P501

The Systematics and Molecular Evolution of the Korean Desmodorid Nematodes

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A systematic study was carried out on the desmodorid nematodes. The specimens were collected from the intertidal and shallow subtidal zones at 86 localities in South Korea during the period from May, 1995 to February, 2004. As a result of the study, 37 species belonging to 13 genera of 2 families were identified and classified, of which 35 species turned out to be new species: *Draconema* n. sp. 1, *Draconema* n. sp. 2, *Draconema* n. sp. 3, Draconematinae n. gen. and n. sp., *Paradraconema* n. sp. 1, *Paradraconema* n. sp. 2, *Paradraconema* n. sp. 3, *Dracograllus* n. sp. 1, *Dracograllus* n. sp. 2, *Dracograllus* n. sp. 3, *Dracograllus* n. sp. 4, *Dracograllus* n. sp. 5, *Dracograllus* n. sp. 6, *Tenuidraconema* n. sp. 1, *Tenuidraconema* n. sp. 2, *Tenuidraconema* n. sp. 3, *Dinetia orientalis* n. sp. 1, *Dinetia* n. sp. 2, *Dinetia* n. sp. 3, *Dracogalerus* n. sp., *Notochaetosoma* n. sp. 1, *Notochaetosoma* n. sp. 2, *Notochaetosoma* n. sp. 3, *Prochaetosoma* n. sp. 1, *Prochaetosoma* n. sp. 2, *Prochaetosoma* n. sp. 3, *Prochaetosoma* n. sp. 4, *Prochaetosoma* n. sp. 5, *Prochaetosoma* n. sp. 6, *Prochaetosoma* n. sp. 7, *Prochaetosoma* n. sp. 8, *Bathyepsilonema* n. sp., *Epsilonema* n. sp., *Leptepsilonema* n. sp., and *Metaglochinema* n. sp., and the following 2 species were new to Korean fauna: *Draconema japonicum* Kito, 1976 and *Dracograllus filipjevi* Allen and Noffsinger, 1978. The keys to all 37 species and higher taxa were provided, and all 37 species were fully described and illustrated. Thirty-five species of total 37 species are tentatively endemic to Korea. The zoogeographical distributions of desmodorid nematofauna are briefly discussed. The molecular evolution of desmodorid nematodes was examined on the basis of the comparison of nearly complete 18S ribosomal DNA sequences. To unravel the phylogenetic position of order Desmodorida within the phylum Nematoda and the relationships among its families and genera, 12 sequences from two orders were determined by direct PCR sequencing techniques. In addition, sequences of 72 species from NCBI were also used in the analysis. Three different methods of phylogenetic reconstruction (maximum parsimony, neighbor-joining and maximum likelihood) showed strong supports for the monophyly of order Desmodorida. This phylogenetic results showed congruence with the traditional monophyletic scheme of order Desmodorida based on morphological characters. In attempt to focus on relationships within the order Desmodorida, restrict analyses of the 24 desmodorid nematodes sequences only were performed with the enoplid nematodes *Enoplus brevis* and *E. meridionale* as outgroups. The phylogenetic tree suggests that the family Desmodoridae is not monophyletic. This result is well accorded with the traditional taxonomic system based on the morphological characters. All members of the family Draconematidae were grouped together as a monophyletic group. This result is well accorded with the views of traditional classification scheme. However, three phylogenetic methods showed that *Epsilonema* sp. of the family Epsilonematidae occupied a well-supported basal position, being inconsistent with morphology-based traditional classification system. In traditional views, the Epsilonematidae has been regarded as a sister group of the family Draconematidae based on the synapomorphic character, such as the presence of ambulatory setae (=stilt setae). To examine the utility of 18S rDNA sequences as a diagnostic molecular marker, thirteen 18S rDNA sequences also were selected and analyzed from the marine desmodorid nematodes (*Paradraconema* n. sp. 1, *Paradraconema* n. sp. 3, *Dracograllus* n. sp. 1, *Dracograllus* n. sp. 5, *Prochaetosoma* n. sp. 1, *Prochaetosoma* n. sp. 2, *Prochaetosoma* n. sp. 4, *Prochaetosoma* n. sp. 7, *Eubostrichus dianae, Eubostrichus parasitiferus, Eubostrichus topiaries, Laxus cosmopolitus, Laxus oneistus*). The inter-specific and intra-specific variation in the sequences of 18S ribosomal DNA was examined among the closely related marine nematodes, which are very similar each other morphologically. 18S rDNA sequence differences between species of different genera ranged from 2.1% to 8.7% and congeneric species differed by 0.2% to 6.2%. There was some variation among genera: 18S rDNA sequence differences among species of *Prochaetosoma* (maximum of 1.0% and minimum of 0.2%) were somewhat less than those among *Eubostrichus* species (maximum of 6.2% and minimum of 3.9%), although there were no significant patterns in divergence of the species among the five genera. According to the results of the analysis on the genetic divergence of desmodorid nematodes, especially *Dracograllus* species, 18S rDNA sequences were 100% identical for the individuals within a conspecific desmodorid nematodes, that is, no intra-specific genetic variation were detected. As a result of the present analysis on the utility of 18S rDNA sequences as a diagnostic molecular marker, we cautiously propose that the 18S rDNA sequence divergence is a good diagnostic molecular marker to identify and discriminate the closely related marine desmodorid nematodes.