	0	0	0	0	0	0
Linaceae	*Tirpitzia sinensis*	0	0	0	2	0	0	4	0	0
Euphorbiaceae	*Triadica rotundifolia*	0	0	0	0	0	0	1	0	0
Euphorbiaceae	*Trigonostemon thyrsoideus*	0	0	0	0	5	0	0	0	0
Ericaceae	*Vaccinium bullatum*	0	0	0	3	0	0	0	0	0
Urticaceae	*Villebrunea frutescens*	0	1	0	0	0	0	0	0	0
Urticaceae	*Villebrunea integrifolia*	0	4	0	0	1	0	0	2	0
Rhamnaceae	*Ziziphus incurva*	1	0	0	0	1	0	0	0	0
Total		**30**	**57**	**53**	**46**	**51**	**44**	**41**	**20**	**83**

R= ridge transects, S= slope transects, V=valley transects.

4.3 Food species for the cao vit gibbon

4.3.1 Food species identified in previous studies

List of CVG food species and sites where the food was observed to be consumed taken from Insua-Cao (2012), Fan et al., (2011), Fan et al., (2015), Thien (2012) and Chan (2006) where an observation note was made.

Family	Species	Eaten by CVGCA groups (Vietnam)	Eaten by BNNR groups (China)
Sapindaceae	*Acer tonkinensis*	yes	yes
Actinidiaceae	*Actinidia indochinensis*	no	yes
Cornaceae	*Alangium kurzii var. latifolium*	no	yes
Sapindaceae	*Allophylus sp.*	yes	no
Vitaceae	*Ampelopsis cantoniensis*	yes	no
Icacinaceae	*Apodytes dimidiate*	yes	no
Moraceae	*Artocarpus hypargyreus*	no	yes
Moraceae	*Artocarpus tonkinensis*	yes	no
Phyllanthaceae	*Baccaurea ramiflora*	yes	no
Fabaceae	*Bauhinia rubrovillosa*	yes	yes
Phyllanthaceae	*Bischofia javanica*	yes	no
Gramineae	*Bonia saxatilis*	yes	no
Sapindaceae	*Boniodendron minius*	yes	no
Phyllanthaceae	*Bridelia ovata*	yes	no
Phyllanthaceae	*Bridelia retusa*	yes	no
Moraceae	*Broussonetia papyrifera*	yes	yes
Malvaceae	*Burretiodendron hsienmu*	no	yes
Arecaceae	*Caryota bacsonensis*	yes	no
Arecaceae	*Caryota maxima*	yes	yes
Arecaceae	*Caryota urens*	yes	no
Celastraceae	*Celastrus orbicullatus*	no	yes
Ulmaceae	*Celtis bungeana*	no	yes
Ulmaceae	*Celtis tetrandra*	yes	no
Ulmaceae	*Celtis timorensis*	yes	no
Euphorbiaceae	*Cephalomappa sinensis*	yes	yes
Rosaceae	*Cerasus sp.*	no	yes
Anacardiaceae	*Choerospondias axillaris*	yes	yes
Lauraceae	*Cinnamomum parthenoxylon*	no	yes
Lauraceae	*Cinnamomum saxatile*	no	yes
Meliaceae	*Cipadessa baccifera*	yes	yes
Rutaceae	*Citrus sp.*	yes	yes
Rutaceae	*Clausena excavata*	no	yes
Ranunculaceae	*Clematis uncinata*	no	yes
Lauraceae	*Cryptocarya lyoniifolia*	yes	no

