
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 Obrienidae 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

(AI = 33) and Cryptolaryngidae (AI = 34); while the second one includes Dryophthoridae (AI = 31), Curculionidae (AI = 32), Scolytidae (AI = 35), and Platypodidae (AI = 44).

The first group has apomorphic state of characters 36, 52, 56, 65, and 111 characters and plesiomorphic state of character 106.

The second group features a notably reduced tegmen (in most species). The families Dryophthoridae and Curculionidae are the most separate in it, while Scolytidae and Platypodidae are the closest (IPR = 31).

Thus, the analysis of the superfamily Curculionoidea allows us to divide its families into three groups corresponding to three evolutionary levels. The first group includes the most primitive family Nemomychidae (AI = 6). The second group is composed of nine families (Anthribidae, Belidae, Oxycorynidae, Eccoptarthridae, Allocorynidae, Rhynchitidae, Attelabidae, Ithyceridae, and Brentidae) with IP from 12 to 24 (the mean IP = 18.2) with mandibles carrying more than two teeth in the incisor area, ventrite 1 framed near the acetabulae, joint tegmen plate, and clawless larval legs. The third (higher) group includes six families (Brachyceridae, Cryptolaryngidae, Dryophthoridae, Curculionidae, Scolytidae, and Platypodidae) with the main IP of 34.8 (from 31 to 44). These families share flat or almost flat eyes, antennal grooves on the snout sides, larval frontal suture not reaching the mandibles, and larval labrum with three bristle pairs. The autapomorphies of the Curculionoidea superfamily include more or less pronounced snout, antennae with a prominent club, and partially sclerotized or completely membranous male tergite 9.

Comparison of this system with the available current phylogenetic systems (Kuschel, 1995; Morrone, 1997; Marvaldi et al., 2002) demonstrates a match in the recognition of independent families Nemomychidae, Anthribidae, Belidae, Attelabidae, Brentidae, and Curculionidae as well as in the order of their splitting off from the main trunk. At the same time, the volume of the families Belidae, Attelabidae, Brentidae, and Curculionidae is smaller. Together with Morrone (1997) and Marvaldi et al. (2002), we recognize the separate family Eccoptarthridae but we consider it a more primitive group similar to the families Belidae and Oxycorynidae, which agrees with the views of Kuschel (1995) who included it into Belidae. This system is most similar to the system of Morrone (1997), which also considers Ithyceridae, Brachyceridae, and Platypodidae as independent families. The main distinction of this system is the recognition of Oxycorynidae, Allocorynidae, Rhynchitidae, Cryptolaryngidae, Dryophthoridae, and Scolytidae as separate families as well as the justification of sequential branching of weevil families from the main trunk.

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