

P505

## Phylogeny of the Myllaenini and Related Taxa (Coleoptera: Staphylinidae: Aleocharinae)

Kee-Jeong Ahn

*Department of Biology, Chungnam National University, Daejeon 305-764*

The beetle family Staphylinidae represents one of the truly remarkable radiations in the history of life; it currently includes over 46,200 described species, placed in 3,200 genera, organized into about 32 subfamilies. All recent works indicate that this is only a small fraction of the true contemporary diversity. Among staphylinids the subfamily Aleocharinae is the largest, most poorly known, and taxonomically the most difficult lineage. It comprises 52 tribes, over 1,000 described and probably valid genera, and over 12,000 described species. Within the Aleocharinae, members of the tribe Myllaenini Ganglbauer and related genera are characterized by unusual styliform mouthparts; the maxillary lobes and labial palpi are particularly elongated and stylet-like. This set of myllaenine-like genera has a confusing taxonomic history. They have been variously classified as comprising several separate tribes, placed with the tribe Pronomaeini Ganglbauer or its equivalent, or they have been taxonomically dispersed among several lineages of riparian or intertidal aleocharines. Consequently, they comprise one of the most complex and confusing staphylinid groups. To date, the tribe Myllaenini and related taxa contains 19 genera, whose phylogenetic relationships have not been tested by modern cladistic methodology. Phylogenetic analysis was performed using NONA 2.0, run within WinClada (Beta) 0.99. Tree search options of HOLD 10000, HOLD/100, MULT\*1000 were used. The data set for phylogenetic analysis comprised 99 characters representing 297 character states derived from adult morphology. Multistate characters were treated as unordered. To test the monophyly of the Myllaenini I included all outgroup and ingroup taxa in the analysis during tree construction in a simultaneous analysis. All cladograms were rooted on *Gymnusa variegata* Kiesenwetter. In order to estimate clade support on a cladogram I calculated Bremer support value and relative Bremer support. Character distributions were studied using WinClada (Beta) 0.99. All illustrated cladograms were prepared using WinClada and edited using Power Point and Word 2002. The analysis resulted in 20 most parsimonious cladograms with length of 584, a consistency index of 0.33 and a retention index of 0.69. The myllaenine lineage consisting of nine genera (*Myllaena* Erichson, *Amazonopora* Pace, *Dimonomera* Cameron, *Bryothinusa* Casey, *Philomina* Blackwelder, *Polypea* Fauvel, *Brachypronomaea* Sawada, *Rothium* Moore and Legner, and *Lautaea* Sawada) is well supported. My new concept of the Myllaenini is based on the synapomorphy of antero-lateral angles of mentum prolonged into spinose processes, a character that is unique throughout the aleocharines to my knowledge. However, inter-generic relationships among Myllaenini were not well resolved, though the genera *Dimonomera*, *Myllaena*, *Bryothinusa* and *Amazonopora* formed a monophyletic group. On the other hand, the analysis agrees on the monophyly of the Pronomaeini Ganglbauer (*Pronomaea* Erichson, *Pseudomniophila* Pace, *Nopromaea* Cameron, and *Tomoxelia* Bernhauer). The tribe Dimonomerini (*Dimonomera* Cameron) is confirmed to be a member of the Myllaenini. Masuriini is a possible sister group of the Myllaenini. *Stylopalpus* Cameron shows a sister group relationship to the Pronomaeini. Several other clades are also consistently recovered. However, phylogenetic relationships of the genus *Dysacrita* Pace are ambiguous. The rogue genus *Diglotta* Champion is not recovered as a member of the Myllaenini or Pronomaeini. On the contrary, it forms a monophyletic clade with the liparocephaline genera *Halorhadinus* Sawada and *Amblopusa* Casey. My phylogenetic analysis provides the opportunity to study the evolutionary trend of gland opening size on abdominal tergite VII among aleocharines. The cladograms confirm that the defensive gland evolved from the absence of a defensive gland in the most primitive aleocharines (Gymnusini and Deinopsini). In addition, the members of the relatively primitive tribes, Trichopseniini and Mesoporini do not have the glands. However, Steidle and Dettner's hypothesis of gradual increase of size of gland opening during diversification of aleocharines is not directly supported by the cladistic analyses. Instead, the cladograms are consistent with the hypothesis that reduced size of the tergal gland openings in the aleocharine tribes Myllaenini, Masuriini and *Dysacrita* are derived conditions. The taxa in these groups have very small defensive glands and small gland openings on tergite VII that comprise less than the half width of tergite VII. Tribe Myllaenini contains several seashore inhabiting genera: *Bryothinusa*, *Brachypronomaea*, *Rothium*, *Lautaea* and *Polypea*. They are found exclusively in the intertidal region. The other four genera, *Myllaena*, *Amazonopora*, *Philomina* and *Dimonomera*, are terrestrial, and primarily associated with freshwater riparian habitats. The evolution of intertidal habitat in the Myllaenini is represented by a single optimization of two origins. The ancient myllaenine genera *Amazonopora*, *Myllaena*, *Dimonomera* and *Philomina* have been recorded from the riparian habitats. Therefore, I hypothesize that ancestors of the Myllaenini appear to have arisen in riparian habitats and colonized intertidal habitats later. However, the low species diversity of most of myllaenine intertidal genera suggests that most have not successfully diversified in the harsh intertidal environment. The genus *Bryothinusa*, with about 26 known species, is the most successful one in terms of the species number and broad distribution.