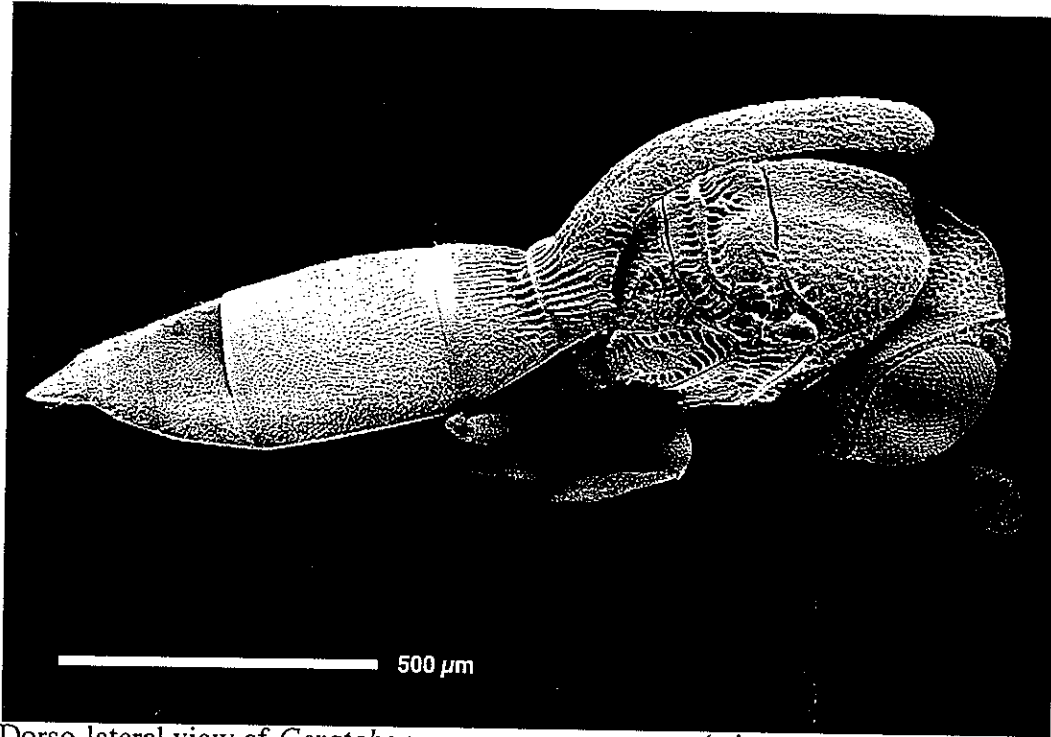


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SYSTEMATICS AND PHYLOGENY OF THE BAEINI (HYMENOPTERA: SCELIONIDAE), WITH SPECIAL REFERENCE TO AUSTRALASIAN FAUNA



Dorso-lateral view of *Ceratobaeus megacerus* sp. nov. (wings removed).

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Summary

Members of the tribe Baeini are endoparasitoids of spider eggs and they are considered to play an important role in regulating spider populations, with some species being responsible for up to 30-40% of egg mortality. Baeines are often highly speciose, with 20-30 species being collected at numerous point localities during this study. This diversity is undoubtedly related to the species richness of spiders at the same sites, given that baeine wasps also appear to be highly host specific. Taxonomically, these wasps are well-known at the generic level, but at species level the group is poorly documented, and the Australian fauna is largely undescribed. Prior to this study there were 86 described species for the Australasian region. The monophyly of Baeini is supported by several characters including their host group, the compact four-segmented antennal clava in females, the mandible being tridentate, and the antennal scape not reaching to the level of the vertex. However, the monophyly of genera are less clear. This study focuses on phylogenetic relationships among genera of Baeini and taxonomy and relationships of *Ceratobaeus* Ashmead, the largest genus in Australasia.

A brief literature review describes the history of taxonomic studies on the group and, in particular, the genus *Ceratobaeus*. This section also reviews the biology of the Baeini and role of Hymenoptera in biodiversity studies.

