

Draft genome of six tropical *Azospirillum argentinense* strains associated with maize and sorghum with potential for plant growth promotion

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ABSTRACT This report presents draft genome sequences of six *Azospirillum argentinense* strains (CMS1626, CMS1630, CMS05, CMS07, CMS11, and CMS18) isolated from maize rhizosphere soil or from sorghum stems grown on oxisols in the Brazilian Cerrado. These diazotrophic strains are promising bioinoculants for sustainable agriculture.

KEYWORDS biostimulants, biological nitrogen fixation, diazotrophs, plant growth-promoting bacteria

Bioinoculants based on plant growth-promoting bacteria are increasingly used to support productive and sustainable agriculture (1, 2). Among them, *Azospirillum* is widely recognized for improving crop productivity through biological nitrogen fixation, enhanced nutrient availability, stress tolerance, and plant growth promotion (3, 4). *Azospirillum* spp. can fix atmospheric nitrogen, reducing dependence on chemical fertilizers (5), and produce phytohormones such as indole-3-acetic acid, which stimulate root development and nutrient uptake (6–8), enhancing plant resilience under suboptimal conditions (8, 9).

Here, we report the draft genome sequences of six *Azospirillum argentinense* strains isolated from maize rhizosphere soil and sorghum stems (Table 1). Samples were collected at the flowering stage from field experiments conducted at the Embrapa Maize and Sorghum Experimental Station in Sete Lagoas, Minas Gerais, Brazil (19°28' S, 44°15' W; 761 m altitude). The soil is classified as a typical dystrophic Red Oxisol (Soil Taxonomy), Cerrado phase (10).

Sorghum stems were harvested, washed, surface-disinfected, and aseptically macerated. Maize plants were collected with roots and adhering soil intact, and the rhizosphere soil was separated (11). For bacterial isolation, 10 g of each sample was suspended in 90 mL sterile saline solution (8.5 g L⁻¹ NaCl), shaken at 150 rpm for 30 min, and allowed to settle for 1 h. Serial dilutions were prepared up to 10⁻⁷.

Aliquots (100 µL) were inoculated into vials containing 5 mL of semi-solid nitrogen-free NFb medium, as described by Baldani and Döbereiner (12), and incubated at 30°C for 5 days. Diazotrophic growth was identified by the formation of a subsurface pellicle. Cultures were purified through approximately five successive transfers in NFb medium, and purity was confirmed on solid potato medium (12).

Strains were cryopreserved at –80°C in glycerol and deposited in the Embrapa Collection of Multifunctional and Phytopathogenic Microorganisms under accession numbers BRM 044320 (CMS18), BRM 044317 (CMS05), BRM 044312 (CMS1630), BRM 044311 (CMS1626), BRM 044318 (CMS07), and BRM 044319 (CMS11).

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TABLE 1 List of bacterial strains, summary of genome features, accession numbers, and general statistics of raw sequences and assembled genomes of *Azospirillum argentinense* strains CMS1626, CMS1630, CMS05, CMS07, CMS11, and CMS18

