

Publication

A fossil-calibrated phylogenomic analysis of *Daphnia* and the Daphniidae**JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 4524515**Author(s)** Cornetti, Luca; Fields, Peter D.; Van Damme, Kay; Ebert, Dieter**Author(s) at UniBasel** [Ebert, Dieter](#) ;**Year** 2019**Title** A fossil-calibrated phylogenomic analysis of *Daphnia* and the Daphniidae**Journal** Molecular Phylogenetics and Evolution**Volume** 137**Pages / Article-Number** 250-262**Keywords** Substitution rates; Fossil records; Tree discrepancy; Gene tree vs species tree; *Daphnia magna*; *Daphnia pulex***Mesh terms** Science & TechnologyLife Sciences & BiomedicineBiochemistry & Molecular BiologyEvolutionary BiologyGenetics & HeredityBiochemistry & Molecular BiologyEvolutionary BiologyGenetics & Heredity

In the post-genomic era, much of phylogenetic analyses still relies on mitochondrial DNA, either alone or in combination with few nuclear genes. Although this approach often makes it possible to construct well-supported trees, it is limited because mtDNA describes the history of a single locus, and nuclear phylogenies based on a few loci may be biased, leading to inaccurate tree topologies and biased estimations of species divergence time. In this study, we perform a phylogenomic analysis of the Daphniidae family (Crustacea: Branchiopoda: Anomopoda) including some of the most frequently studied model organisms (*Daphnia magna* and *D. pulex*) whose phylogenetic relationships have been based primarily on an assessment of a few mtDNA genes. Using high-throughput sequencing, we were able to assemble 38 whole mitochondrial genomes and draft nuclear genomes for 18 species, including at least one species for each known genus of the family Daphniidae. Here we present phylogenies based on 636 nuclear single-copy genes shared among all sampled taxa and based on whole mtDNA genomes. The phylogenies we obtained were highly supported and showed some discrepancies between nuclear and mtDNA based trees at deeper nodes. We also identified a new candidate sister lineage of *Daphnia magna*. Our time-calibrated genomic trees, which we constructed using both fossil records and substitution rates, yielded very different estimates of branching event times compared to those based on mtDNA. By providing multi-locus, fossil-calibrated trees of the Daphniidae, our study contributes to an improved phylogenetic framework for ecological and evolutionary studies that use water fleas as a model system.

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