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# Molecular phylogeny of the aquatic beetle family Noteridae (Coleoptera: Adephaga) with an emphasis on data partitioning strategies

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## ABSTRACT

The first molecular phylogenetic hypothesis for the aquatic beetle family Noteridae is inferred using DNA sequence data from five gene fragments (mitochondrial and nuclear): COI, H3, 16S, 18S, and 28S. Our analysis is the most comprehensive phylogenetic reconstruction of Noteridae to date, and includes 53 species representing all subfamilies, tribes and 16 of the 17 genera within the family. We examine the impact of data partitioning on phylogenetic inference by comparing two different algorithm-based partitioning strategies: one using predefined subsets of the dataset, and another recently introduced method, which uses the *k*-means algorithm to iteratively divide the dataset into clusters of sites evolving at similar rates across sampled loci. We conducted both maximum likelihood and Bayesian inference analyses using these different partitioning schemes. Resulting trees are strongly incongruent with prior classifications of Noteridae. We recover variant tree topologies and support values among the implemented partitioning schemes. Bayes factors calculated with marginal likelihoods of Bayesian analyses support *a priori* partitioning over *k*-means and unpartitioned data strategies. Our study substantiates the importance of data partitioning in phylogenetic inference, and underscores the use of comparative analyses to determine optimal analytical strategies. Our analyses recover Noterini Thomson to be paraphyletic with respect to three other tribes. The genera *Suphisellus* Crotch and *Hydrocanthus* Say are also recovered as paraphyletic. Following the results of the preferred partitioning scheme, we here propose a revised classification of Noteridae, comprising two subfamilies, three tribes and 18 genera. The following taxonomic changes are made: Notomicrinae **sensu n.** (= Phreatodytinae **syn. n.**) is expanded to include the tribe Phreatodytini; Noterini **sensu n.** (= Neohydrocoptini **syn. n.**, Pronoterini **syn. n.**, Tonerini **syn. n.**) is expanded to include all genera of the Noterinae; The genus *Suphisellus* Crotch is expanded to include species of *Pronoterus* Sharp **syn. n.**; and the former subgenus *Sternocanthus* Guignot **stat. rev.** is resurrected from synonymy and elevated to genus rank.

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## 1. Introduction

### 1.1. Overview of Noteridae

Noteridae Thomson (Coleoptera: Adephaga) is a family of aquatic beetles that occurs worldwide (Nilsson, 2005, 2011). Often called the burrowing water beetles, members of the family are small to minute and superficially similar in appearance to their better-known relatives, the Dytiscidae (diving beetles), but are easily distinguished by the noterid platform: an elevated ventral plate on the mesosoma, formed by expansions of the inner metacoxal lamellae (Miller, 2009). With approximately 270 described species (Nilsson, 2011; García et al., 2012; Miller, 2013; Gómez and Miller, 2013; Baca et al., 2014; Baca and Toledo, 2015; Guimarães and Ferreira, 2015; Manuel, 2015), the family is not very diverse, though they can be often found in abundance. Noteridae has been poorly studied in comparison to other adephagan families. Several genera are still in need of revision (Miller, 2009) and many species remain undescribed or known only from their original descriptions, making identifications difficult.

Noteridae was once classified as a subfamily of the Dytiscidae. However, starting with Bertrand (1928:191), the 1900s saw a trend of Noteridae being recognized as a distinct family. Recent phylogenetic analyses of Adephaga support this classification, with other families such as Amphizoidae, Hygrobiidae and Aspidytidae found more closely related to Dytiscidae than Noteridae (e.g. Balke et al., 2008; McKenna et al., 2015; Toussaint et al., 2016).

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### *1.2. Phylogenetic studies of Noteridae*

Noterid representatives have been included in more broadly focused phylogenetic studies of Adephaga (e.g. Ribera et al., 2002; Balke et al., 2008; Toussaint et al., 2016), but few have included sufficient or appropriate sampling to have any bearing on relationships within Noteridae, and nearly all were based on morphology (Beutel and Roughley, 1987; Belkaceme, 1991; Beutel et al., 2006; Miller, 2009; Kato et al., 2010; Dressler et al., 2011; Gómez and Miller, 2013). Morphology-based reconstructions (Figs. 1 and 2), recovered relatively consistent topologies, showing a phyletic grade of noterid tribes in the order of Phreatodytini Ueno, Notomicrini Zimmermann, Tonerini Miller, Neohydrocoptini Zalat et al., Pronoterini Nilsson and Noterini Thomson. Within Noterini, *Noterus* Clairville, *Synchortus* Sharp and *Mesonoterus* Sharp were consistently found to be sister linages to the rest of the noterine genera, for which relationships were often conflicting or unresolved. Miller (2009) was arguably the most comprehensive study of Noteridae. He performed a morphology-based analysis that included some novel characters, and diagnosed all noterid subfamilies, tribes, and genera. The analysis was replicated by Gómez and Miller (2013; Fig. 2B) to place the genus *Prionohydrus* as sister to *Mesonoterus*. Both studies found some slightly shifted or unresolved relationships in Noterini, but otherwise his results were not in strong conflict with previous work. Studies that included larval characters (Beutel et al., 2006, 2008; Dressler et al., 2011; Fig 1) highlighted the fact that immature stages of many noterid genera are unknown, thereby restricting analyses to adult characters to infer relationships.

