Solving mammalian riddles.
A reconstruction of the Tertiary and Quaternary distribution of mammals and their palaeoenvironments in island South-East Asia

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Erik Meijaard

School of Archaeology and Anthropology
The Australian National University

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The Australian National University

Canberra, Australia

Detail of a Ma'a (ceremonial cloth) from Java, early 19th century; from collection Robert Holmgren and Anita Spartus, with permission from the National Gallery of Australia.

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GLOSSARY AND DEFINITIONS

ANOVA = analysis of variance (a statistical technique)

centrifugal evolution = a recurring pattern in the distribution of taxa: a more evolved (derived) taxon is often central, surrounded or flanked by more primitive relatives

Cytochrome *b* gene = part of the mitochondrial DNA

Discriminant Analysis = A statistical technique for situations where one wants to build a predictive model of group membership based on observed characteristics of each case. The procedure generates a set of discriminant functions based on linear combinations of the predictor variables that provide the best discrimination between the groups.

Holocene = 11 Kya to present

Kya = thousand years ago

Kyr = thousand years

Late Pleistocene = period between 128 and 11 Kya (Jablonksi & Whitfort 1999)

LGM = Last Glacial Maximum

m = metre

monophyletic = groups derived from an exclusive common ancestor

mtDNA = mitochondrial DNA

Mya = million years ago

Myr = million years

neretic zone = that part of the ocean which includes both the estuarine zone and the continental shelf; thus neretic deposits are of shallow-water origin.

paraphyletic = groups that have evolved from and include a single ancestral species, but which do not contain all the descendants of that ancestor

PDL = present day level

Principal Components Analysis = A statistical method used in data reduction to identify a small number of factors that explain most of the variance observed in a much larger number of variables

RNA = ribonucleic acid, present in all cells

unconformity = a geological tern referring to a hiatus or break in a sequence

ABSTRACT

Since the mid 19th century, the biogeography of island South-East Asia has been the subject of much study. Early researchers explained many of the species distribution patterns by the rise and fall of sea levels and land. This and the work of other researchers culminated in a theory that emphasized the role of Pleistocene sea level low stands in species evolution. With the advent of newly developed molecular techniques, however, it became clear that many species divergence events had taken place before the Pleistocene and a biogeographical theory focusing on Pleistocene sea level changes was inadequate. In this research, I have developed a new biogeographic model that explains present-day distribution patterns and evolutionary relationships between species. I use this new model to explain 10 'mammalian riddles', i.e. evolutionary or distribution patterns in selected mammal species groups that could not be explained with the existing theories. I developed the new model by analyzing the geological literature for this region, and by mapping palaeogeographical and palaeoenvironmental changes for the last 20 million years. In addition I compiled information on the palaeontological record for the region and on divergence times between taxa using a molecular clock assumption. These phylogenetic data were compared with the palaeomaps to assess whether particular divergence events could be correlated with certain palaeogeographical or palaeoenvironmental changes. The combination of these two information sources has resulted in a much-improved understanding of mammalian evolution in island SE Asia. Using this model it is now possible to relate important palaeoenvironmental events, such as the Late Miocene cooling, an Early–Middle Pliocene highstand, or the emergence and submergence of a land bridge between the Malay Peninsula and Java to evolutionary changes in species. I test the accuracy of the new model by analysing the relationships within several mammal groups using craniometric and molecular analysis. The observed relationships and deduced timing of divergence between taxa could in many cases be explained by the model, which indicates that it is relatively accurate. In addition, with the new model I have been able to find solutions to most mammalian riddles, although these results require further testing. Overall, I therefore believe I have made a significant contribution to the biogeographical understanding of island SE Asia.