Moraceae	*Cudrania cochinchinensis*	yes	yes
Convolvulaceae	*Cuscuta chinensis*	no	yes
Fagaceae	*Cyclobalanopsis glauca*	yes	yes
Sapindaceae	*Dimocarpus fumatus ssp. indochinensis*	yes	no
Dioscoraceae	*Dioscorea persimilis*	yes	no
Ebenaceae	*Diospyros kaki var. silvestris*	yes	yes
Ebenaceae	*Diospyros siderophylla*	no	yes
Menispermaceae	*Diploclisia glaucescens*	yes	yes
Primulaceae	*Embelia undulata*	yes	yes
Juglandaceae	*Engelhardtia roxburghiana*	yes	no
Rosaceae	*Eriobotrya cavaleriei*	yes	yes
Olacacea	*Erythropalum scandens*	yes	no
Rutaceae	*Evodia calcicola*	no	yes
Tiliaceae	*Excentrodendron tonkinense*	yes	yes
Moraceae	*Ficus auriculata*	no	yes
Moraceae	*Ficus cardiophylla*	yes	no
Moraceae	*Ficus cyrtophylla*	yes	yes
Moraceae	*Ficus erecta var. beecheyana*	yes	no
Moraceae	*Ficus glaberrima*	yes	yes
Moraceae	*Ficus heteropleura*	yes	no
Moraceae	*Ficus hookeriana*	yes	yes
Moraceae	*Ficus microcarpa*	yes	yes
Moraceae	*Ficus sagittata*	yes	no
Moraceae	*Ficus talbotii*	yes	no
Moraceae	*Ficus tinctoria ssp. gibbosa*	yes	yes
Moraceae	*Ficus tsangii*	yes	no
Moraceae	*Ficus tuphapensis*	no	yes
Moraceae	*Ficus virens var. virens*	yes	yes
Clusiaceae	*Garcinia bracteata*	yes	yes
Clussiaceae	*Garcinia paucinervis*	yes	yes
Icacinaceae	*Iodes cirrhosa*	yes	no
Icacinaceae	*Iodes vitiginea*	no	yes
Schisandraceae	*Kadsura coccinea*	yes	no
Schisandraceae	*Kadsura heteroclita*	no	yes
Lauraceae	*Litsea monopetala*	yes	no
Lauraceae	*Machilus rehderi*	no	yes
Moraceae	*Maclura cochinchinensis*	yes	yes
Sapotaceae	*Madhuca pasquieri*	yes	yes
Euphorbiaceae	*Mallotus sp.*	no	yes
Apocynaceae	*Melodinus suaveolens*	no	yes
Papilionaceae	*Millettia reticulata*	no	yes
Annonaceae	*Mitrephora maingayi*	yes	no
Myrsinaceae	*Myrsine kwangsiensis*	yes	yes
Lauraceae	*Neolitsea ellipsoidea*	yes	yes

Urticaceae	*Oreocnide frutescens*	no	yes
Bignoniaceae	*Oroxylon indicum*	yes	no
Rubiaceae	*Pavetta hongkongensis*	yes	yes
Anacardiaceae	*Pistacia weinmannifolia*	no	yes
Araceae	*Pothos chinensis*	yes	no
Araceae	*Pothos pilulifer*	yes	yes
Bignoniaceae	*Radermachera boniana*	yes	no
Bignoniaceae	*Radermachera hainanensis*	no	yes
Euphorbiaceae	*Sapium rotundìfolium*	yes	yes
Actinidiaceae	*Saurauia napaulensis*	yes	no
Actinidiaceae	*Saurauia thyrsiflora*	yes	yes
Actinidiaceae	*Saurauia thyrsitlora*	yes	yes
Actinidiaceae	*Saurauia trisyala*	no	yes
Araliaceae	*Schefflera minutistellata*	no	yes
Loranthaceae	*Scurrula parasitica*	no	yes
Sapotaceae	*Sinosideroxylon wightianum*	yes	no
Anacardiaceae	*Spondias lakonensis*	yes	yes
Malvaceae	*Sterculia nobilis*	yes	no
Malvaceae	*Sterculia quadrifida*	yes	no
Vitaceae	*Tetrastigma delavayi*	no	yes
Vitaceae	*Tetrastigma hemsleyanum*	yes	no
Vitaceae	*Tetrastigma hooherii*	yes	no
Vitaceae	*Tetrastigma kwangsiensis*	no	yes
Vitaceae	*Tetrastigma obtectum*	no	yes
Vitaceae	*Tetrastigma planicaule*	yes	yes
Vitaceae	*Tetrastigma pubinerve*	yes	yes
Vitaceae	*Tetrastigma retinervium*	yes	no
Linaceae	*Tirpitzia ovoidea*	no	yes
Meliaceae	*Toona sinensis*	yes	yes
Anacardiaceae	*Toxicodendron succedaneum*	yes	yes
Anacardiaceae	*Toxicodendron wallichii var. microcarpum*	yes	yes
Cucurbitaceae	*Trichosanthes kirilowi*	yes	yes
Cucurbitaceae	*Trichosanthes truncata*	yes	no
Ulmaceae	*Ulmus lanceifolia*	yes	yes
Lamiaceae	*Vitex quinata*	yes	no
Vitaceae	*Vitis sp.*	yes	no
Rhamnaceae	*Ziziphus mauritiana*	no	yes
Rhamnaceae	*Ziziphus pubinervis*	yes	yes
Rhamnaceae	*Ziziphus oenopolia*	yes	no

