



Conference Abstract

Phylogeny of the supertribe Nebriitae (Coleoptera: Carabidae) based on analyses of molecular sequence data--some surprises.

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Abstract

To explore phylogenetic relationships among members of the carabid supertribe Nebriitae, we sampled DNA fragments extracted from adults of 244 nebriite species-group taxa, representing about 25% of known species-group taxa and 93% (38 of 41) of the currently accepted nebriite genus-group taxa. Sequence data were recorded for eight gene fragments (a total of 5654 bases) from nuclear ribosomal, mitochondrial, and nuclear protein coding genes. The resulting phylogeny is based on both individual gene and concatenated gene analyses using Maximum Likelihood and Bayesian methods, which produced nearly identical results. Most nodes are well supported by both high bootstrap and high posterior probability values, and many of them also by unique (autapomorphic) bases.

Many of the previously recognized genus-group taxa are supported as monophyletic, but others are not. Alternative reclassifications that reflect monophyletic groups are still being

considered, based on the molecular analyses along with considerations of ease of group identification and geographical distribution. Of the two alternative reclassifications being considered, one requires the designation of 16 new subgeneric synonymies and the other only nine new subgeneric synonymies plus the recognition of three new subgenera. However, under both schemes, *Nippononebria* Uéno (along with its subgenus, *Vancouveria* Kavanaugh) is re-established as a genus separate from *Nebria* and sister to *Leistus* Frölich; and *Archastes* is embedded within a monophyletic genus *Nebria* and closely related to subgenera *Oreonebria* Daniel and *Orientonebria* Shilenkov. Additional details will be reported in the presentation.

Keywords

Nebriidae, Ground beetles, DNA, taxonomy, molecular phylogenetics, evolutionary tree

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