

Preliminary insight into the molecular phylogeny of Sterrhinae

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Phylogeny of Geometridae in general and Sterrhinae in particular has significantly improved during the last two decades (e.g. Holloway 1994, 1996, 1997, Abraham et al. 2001, Sihvonen & Kaila 2004, Sihvonen 2005). Most of the recent studies on the phylogeny of Geometridae have been conducted primarily on the basis of morphological characters, and only few studies based on the molecular data are available (Abraham et al. 2001, Snäll et al. in press). As several recent findings are in conflict, further research in this area is highly recommended.

We have focussed on resolving the molecular phylogeny of geometrid subfamily Sterrhinae, which comprises more than 110 genera in at least seven tribes. 1530 bp fragment of the mitochondrial cytochrome oxidase gene subunit I was obtained for 28 sterrhine species belonging to nine genera and five tribes. In addition, the same gene fragment was sequenced from six other geometrids belonging to

subfamilies Archiearinae, Geometrinae and Larentiinae, and one drepanid and one noctuid species, which were used as outgroups in phylogenetic analysis. Bayesian phylogenetic analysis of nucleotide data revealed that Sterrhinae is a monophyletic entity, but its exact position in the family Geometridae as well as relationships with other geometrid subfamilies remained unresolved. Two earlier expected evolutionary lineages, “Timandrini lineage” and “Scopulini lineage” within Sterrhinae were approved, as well as the monophyly of most tribes. Since nucleotide variation was too high for MP analysis, amino acid data of COI gene were used for phylogenetic inference instead. MP analysis revealed a phylogenetic tree almost identical to the one obtained by Bayesian analysis, but with poor support in several critical nodes. The results are therefore considered preliminary and final conclusions on the phylogeny of Sterrhinae require additional research.

Evolutionary Relationships of the Emerald Moths of Australia

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The emerald moths, or Geometrinae, comprise one of the six sub-families of the Geometridae (Lepidoptera) and, worldwide, include around 2300 species in 250 genera. They are well-known and recognised by their beautiful green wing colour and slender bodies. The Australian fauna is estimated at 350 species and is diverse in forests and myrtaceous heathlands, but with some unusual arid zone endemics as well.

Australia, with Africa, is the only continent lacking a modern treatment of the Geometrinae and A. J. Turner last reviewed the fauna in 1922. Australia is the centre of diversity for an interesting sub-set of the emeralds, the so-called ‘greys’, recognisable by their mostly dull colouration and robust bodies. This tribe of the Geometrinae, the Pseudoterpnini, may

be pivotal in understanding the evolutionary relationships of the sub-family.

This study builds on a recent large systematic study of the Australian Geometridae. We explore relationships suggested by the latter study between the ‘greys’ and the ‘greens’ and also the Geometrinae and other geometrid sub-families.

Fragments of the nuclear genes 28S D2 and LW Rhodopsin were used to construct a phylogeny for the sub-family. To date approximately 50 taxa have been sequenced for 28S D2, including 15 outgroup and sister group taxa, and a smaller subset of 22 taxa with 4 outgroups, has been sequenced for the LW Rhodopsin fragment. Both trees were well resolved and many clades well supported. Some of the supported relationships obtained, so far, from this