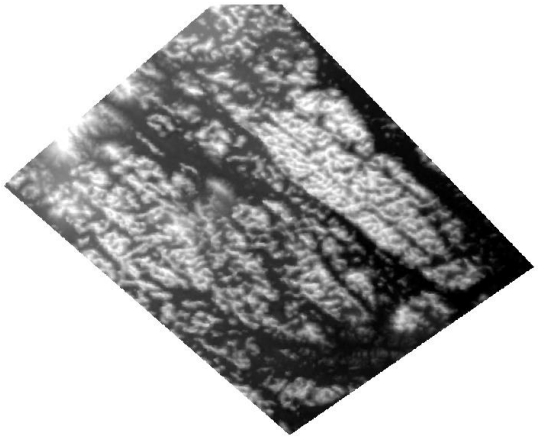
4.3.2 Food species identified in CVGCA, Zone IV and the corridor

Family	Species	CVGCA				Zone IV				Corridor			
		R (n)	S (n)	V (n)	T	R (n)	S (n)	V (n)	T	R (n)	S (n)	V (n)	T
Sapindaceae	*Acer tonkinensis*	17	23	7	**47**	23	6	3	**32**	0	0	0	**0**
Cornaceae	*Alangium kurzii*	0	2	0	**2**	0	1	0	**1**	0	0	0	**0**
Sapindaceae	*Allophylus caudatus*	0	6	14	**20**	0	0	0	**0**	0	0	0	**0**
Phyllanthaceae	*Bischofia javanica*	0	0	7	**7**	0	0	0	**0**	0	0	0	**0**
Phyllanthaceae	*Bridelia ovata*	0	5	1	**6**	0	6	0	**6**	**1**	**0**	**0**	**1**
Moraceae	*Broussonetia papyrifera*	0	0	1	**1**	0	0	0	**0**	0	0	0	**0**
Malvaceae	*Burretiodendron hsienmu*	0	36	13	**49**	3	1	0	**4**	2	1	1	4
Arecaceae	*Caryota bacsonensis*	0	3	2	**5**	0	1	0	**1**	0	0	1	1
Ulmaceae	*Celtis tetrandra*	0	5	5	**10**	5	14	6	**25**	2	1	4	7
Euphorbiaceae	*Cephalomappa sinensis*	0	123	52	**175**	0	21	0	**21**	98	20	0	118
Anacardiaceae	*Choerospondias axillaris*	0	0	0	**0**	1	0	0	**1**	0	0	0	**0**
Meliaceae	*Cipadessa baccifera*	0	0	0	**0**	0	35	19	**54**	0	13	21	34
Rutaceae	*Citrus grandis*	0	0	0	**0**	0	0	2	**2**	0	0	0	**0**
Ebenaceae	*Diospyros kaki*	0	0	0	**0**	0	0	1	**1**	0	0	0	**0**
Juglandaceae	*Engelhardtia roxburghiana*	2	0	0	**2**	12	1	0	**13**	0	0	0	**0**
Olacacea	*Erythropalum scandens*	0	0	9	**9**	2	3	14	**19**	0	0	0	**0**
Moraceae	*Ficus cyrtophylla*	0	0	0	**0**	1	2	4	**7**	1	0	0	1
Euphorbiaceae	*Mallotus barbatus*	8	0	0	**8**	1	4	3	**8**	0	0	0	**0**
Euphorbiaceae	*Mallotus philippinensis*	1	1	0	**2**	4	4	1	**9**	2	2	6	10
Anacardiaceae	*Pistacia weinmannifolia*	6	0	0	**6**	0	0	0	**0**	0	0	0	**0**
Sapotaceae	*Sinosideroxylon wightianum*	19	10	0	**29**	4	7	0	**11**	*2*	9	0	11
Vitaceae	*Tetrastigma obtectum*	0	0	0	**0**	6	27	16	**49**	*0*	3	21	24
Vitaceae	*Tetrastigma planicaule*	0	3	10	**13**	0	0	0	**0**	0	0	0	**0**
Total		**53**	**217**	**121**	**391**	**62**	**133**	**69**	**264**	**108**	**49**	**54**	**211**

