

species *L. plumularia*, and *L. venustata* which is endemic to Kazakhstan. We revealed that *L. venustata* is the most basal taxon in the genus *Lythria*, and that there are two apical groupings of sister taxa: *L. cruentaria* grouped together with *L. sanguinaria*,

and *L. purpuraria* with *L. plumularia*. Conflict between the results of two analyses most probably occurred because of the large amount of homoplasy in the first analysis, which was excluded by the reduction of the dataset in the second analysis.

## DNA barcoding and molecular phylogeny of *Eois* moths (Geometridae) from southern Ecuador

Patrick Strutzenberger, Gunnar Brehm, Florian Bodner, Manuela Zimmermann,  
Martin Wiemers & Konrad Fiedler

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Corresponding author: Dr. Konrad Fiedler, Department of Population Ecology, University of Vienna, Althanstrasse 14 1090 Vienna, Austria; e-mail: konrad.fiedler@univie.ac.at

The genus *Eois* (Larentiinae) comprises an important part of a megadiverse assemblage of geometrid moths in the mountain rainforests of southern Ecuador. Owing to the diversity of morphotypes found in this genus, the abundance of many of its component species, and the close relationships with larval food plants in the genus *Piper*, the genus *Eois* has been chosen as a target for a more detailed investigation of local species diversity, species delimitations, and ecological segregation. COI barcode sequences (676 bp) were generated from approximately 350 individuals to establish an inventory of DNA barcodes from one study area (Reserva Biológica San Francisco). This inventory will be used to match larvae to known adult samples and will be of vital help to extend the currently very limited knowledge about food plant relationships and host specialization. Analyses of barcoding sequence divergence show that when a conservative morphology-based approach in species delimitation is used a few cases arise where maximum within-species distances exceed minimum between-species distances. However, there is a varying degree of evidence for the presence of cryptic species in all of these critical cases, as gained from analyses of elongation factor 1-alpha sequences, phylogenetic analysis and morphological reexamination. Up to 33 previously unrecognized species could be identified with the help of COI barcodes and morphological evidence in addition to at least 10 entirely new species,

thereby increasing the number of *Eois* morphospecies in that small area of Andean mountain forests from 99 to 142. Notably there are no cases where two or more previously known morphospecies had to be lumped (i.e. there was no cryptic polymorphism). Morphospecies were either confirmed or evidence for cryptic species was found. We acquired elongation factor 1-alpha sequences and extended COI sequences of approximately 100 individuals representing at least 70 *Eois* species amounting to a combined sequence dataset of ~2200 bp. Maximum parsimony and Bayesian inference of phylogeny have been employed to estimate relationships within *Eois*. Phylogenetic trees reveal that all included wing-pattern types except for one evolved only once. The exception to this rule occurs in the most basal clade whose species closely resemble those in a clade higher up in the tree. This may represent an ancestral character state or the result of convergent evolution. Additionally it could be determined that species known to feed on *Piper* are spread over most of the major clades within *Eois*, indicating that the host plant relationship with *Piper* is indeed a trait found all over the neotropical members of the genus and not just certain subclades. Within the Larentiinae *Eois* has traditionally been placed close to the Eupitheciini, but there is presently no support for such a placement in our phylogenetic analyses.