

SNP analyses reveal a diverse pool of potential colonists to earthquake-uplifted coastlines

Johnette C Peters¹, Jonathan M Waters², Ludovic Dutoit^{2,3}, Ceridwen I Fraser^{1,3}

1. Fenner School of Environment and Society, Australian National University, Canberra, ACT 2601, Australia
2. Department of Zoology, University of Otago, 340 Great King St, Dunedin 9016, New Zealand
3. Department of Marine Science, University of Otago, PO Box 56, Dunedin 9054, New Zealand

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Corresponding author: Johnette Peters

Address: Fenner School of Environment and Society, Australian National University, Canberra, ACT 2601, Australia

Email: johnette.peters.2@gmail.com

Abstract:

In species that form dense populations, major disturbance events are expected to increase the chance of establishment for immigrant lineages. Real-time tests of the impact of disturbance on patterns of genetic structure are, however, scarce. Central to testing these concepts is determining the pool of potential immigrants dispersing into a disturbed area. In 2016, a 7.8 magnitude earthquake occurred on the South Island of New Zealand. Affecting approximately 100 km of coastline, this quake caused extensive uplift (several metres high), extirpating many intertidal populations, including keystone intertidal kelp species. Following the uplift, we set out to determine the geographic origins of detached kelp specimens which rafted into the disturbed zone. Specifically, we used genotyping-by-sequencing (GBS) approaches to compare beach-cast southern bull-kelp (*Durvillaea antarctica* and *Durvillaea poha*) samples to established populations throughout the species' ranges, and thus infer the geographic origins of potential colonists reaching the disturbed coast. Our findings reveal an ongoing supply of diverse lineages dispersing to the newly uplifted coastline, suggesting potential for establishment of 'exotic' lineages following disturbance. Furthermore, we found that some drifting individuals of each species came from far-distant regions, some >1200 km away. These results show that diverse lineages – in many cases from very distant sources – can compete for new space in the wake of an exceptional disturbance event, illustrating the potential of long-distance dispersal as a key mechanism for re-assembly of coastal ecosystems. Furthermore, our findings demonstrate that high-resolution genomic baselines can be used to robustly assign the provenance of dispersing individuals.

Introduction:

Dispersal, or the movement and subsequent reproduction of individuals (Nathan et al., 2003), is often cited as a key driver for patterns of gene flow, genetic diversity and geographic distribution (Lester et al., 2007; Palumbi, 2003). Recent evidence, however, has suggested that frequent dispersal may not always be effective, with early arriving or pre-existing populations monopolizing available territory, and preventing the establishment of later-arriving individuals (see: De Meester et al., 2002; Fraser et al., 2015; Lester et al., 2007; Mora et al., 2012). This process, variously described as ‘founder takes all’ (Waters et al., 2013) or ‘high-density blocking’ (Hewitt, 2000; Hewitt & Ibrahim, 2001), can result in communities that exhibit high dispersal yet low gene flow (De Meester et al., 2002).

On a global scale, many large-scale recolonization events (e.g. in the wake of deglaciation) have been inferred to have stemmed from long-distance dispersal (LDD) (Hewitt 2000). As a case in point, the rapid postglacial recolonisation of disjunct high-latitude Southern Hemisphere coasts by giant kelp *Macrocystis pyrifera* (Macaya & Zuccarello, 2010) and bull kelp *Durvillaea antarctica* (Fraser et al., 2009b) was apparently underpinned by LDD across the Southern Ocean. The dispersal capacity of plants colonising land made available by volcanic lava flows or retreating glaciers has also been inferred to dramatically influence the diversity of pioneer populations (Litrice et al. 2005). However, despite a growing recognition of the importance of LDD or biogeography (Gillespie et al 2012), most phylogeographic studies have limited ability to infer frequencies of such movement, as unsuccessful dispersal events typically leave no enduring genetic trace. As a result, while LDD is often assumed to be a rare phenomenon, its frequency may be substantially underestimated (see above).

