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Phylogenetic utility of secondary structures of the D2 region of 28S rRNAs of chalcidoids: Non-monophyly of Chalcididae.

Members of the superfamily Chalcidoidea exhibit exceptional ecological, morphological and behavioral diversity. Efforts to achieve a natural (cladistic) classification of Chalcidoidea have been hampered by indeterminate characteristics inherent to this group of insects. Because of their generally small size and life history strategies towards parasitism, chalcidoids have a high potential for reduction or convergence of anatomical structures. Molecular phylogenetics using nucleotide sequences has been one approach to circumvent ambiguities inherent to non-molecular traits of chalcidoids. Analysis based on DNA nucleotide sequences synonymous to the D2 region of 28S rRNA of over 90 chalcidoid taxa from 17 families shows some promise as a tool to help resolve some chalcidoid family and sub-family level affiliations. In addition, RNA secondary structure models of chalcidoid D2s, based on free energy minimisation, provide a framework to confirm alignment of homologous nucleotide positions and provide a series of substructures, such as subhelices, stems, bulges and loops, as an additional aggregate of homologous characters. One of the more surprising inferences from these molecular-based analyses is non-monophyly of the chalcidoid family Chalcididae. Chalcididae are one of the most easily recognised families. Although some features of Chalcididae, such as the distinctive enlarged hind femora, are proposed to be convergent in other families of Chalcidoidea, the monophyly of the family has rarely been questioned. Wijesekara proposed four apomorphic morphological characters to support the group, not including the hind femora, and recognised five subfamilies. To date, molecular assessment of exemplars of Brachymerinae, Haltichellinae, Chalcidinae and Dirhininae suggest monophyly at the subfamily level, but para- or polyphyly at the family level.

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Polybia, paraphyly, and polistine phylogeny.

A cladistic analysis of the subgenera of the polistine genus *Polybia*, and the other genera that construct phragmocytarous nests, is presented. The results clearly indicate paraphyly of *Polybia*, in terms of the genus *Synoecoides*.

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Simultaneous analysis of morphological and molecular data in Hymenoptera.

Principles and methods of simultaneous analysis in cladistics are reviewed, and the first, preliminary, analysis of combined molecular and morphological data on higher level relationships in Hymenoptera is presented to exemplify these principles.