Sprute, Max, Stacy Pirro, Klaus Koepfli, et al. 2026. "Complete Genome Sequence of Laguna Mountains Skipper (*Pyrgus Ruralis Lagunae*)." *Biodiversity Genomes*, May 28. https://doi.org/10.56179/001c.162600.

GENOME SEQUENCING

Complete Genome Sequence of Laguna Mountains Skipper (*Pyrgus ruralis lagunae*)

Max Sprute[1], Stacy Pirro[2], Klaus Koepfli[3], Travis Longcore[1,4], Kendall H. Osborne[5], Tyler Wilson[1], Paige Howorth[6], Jana Johnson[7]

[1] The Urban Wildlands Group, [2] Iridian Genomes, [3] Colossal Biosciences, [4] UCLA Institute of the Environment and Sustainability, [5] Osborne Biological Consulting, [6] San Diego Zoo, [7] Moorpark College (The Teaching Zoo)

https://doi.org/10.56179/001c.162600

Biodiversity Genomes

A complete genome assembly for the endangered *Pyrgus ruralis lagunae* (Laguna Mountains Skipper) (Scott, 1981) is reported here. Illumina short-read sequencing was performed using tissue from a whole specimen of a single deceased individual. The selected specimen was a foundress individual collected directly from the wild population prior to captive propagation, minimizing the potential influence of captive breeding, genetic drift, or artificial selection on genomic patterns. This reference genome is an important resource for studying this endangered lepidopteran.

Methods

Specimen 1302, a female, was collected from the Laguna Mountains population (33.33028, -116.83775) on 12 May 2013 and was maintained in captivity to establish a captive rearing program conducted through The Endangered Butterfly Project at The Teaching Zoo at Moorpark College (Longcore et al. 2014). This work was conducted in accordance with the U.S. Fish and Wildlife Service Carlsbad Fish and Wildlife Office's subpermit, LOS-3761. Geographical and collection data were recorded for the specimen. Husbandry and captive rearing were housed at The Teaching Zoo at Moorpark College.

DNA extraction was performed using the Qiagen DNEasy genomic extraction kit using the standard process. Paired-end sequencing libraries were constructed 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 × 150bp format. The resulting fastq files were trimmed of adapter/primer sequences and low-quality regions with Trimmomatic v0.33 (Bolger et al. 2014). The trimmed sequence was assembled by SPAdes v3.15.4 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras et al. 2021).

Data availability

taxname	accession
Pyrgus ruralis lagunae	PRJNA1356881

Acknowledgements

The authors are grateful to U.S. Fish and Wildlife Service, California Department of Fish and Wildlife, The Urban Wildlands Group, Osborne Biological Consulting, The Teaching Zoo, Moorpark College, San Diego Zoo, and Iridian Genomes for funding, permitting, housing, and fieldwork that made the captive rearing program and subsequent genomic analysis possible.

Funding

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

Submitted: May 28, 2026 EDT. Accepted: May 28, 2026 EDT. Published: May 28, 2026 EDT.

REFERENCES

Bankevich, Anton, Sergey Nurk, Dmitry Antipov, et al. 2012. "SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing." *Journal of Computational Biology*, ahead of print. 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.

Longcore, T., J. Johnson, and K. Osborne. 2014. *Laguna Mountains Skipper Captive Rearing Report*. The Urban Wildlands Group (USFWS Agreement No. 814307J024).

Scott, J. 1981. "New Hesperiidae from California and New Mexico." *Papilio (New Serioes)* 1: 1–3.