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GENOME SEQUENCING

The Complete Genome Sequences of 2 Species of Geukensia (Brachidontinae, Mytilidae)

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Biodiversity Genomes

We present the complete genome sequences of *Geukensia demissa* and *Geukensia granosissima*. Illumina sequencing was performed on genetic material from museum specimens. The reads were assembled using a de novo method followed by a finishing step. The raw and assembled data are available via Genbank.

Introduction

The two extant species of Geukensia are marine bivalve molluscs in the family Mytilidae found in the western Atlantic. We present the assembled genomes of both species from this genus. Tissues were obtained from ethanol-preserved Georgia Museum of Natural History specimens (*G. granosissima*, GMNH-GTIC-14307; *G. demissa*, GMNH-GTIC-14308). Genomic resources for these mussels are of value because they are highly divergent from the genomes of the more commonly-studied Mytilus mussels (Audino, Serb, and Marian 2020), and Geukensia itself plays an important role in maintenance of western Atlantic salt marsh ecosystems (Angelini et al. 2016).

Methods

DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard protocol. A paired-end sequencing library was constructed for each specimen using the Illumina TruSeq kit according to the manufacturer's instructions. The libraries were sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150 bp format. The resulting fastq files were trimmed of adapter/primer sequence and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v2.5 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021).

Results and Data Availability

All data, including raw reads and assembled genome sequence, is available via Genbank. We note that de novo transcriptomic data are also now available for *G. demissa* (Erlenbach and Wares 2023).

Geukensia demissa JARWCS000000000

Geukensia granosissima JAULBM000000000

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