An excellent opportunity to test the scale and frequency of LDD into a disturbed area arose in late 2016, when a 7.8 magnitude earthquake occurred in the Marlborough / Canterbury region of the South Island, New Zealand. This rupture of several faults in the Marlborough fault system and North Canterbury fault zone, was the largest instrumentally recorded New Zealand earthquake (Cesca et al., 2017). The quake caused widespread coastal deformation, with uplift up to ~6 metres, heavily impacting one of New Zealand's most ecologically rich coastlines (Clark et al., 2017), with local to regional extirpation of numerous intertidal-limited taxa, including keystone macroalgae (Clark et al., 2017; Power et al., 2017).

Two species of buoyant southern bull kelp, *Durvillaea antarctica* and *D. poha*, dominate southern New Zealand coastlines, and provide habitat for a range of intertidal species (Edgar & Burton, 2000). Specifically, *D. poha* is endemic to southern New Zealand, with populations known from the South Island as far north as Kaikoura on the east coast, to Fiordland on the west coast, as well as on Stewart Island and the sub-Antarctic Auckland and Snares Islands. Additionally, *D. antarctica* can be found along most of New Zealand's coasts, and as well as in Chile and throughout the sub-Antarctic. A distinctive feature of both species is their honeycombed internal structure, which makes them highly buoyant (Fraser et al., 2009a; Fraser et al., 2012). This buoyancy also means detached individuals can act as rafts (Thiel & Haye, 2006), potentially transporting a range of flora and fauna, including crustaceans (Fraser et al., 2011; Nikula et al., 2010), limpets (Edgar & Burton, 2000), sea-slugs (Cumming et al., 2014) and echinoderms (Waters et al., 2018). Depending on the extent, longevity and direction of strong wind and storm events, detached *D. antarctica* and *D. poha* are capable of dispersing long distances and traversing oceanographic barriers (Garden et al., 2014; Fraser et al. 2018b). Despite this capacity to disperse, and some evidence of dispersal among regions within New Zealand (Bussolini & Waters, 2015), established populations show strong

phylogeographic structure indicative of low gene flow (Collins et al., 2010), possibly as a result of high-density blocking. Indeed, these species are thought to resist gene flow when populations are at high densities, even with frequent dispersal of individuals among distant populations, and thus the potential for ‘turnover’ (genetic change) may depend on large-scale disturbances that effectively liberate new space (Fraser et al. 2018a).

In the aftermath of the Kaikoura 2016 quake, we hypothesised that the apparent local extirpation of intertidal *Durvillaea* communities at some sites would create opportunities for potential establishment of any non-local lineages dispersing into the region. We here set out to determine the sources of dispersing *Durvillaea* (potential colonists) arriving at the newly-uplifted zone, to test the hypothesis that diverse lineages, including individuals from distant locations, are able to disperse to the region. Specifically, we undertook regional phylogenomic analysis of both *D. antarctica* and *D. poha* to determine the origins of dispersing individuals, and predicted that beach-cast rafts arriving on the Kaikoura coast would include lineages distinct from local populations prior to the earthquake. Detection of such lineages would indicate that dispersal can occur to the region from elsewhere. In contrast, detection of local lineages would indicate that some patches might have survived extirpation from the earthquake.

Materials and Methods:

Three sample types were included in this research: beach-cast, newly settled and attached. Beach-cast and newly settled samples were of washed-up (drift) specimens and young, new recruits, respectively, all collected post-earthquake along the uplifted coastline. The samples therefore represent potential colonists – immigrants reaching the disturbed area, and their offspring. The third sample type comprised attached (growing) benthic individuals; these

samples were from established populations across *D. poha* and *D. antarctica*'s respective ranges (both pre- and post-earthquake) and were used as a reference 'baseline' with which to infer source locations of post-earthquake dispersers and colonisers (beach-cast or newly settled).

