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Phylogeny of the subfamily of Ennominae (Lepidoptera, Geometridae): study of the tribes based on both morphological and molecular approaches

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Ennominae comprise the largest of the nine subfamilies of Geometridae with about 9800 described species in approximately 1100 genera that represent 45 % and 55 % respectively of all species and genera of geometrids. This subfamily is widely distributed in the world and the Neotropical component is substantial with 35 % of all ennomines.

There are about 70 family-group names within the Ennominae, but the number of recognized tribes is approximately 30 (Holloway 1994; Beljaev 2003, 2006), with a large concept of the tribe Boarmiini. The subfamily Ennominae is defined primarily on the basis of a very tenuous apomorphy – the loss of vein M2 in the hind wing. Today, the monophyly of Ennominae is uncertain and the relationships between the different tribes isn't enough resolved yet. Recently, several results from morphological studies but also from the first molecular works (in particular Abraham et al. 2001; Young 2006, 2008; Yamamoto & Sota 2007) brought some interesting information to help to a better comprehension of the Ennominae's phylogeny.

The main objective of my work is to propose one or several phylogenetic hypotheses for the systematics of the subfamily Ennominae at tribe level. A global approach is very important to hope to obtain some new and interesting results. So the studied species are chosen among the different biogeographical regions, but are somewhat biased towards Palearctic, Neotropical and Australian fauna due to (un)availability of specimens. Moreover, in taxon-sampling preference is given to type species of type genera of the different tribes, depending on the availability of specimens. Additional species are studied to get a better geographical coverage and a broader taxonomic sample.

This work is based on a double approach – morphological and molecular. The morphological study is based on the analysis of a morpho-anatomic matrix of adult characters, with a particular attention for the thoracic and antero-abdominal region (thoracic sclerites and tympanal organ). The molecular study should be based on several genes (mitochondrial and nuclear), but these genes aren't chosen yet. The Barcode of Life program offers opportunities to work on the mtDNA CO1 region.

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