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**160 SSU rRNA gene of *Soboliphyme baturini* Petrow, 1930 (Nematoda: Dioctophymida) and a reappraisal of molecular bounds of Dorylaimia**

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Molecular phylogenies based on SSU rDNA sequence data suggest that Dorylaimia, along with Enoplia and Chromadoria, constitutes the third mainstream in nematode evolution. Its contents are represented as follows: (Trichinellida (Dorylaimida (Mononchida: Mermithida))). However, high rates of sequence evolution inherent in the trichinellid lineage render this topology unreliable. Novel molecular data on the SSU rRNA gene structure of *Soboliphyme baturini* (Dioctophymida: Soboliphymidae) revealed the fifth lineage within Dorylaimia and provided new information for establishing its internal topology. Maximum parsimony, maximum likelihood and neighbour-joining algorithms with bootstrap replicates consistently inferred *S. baturini* as a sister taxon to Trichinellida. Inclusion of *S. baturini* had a stabilising

affect on the integrity of the Dorylaimia clade through breaking the long branch leading to Trichinellida. Putative molecular synapomorphies reconstructed by parsimony for each node of the tree were analysed on a large dataset of metazoan SSU rDNA sequences to sort out homoplasious characters that may potentially bias parsimony estimations. Strong synapomorphies located in highly conserved parts of the gene support monophyly of all Dorylaimia and suggest the following internal bifurcation pattern: ((Trichinellida: Dioctophymida): (Dorylaimida (Mononchida: Mermithida))). Molecular phylogeny of Dorylaimia juxtaposed with morphological evidence may alter our perception of morphological and ecological change in nematode evolution.