Sampling in uplifted areas

Sampling of beach-cast and newly settled individuals was conducted at four dramatically uplifted sites along the Marlborough / Canterbury coastline: Ward Beach, Wharanui, Waipapa Bay and Kaikoura Peninsula (Table 1, Table S1, and Figure 1). Site surveys, completed following the earthquake, determined areas of extirpation with each site having undergone varying levels of uplift: approximately 1.5 m at Kaikoura, 2.9 m at Ward Beach, 3.0 m at Wharanui, and the maximum uplift of 5.9 m at Waipapa Bay (Figure 1). As detailed in Table 1, at each site small samples (1-2 cm) of frond tissue were collected from each beach-cast *Durvillaea* individual, as well as from any newly settled (young, growing) individuals. Field identification of *Durvillaea* species is complicated by morphological plasticity of some species (Fraser et al. 2012), so species assignments for the two buoyant taxa in the region (*D. antarctica* and *D. poha*) were made only during analysis of genetic data. Sampling was conducted repeatedly at one site, Ward Beach, between June 2017 and January 2018, followed by extensive sampling of all four sites in April 2018. A total of 169 beach-cast samples were collected from Ward Beach, 77 from Wharanui, 18 from Waipapa Bay and one from Kaikoura Peninsula (Table 1). Additionally, one newly-settled, young, attached recruit was sampled at Waipapa Bay and three at Kaikoura. All tissue samples were preserved via desiccation over silica gel beads. For some rafts bearing notably large, attached goose barnacles, *Lepas australis* (a pelagic crustacean indicating long durations drifting at sea: Fraser et. al 2011), the largest barnacle was sampled and preserved via desiccation over silica gel beads.

Measurements of barnacle capitulum length using Vernier calipers were used to estimate minimum rafting time, following Fraser et.al (2011).

DNA extraction

DNA was extracted from all beach-cast and new recruit samples (both those collected in April, 2018, and additional Ward Beach samples) and from 23 attached, possible source populations across New Zealand, Chile, and the sub-Antarctic, including ‘pre-earthquake’ population samples from all four uplifted sites, with those samples collected five days after the quake from kelp still attached to uplifted rocks (Figure 1). Technical replicates were included for some samples, to ensure successful sequencing of those with fewer population replicates (e.g. new recruits) and to confirm the accuracy of phylogenetic analyses.

DNA was initially extracted using the QIAGEN DNeasy PowerPlant Pro kit, with the following modifications, as outlined by Wilson et al. (2016b): small samples of tissue (< 2 mm) were soaked for 24 hours at 65°C in 250 µL of PowerBead solution, 50 µL of PD2 and 3 µL of RNase A. Following soaking, 100 µL of isopropanol was added and samples were incubated at 65°C for a further 30 minutes, vortexing every 10-15 minutes. The samples were lysed for 1-2 minutes at 22/s frequency using a QIAGEN TissueLyser. Subsequent steps followed manufacturers’ protocols, with elution of DNA in 100 µL of elution buffer reloaded / eluted once more for maximum concentration. Additional purification was done using the QIAGEN PowerClean kit, following manufacturers’ protocols, including an additional wash step using 100 % ethanol and a final elution using 100 µL of elution buffer. DNA was stored in a -20°C freezer.

Genotyping procedure

Preparation of genotyping-by-sequencing libraries followed the protocols outlined in Elshire et al. (2011) with modifications. Prior to beginning the protocol, all samples were dried using a vacuum centrifuge at 45°C until evaporated. Samples were then rehydrated with 15 µl of dH₂O. 3 µl of uniquely barcoded PstI adapter stock was added to each sample. Digestion was carried out using PstI-HF and 10x NEB Buffer 4, incubated at 37°C for 2 hours. Adapters were ligated using T4 DNA Ligase in 10x Ligation buffer with incubation at 16°C for 90 minutes followed by 80°C degrees for 30 minutes. DNA was purified using the Qiagen MinElute 96-well PCR purification kit, with modifications including completing two wash steps using 50 µl of dH₂O and using 25 µl of 1x TE for the elution buffer. PCRs were run in an Eppendorf Mastercycler Nexus, with 10 µl of purified post-ligation product and 40 µl of PCR Master Mix (Bioline 2x Taq Master Mix, PCR Primer 1, PCR Primer 2) under the following conditions: 72°C for 5 min, 95°C for 60 s, 28 cycles of 95°C for 30 s, 65°C for 30 s, 72°C for 30s, with a final extension step of 75°C for 5 min. Post purification quantitation was done using a Caliper LabChip GXII Machine, with final DNA concentration calculated for fragments within 200-500 bp range. DNA in this size range was excised from each sample and pooled to ensure normalised concentration of 50 ng of DNA per sample. The pooled library was cleaned using the column clean GenElute PCR Clean-up kit. Paired-end sequencing was carried out on two lanes of a mid-output flowcell in an Illumina NextSeq 500 system (75 bp paired-end).

