

GENOME SEQUENCING

The Complete Genome Sequences of *Iris sibirica* and *Iris virginica* (Iridaceae, Asparagales)

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Biodiversity Genomes

We present the complete genome sequences of *Iris sibirica* and *Iris virginica*. Illumina sequencing was performed on genetic material from individual cultivated specimens. The reads were assembled using a *de novo* method followed by a finishing step. The raw and assembled data are publicly available via Genbank.

Introduction

The genus *Iris* contains ~310 species (IPNI 2023). The species in this genus are perennial plants, growing from creeping rhizomes or bulbs. They are often large and colorful, and commonly grown as decorative garden plants. We present the assembled genome sequences from 2 species. Tissue samples were obtained from individual cultivated specimens.

Methods

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 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

Assembled genome sequences are available via Genbank.

<i>Iris sibirica</i>	JAOTRK000000000
<i>Iris virginica</i>	JAOTQG000000000

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