

161 Phylogeny of Enoplia: parsimony estimations with SSU rDNA sequence data

L. ROUSSINE^{1,*}, P. DE LEY², V.V. ALESHIN¹,
J.R. VANFLETEREN³, D. STURHAN⁴,
A. VIERSTRAETE⁵ and M. BLAXTER⁶

¹*Belozersky Institute of Physico-Chemical Biology, Department of Evolutionary Biochemistry, Moscow State University, 119899 Moscow, Russia*

²*Department of Nematology, University of California, Riverside, CA 92521, USA*

³*University of Ghent, Department of Biology, B-9000 Ghent, Belgium*

⁴*Biologische Bundesanstalt, Institut fuer Nematologie und Wirbeltierkunde, 48161 Muenster, Germany*

⁵*University of Ghent, Department of Biology, B-9000 Ghent, Belgium*

⁶*Institute of Cell, Animal and Population Biology, University of Edinburgh, Edinburgh, EH9 3JT, UK*

**roussine@yandex.ru*

Molecular analyses suggest that Enoplia is the most divergent major clade within the phylum Nematoda. Disparities in rates of sequence evolution between lineages, lack of intermediate taxa to break possible long branches and the limited amount of phylogenetic information shared by sampled taxa make phylogenetic inference for Enoplia a difficult task. The dataset was carefully selected to maximally encompass enoplian biodiversity and utilise basal representatives of other clades, thus breaking long branches at all levels of the tree. It includes several genera for which molecular evidence has not been previously published: *Campydora*, *Leptosomatium*, *Thoracostomopsis*, *Bathylaimus*, *Tripylloides*, *Calyptonema*, *Viscosia*, *Halalaimus*, *Ironus*, *Alaimus*, *Xenella*, *Rhabdode-*

mania, *Tobrilus*, *Aporcelaimellus* and *Nygolaimus*. The data was examined for presence of phylogenetic signal using approaches based on sequential removal of categories of variable sites, with phylogeny reconstruction at each step. This case study proves that the NJ method performs highly inconsistently with this problematic dataset and that bootstrap analyses (both NJ and MP) greatly underestimate repeatability of inferring even basal nodes of the nematode tree. Instead, comparing equally parsimonious topologies obtained in a series of MP runs with a number of statistical tests under the ML optimality criterion allowed the reconstruction of the major lineages within Enoplia.