Myriapoda Phylogeny Based on Nuclear Protein-coding Genes*

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Recent molecular phylogenetic analyses have suggested that myriapods form a monophyletic clade within the phylum Arthropoda and that the four myriapod classes (Chilopoda, Diplopoda, Pauropoda and Symphyla) are also monophyletic respectively. However, their class- and ordinal- level relationships remain unclear. Within morphology-based studies, some results suggest that Diplopoda, Pauropoda and Symphyla form a monophyletic clade (Progoneata), but others do not. In addition morphology-based studies agree that Diplopoda and Pauropoda form a sister clade (Dignatha), while recent molecular-based analyses suggest that Pauropoda is sister to Symphyla. To reveal the phylogenetic relationships among myriapod classes and orders, we sequenced three nuclear protein-coding genes, the catalytic subunit of DNA polymerase delta (DPD1) and the largest and second largest subunits of RNA polymerase II (RPB1 and RPB2) from 19

myriapods representing the four classes (17 orders) and 11 outgroup species. Phylogenetic analyses were performed based on amino acid sequences of the three genes with maximum likelihood (ML) on RAxML and Bayesian inference (BI) on MrBayes. Our results provided strong support for the monophyly of Monomalata composed of Chilopoda, Diplopoda and Pauropoda (Sharov, 1966), suggesting that Symphyla is the sister lineage to all other myriapods. The interordinal relationships within classes were consistent with traditional classification. Our divergence time estimation showed that the split between Symphyla and Monomalata might go back to the early Cambrian. This would imply that the water-to-land transition of myriapods occurred on more than one lineage, because it has been considered that the colonization of land by plants occurred in the Middle Ordovician, and after that animals were adapted to life on land.

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