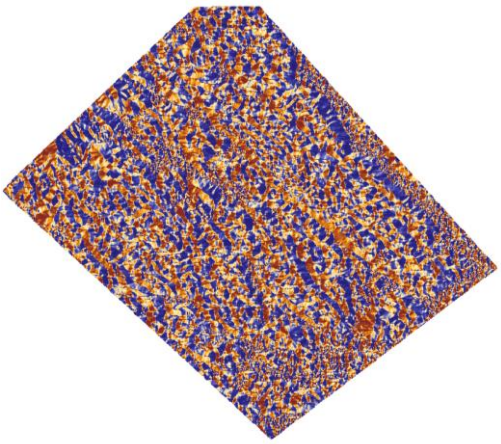
R=ridge, S= slope, V=valley, T=total.

4.4 Results for MaxEnt analysis for the cao vit gibbon

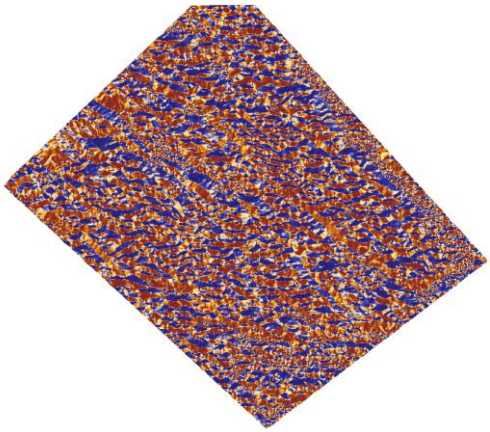
4.4.1 Predictor variables for cao vit gibbon distribution



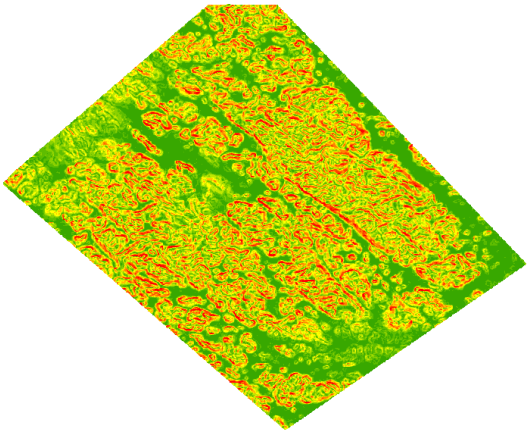
Digital Elevation Model



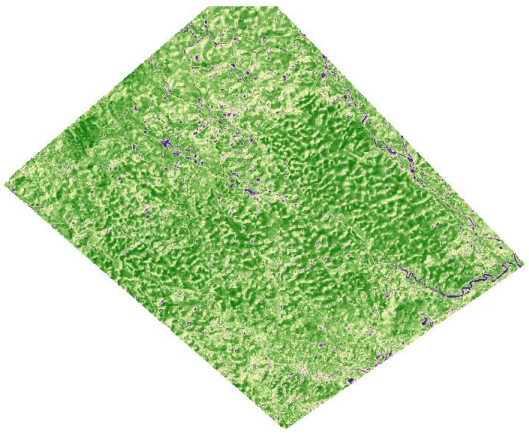
Eastness (Aspect)



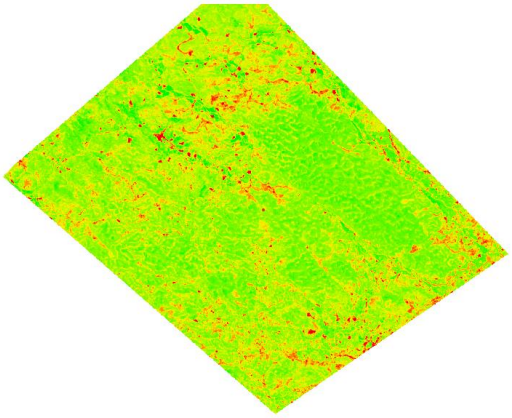
Northness (Aspect)



