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Knowledge of phylogeny is of fundamental importance in evolutionary studies, from the reconstruction of the Tree of Life to revealing and understanding the laws of body plan formation (the evo-devo realm) and to describing the patterns and processes of microevolution. The discipline of phylogenetics has evolved radically in the new millennium, capitalizing on theoretical and methodological breakthroughs in analysis and algorithms, on the exponential increase in molecular data, and on the availability of vast computing power to enter the phylogenomic era. An integral part of contemporary phylogenetics is the development of mathematical models and effective algorithmic solutions to tackle high-complexity computational problems of building evolutionary scenarios across the levels from genes to species, bioinformatics of next-generation sequencing data, and metagenomic assays. A solid methodological framework of phylogenomic analysis is emerging, applying data derived from whole genomes to problems in deep phylogeny, functional genomics, speciation and divergence, large-scale biodiversity studies, and phylogeography. The mission of the 5th Moscow International Conference “Molecular Phylogenetics and Biodiversity Biobanking” (MolPhy-5) is to provide a stimulating platform for the exchange of ideas and experiences in contemporary phylogenetics, evolutionary genomics and conceptually integrated disciplines. This round the program also places emphasis on genomics of biodiversity and aspects of utilizing molecular data for biodiversity research. The acknowledged focus is to bridge new fundamental knowledge with various applications of phylogenetics in metagenomics, barcoding of biological objects, molecular ecology, and epidemiology.

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## Orthonectida and Dicyemida: Two stories of body plan simplification

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Orthonectida and Dicyemida are marine invertebrate parasites with extremely simplified morphological organization. They were previously (in the XIX century) considered as Mesozoa — a transitional link between protists and multicellular animals. With the advent of molecular data, the orthonectids and dicyemids have been firmly placed within Spiralia or Lophotrochozoa; however, the exact phylogeny of the Mesozoan taxa remains difficult to solve even with genomic [1] or transcriptomic data [2] due to the extreme sequence divergence. Some reports recognize monophyly of the “Mesozoa” [2], others reject it [3]. In our 450 gene phylogeny and mitochondrial genome analyses, we have found that Orthonectida and Dicyemida emerged independently within the Lophotrochozoa, with the orthonectids appearing within the crown annelids, and dicyemids as an isolated branch of lophotrochozoans, confirming earlier analyses [3]. The site-heterogeneous substitution model (CAT) is necessary for resolving the orthonectids within the annelid assemblage. In mitochondrial genome analyses, Orthonectida groups with a crown annelid *Lobatocerebrum* sp. Orthonectids are among the taxa that were previously considered as separate phyla or classes (Echiura, Sipuncula, Pogonophora, Vestimentifera, Myzostomida, Lobatocerebridae, and *Diurodrilus*) but are now seen as deviant annelids. Dicyemida do not group with Orthonectida or other Annelida, which suggests that Mesozoa is a polyphyletic taxon.

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