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# Draft Genome Sequences of Nitrogen-Fixing Bradyrhizobia Isolated from Root Nodules of Peanut, *Arachis hypogaea*, Cultivated in Southern Tunisia

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**ABSTRACT** Here, we report the draft genome sequences of two nitrogen-fixing symbionts, *Bradyrhizobium* sp. strain sGM-13 and *Bradyrhizobium* sp. strain sBnM-33, isolated from root nodules of peanut grown on soil samples collected from two regions in South Tunisia. The draft genome sizes of these two strains are  $8.31 \times 10^6$  bp and  $8.97 \times 10^6$  bp, respectively.

Nitrogen-fixing bacteria called rhizobia are known for their ability to form symbioses with a wide range of legumes and convert atmospheric nitrogen into a form that can be assimilated by plants (1). Peanut, *Arachis hypogaea*, is an important oilseed legume originally from South America. Peanut is now cultivated worldwide and forms effective nodules mainly with slow-growing bacteria belonging to the genus *Bradyrhizobium* (2–5). The study of the diversity of symbiotic bacteria nodulating peanut provides a basis for the development of rhizobial inoculants well adapted to the environmental conditions of the local areas of cultivation, which subsequently alleviate the use of synthetic fertilizers (4, 6, 7).

In this study, we report the draft genome sequences of two strains, *Bradyrhizobium* sp. strain sGM-13 and *Bradyrhizobium* sp. strain sBnM-33, symbionts of *Arachis hypogaea*. As a first step, we collected soil samples from two sites in southern Tunisia, one approximately 8 km south of Ben Gardane (33°05'N, 11°14'E) and one approximately 10 km south of Gabès (33°48'N, 10°08'E). Then, we trapped nodulating bacteria from pots containing these soils planted with local varieties of peanut. After cultivation for 7 weeks, plants were harvested and nodules were collected from the roots. Then, the nodules were surface sterilized, crushed, and streaked onto yeast mannitol agar (YMA) medium (8) to isolate the bacteria inside the nodules. The strains isolated were checked for their ability to renodulate their host plant, *Arachis hypogaea*. The isolated strains were identified as *Bradyrhizobium* based on partial sequencing of the 16S rRNA gene using the primers PA (AGAGTTTGATCCTGGCTCAG) and PH (AAGGAGGTGATCCAGCCGCA) (expected insert size, 1,500 bp) (9).

A single colony of each strain was grown in liquid yeast extract mannitol (YEM) medium for 4 days at 28°C. Then, the total genomic DNA was extracted from the two strains using the MasterPure complete DNA and RNA purification kit (Epicentre). Genomic DNA was fragmented by sonication, and fragments were polished, A-tailed, multiplexed, and ligated to Illumina adapters. Libraries were purified with an AMPure XP system and paired-end sequenced in a NovaSeq instrument (library preparation and sequencing subcontracted to Novogene, United Kingdom). Paired-end sequencing generated between 4.4 and 4.5 million reads of  $2 \times 150$  bp. The reads were trimmed and filtered using Trimmomatic version 0.22 (10) with the options ILUMINACLIP:TrueSeq3-PE-2:3:30:10 HEADCROP:6 LEADING:30 TRAILING:30 SLIDINGWINDOW:4:30. Assemblies were then obtained with the SPAdes genome assembler version 3.11.1 (11) using the careful mode. Annotation of the *Bradyrhizobium* sp. sGM-13 and *Bradyrhizobium* sp. sBnM-33 genome sequences was

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**TABLE 1** Characterization of draft genome sequences of *Bradyrhizobium* sp. sGM-13 and *Bradyrhizobium* sp. sBnM-33

Characteristic	Data for:	
	<i>Bradyrhizobium</i> sp. sGM-13	<i>Bradyrhizobium</i> sp. sBnM-33
No. of reads	4,549,384	4,435,615
No. of contigs >200 bp	574	330
No. of genes	7,906	8,678
Draft genome length (bp)	8,309,700	8,966,052
$N_{50}$ (bp)	247,668	121,392
G+C content (%)	62	62
Coverage (×)	129	117
BioSample accession no.	SAMN18828746	SAMN18828747
SRA accession no.	SRR14380225	SRR14380224
Assembly accession no.	JAGWDK000000000	JAGWDJ000000000

performed using Prokka (12). Coverage was calculated with SAMtools mpileup (13) on Burrows-Wheeler Aligner MEM algorithm (BWA-MEM) version 2-generated (14) mapping of the paired-end reads. Information about the two draft genome sequences is listed in Table 1.

The strains sGM-13 and sBnM-33 had average nucleotide identities (ANI; calculated over all coding sequences [CDS] as in <https://img.jgi.doe.gov/docs/ANI.pdf>) of 90.99% and 88.60%, respectively, in relation to the closest species, *Bradyrhizobium retamae* Ro19 (GenBank accession no. [NZ\\_LLYA000000001](https://www.ncbi.nlm.nih.gov/nuccore/NZ_LLYA000000001)) and 89.53% with respect to each other. These values are well below the generally accepted species threshold of 95%, and therefore, they appear to belong to two distinct species (15, 16). These two strains found in the arid soils of southern Tunisia present promising raw materials for the development of bacterial inoculum to improve peanut cultivation in the southern Mediterranean region.

**Data availability.** The raw reads and draft contigs of *Bradyrhizobium* sp. sGM-13 and *Bradyrhizobium* sp. sBnM-33 were deposited at GenBank under the BioProject no. [PRJNA723783](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA723783). The BioSample numbers, raw reads, and assembly GenBank accession numbers are given in Table 1.

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