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**Autor:** Maus, Ch.  
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## INTERNATIONALE ENTOMOLOGEN-TAGUNG BASEL 1999

### **Phylogeny of the genus *Aleochara* (Col.: Staphylinidae) inferred from nuclear and mtDNA sequences**

von Ch. Maus

**Abstract.** A reconstruction of the phylogeny of the genus *Aleochara*, based on nuclear 18s rRNA and mitochondrial COI/II sequence is provided.

**Keywords.** Staphylinidae - *Aleochara* - phylogeny - 18s rRNA, COI/II

The genus *Aleochara* consists of about 400 species and is world-wide distributed. As far as known, all species are parasitoids the larvae of which develop in puparia of cyclorhaphous flies (PESCHKE & FULDNER, 1977, MAUS et al., 1998a) (one exception see below). Several species are important as natural enemies of noxious flies, some are used as biocontrol agents against dipteran pests (references compiled in MAUS et al., 1998a). Many studies have been carried out on the biology, ecology and behavior of *Aleochara* species (e.g. FULDNER, 1960, PESCHKE & HUBERT, 1988, PESCKE, 1990, WRIGHT & MÜLLER, 1989, JONASSON, 1994, and many others). In contrast, very little is known about the phylogeny and evolution of this genus. This lack of knowledge negatively affects subgeneric classification: there are two different, incompatible subgeneric systems, one as used by LIKOVSKY (1974) (based on the system of BERNHAUER & SCHEERPELTZ (1926), with some modifications), the second was established by KLIMASZEWSKI (1984). Both systems are not based on cladistic principles, and both are supposed to contain some non-monophyletic groups.

As previous studies revealed (MAUS, 1996, MAUS, 1998b), construction of a phylogenetic system of *Aleochara* by means of morphological characters is difficult due to the scarcity of characteristics suitable for reconstruction of phylogenetic relationships, and frequency of homoplasies in this group. Therefore, in this study DNA sequences are used in order to infer the phylogeny of *Aleochara*. I use a 1500 bp fragment of the nuclear 18S rRNA gene and a 2000 bp fragment of the mitochondrial COI/II genes. The sequences of the more conservative 18S rRNA gene allow to resolve the deeper branches in the resulting tree, the faster evolving COI/II sequences provide a better resolution of the relationships among more closely related taxa.

Here I present the provisional results of this study. The inferences outlined here are based on the 18S rRNA data. At present, 45 *Aleochara* species are included in the analysis (some of them with two individuals from different parts of the geographic range), as well as 9 Aleocharinae and 1 Silphidae as outgroup species. A maximum parsimony analysis of the 18S data resulted in 28 trees. The strict consensus of these trees (Fig. 1) shows several major discrepancies to current taxonomic classifications.

