

Hexapod Phylogeny based on Three Nuclear Protein-coding Genes*

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Hexapods are the most diverse group of contemporary animals in the world. Phylogenetic relationships are the most important information for understanding of the diversity and evolution of hexapods. Many attempts to resolve the phylogenetic relationships of higher groups of hexapods have been made based on both morphological and molecular evidence; nonetheless the interordinal relationships of hexapods remain unclear or are controversial. We have performed phylogenetic analyses of Hexapoda based on the protein sequences of three orthologous nuclear genes encoding the catalytic subunit of DNA polymerase delta (DPD1) and the largest and second largest subunits of RNA polymerase II (RPB1 and RPB2) from 64 species including 55 representatives of all hexapod orders, 6 crustaceans, 1 myriapod and 2 chelicerates. As a result, Ectognatha, Palaeoptera, Neoptera, Polyneoptera, and Holometabola were each confirmed to be monophyletic with robust support, but monophyly was not supported for Entognatha (Protura + Collembola + Diplura), Ellipura (Protura + Collembola), or Nonoculata (Protura + Diplura). Instead, our results showed that Protura is the sister lineage to all other hexapods and that

Diplura or Diplura + Collembola is closely related to Ectognatha, suggesting the paraphyly of Entognatha. It may be worthy to emphasize that our results provided the first molecular evidence to strongly support the monophyly of Polyneoptera. In addition, the dataset allowed almost complete elucidation of the interordinal phylogenetic relationships of holometabolous insects. Therefore, the use of the amino acid sequences of these nuclear genes is clearly an effective approach for resolving the relationships of higher groups of hexapods, and probably can be considered for phylogenetic analyses of other arthropod groups.

References

- Ishiwata K., G. Sasaki, J. Ogawa, T. Miyata and Z.-H. Su (2011)
Phylogenetic relationships among insect orders based on three nuclear protein-coding gene sequences. *Molecular Phylogenetics and Evolution*, **58**, 169–180.
- Sasaki G., K. Ishiwata, R. Machida, T. Miyata and Z.-H. Su (2013)
Molecular phylogenetic analyses support the monophyly of Hexapoda and suggest the paraphyly of Entognatha. *BMC Evolutionary Biology*, **13**, 236.

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