

Title

Processing rotifer sequences for phylogenetic analysis and unraveling evolutionary relationships

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Abstract

Rotifers make up a phylum of microscopic and near-microscopic invertebrate animals. These aquatic organisms have long captivated researchers with their unique biology and ecological significance. In recent times, advancements in the field of molecular biology have opened new avenues for gaining a better understanding of the evolutionary past of these animals, but rotifers still lack resolved phylogenies at most taxonomic levels. To reconstruct the evolutionary relationships among rotifer species, genetic biomarkers are used. To isolate these biomarkers DNA extraction and sequencing are used. High-throughput sequencing has revolutionized the field by providing extensive genetic data from various rotifer species, primarily targeting genetic markers such as nuclear 18S rRNA and internal transcribed spacer regions and mitochondrial COI. Alignment algorithms are then employed to align sequences, facilitating the comparison of genetic variation and shared ancestry among species. Phylogenetic trees are constructed using various inference methods, such as maximum likelihood and Bayesian analysis to estimate the evolutionary relationships among rotifers. The resulting phylogenetic trees offer insights into the evolutionary history, biogeography, and diversification of rotifers, shedding light on their adaptation to various environments and ecological roles. Here we developed a simple Python script to facilitate a rigorous quality control process, including trimming, filtering, and error correction. This script was used in processing the 146 sequencing results to ensure reliable downstream results.