

Supplementary Materials

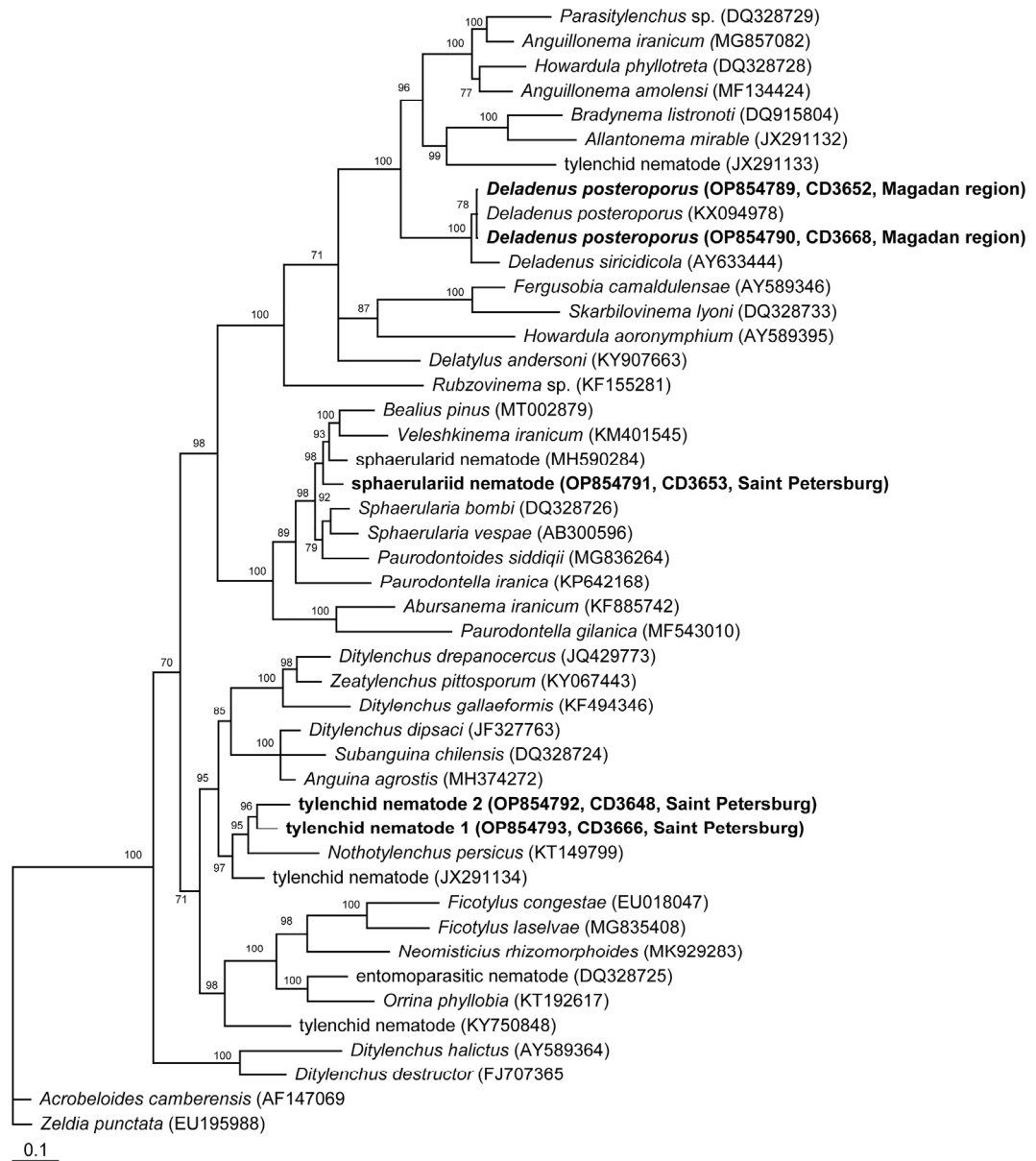


Figure S1: Phylogenetic positions of studied samples within some species from the order Tylenchida nematodes as inferred from Bayesian analysis of the D2-D3 of 28S rRNA (ntax=46 nchar=987) gene sequences. Posterior probability values more than 70% are given on appropriate clades. New sequences are indicated in bold.