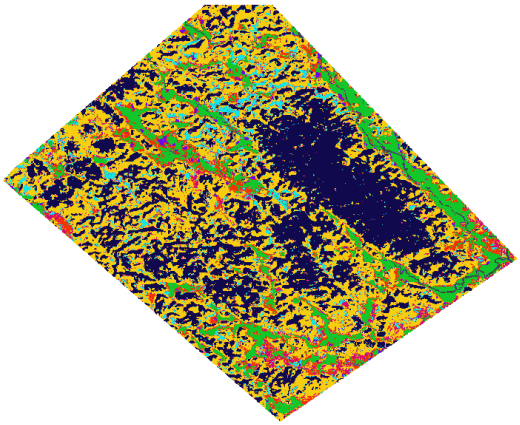
Slope



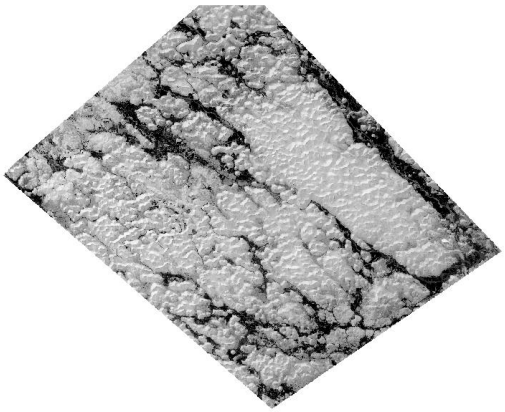
Normalised Difference Vegetation Index



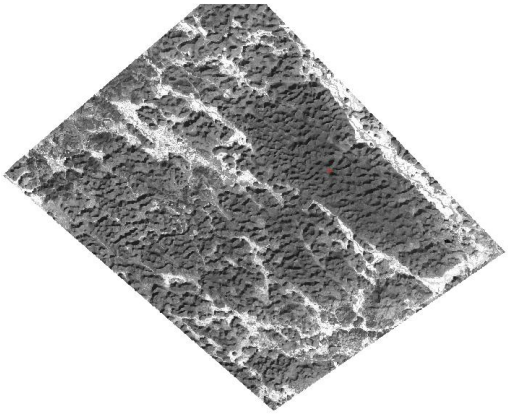
Normalised Difference Moisture Index



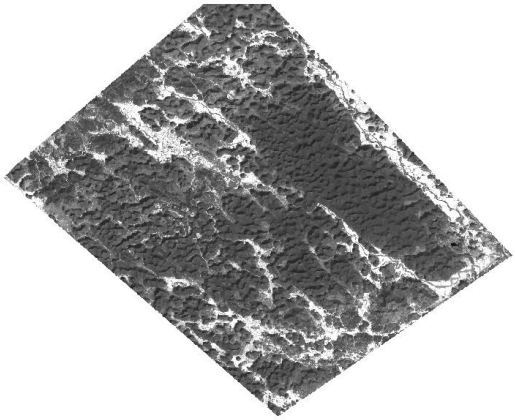
Land use and land cover



SPOT6 Band 1 (blue)

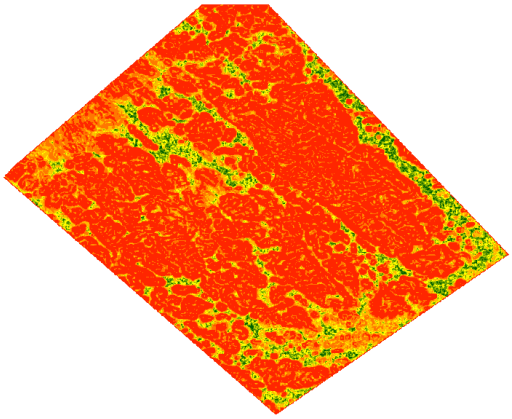


SPOT6 Band 2 (green)



SPOT6 Band 3 (red)

SPOT6 Band 4 (near-infrared)



