

GENOME SEQUENCING

The Complete Genome Sequences of Four Species of *Adansonia* (Malvaceae, Malvales)

Stephen Woods¹, Stacy Pirro²

¹ California Baobabs, Simi Valley, CA, ² Iridian Genomes

<https://doi.org/10.56179/001c.136969>

Biodiversity Genomes

We present the complete genome sequences of four species of Baobabs: *Adansonia grandidieri*, *Adansonia gregorii*, *Adansonia madagascariensis*, *Adansonia rubrostipa*. Illumina sequencing was performed on DNA extracted from single leaves. The reads were assembled using a *de novo* method followed by a finishing step. The raw data and assembled genomes are available in Genbank.

Methods

Single leaves from trees grown from wild-collected seeds were sampled. DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard protocol. 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

All data is available via Genbank.

taxname	raw_reads	assembled_genome
<i>Adansonia grandidieri</i>	SRR28509440	JBBYHK000000000
<i>Adansonia gregorii</i>	SRR28509443	JBBYHO000000000
<i>Adansonia madagascariensis</i>	SRR28509442	JBBYHL000000000
<i>Adansonia rubrostipa</i>	SRR28509441	JBBYHM000000000

Funding

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

Submitted: April 18, 2025 EDT. Accepted: April 24, 2025 EDT. Published: April 24, 2025 EDT.

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>.