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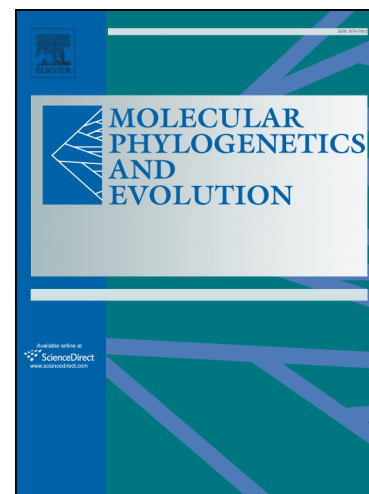
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Molecular data reveal a tropical freshwater origin of Naidinae (Annelida, Clitellata, Naididae)

Christer Erséus^{a,*}, Ida Envall^{b,c}, Pierre De Wit^d, Lena M. Gustavsson^c

^aDepartment of Biological and Environmental Sciences, University of Gothenburg, Box 463, SE-405 30 Göteborg, Sweden

^bDepartment of Zoology, Stockholm University, SE-106 91 Stockholm, Sweden

^cDepartment of Zoology, Swedish Museum of Natural History, Box 50007, SE-104 05 Stockholm, Sweden

^dDepartment of Marine Sciences, University of Gothenburg, Sven Lovén Centre for Marine Sciences Tjärnö, Hättebacksvägen 7, SE-452 96 Strömstad, Sweden

*Corresponding author: christer.erseus@bioenv.gu.se

Abstract

The phylogenetic relationships within Naidinae (Annelida, Clitellata, Naididae) were investigated, using six molecular markers, both mitochondrial (12S rDNA, 16S rDNA, the COI gene) and nuclear (18S rDNA, 28S rDNA, the ITS region). Thirty-seven nominal species, representing 16 of the 22 genera recognized in the subfamily, were included, and the *Nais communis/variabilis* species complex was represented by six different morphotypes. Ten other species of Naididae were selected as outgroups. The data were analysed by Bayesian inference and Maximum Likelihood. The phylogeny corroborates monophyly of the Naidinae, and the separate status of the genus *Pristina* (Pristininae) and the Opistocystinae.

Relationships within Naidinae are largely well supported, but in some parts unexpected: (1) A clade containing the largely tropical genera *Dero* and *Branchiodrilus* is sister to the rest of the subfamily, and together with a third tropical genus, *Allonais*, they form a basal paraphyly. All these genera show morphological adaptations to environmental hypoxia, leading to the conclusion that Naidinae originated in tropical freshwaters. (2) The genera *Dero*, *Nais* and *Piguetiella* are paraphyletic. (3) At least *Branchiodrilus*, *Paranaïs*, *Chaetogaster*, *Nais*, *Stylaria* appear to contain cryptic species. Morphological characters, especially those associated with chaetae, are to a great extent homoplastic within Naidinae, which certainly has contributed to the overall taxonomic confusion of this subfamily.

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