

several morphological features, particularly the paraphyly of *Euhognatha* in light of the presence of an unpaired *corpus allatum*; and future studies will need to more fully examine molecular support for these relationships in light of morphological characters. Patterns of geographical distribution are consistent with early diversification of basal lineages prior to the break up of Pangea, the survival of only two lineages (progenitors of Notonemouridae and Antarcto-

perlaria) on Gondwanaland, and the more recent invasion of South America and sub-Saharan Africa by small groups of Perlidae.

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Phylogenetics of Embioptera (= Embiidina)

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Introduction

Embioptera is an interesting order comprising relatively uncommon, relictual, pseudosocial insects. Phylogenetic studies of the Embioptera are still in their infancy. Despite the small size of the order – with close to 350 described species (ROSS 2001, 2003a, 2003b) – there are no explicit proposals about the relationships between families and there is no reason to believe that currently recognized families are monophyletic units. Rather, a preliminary cladistic study on the classification of the order (SZUMIK 1996) and subsequent analyses at the family level (SZUMIK 1994, 1998) show that many of the currently recognized higher groups are not monophyletic.

Most of the groups in the order have been recognized almost solely on the basis of male terminalia. These display an enormous variety of processes, modified for copulation, and this has kept other potentially informative structures almost completely ignored in traditional classifications of Embioptera.

Given this situation, a morphological and molecular analysis including all the potentially useful characters and many taxa representing all the major groups is strongly needed.

Data and scope

Our morphological analysis includes 57 genera from 8 families, represented by 157 species. This sample represents about 70 % of the described embiid genera, and about 45 % of the known species. 182 morphological characters were scored: 29 cephalic, 53 thoracic and abdominal, and 100 from terminalia. These are characters that vary between apparently distant groups as well as characters that only distinguish genera or groups of genera that seem to be closely related. The molecular data set we analyzed consists of sequences for 16S, 18S and 28S rDNA and COI for 22 species from 6 families and 15 genera. The trees were rooted on the 'primitive' embiopteran *Clothoda*; given this, the monophyly and phylogenetic position of Clothodidae is obviously not tested here.

Results

The resulting trees from the morphological and from the combined data set have well resolved basal clades; in other words, they have a good resolution of the higher groups. In both cases (morphological and combined analyses) only 3

of the 8 families result clearly as monophyletic: Teratembidae, Anisembidae and Australembidae. Notoligotomidae (from Java and Australia) results included in the American-African Archembidae, with these two families together forming a monophyletic group which is ambiguous in the combined data set but supported in the morphological analysis. Embidae appears non-monophyletic in both analyses; some of its African genera are grouped with the Australembidae.

The major difference between the morphological and the combined analyses is that in the former Teratembidae + Oligotomidae result as the sister group of the remaining non-clothodid Embioptera, while in the latter the Anisembidae take this position.

Conclusion

The results indicate that many non-male-terminalia characters are also very informative; many of them support major groups. Given that some groups (like Archembidae) are not well supported by the molecular data, the combined data set needs to be expanded in several ways (e.g., including more taxa in the DNA data set, and including internal morphology and maternal behavior in the morphological data set).

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