GENOME SEQUENCING

The Complete Genome Sequences of 34 Brush-footed Butterflies (Nymphalidae, Lepidoptera)

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Biodiversity Genomes

We present complete genome sequences of 34 butterflies in the Nymphalidae family.

Methods

Tissues from single, wild-collected individuals were used for this study. 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, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v3.15.4 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021).

Results and Data Availability

All genomes are available on Genbank:

Charaxes varanes	JANCMC000000000
Danaus melanippus	JAAAKD000000000
Dione vanillae	JBCHJV000000000
Doxocopa laurentia	JAOPTZ000000000
Dryas iulia	JBCHJX000000000
Eueides isabella	JBCGHP000000000
Eueides lampeto	JBCGHS000000000
Eueides vibilia	JBCHJZ000000000
Heliconius antiochus	JBCGCW000000000
Heliconius atthis	JBDJHX000000000
Heliconius burneyi	JBCHJY000000000
Heliconius charithonia	JAXGGO000000000
Heliconius clysonymus	JBCGHO000000000
Heliconius congener	JBCGCV000000000
Heliconius demeter	JBCHJW000000000
Heliconius doris	JBCGHR000000000
Heliconius egeria	JBCGHQ000000000
Heliconius eleuchia	JBCGHN000000000
Heliconius elevatus	JBCGHU000000000
Heliconius eratosignis	JBCHVV000000000

Heliconius hewitsoni	JBCHKA000000000
Heliconius leucadia	JBCHVU000000000
Heliconius numata	JBCHWA000000000
Heliconius pardalinus	JBCHVS000000000
Heliconius peruvianus	JBCHVZ000000000
Heliconius sapho	JBCHVT000000000
Heliconius sara	JBCHVQ000000000
Heliconius timareta	JBDJHW000000000
Heliconius wallacei	JBCHVR000000000
Heliconius xanthocles	JBCHVX000000000
Hypolimnas misippus	JAOPJQ000000000
Junonia oenone	JAPEIZ000000000
Neptis clinioides	JAOPUB000000000
Taenaris catops	WURW00000000

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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.

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Kieras, M., K. O'Neill, and S. Pirro. 2021. "Zanfona, a Genome Assembly Finishing Tool for Paired-End Illumina Reads." 2021. https://github.com/zanfona734/zanfona.