The Complete Genome Sequence of *Telfairia occidentalis,* the African Fluted Pumpkin

Stacy Pirro[1], Olawole Obembe[2] [a]

[1] Biodiversity, Iridian Genomes, [2] Department of Biological Sciences, Covenant University

Biodiversity Genomes

Telfairia occidentalis is a tropical vine grown in West Africa as a leaf vegetable and for its edible seeds. We present the whole genome sequence of this species. Illumina sequencing was performed on a leaf tissue sample from a single cultivated 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 (SRR14834394) and Genome Assembly (JAOANK000000000).

Introduction

Telfairia occidentalis (Cucurbitaceae, Cucurbitales), commonly known as the fluted pumpkin, grows in several countries in West Africa but is mainly cultivated in southeastern Nigeria and it is used primarily in soups and herbal medicines. The cultivated plant is a drought-tolerant, dioecious perennial. The fruit is inedible but the seeds are high in protein and fat. The leaves and seeds are consumed by an estimated 30 to 35 million people indigenous people in Nigeria.

The fruit of this species is quite large. One study documented a range of 16–105 centimetres (6.3–41.3 in) in length, and an average of 9 cm in diameter. Each gourd contains approximately 200 large seeds. The flowers grow in sets of five, with creamy-white and dark red petals, contrasting with the yellow color of the ripe fruit (Okoli and Mgbeogu 1983).

Methods

Leaf tissue from a single cultivated plant was used for this study. 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

a   Olawole O. Obembe, Ph.D
    Professor and UNESCO Chair-holder
    Department of Biological Sciences
    College of Science and Technology
    Covenant University, PMB 1023
    Ota Canaan Land, Ogun State
    Nigeria.
    +2348130928965

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

The genome assembly yielded a total sequence length of 768,820,061 bp.

Raw genome data

https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR14834394

Assembled genome

https://www.ncbi.nlm.nih.gov/nuccore/JAOANK000000000

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