

ABSTRACT

Subfamilies Rygmodinae and Sphaeridiinae together form approximately one third of the extant diversity within the family Hydrophilidae (Coleoptera: Polyphaga). Members of both these subfamilies inhabit wide spectrum of aquatic and terrestrial environments including specialized habitats such as phytotelmata, carrion or termite nests. So far, habitat shifts within these subfamilies have been only tested with a limited amount of taxa at the family level. Using a broader sampling and Bayesian and maximum likelihood methods, genus-level molecular phylogenetic analysis and divergence dating were performed. The dataset included 96 taxa, representing all major clades (genus groups) in both subfamilies, sequenced for two mitochondrial and two nuclear genes. A single shift from the aquatic to terrestrial environment in the Middle Jurassic was suggested, thus revealing both subfamilies and all tribes as ancestrally inhabiting decaying plant material and leaf litter. Secondary returns to aquatic habitats were suggested for two lineages of the Rygmodinae and several lineages belonging to tribes Coelostomatini and Megasternini. A single shift to flowers was revealed in the subfamily Rygmodinae. Similarly, single independent shifts to the inquiline lifestyle in tribes Omicrini and Megasternini were revealed. In contrast, shift to dung + carrion occurred multiple times in the subfamily Rygmodinae and tribe Megasternini, and once in an ancestor of the tribe Sphaeridiini. Results of the diversification analysis agree with those performed at family level, with a single increase revealed in the Megasternini and not corresponding to any habitat shift. Morphological characters supposed to be adaptations to the aquatic lifestyle (ventral hydrophobic pubescence, presence of trichobothria) were coded for all terminal taxa and tested for their correlation with habitat and for possible correlated evolution, in both cases using phylogenetic comparative methods. Results showed similar trait values in closely related taxa rather than in taxa sharing the same habitat, and little correlation between particular characters.