Topographic Ruggedness Index

4.4.2 Pearson's correlation of variables for cao vit gibbon MaxEnt analysis

	Eastness	NDMI	NDVI	Northness	Spot6 band1 (Blue)	Spot6 band2 (Green)	Spot6 band3 (Red)	Spot6 band4 (NIR)	DEM	Slope	TRI
Eastness	1										
NDMI	0.060	1									
NDVI	0.297	0.650	1								
Northness	0.087	-0.027	-0.201	1							
Spot6 band 1 (Blue)	0.106	-0.193	-0.129	-0.112	1						
Spot6 band2 (Green)	0.156	-0.156	0.002	-0.209	0.957*	1					
Spot6 band3 (Red)	0.094	-0.126	-0.074	-0.101	0.969*	0.953*	1				
Spot6 band4 (NIR)	0.305	0.143	0.606	-0.465	0.133	0.335	0.119	1			
DEM	-0.007	0.220	0.139	-0.018	-0.547	-0.514	-0.505	-0.007	1		
Slope	-0.020	0.189	0.102	0.059	-0.561	-0.568	-0.570	-0.072	0.446	1	
TRI	-0.010	0.023	0.002	0.022	-0.117	-0.117	-0.117	-0.028	0.104	0.241	1

*Strong correlation where -0.7<r>0.7

4.4.3 MaxEnt model results

4.4.3.1 *Results of models with feature class and regularisation multiplier variations*

Feature type	Test #	Regularisation multiplier	Number of variables	Training AUC	Test AUC	AUC Difference	Highest contributing variables	Lowest contributing variables	Negative test gain
Quadratic-only	1	0.25	10	0.909	0.848	0.061	Land use and NDMI	TRI, Eastness, Northness	Spot Band 4, NDVI
	2	0.5	10	0.906	0.849	0.057	Land use and NDMI	TRI, NDVI, Eastness, Northness	Spot Band 4, NDVI
	3	1	10	0.902	0.849	0.053	Land use and NDMI	TRI, NDVI, Eastness, Northness	Spot Band 4, NDVI
	4	2	10	0.896	0.847	0.049	Land use and NDMI	TRI, Slope, NDVI, Eastness, Northness, DEM	Spot Band 4, NDVI
Best performing test rerun	5	2	8	0.89	0.852	0.038	Land use and NDMI	TRI, Slope, Eastness, Northness, DEM	-
Hinge	6	0.25	10	0.972	0.765	0.207	Land use and NDVI	TRI	NDVI, Northness, Slope, Spot6 Band4, TRI
	7	0.5	10	0.945	0.828	0.117	Land use and NDVI	TRI	NDVI, Northness, Slope, Spot6 Band4, TRI
	8	1	10	0.932	0.836	0.096	Land use and NDVI	TRI	NDVI, Northness, Slope, Spot6 Band4, TRI
	9	2	10	0.902	0.823	0.079	Land use and NDVI	DEM, NDMI, Spot6 Band4, TRI, Slope	NDVI, Northness, Slope, Spot6 Band4
Best performing test rerun	10	2	6	0.890	0.855	0.035	Land use	TRI, Spot Band1	NDMI
Quadratic and Hinge	11	0.25	10	0.972	0.771	0.201	Land use and NDVI	TRI, DEM	Eastness, NDVI, Northness, Slope, Spot6 Band4, TRI