Filtering procedures and source population assignment analyses

GBS data were analysed using the Stacks 2.1 pipeline (Catchen et al., 2013). Sequencing data from an additional 96 samples of *D. antarctica* from across its international range (from

Fraser et al., 2018b) were included as possible source populations (full sample map shown in Figure 1). Sequence filtering was carried out as follows. Fragments were demultiplexed using Axe (Murray & Borevitz, 2017), quality-assessed using fastQC (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc>) and trimmed to 65 bases. With no suitable reference genome, de novo sequence alignment was employed. In ustacks, minimum depth of coverage (m) was set to five, with the maximum distance between stacks (M) at three and maximum difference (in nucleotides) allowed between stacks (N) at 5 (M+2). In cstacks, the number of mismatches (n) was set to four. To be considered, loci had to be present in two population groups, meet a minor allele frequency (min_maf) of 0.05 with a minimum percentage of individuals in a population (r) set to 20%, meaning each locus had to be present in 20% of individuals. IQ-TREE (Nguyen et al., 2015) was used to create phylogenetic trees with model testing using ModelFinder (Kalyaanamoorthy et al., 2017). Trees were built from data sets that excluded or included the drift samples, in the former case to enable verification of phylogeographic structure, and in the latter case to infer source population of drift material. Bootstrapping was set at 5000 bootstraps with UFBoot (Minh et al., 2013) enabled to reduce bias through the overestimation of branch support (maximum iterations of 3000, with interval checks every 250 iterations). Phylogenetic trees were visualised with FigTree v1.4.3 (<http://tree.bio.ed.ac.uk/software/figtree/>). Beach-cast samples were also assigned a source population based on proximity to sequences from a given established population in the tree.

To complement phylogenetic-based source population assignment, we analysed both species independently using fastSTRUCTURE v1.0 (Raj et al. 2014). SNPs genotyped for less than 60% of the total samples in each of the species were removed using R (R Core Team, 2018) via the package *adegenet* (Jombard & Ahmed, 2011). This filter was selected as

fastSTRUCTURE does not handle large amounts of missing data well, and so was not suited to the more relaxed data set used in our phylogenetic analyses. FastSTRUCTURE v1.0 was run for $K = 2$ to $K = 10$ without location priors. Results were visualised using the R package *pophelper* (Francis 2017).

Results:

Some samples failed quality checks at various stages of the process, including DNA extraction, GBS library preparation, and sequence filtering. Of the 397 samples pooled in the GBS library, 331 were retained following bioinformatic filtering. With the inclusion of 96 additional *D. antarctica* data (from Fraser et al., 2018b), the resulting data set included 427 samples for analysis (including 32 technical replicates: TR), with 103,881 informative sites. Excluding technical replicates, 201 samples were beach-cast, 3 were newly settled, and 191 were samples from attached populations.

Of the 201 beach-cast samples sequenced, 91 % (183) were *D. antarctica* and 9 % (18) were *D. poha*. While the vast majority (187) of attached samples fell into unambiguous phylogenetic groupings, three did not group closely with any of the main clades, possibly representing hybrid individuals or contaminated samples. Although these samples were not excluded (Figure 2), their provenance could not be determined, and they were therefore not considered further in our interpretation of results. The phylogenetic groupings of source samples were supported by previous mtDNA (COI) analyses (Bussolini & Waters, 2015; Fraser et al., 2010), and by the trees produced from our SNP data sets that excluded drift samples (Supplementary Fig. S1), which show the same broad topologies and regional groupings as the trees that included drift samples (Figs 2 and 3).

