

ZOOLOGY

Phylogenetic Reconstruction of Weevil Superfamily Curculionoidea (Coleoptera) Using the SYNAP Method

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Abstract—Phylogenetic relationships within the superfamily Curculionoidea were reconstructed. Autapomorphies of the superfamily Curculionoidea include more or less pronounced snout, clubbed antennae, and partially sclerotized or completely membranous male tergite 9. Weevil families can be divided into three groups. The first group includes the most primitive family Nemonychidae. The second group includes nine families (Anthribidae, Belidae, Oxycorynidae, Eccoptarthridae, Allocorynidae, Rhynchitidae, Attelabidae, Ithyceridae, and Brentidae). The third (“higher”) group includes six families (Brachyceridae, Cryptolaryngidae, Dryophthoridae, Curculionidae, Scolytidae, and Platypodidae).

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The problem of phylogenetic relationships between families of the superfamily Curculionoidea and of their number remains the key problems in weevil research. Phylogenetic reconstruction of Curculionoidea is complicated, on the one hand, by the ancient origin of this family known from the late Jurassic period (Ponomarenko and Kireichuk, 2003) and, on the other hand, by a huge number of the constituent taxa (about 60000 species and over 6000 genera). Triassic Obrieniidae have been recently excluded from the considered superfamily (Legalov, 2002).

Many attempts were made to develop a natural system of the superfamily. Nearly all authors recognize the families Nemonychidae, Anthribidae, Curculionidae, and recently described Eccoptarthridae (Arnoldi, 1977; Thompson, 1992; Kuschel, 1995). Most systems also include the families Belidae, Oxycorynidae, Attelabidae, Ithyceridae, Apionidae, and Brentidae. However, the volume of the families Belidae, Oxycorynidae, Attelabidae, Apionidae, Brentidae, and particularly Curculionidae is ambiguous. Some authors recognize Allocorynidae, Rhynchitidae, Brachyceridae, Dryophthoridae, Scolytidae, Platypodidae, Cimberididae, Urodontidae, Aglycyderidae, Raymondionymidae, Cryptolaryngidae, Antliarhinidae, Eurhynchidae, Pterocolidae, Eirrhinidae, Nanophyidae, and Barididae as independent families.

Two trends can be traced in the development of the weevil system: phenetic and phylogenetic. The similarity-based phenetic systems relying on both symplesiomorphies and synapomorphies have a higher number of families in the Curculionoidea superfamily, which is quite significant in recent publications (Thompson, 1992; Zimmermann, 1993a, 1993b, 1994; Zherikhin

and Gratshev, 1995; Alonso-Zarazaga and Lyal, 1999). The relationship-based phylogenetic systems (Rasnitsyn, 2002) relying on synapomorphies starting from Crowson’s works usually have a low number of families (Crowson, 1955, 1981, 1984, 1985, 1986; Kuschel, 1995; Morrone, 1997; Marvaldi et al., 2002).

MATERIALS AND METHODS

The cladistic method was used in this work (Pavlinov, 1989, 1990; Rasnitsyn, 2002). Cladogram generation using the Hennig86 and Phylip software was rejected since an explanation of calculations underlying diagram plotting was required. PAUP 2.4.1 and SYNAP 420 yielded similar results, particularly, for weighed characters. However, SYNAP not only marked the branches with phylogenetic events and allowed tracing of the calculation progress but also generated two additional parameters (the advancement index and the index of phylogenetic relationship), which substantiated the use of this software for the phylogenetic reconstruction (Baikov, 1999). The following abbreviations are used in this work: advancement index (AI), sum of advanced characters; and index of phylogenetic relationship (IPR), AI minus unique advanced characters. In the case of equal IPRs, polytomy (merging of equivalent nodes), emergence of a new unique character, and minimum reversions were preferred. No matrix optimization was carried out. The reversion value was taken as -1 . Character states: 0, plesiomorphic; 1, apomorphic. Step-by-step protocols of phylogenetic reconstruction were published elsewhere (Legalov, 2003). Sixteen weevil families with marked apomorphic characters were considered. These families included extinct forms. The previous analysis of the