



New insights on the phylogenetic relationships of the Proseriata (Platyhelminthes), with proposal of a new genus of the family Coelognoporidae

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Abstract

Proseriata is a diverse and species-rich taxon of Neophora (Platyhelminthes). The group is divided into two morphologically well-characterised taxa: Lithophora and Unguiphora. Previous molecular analyses, aimed at ascertaining in-group relationships of the Proseriata, were equivocal in supporting the monophyly of the Lithophora, and of one of its families, the Coelognoporidae. Here we present a new phylogeny of the Proseriata, based on complete ssrDNA and partial (D1-D6) lsrDNA. The analysis includes 36 proseriate species. 13 new sequences from seven species are used, four of which from species of the Coelognoporidae and one from a new species of the recently established family Calviriidae. Phylogenetic analysis was performed using Bayesian Inference (BI), maximum likelihood (ML) and maximum parsimony (MP). Clades were considered to have high nodal support if BI posterior probability and ML and MP bootstrap percentages were $\geq 90\%$. The resulting cladogram strongly supports the monophyly of the Lithophora. In addition, the monophyly of the Coelognoporidae and their inclusion in the Lithophora are corroborated. Within the Lithophora, two sister clades are supported, including Coelognoporidae+Calviriidae, and Otoplanidae+Archimonocelididae+Monocelididae respectively. In the Coelognoporidae, there was a poor correspondence between estimates of phylogeny and the monophyly of genera, suggesting the family is in need of systematic revision. Current morphology-based systematic arrangements of Otoplanidae and Monocelididae are not supported by molecular results. The enigmatic taxon *Ciliopharyngiella* (formerly included in the Rhabdozoa) clusters with the Unguiphora, although with low support. One new species of Coelognoporidae (*Parainvenusta englarorum* n. gen n. sp.) is described and discussed in the appendix.

Key words: phylogeny; taxonomy; ssrDNA; lsrDNA; Unguiphora; Lithophora; *Ciliopharyngiella*

Introduction

The first comprehensive molecular study specifically designed to assess both in-group and out-group phylogenetic relationships of the Proseriata, a species-rich and widespread taxon of Neophoran flatworms, left two major problems unsolved. In fact, the monophyly of the Proseriata themselves and of one of its major subtaxa, the Lithophora were unsupported by the molecular trees obtained (Littlewood *et al.*, 2000). These results were in stark contrast with most of the morphology-based phylogenies of the group, which instead clearly supported their monophyly (Sopott-Ehlers, 1985; Ehlers, 1985; Ehlers & Sopott-Ehlers, 1990). However, molecular data partially agreed with alternative, morphology based reconstructions, which hypothesized paraphyletic Lithophora (Martens & Schockaert, 1988) and Proseriata (Brüggemann, 1986).