

GENOME SEQUENCING

The Complete Genome Sequences of Carludovica palmata Ruiz & Pavón and C. drudei Mast.

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Biodiversity Genomes

We present the complete genome sequences of Carludovica palmata Ruiz & Pavón and C. drudei Mast., which are pseudopalms used to weave Panama hats.

Methods

An individual seedling derived from *in vitro* culture of each species was used to extract genomic DNA using a commercially available kit (DNeasy Plant Mini kit, Qiagen) following the manufacturer's protocol. Paired-end sequencing libraries were prepared with the Illumina TruSeq kit according to the manufacturer's instructions and subsequently sequenced on an Illumina NovaSeq 6000 platform in paired-end mode (format 2×150 bp). During assembly, the resulting FASTQ files were uploaded to the Huitzilin high-performance computing cluster (INECOL), where adapter and primer sequences, as well as low-quality regions, were removed using fastp v0.23.4 (Chen et al. 2018). High-quality paired-end reads were then assembled with SPAdes v3.13.0 (Bankevich et al. 2012).

Results and Data Availability

Taxname	Accession
Carludovica palmata Ruiz & Pavón	PRJNA1314624
Carludovica drudei Mast.	PRJNA1356871

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