

GENOME SEQUENCING

The Complete Genome Sequence of *Vachellia tortilis* subsp. *raddiana*, the Umbrella Thorn Acacia (Fabaceae, Fabales)

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We present the first high-quality genome assembly of *Vachellia tortilis* subsp. *raddiana* (Savi) Brenan, a keystone tree species of the circum-Saharan region. Plant material used for genome sequencing was collected from Taidalt, a small town near Guelmim in southern Morocco. Using Illumina paired-end sequencing, a scaffold-level genome assembly was generated, providing a foundational genomic resource for this ecologically critical taxon.

Introduction

Vachellia tortilis subsp. *raddiana* (Savi) Brenan is a keystone species of arid and semi-arid ecosystems across Africa and the Middle East, where it contributes significantly to ecosystem stability and local livelihoods (Hnini et al. 2023). Its ecological success relies on strong adaptive traits, including a deep root system and efficient hydraulic functioning, enabling survival under extremely low precipitation regimes (20–200 mm annually) (Abdallah et al. 2012). Beyond its ecological role, the species is also recognized for its richness in bioactive secondary metabolites such as flavonoids, phenolic acids, and tannins which support its widespread use in traditional medicine (Akapo et al. 2025). However, despite this dual ecological and pharmacological importance, genomic resources for *V. tortilis* remain limited. This gap constrains our understanding of both its associated microbiota and the biosynthetic pathways underlying its metabolic potential, highlighting the need for integrative genomic approaches. In this context, we report the genome sequence of *V. t.* subsp. *raddiana*, providing a foundational resource for future studies in conservation genomics and biotechnological valorization.

Methods

Leaf tissue was collected from a wild tree in Morocco. DNA extraction was performed using the Qiagen DNEasy genomic extraction kit using the standard process. Paired-end sequencing libraries were constructed using the Illumina TruSeq kit according to the manufacturer's instructions. The 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 sequence was assembled by SPAdes v3.15.4 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras et al. 2021).

Data Availability

The genome assembly size was 234.6 MB with 16,879 scaffolds/contigs, and 35.5% GC.

Taxname	accession
<i>Vachellia tortilis</i>	JBVAGF000000000

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