

GENOME SEQUENCING

The complete genome sequences of three species of Mountain Avens (*Dryas*, Rosaceae)

Dawson White¹, Stacy Pirro²

¹ Negaunee Integrative Research Center, Field Museum, ² Biodiversity, Iridian Genomes

Keywords: dryas, genomes

<https://doi.org/10.56179/001c.40366>

Biodiversity Genomes

We present the whole genome sequences of *Dryas alaskensis*, *D. ajanensis*, and *D. integrifolia* from plants collected from interior Alaska. We performed deep Illumina sequencing of a single leaf of each voucher. The sequence reads were then *de novo* assembled and conserved regions across all preassemblies were used to join contigs in a finishing step. The raw and assembled data is publicly available via Genbank.

Introduction

Mountain Avens (*Dryas* spp. Rosaceae) is a circumpolar genus of about fifteen species of wind-dispersed, self-incompatible dwarf shrubs that are distributed throughout the Arctic and Alpine regions of the northern hemisphere (Springer and Parfitt 2015; <http://www.itis.gov>). *Dryas* is primarily referenced as a classic palynological indicator of past climate (i.e. Younger Dryas stadial). As an abundant and charismatic floristic element of arctic ecosystems, species of *Dryas* are the official plants of the Northwest Territories, Canada and Iceland.

Here we present the first genome assemblies for three species of *Dryas* occurring in interior Alaska. The taxonomy of *Dryas* is in desperate need of taxonomic revision. The nomenclature we use here follows the Flora of North America (Springer and Parfitt 2015).

Dryas alaskensis Porsild (DAL) grows in Alaska and the Yukon Territories and *D. ajanensis* ssp. *beringensis* Jurtzev (DAJ) occurs from the Northwest Territories into Chukotka Autonomous Okrug, Russia. The ecology of DAL and *D. ajanensis* ssp. *beringensis* (DAJ) has been carefully studied to understand how they have persisted in sympatry. The two species are readily distinguished by differences in leaf size and leaf pubescence as well as microhabitat, with DAL occupying moist, 'snowbed' sites and DAJ occupying dry, rocky, exposed, 'fellfield' sites (McGraw and Antonovics 1983). The species have distinct flowering times and significant genetic differentiation as interpreted from allozyme (Max, Mouchaty, and Schwaegerle 1999) and genotyping by sequencing data (Stasinski et al. 2021). The third species, *D. integrifolia* Vahl., is widely distributed in Alaska, Canada, and the Russian far-east.

A genome for the other North American species, *Dryas drummondii* was published in 2018 as part of an investigation into the biology of nitrogen fixation in root nodules (Griesmann et al. 2018). These genome assemblies will add to the growing resources available to study this phenomenon as well as the taxonomy, ecology, evolution, and conservation of *Dryas* plants.

Methods

Leaf tissue from wild plants was extracted using the Qiagen Plant DNAeasy kit according to the manufacturer's instructions. 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 (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

Raw sequence reads and assembled genomes were deposited to Genbank's SRA and Genomes submission pipelines.

species	genome size	N50	SRA	genome
<i>Dryas alaskensis</i>	204,362,168	13.449 KB	SRR14834469	JAOTQX000000000
<i>Dryas integrifolia</i>	211,994,740	15.434 KB	SRR14834464	JAOTRM000000000
<i>Dryas octopetala</i>	228,063,777	11.214 KB	SRR14835741	JAOTQF000000000

Funding

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

Dawson White is supported by the Grainger Bioinformatics Center at the Field Museum and an NSF Postdoctoral Fellowship in Biology, award 2010821.

Submitted: November 04, 2022 EST, Accepted: November 07, 2022 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>.
- Griesmann, Maximilian, Yue Chang, Xin Liu, Yue Song, Georg Haberer, Matthew B. Crook, Benjamin Billault-Penneteau, et al. 2018. “Phylogenomics Reveals Multiple Losses of Nitrogen-Fixing Root Nodule Symbiosis.” *Science* 361 (6398): eaat1743. <https://doi.org/10.1126/science.aat1743>.
- 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>.
- Max, Karen N., Suzette K. Mouchaty, and Kent E. Schwaegerle. 1999. “Allozyme and Morphological Variation in Two Subspecies of *Dryas Octopetala* (Rosaceae) in Alaska.” *American Journal of Botany* 86 (11): 1637–44. <https://doi.org/10.2307/2656800>.
- McGraw, J. B., and J. Antonovics. 1983. “Experimental Ecology of *Dryas Octopetala* Ecotypes: I. Ecotypic Differentiation and Life-Cycle Stages of Selection.” *Journal of Ecology* 71 (3): 879. <https://doi.org/10.2307/2259599>.
- Springer, Joshua C., and Bruce D. Parfitt. 2015. “Dryas.” In *Flora of North America North of Mexico [Online]*, edited by Flora of North America Editorial Committee 1993+. New York and Oxford: Oxford University Press. http://www.efloras.org/florataxon.aspx?flora_id=1&taxon_id=110971.
- Stasinski, Lance, Dawson M. White, Peter R. Nelson, Richard H. Ree, and José Eduardo Meireles. 2021. “Reading Light: Leaf Spectra Capture Fine-scale Diversity of Closely Related, Hybridizing Arctic Shrubs.” *New Phytologist* 232 (6): 2283–94. <https://doi.org/10.1111/nph.17731>.