Noterids have also been included in several molecular phylogenies (e.g. Ribera et al., 2002; Balke et al., 2005, 2008 (Fig. 1E);

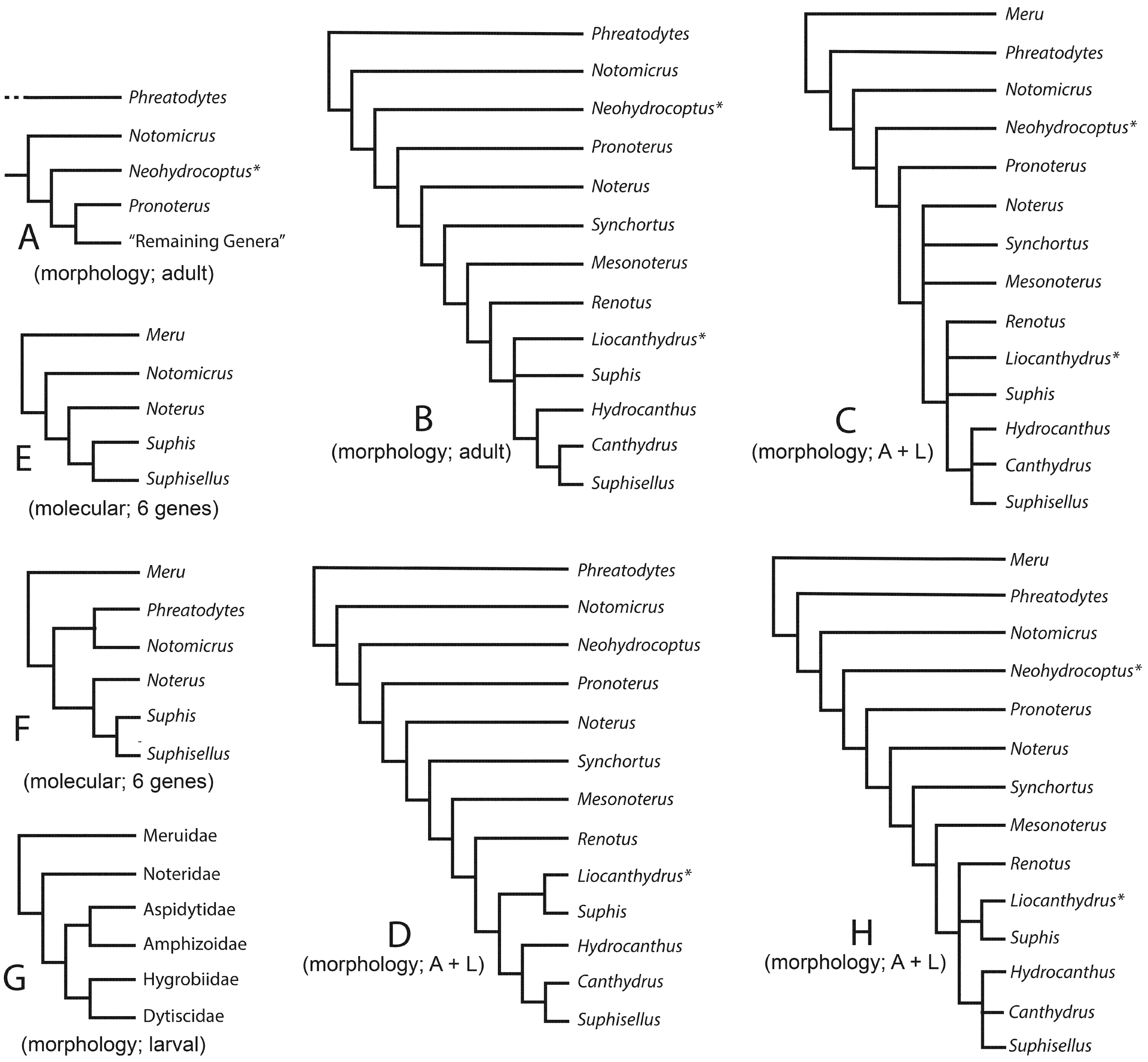

**Fig. 1.** Previous phylogenetic reconstructions/hypotheses of Noteridae (A) Beutel and Roughley (1987); (B) Belkaceme (1991); (C) Beutel et al. (2006); (D) Beutel et al. (2008); (E) Balke et al. (2008); (F). Kato et al. (2010); (G) Alarie et al., 2011; and (H) Dressler et al. (2011). Captions in parentheses denote type data inferred for respective reconstruction; A + L indicates that both adult and larval morphological characters were used. Asterisks (*) indicates taxon name changed to follow recently published taxonomic actions.

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