

GENOME SEQUENCING

The complete genome sequences of 13 species of *Catopsis* (Bromeliaceae, Poales)

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Biodiversity Genomes

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Introduction

Catopsis is a genus of entirely epiphytic bromeliads (family Bromeliaceae) distributed throughout southern Mexico, Central America, the Caribbean, and northern South America. Species occupy diverse habitats ranging from cloud forests and mangroves to seasonally dry forests, with plants that are characterized by their funnel-shaped to tubular rosettes, hyaline leaf margins, and seeds bearing comose appendages attached to the apex (Smith and Downs 1977). Phylogenetic studies have resolved *Catopsis* as sister to the remaining lineages of Tillandsioideae, placing the genus in a pivotal position for understanding the evolutionary history of the subfamily and its position within the Bromeliaceae (Barfuss et al. 2016).

Several species exhibit unusual ecological and reproductive traits that have attracted longstanding interest. Most notably, *C. berteroniana* (Schult. & Schult.f.) Mez is considered protocarnivorous, relying on UV-reflective epicuticular waxes to disorient and trap flying insects, a nutritional strategy linked to the phosphorus- and potassium-poor conditions of its exposed epiphytic habitat (Gonsiska 2010; Benzing 2023). Reproductive systems within *Catopsis* are unusually diverse, with approximately half of the species reported as dioecious and the remainder possessing bisexual flowers (Benzing 2000). Despite the distinctive reproductive biology in *Catopsis*, genomic resources for the genus remain scarce. Here, we present genome assemblies for 13 species: *C. delicatula* L.B.Sm., *C. floribunda* (Brongn.) L.B.Sm., *C. juncifolia* Mez & Wercklé, *C. micrantha* L.B.Sm., *C. minimiflora* Matuda, *C. morreniana* Mez, *C. nitida* Griseb., *C. nutans* Griseb., *C. occulta* Mart.-Correa, Espejo & López-Ferr., *C. paniculata* hort. ex Gentil, *C. pisiformis* Rauh, *C. sessiliflora* Mez, and *C. wangerinii* Mez & Wercklé (Figure 1), representing the most comprehensive genomic sampling of the genus to date.

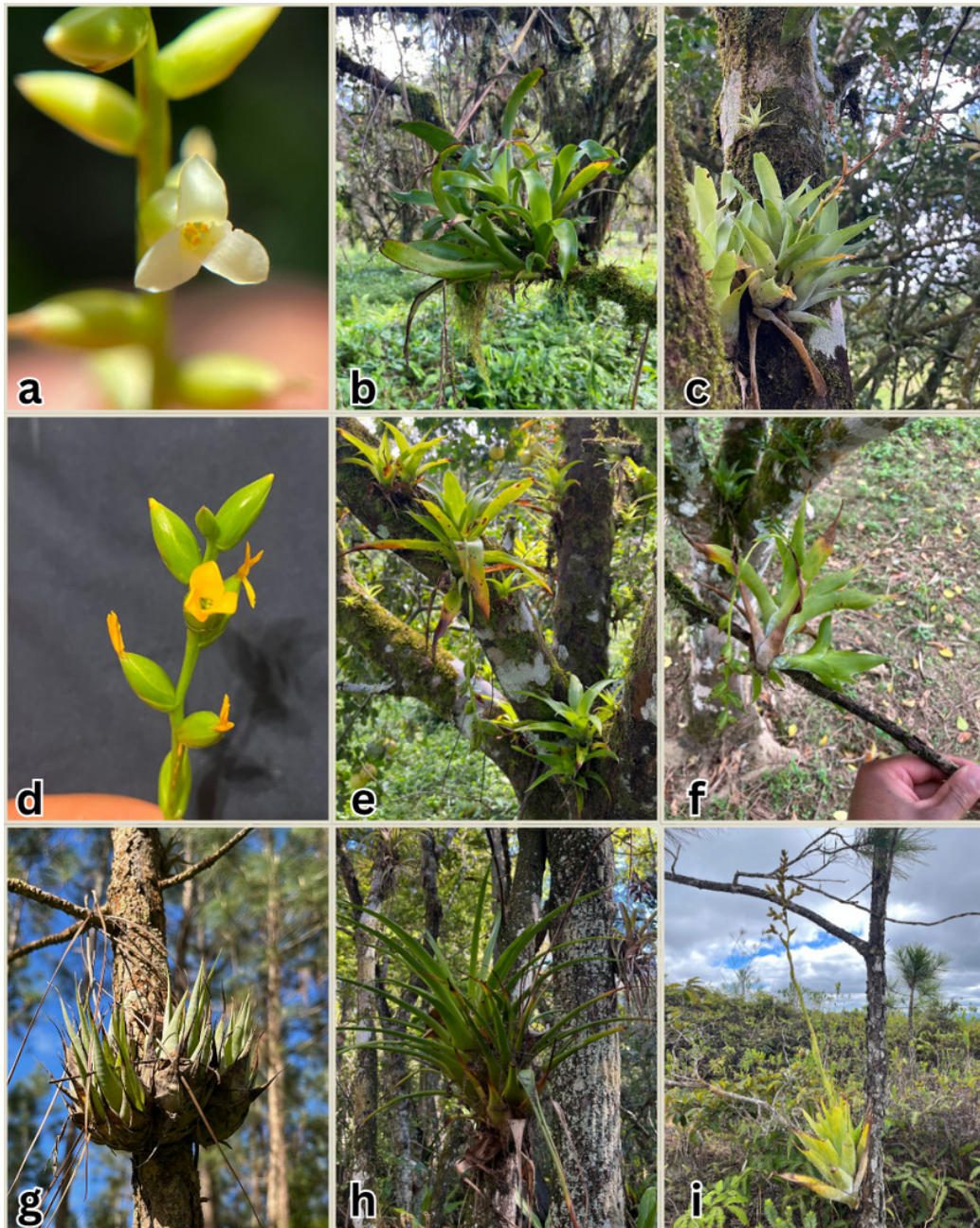


Figure 1. Reproductive and vegetative morphology of selected *Catopsis* species.