Strain ID	CMS1626	CMS1630	CMS05	CMS07	CMS11	CMS18
Best match (type species)	<i>A. argentinense</i>	<i>A. argentinense</i>	<i>A. argentinense</i>	<i>A. argentinense</i>	<i>A. argentinense</i>	<i>A. argentinense</i>
Fast ANI placement (%)	98.54	98.62	98.54	98.56	98.57	98.92
Fast ANI reference (NCBI)	Az39	Az39	Az39	Az39	Az39	Az39
Library size	13,640,092	13,656,034	13,649,444	13,686,604	13,698,520	13,666,770
Number of contigs	164	193	155	167	153	159
Genome size (bp)	7,755,591	7,331,621	7,474,862	7,476,534	7,413,709	7,472,015
Total sequence length (bp)	13,640,092	13,656,034	13,649,444	13,686,604	13,698,520	13,666,770
Total unappended length (bp)	7,726,501	7,331,521	7,474,666	7,457,545	7,384,753	7,452,289
N50 (kb)	271.131	302.722	403.991	428.079	496.634	271.160
G + C content (%)	68.43	68.64	68.54	68.54	68.68	68.66
Genes (CDS)	6954	6497	6602	6602	6564	6578
Non-coding (RNA)	97	104	104	103	99	104
Genome completeness (%)	99.2%	99.2%	99.2%	99.2%	99.2%	99.2%
Genome contamination (%)	3.29	3.07	4.61	4.61	3.73	3.51
Coverage (x)	248	265	254	259	263	256
SRA identifiers	SRS24755893	SRS27295600	SRS24719299	SRS24752666	SRS24761364	SRS24755893
Genome assembly (NCBI)	GCA_054048325.1	GCA_054048285.1	GCA_054048425.1	GCA_054065635.1	GCA_054504525.1	GCA_054048405.1
BioSample ID	SAMN47891599	SAMN47891619	SAMN47891644	SAMN47891646	SAMN44516662	SAMN47891450
GenBank accession number	JBSVFC010000001.1	JBSVFE010000001.1	JBSVFF010000001.1	JBSVFB010000001.1	JBIUFN010000001.1	JBSVFD010000001.1
Strain	BRM 044311	BRM 044312	BRM 044317	BRM 044318	BRM 044319	BRM 044320
Isolate name alias	CMPC 1821	CMPC 1822	CMPC 1827	CMPC 1828	CMPC 1829	CMPC 1830
Country/state/municipality	Brazil/MG/Sete Lagoas	Brazil/MG/Sete Lagoas	Brazil/MG/Sete Lagoas	Brazil/MG/Sete Lagoas	Brazil/MG/Sete Lagoas	Brazil/MG/Sete Lagoas
Geographic location	19° 28'S, 44° 15'W	19° 28'S, 44° 15'W	19° 28'S, 44° 15'W	19° 28'S, 44° 15'W	19° 28'S, 44° 15'W	19° 28'S, 44° 15'W
Biome	Cerrado	Cerrado	Cerrado	Cerrado	Cerrado	Cerrado
Collection date	2011	2012	1996	1996	1996	1996
Host	Sorghum stem	Sorghum stem	Maize rhizosphere soil	Maize rhizosphere soil	Maize rhizosphere soil	Maize rhizosphere soil
Isolation medium	NFb	NFb	NFb	NFb	NFb	NFb

Genomic DNA was extracted from cultures grown in Luria-Bertani medium (28°C, 24 h, 150 rpm) using the Wizard Genomic DNA Purification Kit (Promega, USA) and quantified with a Qubit 2.0 fluorometer (Life Technologies, USA). Whole-genome sequencing libraries were prepared following the BGISEQ-500 protocol described by Huang et al. (13), including DNA fragmentation and size selection (200–400 bp) using Agencourt AMPure XP magnetic beads (Beckman Coulter, USA). Libraries were sequenced on a BGISEQ-500 platform (150-bp paired-end) at BGI (Shenzhen, China), and base calling was performed using the platform's internal software.

Low-quality reads (Phred score <20) were removed using Trimmomatic v0.38 (14). Genome assembly was performed with SPAdes v3.12.0 (15), and assembly quality and completeness were assessed using Quast v5.0.2 (16) and BUSCO v5.3.1 (17), respectively. Genomes were annotated with the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline v6.6 (18). Species identification was conducted using TYGS v39.1 (19) against type strains in the RefSeq database (October 2024) and confirmed using fastANI v1.34 (20) against *A. argentinense* Az39 (NZ_CP007793.1). General genome features and ANI results are summarized in Table 1. All software was used with default parameters.

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DATA AVAILABILITY

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under BioProject [PRJNA1180210](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1180210), with accession [JBIUFN000000000](https://www.ncbi.nlm.nih.gov/nuccore/JBIUFN000000000), and BioSample accessions [SAMN47891599](https://www.ncbi.nlm.nih.gov/biosample/SAMN47891599), [SAMN47891619](https://www.ncbi.nlm.nih.gov/biosample/SAMN47891619), [SAMN47891644](https://www.ncbi.nlm.nih.gov/biosample/SAMN47891644), [SAMN47891646](https://www.ncbi.nlm.nih.gov/biosample/SAMN47891646), [SAMN44516662](https://www.ncbi.nlm.nih.gov/biosample/SAMN44516662), and [SAMN47891450](https://www.ncbi.nlm.nih.gov/biosample/SAMN47891450) for strains CMS1626, CMS1630, CMS05, CMS07, CMS11, and CMS18, respectively. The raw reads were deposited in the SRA database and can be accessed under the numbers [SRS24755893](https://www.ncbi.nlm.nih.gov/sra/SRS24755893) (CMS1626), [SRS27295600](https://www.ncbi.nlm.nih.gov/sra/SRS27295600) (CMS1630), [SRS24719299](https://www.ncbi.nlm.nih.gov/sra/SRS24719299) (CMS05), [SRS24752666](https://www.ncbi.nlm.nih.gov/sra/SRS24752666) (CMS07), [SRS24761364](https://www.ncbi.nlm.nih.gov/sra/SRS24761364) (CMS11), and [SRS24755893](https://www.ncbi.nlm.nih.gov/sra/SRS24755893) (CMS18).

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