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GENOME SEQUENCING

The Complete Genome Sequence of the Moroccan endemic plant *Artemisia ifranensis* (Asteraceae, Asterales)

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Biodiversity Genomes

We present the whole genome sequence of *Artemisia ifranensis*, an endemic species to Morocco. Illumina paired-end reads were assembled by a de novo method followed by a finishing step. The raw and assembled data are publicly available via GenBank: Sequence Read Archive (SRR28896299) and assembled genome (JBEUCH000000000).

Methods

A single wild-collected specimen from the Middle Atlas in Morocco was used for sequencing. DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard process. A paired-end sequencing library was constructed using the Illumina TruSeq kit according to the manufacturer's instructions. The library was sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150 bp format. The resulting fastq files were trimmed of adapter/primer sequences and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v2.5 (Bankevich, Nurk, Antipov, et al. 2012) followed by a finishing step using Zanfona v1.0 (Kieras 2021) to make additional contig joins based on conserved regions in related species.

Data availability

Raw and assembled data are publicly available via GenBank.

taxname	raw_reads	assembled_genome
Artemisia ifranensis (TaxID:1903206)	SRR28896299	JBEUCH000000000

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