

Title

Identifying UCEs to design baits for phylogenetic analysis of monogonont rotifers

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Abstract

Rotifers, the microscopic invertebrates, play essential roles in freshwater ecosystems. With approximately 2,200 known species and many more awaiting discovery, comprehending the genetic diversity and evolutionary history of rotifers poses a daunting challenge with past attempts using traditional genes (e.g., 18S RNA, COI) resulting in an unresolved phylogeny of the phylum. In this study, we harness the power of Ultra-Conserved Elements (UCEs) as indispensable molecular markers. These highly conserved DNA sequences transcend species boundaries, offering a promising avenue for unraveling the intricate genetic landscape of rotifers. Our goal is to revolutionize rotifer species identification and clarify evolutionary relationships. To identify the UCEs, we employed the versatile Phyluce software package, known for its comprehensive workflow that encompasses preprocessing, aligning the base genome, conserved locus identification, conserved locus validation, and final bait design. This workflow seamlessly identifies and processes UCEs, unveiling their pivotal role in our research. Beyond identification, Phyluce's bioinformatics tools empowered us to pinpoint target loci of UCEs with precision. In our study encompassing 15 rotifer species, we successfully identified a total of 258 target loci. These target loci will serve as the foundation upon which we will design baits—customized sequences for capturing UCE loci. This crucial step represents a strategic leap forward in our exploration of rotifer species complexity.