

57. ON THE EVOLUTION OF THE PHYLUM NEMATODA

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Phylogenetic trees were constructed for the phylum Nematoda using the (nearly) full-length small subunit (SSU) rDNA sequences (~1700 bp) of 341 nematode species. The trees were constructed using neighbor-joining, maximum parsimony and Bayesian methods. Five major clades could be reconstructed with a good resolution between and –except for the Dorylaimida – within these clades. For the order Dorylaimida, separate trees were constructed using partial large subunit (LSU) rDNA sequences (~1050 bp). These trees showed that well-represented dorylaimid families often were paraphyletic. A closer analysis of the SSU trees revealed there was a large difference in relative evolutionary rates between the different clades. The younger clades (including *e.g.* the Rhabditidae and Tylenchida) evolved at a rate that could be twice as high as that of the older clades (including *e.g.* the Enoplida and Dorylaimida). Tests showed this difference to be highly significant. The development of plant feeding and fungal feeding during evolution appeared to be correlated with each other. We looked whether the hypothesis that plant was derived from fungal feeding could be corroborated with our tree. Plotting the feeding types in our tree revealed that this was likely to be the case for the Tylenchida and Aphelenchida. The plant feeding Longidoridae and Trichodoridae were also closely associated with fungal feeders, but it could not be inferred with certainty whether the ancestors of these families were likely to be fungal feeders.