PHYLOGENY OF THE COLEOPTERA BASED ON MORPHOLOGICAL CHARACTERS OF ADULTS AND LARVAE

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Abstract.— In order to infer phylogenetic relationships within the extraordinarily species-rich order Coleoptera, a cladistic analysis is performed, in which 516 adult and larval morphological characters are scored for 359 beetle taxa, representing 314 families or subfamilies plus seven outgroup taxa representing seven holometabolan orders. Many morphological features are discussed at length with accompanying illustrations, and an attempt is made to homologize these and employ a uniform set of terms throughout the order. The resulting data matrix is analyzed using the parsimony ratchet in conjunction with implied weighting. The resulting most parsimonious tree found the order Strepsiptera to be sister to Coleoptera, each of the four coleopteran suborders to be monophyletic and subordinal relationships as follows: (Archostemata + Adephaga) + (Myxophaga + Polyphaga), but without significant support for either clade. The topology of the remainder of the tree is consistent with many prior molecular and morphological analyses, with the monophyly of superfamilies Hydrophiloidea (sensu lato), Scarabaeoidea and Curculionoidea and many currently recognized families and subfamilies are well supported, with weaker support for Elateroidea, Cucujiformia and Phytophaga.

Key words.— Coleoptera, beetles, morphology, phylogeny, classification.

INTRODUCTION

Beetles (order Coleoptera) are an extraordinarily species-rich group, comprising over 360,000 described species (Bouchard \textit{et al.} 2009), of tremendous morphological and ecological diversity with a history dating back at least to the Permian (Ponomarenko 1995). As such, beetles represent an excellent system for addressing a broad spectrum of evolutionary questions, particularly those pertaining to causes and correlates of diversification. Although many efforts have been made to explain this spectacular evolutionary radiation, relatively few attempts have been made to infer the phylogeny of beetles as a whole; of these, all recent attempts have relied on molecular data alone (Hunt \textit{et al.} 2007, Maddison \textit{et al.} 2009, Song \textit{et al}. ...