

GENOME SEQUENCING

The Complete Genome Sequence of *Ginkgo biloba* (Ginkgoaceae, Ginkgoales), the Maidenhair Tree

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Biodiversity Genomes

Ginkgo biloba is the only extant member of the order Ginkgoales. Fossils similar to this species extend back to the Middle Jurassic approximately 170 million years ago. Ginkgo trees are native to deciduous forests in China but are cultivated throughout North America, Europe, and Asia. We present the whole genome sequence of this species. Illumina sequencing was performed on a leaf tissue sample from a single cultivated plant. The reads were assembled using a de novo method followed by a series of references from related species for finishing. The raw and assembled data is publicly available via Genbank: Sequence Read Archive (SRR22349630) and Genome Assembly (JANKJI000000000).

Introduction

Ginkgo biloba, commonly known as the maidenhair tree, is native to deciduous forests in China. It is the last living species in the order Ginkgoales, which first appeared over 290 million years ago. The tree was cultivated early in human history and remains commonly planted.

Ginkgos are large trees, normally reaching a height of 20–35 m, with some specimens in China being over 50 m tall. The combination of resistance to disease, insect-resistant wood, and the ability to form aerial roots and sprouts makes ginkgos durable, with some specimens claimed to be more than 2,500 years old. The leaves are unique among seed plants, being fan-shaped with veins radiating out into the leaf blade, sometimes bifurcating. Ginkgo prefers full sun and grows best in environments that are well-watered and well-drained. The species shows a preference for disturbed sites.

Ginkgo leaf extract is commonly used as a dietary supplement, and has been demonstrated to have a medicinal and pharmacological properties (Noor-E-Tabassum et al. 2022).

Methods

Leaf tissue from a single cultivated plant was used for this study. 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 × 150bp 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 et al. 2012) followed by a finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021).

Results and Data Availability

Raw reads and assembled genome sequence are available via Genbank.

The genome assembly yielded a total sequence length of 2,638,059,399 bp and an N50 of 181 Mb.

Raw genome data

https://trace.ncbi.nlm.nih.gov/Traces/?view=run_browser&acc=SRR22349630

Assembled genome

<https://www.ncbi.nlm.nih.gov/nucleotide/JANKJI000000000>

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