Within *D. antarctica*, four regional phylogeographic groupings were resolved (Figure 2, Table 2), including a Chilean clade, a Chatham Islands clade, and two New Zealand groups, with a northern NZ clade (populations north of Banks Peninsula), and a southern NZ / sub-Antarctic group (populations south of Banks Peninsula). No beach-cast / new recruit *D. antarctica* samples retrieved from the uplifted sites showed phylogenetic affinity with Chile, the Chatham Islands or the broader (non-New Zealand region) sub-Antarctic clades. In total, 150 beach-cast samples were identified as belonging to the northern NZ clade, whereas 33 clearly grouped with southern NZ or NZ sub-Antarctic specimens (Table 2). For the northern clade, many beach-cast samples were similar to pre-earthquake lineages from the uplifted region. Although individual site provenance could not be resolved, some regional groups were apparent, with clades for Marlborough / Canterbury region (Cape Campbell, Ward Beach, Wharanui and Waipapa Bay), Kaikoura region (Kaikoura, Oaro, Rakanui), and Banks Peninsula (Figures 2 and 4, Table 3). Two new recruits also grouped with NZ northern populations, with similarities to the pre-earthquake populations; one Kaikoura colonist grouped with Kaikoura source samples and the Waipapa Bay colonist grouped with pre-quake Waipapa Bay populations. Considerably fewer beach-cast samples fell within the southern and sub-Antarctic clade for *D. antarctica*. As some reference (attached) populations from this remote southern region were not successfully sequenced, precise source locations within this region are sometimes unclear, with samples thus broadly binned into either Otago or Tautuku clusters (successfully sequenced samples from attached populations are shown in Supplementary Table S1). Some beach-cast samples clearly have distant origins, grouping with sub-Antarctic Snares and Auckland Islands lineages (approximately 900 km and 1200 km away, respectively).

For *D. poha*, 18 beach-cast samples were inferred to have reached the uplifted area from northern, southern and sub-Antarctic sources (Tables 2 and 3, Figures 3 and 4). No pre-earthquake samples of this species from uplifted sites north of Oaro were detected in our genomic analyses (desiccated uplifted samples tentatively assigned to *D. poha* in the field in fact grouped with *D. antarctica*) (Figure 3). A new recruit collected from Kaikoura in 2018 was genetically similar to remnant attached populations of *D. poha* at Kaikoura collected in 2018, and to pre-quake populations in the region. The majority of samples, however, had southern NZ or sub-Antarctic origins, including samples from Fiordland along the west coast (approximately 1200 km away). Samples of large *L. australis* found on two *D. poha* rafts originating from Fiordland, had capitulum lengths of 24 mm and 30 mm respectively, indicating rafting times of 50 to 60 days. In total, 68% of *D. poha* rafts arrived from distant populations, at least several hundreds of kilometres to the south (Figure 4).

FastSTRUCTURE results supported the source population assignments inferred from the phylogenetic analyses. When SNPs genotyped in at least 60% of samples were retained, the *D. poha* data set comprised 3719 loci, and the *D. antarctica* data set comprised 3126 loci. Beach-cast *D. poha* from Ward Beach, Wharanui and Waipapa Bay clustered predominantly with the southern New Zealand populations of Otago, Tautuku and Fiordland, with some sub-Antarctic samples detected, whereas beach-cast samples from Kaikoura cluster with local attached populations. These conclusions were supported across several K values (Supplementary Figure S2). Likewise, for *D. antarctica*, fastSTRUCTURE analyses support the phylogenetic analyses (Figure 5B), with the majority of beach-cast samples being of local (northern New Zealand, north of the Canterbury Bight) origin, but with some samples clustering with sub-Antarctic and southern New Zealand source populations. Comparable results were obtained using an 80% filter, albeit with far fewer loci retained (data not shown).

