琉球大学学術リポジトリ

Resolving species limits within Dicranosepsis

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: Hwang, Wei Song
	メールアドレス:
	所属:
URL	http://hdl.handle.net/20.500.12000/8763

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 Habitat diversity was not shown to play a major role until the usage of choros (K) which superceded island area as the best predictor of species distribution.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.

### Poster -10

### **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.

### Poster -11

### 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 noncalcareous substrates. This spatial structure restricts gene flow between isolated karsts, with the result that certain taxonomic groups exhibit high endemicity 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)