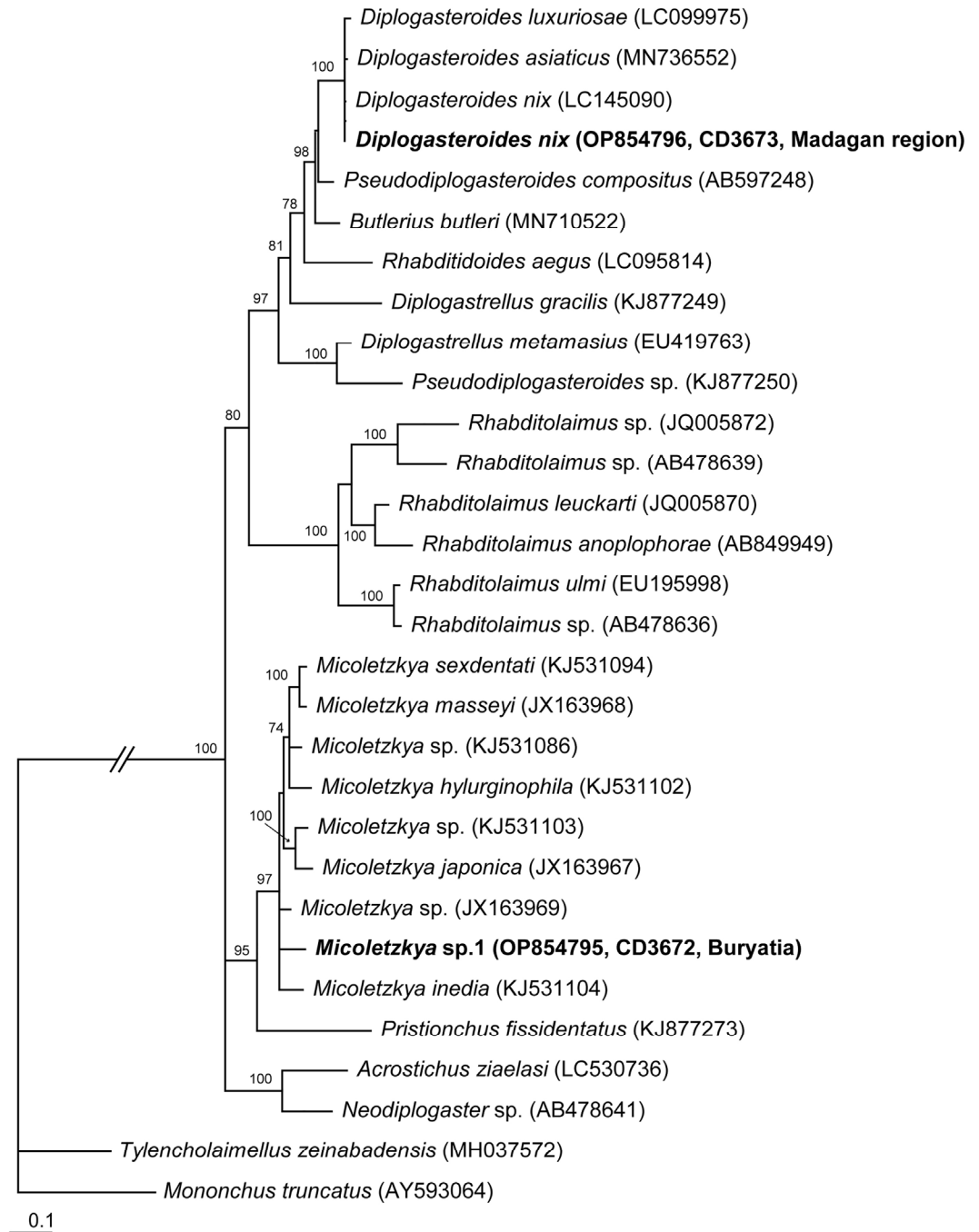


Figure S2: Phylogenetic positions of studied samples within some species from Diplogastridae as inferred from Bayesian analysis of the D2-D3 of 28S rRNA (ntax=31 nchar=794) gene sequences. Posterior probability values more than 70% are given on appropriate clades. New sequences are indicated in bold.