Discussion:

Dispersal of both *D. antarctica* and *D. poha* to the uplifted areas on the Marlborough / Canterbury coastline was detected from a wide range of source populations (including Fiordland, and the Snares and Auckland Islands), with some voyages inferred to have been greater than 1200 km. Intriguingly, however, most beach-cast *D. antarctica* in the uplifted areas were found to be closely related to local populations north of Banks Peninsula, and to pre-earthquake populations at uplifted sites, contrary to our expectations if local populations had been completely extirpated. For *D. antarctica*, therefore, the mortality of bull-kelp populations was perhaps not as complete as initially thought, with pockets of surviving kelp still providing potential colonists to uplifted areas. The survival of such populations, possibly on off-shore reefs and outcrops, would not be altogether surprising, because although the visual assessment of macroalgal mortality appeared widespread, the extent of the uplift was highly variable along the coastline (Clark et al., 2017). If such relictual *Durvillaea* populations do exist, these patches would be likely to hold far more adults than are arriving to the area via rafting, weighing the probability of recolonisation in the favour of local versus immigrant lineages (Fraser et al. 2018a). The ‘clean slate’ of the uplifted coastlines should nonetheless offer considerably improved opportunities for colonisation, in the years following the earthquake, to the diverse lineages reaching the area from further away, which could facilitate turnover.

Passive dispersal at sea is heavily influenced by ocean currents, and several studies have inferred dispersal routes of kelp (and associated organisms) that are consistent with predominant regional oceanographic processes (see Chiswell, 2009; Collins et al., 2010). Likewise, our results showed that most drift kelp came from the south, presumably driven by the Southland Current (as seen in Collins et al., 2010; Bussolini & Waters, 2015).

Unfortunately, although samples from some North Island populations were included in our research, no sequences from these were retained following quality filtering, making it impossible to infer any notable southward movement. Nonetheless, as most drift samples grouped closely with populations that *were* retained throughout the analyses, it seems unlikely that many (if any) samples came from the North Island. The size of goose barnacles on samples from Fiordland, which indicate rafting times of perhaps 50 - 60 days, suggests average travel speeds of over 0.2 ms^{-1} , which are plausible given the comparable estimates of kelp rafting speeds in the New Zealand region (0.2 ms^{-1} : Fraser et al. 2011; $0.3\text{-}0.6 \text{ ms}^{-1}$: Waters and Craw 2018) and the greater Southern Ocean (0.4 ms^{-1} : Fraser et al. 2018b).

For both *D. antarctica* and *D. poha*, these genomic analyses were able to provide much greater resolution of geographic variation than previous, single- or multi-locus analyses of the species. Indeed, previous work using mitochondrial, nuclear and chloroplast genes showed almost no site- or region-specific variation among all sites for *D. poha* (Fraser et al. 2012), whereas our GBS data resolve differences among localities (e.g. Otago, Stewart Island and Fiordland), and can distinguish sub-Antarctic island populations (Figure 2). Likewise, whereas single- or multi-locus data were previously only able to determine the broad, regional origin of drift kelp (e.g. northern, southern or sub-Antarctic New Zealand: Collins et al. 2010; Bussolini & Waters 2015), our GBS analyses can resolve origin to within ten to 100 kilometres. The power of these genome-wide analyses to show the origin of dispersing individuals is further highlighted by a recent study of *D. antarctica* reaching Antarctica, with GBS data revealing that two individuals had drifted more than 20,000 km from separate, genomically distinct sub-Antarctic islands (Fraser et al. 2018b).

As macroalgal rafts and stands support a range of intertidal species (Cumming et al., 2014; Morton & Miller, 1968; Thiel & Haye, 2006), the quick recovery of these species has

implications for the timing of re-establishment of a range of dependent species, including invertebrate animals, that rely on *Durvillaea* for food, shelter, protection and passive dispersal (Edgar & Burton, 2000; Smith, 2002). As *Durvillaea* populations continue to recover, the ongoing dispersal of organisms via rafting could therefore result in shifts in the local communities, including changes in species diversity and abundance of epibiotic invertebrates. We expect that there will be a cascade of recolonisation events involving intertidal taxa following establishment of the first large kelp species, and that different taxa could come from different source populations representing sequential waves of dispersal.

