

Cost-efficient population genomic investigation of *Daphnia longispina* complex resting eggs using whole genome amplification and pre-sequencing screening

Jana Nickel¹ and Mathilde Cordellier¹

¹Universität Hamburg

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Abstract

Resting stages of aquatic organisms that accumulate in the sediment over time are an exceptional resource that allows direct insights into past populations and addressing evolutionary questions. This is of particular interest in taxa that have recently faced environmental changes such as the *Daphnia longispina* species complex, a keystone zooplankton group in European freshwater ecosystems. However, genomic analysis might be challenging as many of these resting stages are very small and the DNA might be degraded. To reliably allow the resequencing of single *Daphnia* resting eggs from different sediment layers and characterize genomic changes through time, we performed whole genome amplification to obtain DNA amounts suitable for genome re-sequencing and tested multiple protocols involving egg isolation, whole genome amplification kits and library preparation. A pre-sequencing contamination screening was developed to quickly assess possible contamination. In total, we successfully amplified and sequenced nine genomes from *Daphnia* resting eggs that could be identified as *Daphnia longispina* species. We analyzed the genome coverage and SNP calling of these samples to optimize this method for future projects involving population genomic investigation of the resting egg bank.

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