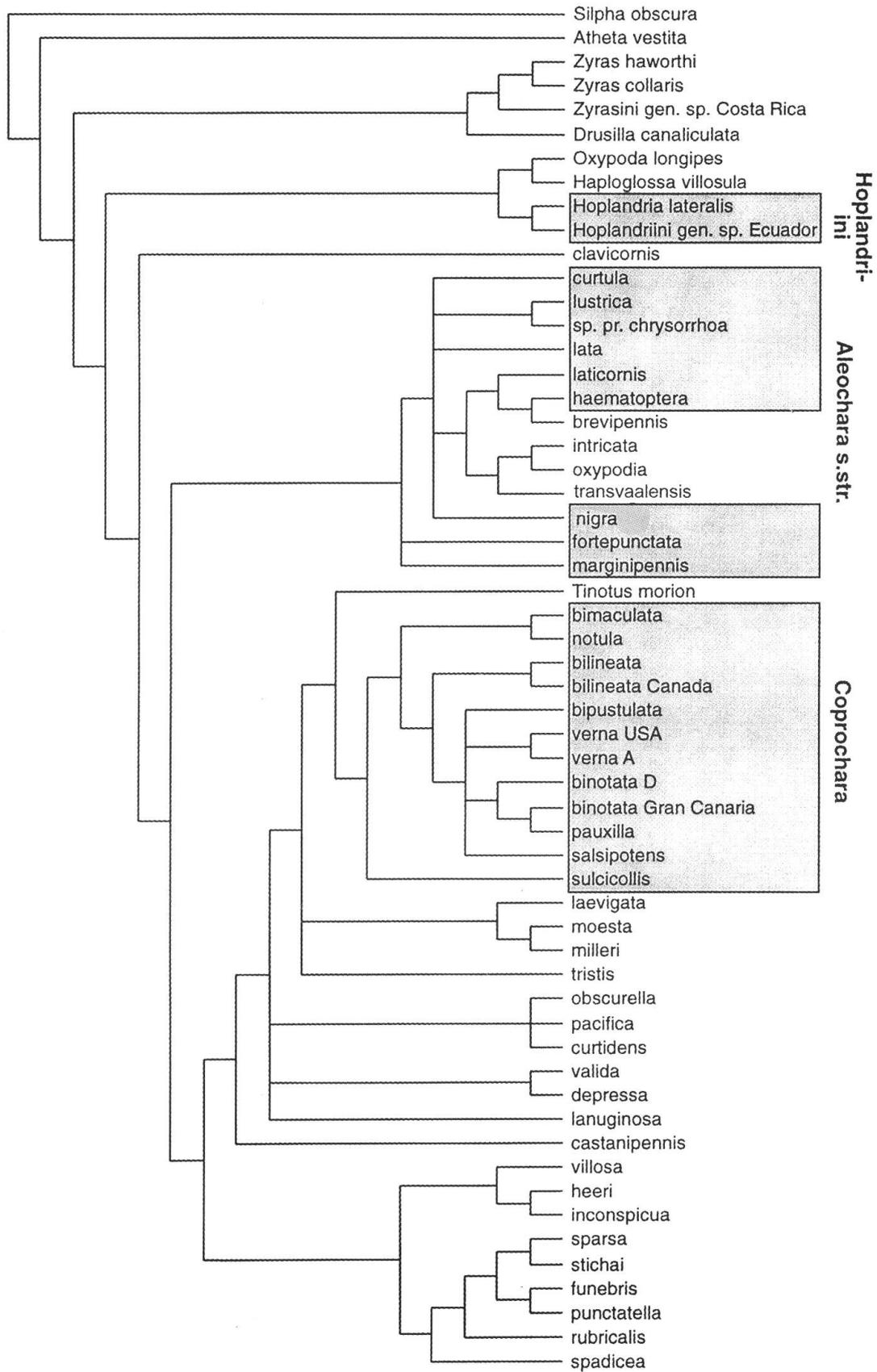


Fig. 1: Phylogenetic tree of *Aleochara* based on 18S rRNA sequences (strict consensus). Species quoted without generic names belong to the genus *Aleochara*.

The tribe Hoplandriini which was previously supposed to be the sister group of the Aleocharini is apparently more closely related to the Oxypodini than to the Aleocharini. *Tinotus morion* which was formerly thought to be a Hoplandriine is placed among the *Aleochara* species. The genus *Aleochara* proved to be monophyletic. Within the genus, *A. clavicornis* which is the only known non-parasitoid species (PESCHKE et al., 1996), branches off most basally; this supports the assumption that it is a very primitive representative of the genus. The next branch divides the genus into two larger groups. The first contains species of the subgenus *Aleochara* s.str. (including *Euryodma*), and *Xenochara* s.str. and *Baryodma*. The second main branch leads to an assemblage of several subgenera which partially turn out to be monophyletic (e.g. *Coprochara*, *Emplenota*, *Maseochara*) while others are shown to be para- or polyphyla (e.g. *Polychara*, *Baryodma*, *Xenochara* s.l., *Calochara*). Some striking cases of analogous character evolution are suggested; for example, there is no close relationship between each of the morphologically extremely similar species pairs *A. salsipotens* and *A. sulcicollis*, and *A. intricata* and *A. milleri*. The two former species are both specialised seashore-dwellers, *A. salsipotens* in South Africa and *A. sulcicollis* on the American Pacific Coast; the conspicuous morphological similarity must be explained as convergent adaptation to a specific environment. On the other hand, close relationships are revealed e.g. for *A. spadicea*, *A. punctatella*, and the *A. sparsa* group, which share very few morphological similarities, probably as a consequence of divergent adaptations to very particular bionomics of these species (life at sea shores in *A. punctatella*, in mole nests in *A. spadicea*).

The results outlined here show that the subgeneric system of *Aleochara* needs to be revised in order to create a phylogenetic classification; some modifications suggested by the molecular data are supported by available data on the biology of the species, other changes indicated here still need support from independent datasets, e.g. morphological characteristics, before conclusions should be drawn. Knowledge of the phylogeny of *Aleochara* will make it possible to interpret biological, ecological and biochemical data newly based on an evolutionary background. Finally, knowledge of phylogenetic relationships may help applied entomology in evaluating further *Aleochara* species as potential biocontrol agents against noxious flies.

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**Author's address :**

Dipl.-Biol. Christian Maus  
Institut für Biologie I (Zoologie)  
Hauptstr. 1  
D - 79104 Freiburg  
GERMANY