Triant, Deborah, and Stacy Pirro. 2023. "The Complete Genome Sequences of 9 Species of Swallowtail Butterflies (Papilionidae, Lepidoptera)." *Biodiversity Genomes*, March. https://doi.org/10.56179/001c.73927.

GENOME SEQUENCING

The Complete Genome Sequences of 9 Species of Swallowtail Butterflies (Papilionidae, Lepidoptera)

Deborah Triant[1], Stacy Pirro[2]

[1] Department of Biochemistry & Molecular Genetics, University of Virginia, [2] Biodiversity, Iridian Genomes

https://doi.org/10.56179/001c.73927

Biodiversity Genomes

We present the complete genome sequences of 9 species of Papilionidae from 3 genera (Graphium, Ornithoptera, Papilio). Illumina sequencing was performed on genetic material from individual wild-caught specimens. The reads were assembled using a de novo method followed by a finishing step. The raw and assembled data are publicly available via Genbank.

Introduction

The Papilionidae include ~550 extant species in 31 genera (Reed and Sperling 2006). The species in this family are often large and colorful, and can be found on every continent except Antarctica. We present the assembled genome sequences from 9 extant species. Tissue samples were obtained from single wild-caught specimens. More detailed information about the specimen used for each species can be found in the Biosample linked to each genome assembly in Genbank (Table 1).

Methods

DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard process. 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 using default settings (Bolger, Lohse, and Usadel 2014). The trimmed reads were assembled by SPAdes v2.5 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021), with default settings used for both.

Results and Data Availability

Table 1. Assembled genome sequences are available via Genbank.

Species	GenBank Project	Assembly
Graphium colonna	JAOCPS000000000	ASM2550542v1
Graphium doson	WUAN00000000	ASM1404840v2
Graphium evemon	JAOPJC000000000	ASM2577437v1
Ornithoptera priamus	WYDZ00000000	ASM1131775v2
Papilio bianor	JAAOEG000000000	ASM1176362v2
Papilio gigon	JAODUI000000000	ASM2756399v1
Papilio helenus	JAOCNA000000000	ASM2654667v1
Papilio memnon	JAOPJP000000000	ASM2712267v1
Papilio polyxenes	JAOPJD000000000	ASM2616782v1

Funding

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

Submitted: March 24, 2023 EDT, Accepted: March 26, 2023 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.

Reed, Robert D., and Felix A.H. Sperling. 2006. "Papilionidae. The Swallowtail Butterflies. Version 07 July 2006." The Tree of Life Web Project. 2006. http://tolweb.org/Papilionidae/12177/2006.07.07.