Title

Identifying UCEs for Stepwise Phylogenetic Analysis of Gnesiotrocha and Ploima Rotifers

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Abstract

Rotifers play a vital ecological role in freshwater systems, yet their phylogenetic relationships remain largely unresolved due to the limitations of traditional genetic markers like 18S RNA and COI. This study leverages the power of Ultra-Conserved Elements (UCEs) to provide a more refined understanding of rotifer evolution. We employed a novel, stepwise approach to UCE identification, analyzing the entire rotifer group of 15 species before conducting subgroup-specific investigations on Gnesiotrocha (3 species) and Ploima (12 species). Gnesiotrocha represents one of the most morphologically diverse rotifer groups, while Ploima encompasses a wide range of species critical to ecosystem functioning. By performing separate analyses on these two subgroups, we aimed to uncover conserved loci that may have been overlooked in broader analyses. Using the Phyluce software package, we identified 2,323 conserved loci and 10,134 probes across all rotifers. Further analysis revealed 2,230 loci in Gnesiotrocha and 199 loci in Ploima, showcasing the enhanced phylogenetic resolution achieved through targeted subgroup analysis. Our findings underscore the importance of using subgroup-specific UCE analysis to capture the complexity of rotifer evolution and suggest that this approach can serve as a valuable framework for future studies on other invertebrate lineages.