Table 4.4.3.1 continued

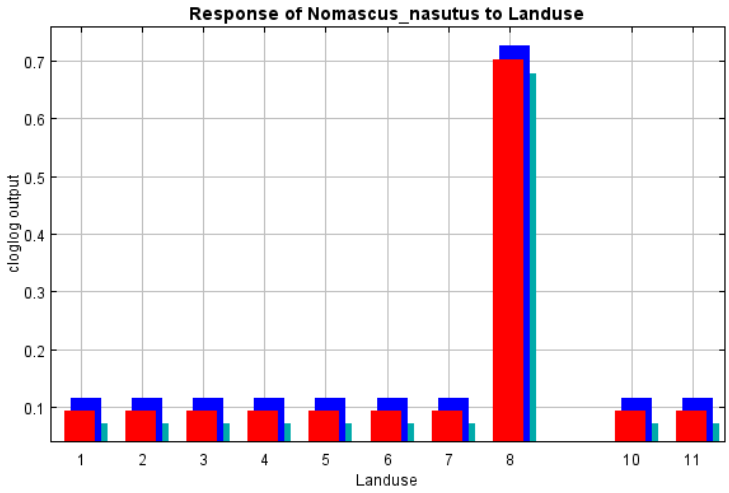
	12	0.5	10	0.948	0.832	0.116	Land use and NDVI	TRI, DEM, Slope	Eastness, NDVI, Northness, Slope, Spot6 Band4
	13	1	10	0.934	0.844	0.090	Land use and NDVI	TRI	Eastness, NDVI, Northness, Slope, Spot6 Band4, TRI
	14	2	10	0.902	0.836	0.066	Land use and NDVI	Northness, TRI, Slope, DEM	NDVI, Northness, Slope, Spot6 Band4
Best performing test rerun	15	2	6	0.892	0.855	0.037	Land use and NDMI	TRI, DEM	-
Automatic	16	0.25	10	0.972	0.772	0.200	Land use and NDVI	TRI	Eastness, NDVI, Northness, Slope, Spot6 Band4, TRI
	17	0.5	10	0.948	0.833	0.115	Land use and NDVI	TRI, DEM	Eastness, NDVI, Northness, Slope, Spot6 Band4, TRI
	18	1	10	0.935	0.846	0.089	Land use and NDVI	TRI, DEM, Slope	Eastness, NDVI, Northness, Slope, Spot6 Band4, TRI
	19	2	10	0.902	0.838	0.064	Land use and NDVI	Northness, Slope, DEM	NDVI, Northness, Slope, Spot6 Band4
Best performing test rerun	20	2	6	0.893	0.856	0.037	Land use and NDVI	DEM	-

4.4.3.2 *Top performing model comparison for cao vit gibbon*

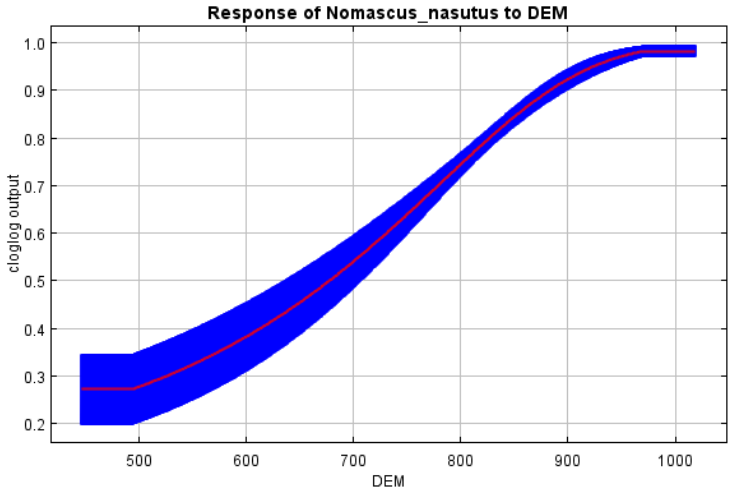
Feature Type	Test #	Number of variables	Number of replications	Regularisation multiplier	Mean AUC	Standard deviation
Hinge	10	6	10	2	0.871	±0.058
Quadratic and Hinge	15	6	10	2	0.874	±0.059

4.4.3.3 *Response curves of predictor variables for top performing model for cao vit gibbon distribution*

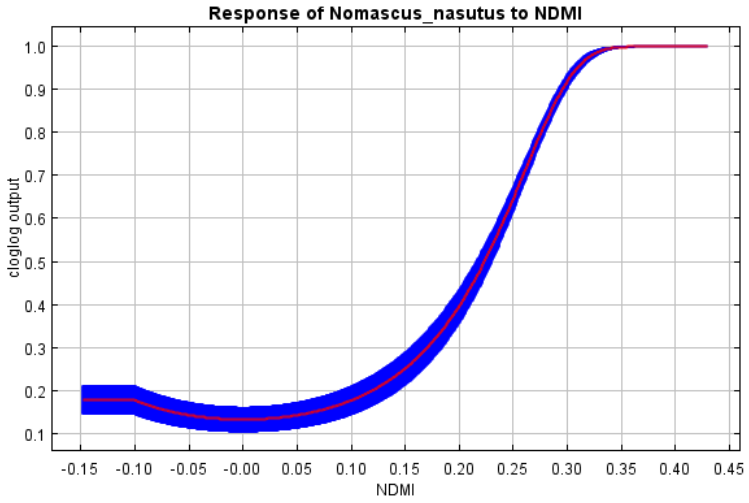
Response curves in order of highest to lowest per cent contribution to model



