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GENOME SEQUENCING

The complete genome sequence of Apodemia mormo langei, Lange's Metalmark Butterfly

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Biodiversity Genomes

A complete genome assembly for the endangered Apodemia mormo langei (Lange's Metalmark Butterfly) (Comstock, J.A. 1938) is reported here. Illumina short-read sequencing was performed using tissue from 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 presumably extinct dune-endemic butterfly.

Methods

Specimen 1703, a female *Apodemia mormo langei*, was collected from the Antioch Dunes population during the 2017 flight season at 10:02 AM (38.01348, -121.78278) and was maintained in captivity as part of conservation breeding efforts conducted through The Endangered Butterfly Project at The Teaching Zoo at Moorpark College (Johnson et al. 2017). This work was conducted in accordance with applicable federal and state permits # FWSADNWR-1. Letter of Authorization from Fish and Wildlife LOA-06.

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

Apodemia mormo langei	JBYHFJ000000000

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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.

Comstock, J. A. 1938. "A New Race of Apodemia Mormo from California." *Bulletin of the Southern California Academy of Sciences* 37 (2): 91–92.

Johnson, J., T. Wilson, J. Terry, et al. 2017. *Two Year Report: Captive Rearing of Lange's Mealmark Buttrfly, Fall 2015 - Fall 2017*. The Urban Wildlands Group (USFWS Agreement No. 80270-B-G617).

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.