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GENOME SEQUENCING

The Complete Genome Sequence of *Erigeron philadelphicus,* the Philadelphia Fleabane

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Biodiversity Genomes

The Philadelphia Fleabane (*Erigeron philadelphicus*) is a common flower across North America, growing along roadsides and in fields and woodlands. Each plant has 3 to 35 small daisy-like flowers at the top of the plant. Flowers are 0.5 - 0.8" across, with 150 or more pink to white thread-like petals and a yellow center disk. We present the whole genome sequence of this species. Illumina sequencing was performed on a single leaf from a wild-collected plant. The reads were assembled using a *de novo* method followed by a series of references from related species for finishing. The raw and assembled data is publicly available via Genbank: Sequence Read Archive (SRR13004263) and Assembly (GCA_024320915).

Introduction

The Philadelphia Fleabane (*Erigeron philadelphicus*) is a biennial or short-lived perennial. It is 1 - 2.5' tall and usually unbranched, except toward the inflorescence. Initially, there is a low rosette of basal leaves that disappears when the plant bolts during the spring. The central stem and upper stems are light green, multiangular-terete, and sparsely to moderately covered with spreading white hairs. Alternate leaves occur along the entire length of these stems, becoming smaller in size and more sparse as they ascend. These leaves are up to 3¾" long and 1¼" across; they are ovate, lanceolate, oblanceolate, or narrowly elliptic in shape. The leaf margins are often short-ciliate; upper leaves usually have entire (toothless) margins, while lower leaves are usually sparingly toothed, especially toward their tips. All of these leaves clasp the stems at their bases to a greater or less extent. Both the upper and lower leaf surfaces are light to medium green and sparsely short-pubescent to nearly glabrous. The central stem terminates in a panicle of flowerheads that is somewhat flat-headed. In addition, smaller panicles or clusters of flowerheads may develop from the axils of upper leaves. The branches and peduncles of these flowerheads are similar to the stems, except their hairs are shorter. There are often solitary leafy bracts up to 1" long where the branches of an inflorescence divide; these bracts are narrowly lanceolate (Spellenberg 2007).

Each daisy-like flowerhead is ½–¾" across, consisting of 100-300 ray florets that surround a dense head of disk florets. The petaloid rays of the flowerhead are white (less often light pink or light violet), linear in shape, and densely distributed. The corollas of the disk florets are 2-3 mm. long, yellow, and narrowly tubular in shape. Surrounding the cup-like base of each flowerhead, there are numerous appressed phyllaries in a single overlapping series. Individual phyllaries are light green, linear in shape, and sparsely short-pubescent. The blooming period occurs from late spring to mid-summer, lasting about 1–1½ months. There is either a mild floral fragrance or none. Afterwards, this plant tends to die down for the remainder of the summer. The florets are replaced by achenes with small tufts of white bristly hair; they are distributed by the wind. The narrow achenes are 0.5–1 mm. long. The root system is shallow and fibrous, sometimes forming a small caudex on older plants. Colonies of plants occasionally occur at favorable sites.

The nectar and pollen of the flowerheads attract a variety of insects, including a variety of bees, butterflies, moths, and flies.

Methods

Leaf tissue from a single individual was collected in Bethesda, MD, USA.

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 (Kieras, O'Neill, and Pirro 2021).

Results

The genome assembly yielded a total sequence length of 619,561,997 bp over 213,738 scaffolds.

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Data availability

Raw and assembled data is publicly available via GenBank:

RAW GENOME DATA

https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR13004263

ASSEMBLED GENOME

https://www.ncbi.nlm.nih.gov/assembly/GCA_024320915

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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., K. O’Neill, and S. Pirro. 2021. *Zanfona, a genome assembly finishing tool for paired-end Illumina reads*. https://github.com/zanfona734/zanfona.

Spellenberg, R. 2007. *National Audubon Society Field Guide to North American Wildflowers, Western Region*. New York: Knopf.