A Critique on Naomi’s Phylogeny and Higher Classification of Staphylinidae and Allies (Coleoptera)

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A phylogenetic analysis and new family-level classification of Staphylinidae and allied families, proposed by Naomi in 1985, is critically reviewed. Although some of his new characters are found promising, examples are given of numerous problems with the phylogenetic analysis, including inadequate sampling, arbitrary use of the concept of “underlying autapomorphy,” and careless gathering and analysis of data. The resulting radically new division of Staphylinidae into 3 families (the names of 2 of which are junior synonyms) is not justified by Naomi’s analysis, and his classification is rejected.

1 Introduction

Staphylinidae, along with the related “traditional” families Pselaphidae, Dasyceridae, Silphidae, Scaphidiidae, and Scydmaenidae, form a probably monophyletic lineage within the beetle superfamilia Staphylinoidea [Lawrence & Newton 1982]. Together, these families include over 3,000 genera and 45,000 named species, or over a tenth of the ordo Coleoptera. Most of these species have short elytra that expose much of the abdomen, hence the informal name “Brachelytra” that is often applied to them (despite the numerous exceptions).

Various revisions to the traditional classification of Staphylinidae [e.g., as represented by Blackwelder 1952] have been proposed, for example Coiffait’s [1972] highly split ten-family arrangement and Moore’s [1964] somewhat idiosyncratic subfamily scheme. The proponents of these arrangements did not claim any theoretical (e.g., phylogenetic) justification for them, however.

In recent decades, attempts have been made to group the staphylinid subfamilies on the basis of their inferred relationships, as in Tikhomirova’s [1973] morphological and ecological study of Staphylinidae. Other studies [Crowson 1955, Kasule 1966, Lawrence & Newton 1982] have suggested some of the same groupings, but have also recognized that the familia Staphylinae in the traditional sense is probably paraphyletic, with some or all of the other smaller families of Brachelytra being related to various subgroups of Staphylinidae. None of the studies mentioned has presented a detailed phylogenetic analysis of the higher taxa, and none has proposed any dramatic formal changes in the family-level classification, at least partly because of difficulties in resolving basal relationships in this large group. Lack of concordance between elytral length and various other adult structures, and between adult and larval characters, are among these many difficulties. Thus, a well-documented highly resolved phylogenetic analysis of the Brachelytra and a new phylogenetically-based classification of the group based on it are badly needed.

Recently, Dr Shun-Ichiro Naomi [1985] presented the most detailed phylogenetic analysis yet published for the Brachelytra, treated down to the subfamily level. Naomi’s analytical methods were ostensibly