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Evolutionary transitions within Chalcidoidea inferred from analysis of 28S-D2 rDNA.

Economically and ecologically, Chalcidoidea are one of the most important groups of insects that control natural and pest insect populations. They are also one of the largest and least-known groups of Hymenoptera, with an estimated 60,000 to 100,000 species distributed in what are now 20 families and 89 subfamilies. Monophyly of many of the family groups has not been determined, and some of the largest families are almost certainly paraphyletic, if not polyphyletic. The higher classification of Chalcidoidea is not resolved, and no cladistic hypothesis based on character evidence has been presented. Extreme variation and convergence of behavioral and morphological traits across the superfamily have made it difficult to score these attributes reliably to develop such a hypothesis. Molecular approaches have been applied to a few taxa, often with disparate results, although in most cases few taxa have been analysed and often the outgroups were inappropriate. Preliminary analysis of nucleotide sequences of DNA synonymous to the D2 expansion region of 28S ribosomal RNA (28S-D2) demonstrate an appropriate degree of variation to study relationships of tribes, subfamilies and families of Chalcidoidea. Reasonable hypotheses of relationships were derived from 28S-D2 data for about 94 chalcidoid taxa, representing 17 families and 13 subfamilies, in which trees were calculated using unweighted parsimony and successive approximations character weighting. In some cases the results are highly congruent with morphological data, for example, Mymaridae are consistently placed as the sister group of the remaining Chalcidoidea. In others, groups traditionally regarded as monophyletic, for example, Aphelinidae and Chalcididae, are only treated as monophyletic at the subfamily level, but never at the family level. Using these preliminary results, some of the biological and evolutionary considerations within Chalcidoidea are explored.

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Relationships of eucharitids and perilampids: Where do we go from here?

New evidence for the behavioural and geographic evolution of Oraseminae is presented based on data from the South Africa genus *Timioderus*, which in its recent taxonomic history has been variably placed in Perilampidae and Eucharitidae. The eucharitid-perilampid complex is comprised of 6 subfamilies of uncertain relationships. Eucharitidae s.s. (Eucharitinae + Oraseminae) are monophyletic. Perilampidae (Perilampinae + Chrysolampinae) are paraphyletic or polyphyletic with regards to Eucharitidae, Akapalinae and Philomidinae. Parsimony analysis of the combined adult and larval data sets using a hypothetical ancestor as the outgroup suggest the following subfamilial relationships: (Chrysolampinae + (Philomidinae + (Perilampinae + (Akapalinae + (Oraseminae + Eucharitinae))))). The association of these subfamilies as a monophyletic assemblage within Chalcidoidea is based almost entirely on features of the first-instar planidial larva. However, evidence from the 28S-D2 rDNA region does not support a close relationship between Eucharitidae and Perilampidae. If true, how would this affect our assumptions of behavioural and morphological evolution of the Oraseminae and other Eucharitidae?