Procko, Carl, Joanne Chory, and Stacy Pirro. 2023. "The Genome Sequences of 17 Species of Carnivorous Plants." *Biodiversity Genomes*, November. https://doi.org/10.56179/001c.90164.

GENOME SEQUENCING

The Genome Sequences of 17 Species of Carnivorous Plants

Carl Procko[1], Joanne Chory[1,2], Stacy Pirro[3]

[1] Plant Biology Laboratory, Salk Institute for Biological Studies, [2] Howard Hughes Medical Institute, [3] Iridian Genomes

https://doi.org/10.56179/001c.90164

Biodiversity Genomes

We present the genome sequences of 17 species of carnivorous plants. Illumina sequencing was performed on genetic material from cultivated individuals. The reads were assembled using a de novo method followed by a finishing step. The raw and assembled data are available via Genbank.

Introduction

Carnivorous plants derive nutrients from catching and digesting small animals, such as insects and other arthropods. This adaptation allows them to grow in nutrient-poor soils. Strikingly, plant carnivory has at least 11 independent evolutionary origins spread across distantly related genera (Fleischmann et al. 2018; Lin et al. 2021), making them and their genomes useful models for the study of convergent evolution.

Here, we provide genome sequences of carnivorous plants from three different plant orders representing three different evolutionary trajectories to carnivory (Fleischmann et al. 2018). These include trumpet pitcher plants of the order Ericales (including members of each of the genera *Darlingtonia*, *Sarracenia* and *Heliamphora*); butterworts (genus *Pinguicula*) of the order Lamiales; and notable species of the order Caryophyllales, including a species of tropical pitcher plant of the *Nepenthes* genus, sundews of the genus *Drosera*, and the Venus flytrap (*Dionaea muscipula*). The modified leaves of these species represent diverse prey-trapping mechanisms, including adhesive, pitfall and snap traps. In addition to previously published carnivorous plant genomes (for example, Palfalvi et al. 2020; and Gao et al. 2023), these sequences provide a resource to the community to better understand the evolution of these most unusual and charismatic plants.

Methods

DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard protocol. A paired-end sequencing library was constructed for each specimen 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 × 150 bp 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 (Kieras, O'Neill, and Pirro 2021).

Results and Data Availability

All data, including raw reads and assembled genome sequence, is available via Genbank.

Darlingtonia californica	JAUBWS000000000
Dionaea muscipula	JAOWBR000000000
Drosera spatulata	JAOVYX000000000
Drosera tokaiensis	JAOYUI000000000
Heliamphora ciliata	JAUMHN000000000
Heliamphora exappendiculata	JAOTRH000000000
Heliamphora pulchella	JAULJZ000000000
Nepenthes alata	JAOVVI000000000
Pinguicula moranensis	JAOWBN000000000
Pinguicula primuliflora	JAOYMZ000000000
Sarracenia alabamensis	JAULLH000000000
Sarracenia alata	JAPEKV000000000
Sarracenia flava	JAULLH000000000
Sarracenia leucophylla	JAULLG000000000
Sarracenia minor	JAULLD000000000
Sarracenia psittacina	JAUZSS000000000
Sarracenia purpurea	JAULLE000000000

……

Funding

Funding for genome sequencing was provided by Iridian Genomes, grant# IRGEN_RG_2021-1345 Genomic Studies of Eukaryotic Taxa. This work was further supported by National Institutes of Health award 5R35GM122604 (J.C.) and the Howard Hughes Medical Institute (J.C.).

Submitted: November 10, 2023 EST, Accepted: November 14, 2023 EST

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.

Fleischmann, Andreas, Jan Schlauer, Stephen A. Smith, and Thomas J. Givnish. 2018. "Evolution of Carnivory in Angiosperms." In *Carnivorous Plants: Physiology, Ecology, and Evolution*, edited by Aaron Ellison and Lubomir Adamec, 22–41. United Kingdom: Oxford University Press. https://doi.org/10.1093/oso/9780198779841.003.0003.

Gao, Yuan, Hao-Bin Liao, Ting-Hong Liu, Jia-Ming Wu, Zheng-Feng Wang, and Hong-Lin Cao. 2023. "Draft Genome and Transcriptome of Nepenthes Mirabilis, a Carnivorous Plant in China." *BMC Genomic Data* 24 (1): 2110118612863-023-01126–5. https://doi.org/10.1186/s12863-023-01126-5.

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.

Lin, Qianshi, Cécile Ané, Thomas J. Givnish, and Sean W. Graham. 2021. "A New Carnivorous Plant Lineage (*Triantha*) with a Unique Sticky-Inflorescence Trap." *Proceedings of the National Academy of Sciences* 118 (33): e2022724118. https://doi.org/10.1073/pnas.2022724118.

Palfalvi, Gergo, Thomas Hackl, Niklas Terhoeven, Tomoko F. Shibata, Tomoaki Nishiyama, Markus Ankenbrand, Dirk Becker, et al. 2020. "Genomes of the Venus Flytrap and Close Relatives Unveil the Roots of Plant Carnivory." *Current Biology* 30 (12): 2312-2320.e2315. https://doi.org/10.1016/j.cub.2020.04.051.