A detailed treatment of the external morphology of the genus is presented and explains characters and terminology used in the taxonomic revision and phylogenetic analysis. A section on methods then follows and describes the techniques used for collection and identification of material, the use of the field emission scanning electron microscopy (FESEM), and electronic editing of images. A detailed discussion of the methods adopted for phylogenetic analyses, and the workings of the parsimony program PAUP, is also presented.

Two series of analyses were conducted, one for relationships among genera of Baeini and the other for exemplar species of *Ceratobaeus*. For generic level relationships, 49 in-group taxa were selected, including 27 species of Australasian *Ceratobaeus*, as well as an additional 19 taxa from six other Australasian genera and three species of uncertain generic status. *Sparasion* and *Nixonia* were used as out-groups. A data matrix was compiled using MacClade (version 3.07) for these 51 taxa and 35 informative characters. Four of these characters were treated quantitatively while the others were divided into discrete states. The data matrix was analysed using the Random addition sequence of PAUP with 300 replications and TBR branch swapping algorithm. The

resultant trees were further analysed by using successive weighting according to the maximum value of the rescaled consistency index (RC) with all multi-state characters transformed into additive binary characters.

These analyses show the largest genera, *Idris* Foerster and *Ceratobaeus*, are polyphyletic. However, three smaller genera are putatively monophyletic and have identifiable synapomorphies: *Baeus* Haliday is apterous, with a fusiform body and the metanotum greatly reduced; *Odontacolus* Kieffer has a laterally compressed metasomal horn and pedunculate metasoma, and *Hickmanella* Austin has long sparse pilosity covering the body. The status of *Mirobaeus* Dodd and *Mirobaeoides* Dodd are less clear but they fall within a tight clade containing the majority of reduced-winged taxa. Femoral spines, a character previously used to diagnose *Mirobaeoides*, was found to be homoplasious, as were wing reduction, presence of metasomal horn, and a fused antennal clava. Although these results are somewhat preliminary, they indicate that baeine genera are in urgent need of more broad-ranging phylogenetic studies on a world wide basis.

Although *Ceratobaeus* is shown not to be monophyletic, it is one of the most easily recognised genera of Scelionidae because of the presence of a cylindrical metasomal horn in females. This horn provides a space for the elongate, internally retractable ovipositor, and its size and morphology are undoubtedly linked to the radiation of the genus in exploiting different hosts and, ultimately, to their high degree of host specificity. For this reason *Ceratobaeus* is maintained as a genus of convenience until generic boundaries within the Baeini are better resolved and a stable classification can be proposed.

Relationships among species of *Ceratobaeus* were examined for 55 exemplar species. *Sparasion*, *Nixonia* and the most basal species of *Idris* from the generic level analysis were used as out-groups. An analysis using 48 informative characters was conducted, 46 of which were the same as in the generic level analysis. Ten characters were treated quantitatively while the remaining 38 were divided into discrete states. The heuristic analysis was largely unresolved because of the high level of homoplasy and so a successive weighting analysis was conducted. This analysis generated almost completely resolved tree, and the resultant monophyletic clades were used to determine a species-group classification. Twenty-eight such groups are proposed with the remaining 79 species (not included in the analysis) being assigned to these species-groups based on the synapomorphies for each clade.

Ceratobaeus is revised for the Australasian region, with a total of 133 species being recorded and described for the Australasian region, of which 101 are recognised as new. Illustrated keys to

species-groups and species based on females are presented and, where possible, notes on their biology and host relationships are also provided.

The results of this study are discussed in regard to the inadequacy of morphological data to determine phylogenetic relationships within the Baeini, and their potential as a target taxon for biodiversity studies. Although this study has by no means exhausted the likelihood of finding characters useful for phylogenetic analysis, it is also clear from this work that morphological characters will probably not fully resolve relationships within this tribe because of the extremely high level of homoplasy. In this respect the role of other data sets, such as those generated by molecular systematics, is discussed as a means of solving generic level relationships with the tribe, and scelionids in general.