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Insular biogeography of web-building spiders on small tropical islands surrounding Singapore

メタデータ	言語: 出版者: 琉球大学21世紀COEプログラム 公開日: 2009-01-07 キーワード (Ja): キーワード (En): 作成者: Lim, Adrian L., Li, Daiqin メールアドレス: 所属:
URL	http://hdl.handle.net/20.500.12000/8762

described from each region, and each of these three taxa may be a cluster of related taxa. The distribution of *T. syrichta* conforms well to the Ice Age landmass Greater Mindanao. The distribution of the *T. tarsier*-complex covers the Ice Age landmass of Sulawesi, and extends to discontinuous island groups, possibly indicating a relatively ancient dispersal throughout the proto-Sulawesi archipelago. The distribution of *T. bancanus* is limited to a greatly reduced subset of Sundaland, and may indicate a Holocene range expansion from a Pleistocene refuge in Borneo. The alpha-level taxonomy of the *T. tarsier*-complex is reviewed. Acoustic evidence provides a hypothesis of at least 17 distinct taxa, 16 known acoustic forms plus the enigmatic *T. pumilus*. The distribution of tarsier acoustic forms conforms to empirical biological and geological data to form a compelling biogeographic hypothesis for Sulawesi. Congruence among tarsier acoustic, genetic, and morphologic data is reviewed. One implication for conservation is that biodiversity in Sulawesi may be underestimated by as much as an order of magnitude. Rigorous testing of the hypothesis of so many new taxa will require a large investment of resources and time, but regrettably, current rates of deforestation indicate that time may be of short supply.

Poster -8

Cryptic species: What we don't know might hurt us

David Bickford

*Department of Biological Science, National University of Singapore, 14, Science Drive 4,
Singapore 117543, Republic of Singapore*

The taxonomic challenge posed by cryptic species has been recognized for nearly 300 years, but the advent of relatively inexpensive and rapid DNA sequencing has given biologists a powerful new tool for detecting and differentiating morphologically similar species. Here, we synthesize the literature on cryptic and sibling species and discuss trends in their discovery. However, a lack of systematic studies leaves open the tantalizing questions such as whether cryptic species are more common in particular habitats, latitudes or taxonomic groups. Such uncertainties could have profound implications for evolutionary theory, biogeography planning and conservation planning.

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Adrian L. Lim and Daiqin Li

*Department of Biological Science, National University of Singapore, 14, Science Drive 4,
Singapore 117543, Republic of Singapore*

The main objective of this study was to investigate biogeographical effects that influenced the distribution and assemblage of web-building spiders on small tropical islands off Singapore in order to understand how this group of arthropods responded to biogeographical, environmental and human factors. Fifteen islands were sampled for web-building spiders. Correlation analysis, simple linear and multiple regressions, nestedness index and choros (*K*) model were used to test the six specific predictions that (1) area is the best predictor of species/genus richness at both community and specific/generic levels; (2) there is no correlation between island size and population density; (3) web-building spiders are non-randomly distributed on the islands and exist as nested subsets; (4) there is a correlation between environmental variables and web-building spider species/genus distribution; (5) body size (chelicerae to end of abdomen) of female insular *Nephila pilipes* increases with increasing island area; and (6) the choros (*K*) (Triantis *et al.*, 2003) model offers a better-fit than the classic species-area one.

Area *per se* was found to be the most significant factor accounting for web-building spider assemblage at both community and specific/generic levels. Contrary to the theory of Island Biogeography, there was a positive correlation between island size and population density. Web-building spiders were

also found to be non-randomly distributed on islands, suggesting that smaller islands were sustained in a subset of a more complete one found on larger islands. CCA results showed that spiders were associated with specific environmental variables. A majority of them apparently preferred sites with bigger trees with more canopy cover. Furthermore, the body size of *N. pilipes* females was significantly correlated to island area and distance from Malaysia, the assumed source island for web-building spiders. A larger island and sites found closer to Malaysia harboured greater species richness. Finally, the *K* model provided an improved goodness-of-fit to account for the spider data.

We concluded that many factors could account for the distribution of web-building spiders on these small tropical islands but island area *per se* is the most important factor. Habitat diversity was not shown to play a major role until the usage of choros (*K*) which superceded island area as the best predictor of species distribution. Moreover, conservational strategies should accorded highest protection priority to the bigger islands, i.e. Pulau Ubin as it not only has the highest species richness but also contains many other species not recorded on other islands, and the responses of individual species must also be studied before embarking on a conservation project.

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Resolving species limits within *Dicranosepsis*

Hwang Wei Song

*Department of Biological Science, National University of Singapore, 14, Science Drive 4,
Singapore 117543, Republic of Singapore*

Dicranosepsis is the most speciose genus of black scavenger fly (Sepsidae) in South-east Asia. Species limits are problematic for species with few morphologically diagnostic features and cases of cryptic species are suspected to exist within the species currently listed as 'widespread'. Here the use of morphology, DNA and reproductive isolation tests is adopted to help resolve species limits and to test recently proposed methods in DNA taxonomy. The overall level of congruence between morphological and molecular data is low due to greatly differing rates of speciation in different *Dicranosepsis* species. The different rates are not well reflected in COI sequences. DNA taxonomy methods are thus not satisfactory in delimiting species. In contrast, consistent results between morphology and reproductive isolation support the relevance of foreleg morphology for species delimitation within *Dicranosepsis*. Cases of peripatric speciation and rapid speciation are discussed and widespread species are documented that have few morphological modifications but large COI divergences. Cryptic species are not described here because of a lack of reproductive isolation evidence.

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Biogeographical patterns of molluscs on tropical limestone karst 'islands'

Reuben Clements

*Department of Biological Science, National University of Singapore, 14, Science Drive 4,
Singapore 117543, Republic of Singapore*

Limestone karst outcrops are *de facto* terrestrial islands because they are isolated from one other by non-calcareous substrates. This spatial structure restricts gene flow between isolated karsts, with the result that certain taxonomic groups exhibit high endemism via allopatric and/or parapatric modes of speciation. For terrestrial molluscs, tropical karsts are generally considered evolutionary hotspots for speciation. However, there is a paucity of biogeographical studies on karst malacofaunas in general. Using molluscan species data we: (1) identified correlates of endemism from a set of important biogeographical factors (i.e., karst area, isolation, surrounding soil type and geological age); and (2) investigated how species compositions varied among different karsts in two biogeographical regions (Peninsular Malaysia and Sabah, Malaysian Borneo). Generalized linear mixed-effect models (GLMM)