

ZOOGEOGRAPHIC NOTES ON SPIDERS OF THE FAMILY LIPHISTIIDAE

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About 90 species of spiders were described under the family Liphistiidae, being 40 heptathelines and 50 liphistiines, all from East Asia. Localities of these species are dotted on a map. The former subfamily is distributed in the northeastern part of the range of the family, including Southwest Japan, China and Vietnam, while the latter ranges in the southwestern part, i.e., eastern Burma, Thailand, the Peninsular Malaysia and Sumatra and Indonesia. At the first sight, both ranges are separated by the Mekong valley, without overlapping each other. Although information from Laos and Cambodia is lacking, some suppositions on possible origin of this allopatry are presented.

Poster, Tuesday 7th

A CLADISTIC ANALYSIS OF THE STYGNICRANAINAE ROEWER: PRELIMINARY RESULTS (OPILIONES: CRANAIDAE)

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A character survey compiling the morphological information of the subfamily Stygnicranainae is done with the purpose of testing the monophyly of this subfamily. All known species of the subfamily are included in a matrix of 34 characters. Two new species of *Stygnicranus* Roewer from Colombia and a new genus from Ecuador, believed to be closely related to this subfamily, are also included. Parsimony analysis under implied weights recovered a monophyletic Stygnicranainae including *Tryferos* Roewer, *Stygnicranus* and the new genus nested within it. Within outgroups, the two largest subfamilies of Cranidae, Cranainae and Prostygnae, represent paraphyletic groups (grades), while Heterocranainae is a superfluous subfamily, including only the genus *Heterocranus* Roewer. The character sustaining the monophyly of Stygnicranainae is an elongated pedipalpal femur, which according to previous work by Kury, probably evolved a number of times within Opiliones. Practically all representative genera chosen for outgroups seems highly autapomorphic offshoots eliciting a grade in this family. Maybe, dropping altogether the subfamilial divisions of the Cranidae, the division in genera will better reflect the branching structure of the phylogenetic tree.

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