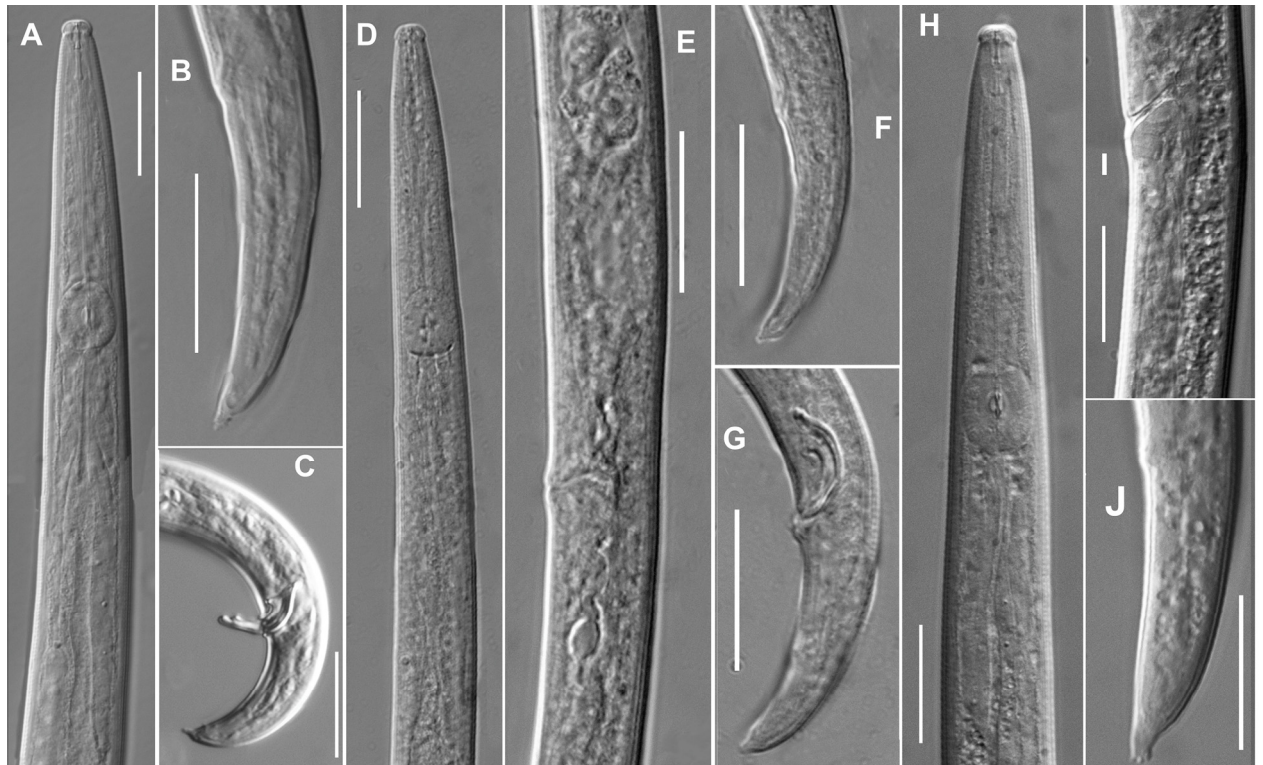


Figure S4: Anterior body end, male and female tails. A-C – *Aphelenchoides* sp.1 (CD3645); D-G – *Aphelenchoides heidelbergi* (CD3663); H-J – *Laimaphelenchus* sp1. (CD3674). Scale - 20 μ m.



Figure S5: Anterior body end, male and female tails. A-C – *Bursaphelenchus fraudulentus* (CD3644); D-F – *B. eremus* (CD2936); G-I - *B. mucronatus* (CD3642). Scale - 20 μ m.

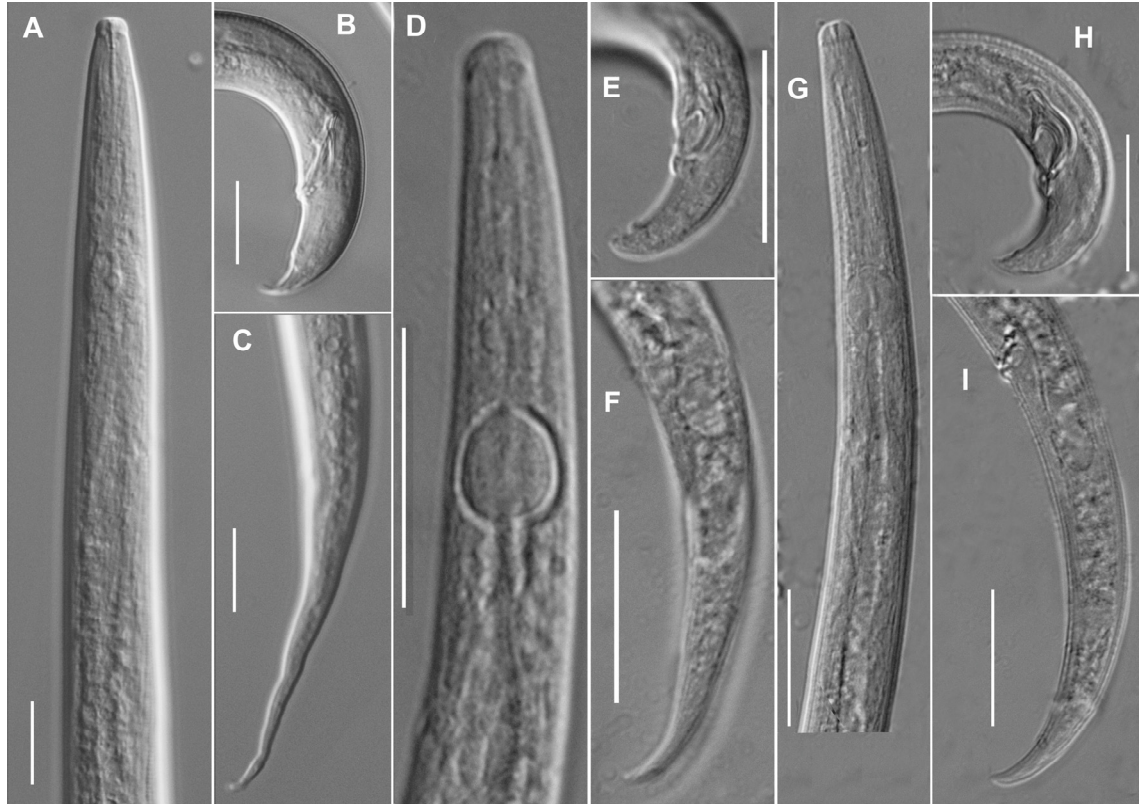


Figure S6: Anterior body end, male and female tails. A-C – *Bursaphelenchus willibaldi* (CD3664); D-F – *Cryptaphelenchus* sp.3 (CD3658); G-I – *Cryptaphelenchus* sp.1 (CD3655). Scale - 20 μm.