(A) Staminate flower of *C. sessiliflora*. (B) Epiphytic individual of *C. sessiliflora* in its natural habitat. (C) Vegetative rosettes of *C. morreniana* growing on a tree trunk. (D) Hermaphroditic flower of *C. nutans*. (E) *Catopsis nutans* in its natural habitat. (F) *Catopsis nutans* established on a small branch, highlighting twig epiphyte habit. (G) Juvenile individuals of *C. floribunda*. (H) Mature individual of *C. floribunda*. (I) Flowering individual of *C. berteroniana*.

Methods

Leaves from herbarium vouchers were used for DNA extraction and sequencing, using approximately 10-15 mg of leaf tissue per extraction. Each DNA extraction was performed using the Qiagen DNEasy genomic extraction kit using the manufacturer's protocol. Paired-end sequencing libraries were constructed using the Illumina TruSeq kit according to the manufacturer's instructions. Libraries were sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150bp format. The resulting fastq files

were trimmed of adapter/primer sequences and low-quality regions with Trimmomatic v0.33 (Bolger et al. 2014). The trimmed sequences were assembled by SPAdes v3.15.4 (Bankevich et al. 2012), screened for foreign contaminants with FCS (Astashyn et al. 2024), followed by a finishing step using Zanfona (Kieras et al. 2021) to scaffold newly generated assemblies based on available genomes from related species. Raw sequencing reads were uploaded to the Sequence Read Archive.

Results and Data Availability

Sequencing files and scaffolded genome assemblies are available on NCBI with the accession numbers listed in [Table 1](#).

Table 1. Species name, herbarium voucher, and accession number for each genome assembly generated.

Taxon	Herbarium Voucher	SRA Accession
<i>Catopsis delicatula</i> L.B.Sm.	NY03854207	SRR38611126
<i>Catopsis floribunda</i> (Brongn.) L.B.Sm.	NY010807173	SRR32988703
<i>Catopsis juncifolia</i> Mez & Wercklé	MO671256	SRR32984321
<i>Catopsis micrantha</i> L.B.Sm.	MO3515985	SRR38612148
<i>Catopsis minimiflora</i> Matuda	MO6718389	SRR32984528
<i>Catopsis morreniana</i> Mez	NY03854226	SRR35004682
<i>Catopsis nitida</i> Griseb.	MO6712158	SRR32974587
<i>Catopsis nutans</i> Griseb.	MO4971250	SRR32974602
<i>Catopsis occulta</i> Mart.-Correa, Espejo & López-Ferr.	MO2309515	SRR38611127
<i>Catopsis paniculata</i> hort. ex Gentil	NY04249030	SRR32988766
<i>Catopsis pisiformis</i> Rauh	MO2622832	SRR38612147
<i>Catopsis sessiliflora</i> Mez	NY04249005	SRR38611111
<i>Catopsis wangerinii</i> Mez & Wercklé	MO6700579	SRR33339433

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REFERENCES

- Astashyn, A., E. S. Tvedte, D. Sweeney, et al. 2024. “Rapid and Sensitive Detection of Genome Contamination at Scale with FCS-GX.” *Genome Biology* 25: 60. <https://doi.org/10.1186/s13059-024-03198-7>.
- Bankevich, A., S. Nurk, D. Antipov, 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>.
- Barfuss, M. H. J., W. Till, E. M. C. Leme, et al. 2016. “Taxonomic Revision of Bromeliaceae Subfam. Tillandsioideae Based on a Multi-Locus DNA Sequence Phylogeny and Morphology.” *Phytotaxa* 279 (1): 1. <https://doi.org/10.11646/phytotaxa.279.1.1>.
- Benzing, D. H. 2000. *Bromeliaceae: Profile of an Adaptive Radiation*. Cambridge University Press. <https://doi.org/10.1017/CBO9780511565175>.
- Benzing, D. H. 2023. “Bromeliaceae: A Brief Profile and Some Topics That Warrant Further Inquiry.” *Selbyana* 34: 1–79.
- Bolger, A. M., M. Lohse, and B. Usadel. 2014. “Trimmomatic: A Flexible Trimmer for Illumina Sequence Data.” *Bioinformatics* 30 (15): 2114–20. <https://doi.org/10.1093/bioinformatics/btu170>.
- Gonsiska, P. A. 2010. *Aspects of the Evolutionary Ecology of the Genus Catopsis (Bromeliaceae)*. Vol. 72.
- 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>.
- Smith, L. B., and R. J. Downs. 1977. “Tillandsioideae (Bromeliaceae).” *Flora Neotropica* 14 (2): 663–1492.