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Molecular phylogeny of psyllids: implications for the classification

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Abstract

Jumping plant-lice biology shows very interesting aspects with regards to insect-plant co-evolution, as revealed by their mono- or oligophagous habits. However, the phylogenetic relationships between higher taxa are not documented. We present here the most recent phylogeny of the world fauna based on a large sampling of complete 18S rRNA gene of representatives of the 6 known families, 17 subfamilies and 40 genera. Results show an original basal division of the superfamily into two main groups, inside which major subgroups are recognized.

Key words: Hemiptera, Psylloidea, phylogeny, 18S rRNA, host-plant relationships.

Introduction

Phylogenetic knowledge in Psylloidea is still very poor, while recent taxonomic and systematic studies have enhanced substantially the classification of the superfamily (Burckhardt, 2005). However, this knowledge is uneven with regard to taxa and biogeographical regions. The paper gives the results of cladistic analyses of molecular data (18S rRNA) in psyllids, covering the world fauna.

Materials and methods

Complete sequences of the 18S rRNA gene have been aligned using the secondary structure model of Ouvrard *et al*. (2000). The sampling contains ca. 80 species belonging to 40 genera, covering 17 subfamilies and all of the 6 families currently recognized.

Results and discussion

Phylogenetic relationships at a high taxonomic level, as well as evolutionary trends, are discussed. Psyllids appear to be divided into two branches, one branch grouping the Phacopteronidae, the Spondyliaspidinae, the Rhinocolinae, the Aphalarinae, the Carsidaridae and the Homotomidae, and the other branch grouping the Euphyllurinae, the Paurocephalinae, the Calophyidae, the Psyllinae/Arytaininae, the Ciriacreminae, the Acizziinae and the Triozidae. Among these clades, some relationships, e.g. those of the Triozidae, remain unclear and the use of new genes must be considered. Despite the observed high level of homoplasy of morphological characters in psyllids in general, we show that some clades are also supported by morphological (mostly nymphal) characters.

Conclusion

Psyllids are potentially a good model group for investigating co-speciation with their host plants as well as biogeographical patterns due to their narrow host and geographical ranges. Such a phylogeny will help in describing major evolutionary trends in psyllids. Also, this phylogenetic frame will be used to establish a more natural higher classification of the superfamily.

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References

BURCKHARDT D., 2005.- Biology, Ecology, and Evolution of Gall-inducing Psyllids (Hemiptera: Psylloidea), pp. 143-157. In: *Biology, Ecology, and Evolution of Gall-inducing Arthropods* (RAMAN A., SCHAEFER C. W., WITHERS T. M., Eds).- Science Publishers Inc., Enfield, USA.

OUVRARD D., CAMPBELL B. C., BOURGOIN T., CHAN K. L., 2000.- 18S rRNA secondary structure model and phylogenetic position of Peloridiidae (Insecta, Hemiptera).- *Molecular Phylogenetics and Evolution*, 16 (3): 403-417.

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