

GENOME SEQUENCING

The Complete Genome Sequence of *Polystichum acrostichoides* (Dryopteridaceae, Polypodiales)

Sana Raoui^{1,2}, Stacy Pirro³, Saaïd Amzazi², Hassan Ghazal^{1,4}

¹ Laboratory of Genomics and Bioinformatics, Faculty of Pharmacy, Mohammed VI University of Health Sciences, ² Laboratory of Human Pathologies Biology, Department of Biology, Mohammed V University, ³ Biodiversity, Iridian Genomes, ⁴ National Center for Scientific and Technical Research

Keywords: fern, genome, assembly

<https://doi.org/10.56179/001c.55604>

Biodiversity Genomes

Polystichum acrostichoides is a perennial, evergreen fern, commonly found in woodlands, stream banks, and rocky slopes in eastern North America. We present the whole genome sequence of this species. Illumina sequencing was performed on a leaf tissue sample from a single plant collected in Maryland, USA. The reads were assembled using a *de novo* method followed by a finishing step using series of references from related species. The raw and assembled data are publicly available via GenBank: Sequence Read Archive (SRR18053988) and Genome Assembly (JAOYMV000000000).

Introduction

Polystichum acrostichoides is a perennial, evergreen fern native to eastern North America, from Nova Scotia west to Minnesota and south to Florida and eastern Texas. It is one of the most common ferns in eastern North America, being found in moist and shady habitats in woodlands, stream banks and rocky slopes. This species has a tufted, clumping habit, with its fronds arising from a central growth point.

Methods

Leaf tissue from a single plant collected in Maryland, USA 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

The genome assembly yielded a total sequence length of 450,652,285 bp.

Raw genome data

https://trace.ncbi.nlm.nih.gov/Traces/?view=run_browser&acc=SRR18053988

Assembled genome

<https://www.ncbi.nlm.nih.gov/nuccore/JAOYMV000000000>

Funding

Funding was provided by Iridian Genomes, grant# IRGEN_RG_2021-1345 Genomic Studies of Eukaryotic Taxa.

Submitted: October 25, 2022 EST, Accepted: November 12, 2022 EST



This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International License (CCBY-SA-4.0). View this license's legal deed at <https://creativecommons.org/licenses/by-sa/4.0> and legal code at <https://creativecommons.org/licenses/by-sa/4.0/legalcode> for more information.

REFERENCES

- Bankevich, Anton, Sergey Nurk, Dmitry Antipov, Alexey A. Gurevich, Mikhail Dvorkin, Alexander S. Kulikov, Valery M. Lesin, et al. 2012. “SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing.” *Journal of Computational Biology* 19 (5): 455–77. <https://doi.org/10.1089/cmb.2012.0021>.
- Bolger, Anthony M., Marc Lohse, and Bjoern Usadel. 2014. “Trimmomatic: A Flexible Trimmer for Illumina Sequence Data.” *Bioinformatics* 30 (15): 2114–20. <https://doi.org/10.1093/bioinformatics/btu170>.
- Kieras, M., K. O’Neill, and S. Pirro. 2021. *Zanfona, a genome assembly finishing tool for paired-end Illumina reads*. <https://github.com/zanfona734/zanfona>.