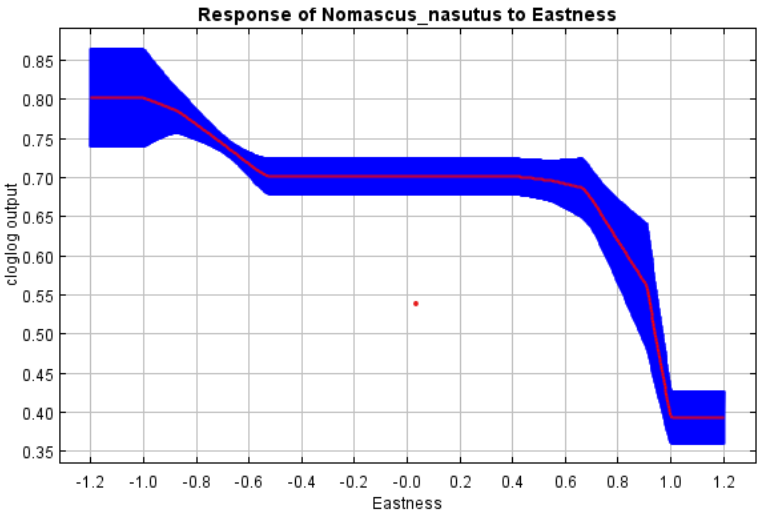
A Land use 80.9% contribution



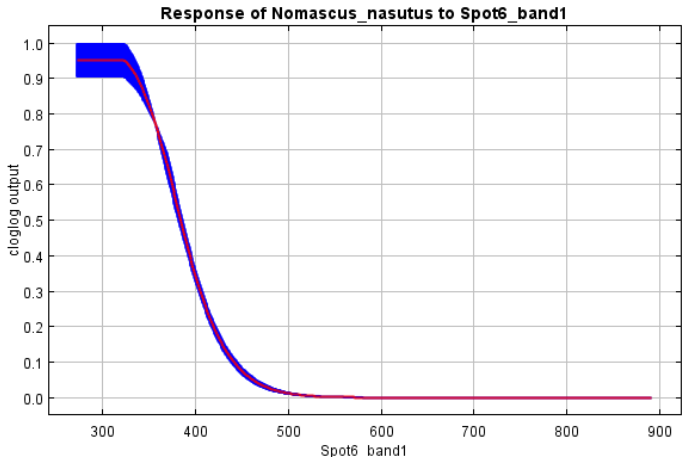
B DEM 9.2% contribution Categories: 1- water, 2- urban, 3- rice field, 4- crops, 5- grass and shrubs, 6- orchards, 7- barren (limestone), 8- evergreen broadleaf forest, 9- coniferous Forest, 10- deciduous forest, 11- plantation forest, 12 – mangroves



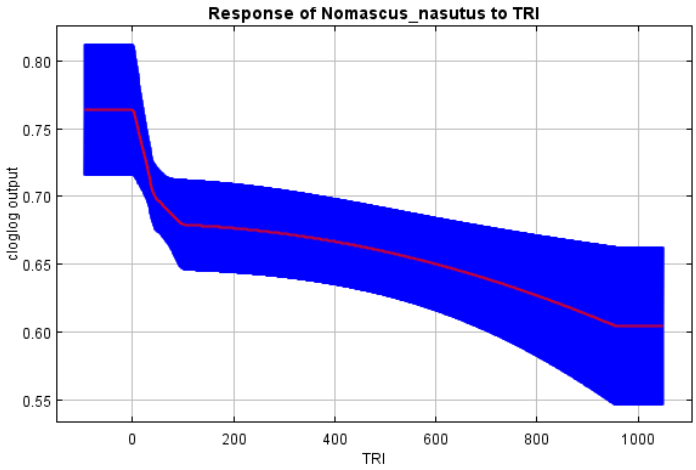
C NDMI 7.3% contribution



D Eastness 2.3% contribution



E Spot6 Band 1 (Blue) 0.2% contribution



F TRI 0.1% contribution