Our phylogenomic analyses suggest that *D. poha* has previously experienced a range expansion, originating in the sub-Antarctic islands, and later extending northward to mainland New Zealand. The strong relationship between Oaro, near Kaikoura, and far-distant Stewart Island also suggests that these north Canterbury populations may be the result of a recent expansion from New Zealand's south. Phylogeographic studies of kelp-associated sea slugs (*Onchidella*) also found Kaikoura populations to be a northern outlier in the genus' distributional range, closely related to populations found on Stewart Island (Cumming et al., 2014). Therefore, the colonisation of the north Canterbury region, by both *D. poha* and associated holdfast invertebrates, may be the result of recent successful dispersal events, perhaps facilitated by an earlier disturbance event that affected Oaro (e.g. earthquake, tsunami, or major landslide). Interestingly, genomic data suggest that predominantly *D. antarctica* (rather than *D. poha*) occurred at the sampled sites north of Oaro prior to the earthquake, despite detection of plants that were apparently morphologically similar to *D. poha* (wide blades; short, stout stipes; orange colouration: Fraser et al. 2012) in the days following the quake. Morphological plasticity, a common trait for seaweed species (e.g. *Ulva*: Leskinen et al., 2004, and *Macrocystis*: Demes et al., 2009), might explain this apparent

finding, with *D. antarctica* individuals perhaps filling the *D. poha* niche. The removal by uplift of the *D. antarctica* potentially occupying the *D. poha* niche could thus allow for further northward expansion of this species. Recent research, however, indicates that extreme changes in temperature can lead to extensive die-off of *D. poha* (Thomsen et al. 2019). This species might, therefore, have a lower tolerance for high temperatures than *D. antarctica*, perhaps explaining its relatively restricted, more southern range.

Understanding how frequently and effectively species disperse has critical implications for evolution and conservation ecology (Fraser et al., 2015), including for predicting species response to environmental change (Nathan et al., 2003). High-resolution genomic analyses offer unprecedented potential for research on dispersal and connectivity – with adequate sampling of established populations, we can now robustly infer the sources of dispersing individuals. With current predictions suggesting an increasingly erratic disturbance regime, understanding how effectively marine taxa disperse is a key component of predicting the impacts of environmental change on coastal ecosystems.

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Data Accessibility Statement

Raw sequencing, SNP data and metadata are available at Dryad

<https://doi.org/10.5061/dryad.573n5tb3m>.

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Tables

Table 1. Number of samples collected across the uplift zone, including the uplift and location of each site and the number of beach-cast and new-recruit samples.

| Site | Uplift (metres) | Latitude/Longitude | Month/Year | <i>n</i> sampled | |
|--------------------|--------------------|--------------------|------------|------------------|---------------|
| | | | | Beach-cast | Newly Settled |
| Ward Beach | 2.9 | -41.844, 174.194 | 06/17 | 6 | 0 |
| | | | 07/17 | 10 | 0 |
| | | | 08/17 | 6 | 0 |
| | | | 10/17 | 3 | 0 |
| | | | 12/17 | 22 | 0 |
| | | | 01/18 | 26 | 0 |
| | | | 04/18 | 96 | 0 |
| Wharanui | 3.0 | -41.930, 174.097 | 04/18 | 77 | 0 |
| Waipapa Bay | 5.9 | -42.206, 173.877 | 04/18 | 18 | 1 |
| Kaikoura Peninsula | 1.5 | -42.421, 173.723 | 04/18 | 1 | 2 |

Table 2. Five broad phylogeographic groupings of ‘attached’ benthic *Durvillaea* samples recovered from phylogenetic analysis of the complete GBS data set.

| Species | Clade | Attached (<i>n</i>) | Beach-cast (<i>n</i>) | Newly settled (<i>n</i>) | Total |
|----------------------|-----------------------|--------------------------|----------------------------|-------------------------------|-------|
| <i>D. antarctica</i> | NZ North | 45 | 150 | 2 | 197 |
| | NZ South / NZ sub-Ant | 27 | 33 | 0 | 59 |
| | Broader sub-Antarctic | 65 | 0 | 0 | 65 |
| | Chile | 4 | 0 | 0 | 4 |
| <i>D. poha</i> | <i>D. poha</i> | 46 | 18 | 1 | 65 |
| Unconfirmed | Ungrouped | 3 | 0 | 0 | 3 |

Table 3. Inferred sources of beach-cast *D. antarctica* and *D. poha* rafts sampled at four tectonically-uplifted coastal sites in northeast South Island, New Zealand.

