

GENOME SEQUENCING

The Complete Genome Sequence of *Actias luna* (Saturniidae, Lepidoptera), the luna moth

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Biodiversity Genomes

Actias luna, the luna moth, is a Nearctic species in the family Saturniidae, the giant silk moths. Known for its large size, bright green wings and elongated tails, it is found in Eastern North America, from east of the Great Plains in the United States, and from Saskatchewan eastward through central Quebec to Nova Scotia in Canada. We present the complete genome sequence of this species. Raw read data and the assembled genome are available in Genbank.

Methods

A single wild-caught specimen was used for this study. 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 × 150bp 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 v1.0 (Kieras 2021) to make additional contig joins based on conserved regions in related species.

Data availability

Raw and assembled data is publicly available via GenBank:

RAW GENOME DATA

https://trace.ncbi.nlm.nih.gov/Traces/?view=run_browser&acc=SRR6873685

ASSEMBLED GENOME

<https://www.ncbi.nlm.nih.gov/nuccore/WUCQ00000000>

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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>.
- 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. 2021. *Zanfona, a genome finishing process for use with paired-end short reads*. <https://github.com/zanfona734/zanfona>.