

GENOME SEQUENCING

# The Complete Genome Sequences of two Species of Stegodyphus Spiders (Araneae: Eresidae)

Timothy J. Colston<sup>1,2</sup>, Steven T. Cassidy<sup>3</sup>, Kara J. M. Taylor<sup>4</sup>, Stacy Pirro<sup>5</sup>, Martha Haufiku<sup>6</sup>, Tresia Kavili<sup>7</sup>, Seth J. Eiseb<sup>7</sup>, Carl N. Keiser<sup>4</sup>

<sup>1</sup> Biology Department, University of Puerto Rico at Mayaguez, <sup>2</sup> Genomic Resources Collection, University of Puerto Rico at Mayaguez, <sup>3</sup> Department of Biology, University of Florida, Gainesville, FL, <sup>4</sup> Department of Biology, University of Florida, Gainesville, FL, 32611, <sup>5</sup> Iridian Genomes, <sup>6</sup> 5. Department of Environmental Science, University of Namibia, Windhoek, Namibia, <sup>7</sup> Department of Environmental Science, University of Namibia, Windhoek, Namibia

<https://doi.org/10.56179/001c.123740>

---

## Biodiversity Genomes

---

We present the complete genome sequences of *Stegodyphus bicolor* and *Stegodyphus dumicola*. Illumina sequencing was performed on genetic material from specimens collected in Namibia in March 2023. The reads were assembled using a *de novo* method followed by a finishing step. The raw and assembled data are publicly available via Genbank.

## Methods

DNA extraction was performed using the Qiagen DNeasy genomic extraction kit using the standard protocol. A paired-end sequencing library was constructed for each specimen using the Illumina TruSeq kit according to the manufacturer's instructions. The libraries were 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

Genome data is available through Genbank:

Species	Genome record
<i>Stegodyphus bicolor</i>	JBFSWU000000000
<i>Stegodyphus dumicola</i>	JBFSWV000000000

Specimen information can be found at Spider Parasite Digital Research Collection. Occurrence dataset (ID: 8be51fa1-6dec-44d6-9e3b-a748c7463c45) <https://ecdysis.org/collections/misc/collprofiles.php?collid=93>.

.....

## ***Funding***

Funding for genome sequencing was provided by Iridian Genomes, grant# IRGEN\_RG\_2021-1345 Genomic Studies of Eukaryotic Taxa. Specimen collection was funded by the Department of Biology at the University of Florida (Research/export permits: RCIV00022018, Authorization 202302008, from the Namibia National Commission on Research, Science, and Technology).

Submitted: September 01, 2024 EDT, Accepted: September 16, 2024 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>.