D. antarctica

| Sources | Region | Uplifted Sites | | Wharanui | Waipapa Bay | Kaikoura Peninsula |
|-----------------------------|--------------------------|-----------------|-----------------|-----------|-------------|--------------------|
| | | Ward Beach 2017 | Ward Beach 2018 | | | |
| Cape Campbell | Marlborough / Canterbury | 0 | 13 | 0 | 0 | 0 |
| Ward Beach | Marlborough / Canterbury | 1 | 52 | 0 | 0 | 0 |
| Wharanui | Marlborough / Canterbury | 3 | 0 | 51 | 0 | 0 |
| Waipapa Bay | Marlborough / Canterbury | 0 | 0 | 0 | 4* | 0 |
| Kaikoura | Kaikoura region | 1 | 3 | 0 | 0 | 2* |
| Rakanui / Oaro / Manuka Bay | Kaikoura region | 2 | 7 | 1 | 4 | 0 |
| Banks Peninsula | Banks Peninsula | 2 | 3 | 2 | 1 | 0 |
| North Otago/Dunedin | Otago | 6 | 5 | 0 | 0 | 0 |
| Tautuku | Tautuku | 7 | 7 | 3 | 0 | 0 |
| Snares Islands | Sub-Antarctic | 1 | 3 | 0 | 0 | 0 |
| Auckland Islands | Sub-Antarctic | 1 | 0 | 0 | 0 | 0 |
| Total | | 24 | 93 | 57 | 9 | 2 |

D. poha

| | | | | | | |
|---------------------|-----------------|----------|----------|----------|----------|----------|
| Kaikoura / Oaro | Kaikoura Region | 0 | 0 | 1 | 4 | 1* |
| North Otago/Dunedin | Otago | 0 | 1 | 0 | 1 | 0 |
| Tautuku | Tautuku | 2 | 0 | 0 | 0 | 0 |
| Fiordland | Fiordland | 2 | 1 | 3 | 1 | 0 |
| Sub-Antarctic | Sub-Antarctic | 2 | 0 | 0 | 0 | 0 |
| Total | | 6 | 2 | 4 | 6 | 1 |

Figure Legends

Figure 1: Map of the southern hemisphere with locations for sequenced *Durvillaea* samples from attached populations. The earthquake-uplifted zone is highlighted in red text, with respective uplift in metres shown. Inset map shows samples from Chile and the broader sub-Antarctic. Individual site names and locations, as well as number of samples extracted and successfully sequenced can be found in supporting information.

Figure 2: Phylogenetic structure of *Durvillaea antarctica*, with five groupings corresponding to northern NZ, Chatham Is., southern NZ and NZ sub-Antarctic, broader sub-Antarctic, and Chile. Black dots indicate ungrouped individuals. Lighter-toned, red branches indicate beach-cast samples, and black branches indicate attached samples from established populations (blue pointers show sites names for these samples). Outlined red pointers indicate where newly settled recruits fell within the tree. Bootstrap values of 90-100 % for major branches are shown by thick black lines. Inset photograph shows drift *D. antarctica* close to uplifted coast at Waipapa Bay.

Figure 3: Phylogenetic structure of all *Durvillaea poha* samples. Lighter-toned / red branches indicate beach-cast samples, and black branches indicate attached samples from established populations (blue pointers show sites names for these samples). Outlined-red pointer indicates where a newly settled recruit fell within the tree. Bootstrap values of 90-100 % for major branches are shown by thick black lines. Inset photograph shows beach-cast *D. poha* at an uplifted site.

Figure 4: Inferred origins of beach-cast and new recruit samples at uplifted sites, according to species. Sample numbers are indicated below each pie chart. The Ward Beach samples shown here include collections from both 2017 and 2018. Sites with new recruits are indicated by asterisks.

Figure 5: fastSTRUCTURE analysis of A) *D. poha* (K = 9) and B) *D. antarctica* (K = 10), with beach-cast and attached samples in separate, adjacent plots.