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GENOME SEQUENCING

The complete genome sequences of 17 tree species of Fabaceae (Fabales, Magnoliopsida)

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Biodiversity Genomes

We present complete genome sequences for 15 Amazonian tree species from the genus *Eperua* along with two African tree species from the closely related genus *Eurypetalum*. The species are: *Eperua bijuga* Mart. ex Benth., *Eperua cerradoensis* Fortes, G.S.da Silva & Mansano, *Eperua duckeana* R.S.Cowan, *Eperua falcata* Aubl., *Eperua froesii* Fortes, Aymard, ter Steege & Mansanogl, *Eperua glabra* R.S.Cowan, *Eperua glabriflora* (Ducke) R.S.Cowan, *Eperua grandiflora* (Aubl.) Baill., *Eperua leucantha* Benth., *Eperua manausensis* Fortes & Mansano, *Eperua oleifera* Ducke, *Eperua purpurea* Benth., *Eperua rubiginosa* Miq., *Eperua schomburgkiana* Benth., *Eperua venosa* R.S.Cowan, *Eurypetalum tessmannii* Harms, and *Eurypetalum unijugum* Harms.

Introduction

The taxonomic and genomic diversity Amazonia trees remains poorly understood (ter Steege et al. 2016; Cardoso et al. 2017). For many known species, foundational knowledge on taxonomy, ecology, and genetics is lacking. Taxonomic revisions and phylogenetic studies are essential to address these gaps, clarifying species delimitation, distribution, evolutionary history, and biogeography. Recent taxonomic (Romero-González and Aymard 2019; Fortes, Reis, et al. 2023; Fortes, Da Silva, et al. 2023) and phylogenetic (ter Steege et al. 2023; Fortes et al. 2025) studies on the tree genus *Eperua* (Leguminosae) exemplify this, leading to the recognition and naming of four new species; the publication of an updated identification key; and the revelation of new insights into the evolutionary history of the group which highlight the role of Amazonian white-sand forests and the impact of pollinator shifts on speciation and morphological diversification of this lineage. To support ongoing and future studies, we present genome assemblies for 15 of the 19 accepted *Eperua* species plus two closely related species of *Eurypetalum*, therein providing a significant contribution to the genomic resources available for tropical trees and particular the African Fabaceae.

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
Eperua bijuga	IAN201278	SRR33697102
Eperua cerradoensis	IAN201061	SRR35007291
Eperua duckeana	RB01458703	SRR33693803
Eperua falcata	RB01459756	SRR37084212
Eperua froesii	IAN117052	SRR35007329
Eperua glabra	US00242958	SRR33697116
Eperua glabriflora	RB01459756	SRR33693768
Eperua grandiflora	US00508872	SRR35007165
Eperua leucantha	US00501048	SRR35007164
Eperua manausensis	RB01458706	SRR35921131
Eperua oleifera	INPA0293610	SRR33697461
Eperua purpurea	US00963721	SRR33326255
Eperua rubiginosa	RB01460614	SRR33325002
Eperua schomburgkiana	US00889813	SRR33339764
Eperua venosa	US00243020	SRR33339528
Eurypetalum tessmannii	US1188000	SRR35007173
Eurypetalum unijugum	K001091352	SRR33694675

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