



# Draft Genome Sequence of Plant Growth-Promoting Drought-Tolerant *Bacillus* sp. Strain CMAA 1363 Isolated from the Brazilian Caatinga Biome

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**ABSTRACT** The strain of *Bacillus* sp. CMAA 1363 was isolated from the Brazilian Caatinga biome and showed plant growth-promoting traits and ability to promote maize growth under drought stress. Sequencing revealed genes involved in stress response and plant growth promotion. These genomic features might aid in the protection of plants against the negative effects imposed by drought.

Strain CMAA 1363 was originally recovered from the rhizosphere of *Cereus jamacaru*, a cactus found in a unique Brazilian semiarid biome called Caatinga (3 to 17°S to 35 to 45°W). This strain showed plant growth-promoting traits and the ability to promote maize growth under drought stress (1), and it displayed 99.6% 16S rRNA gene similarity to *Bacillus aryabhattai*, a Gram-positive bacterium that has been recently described by Shivaji et al. (2). Genomic DNA was extracted from a pure culture grown overnight on tryptic soy broth (TSB) medium using the PureLink genomic kit (Life Technologies, Inc.). Whole-genome sequencing was performed using the Ion Torrent (PGM) platform, according to the manufacturer's protocol. Genome sequence was *de novo* assembled using MIRA version 4, CLC Genomics Workbench version 5.5.1, and SeqMan NGen version 4.0.0 packages. The obtained contigs were integrated using CISA, according to Santos et al. (3).

The genome size corresponded to 3,656,253 bp, with 135× coverage. Data were assembled using *Bacillus aryabhattai* strain T61 (GenBank accession no. NZ\_KQ087173) (Yan et al. [4]) as a reference and analyzed by Rapid Annotations using Subsystems Technology (RAST) (5). The genome size was found to be 4,956,314 bp, allocated into 10 contigs, comprising 5,339 coding sequences, 414 subsystems, and 63 RNA genes. A total of 126 genes involved in stress response were found. Forty-one genes involved in cell wall and capsule were found, with seven of them being related to capsular and extracellular polysaccharide biosynthesis. Also, six genes related to auxin biosynthesis and 529 genes related to amino acids and derivatives were found. As previously mentioned, the closest species is *Bacillus aryabhattai*, which has been reported as temperature and drought tolerant (6), and its genome revealed adaptations to the Tibetan plateau, which has high altitude, high UV radiation, and limited oxygen and temperature variations (4). Some of these characteristics (high UV radiation and temperature variation) may be similar to those found in the Caatinga biome, enabling the survival of this strain under such conditions. Furthermore, some genomic features, such as amino acids, exopolysaccharides, and indole-3-acetic acid (IAA) biosynthesis, might aid in plant growth promotion and protection against negative effects imposed by drought.

**Accession number(s).** The partial genome sequence of *Bacillus* sp. CMAA 1363 has been ascribed to the whole-genome shotgun project deposited at DDBJ/ENA/GenBank

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## REFERENCES

1. Kavamura VN, Santos SN, Silva JL, Parma MM, Ávila LA, Visconti A, Zucchi TD, Taketani RG, Andreote FD, Melo IS. 2013. Screening of Brazilian cacti rhizobacteria for plant growth promotion under drought. *Microbiol Res* 168:183–191. <https://doi.org/10.1016/j.micres.2012.12.002>.
2. Shivaji S, Chaturvedi P, Begum Z, Pindi PK, Manorama R, Padmanaban DA, Shouche YS, Pawar S, Vaishampayan P, Dutt CB, Datta GN, Manchanda RK, Rao UR, Bhargava PM, Narlikar JV. 2009. *Janibacter hoylei* sp. nov., *Bacillus isronensis* sp. nov. and *Bacillus aryabhatai* sp. nov., isolated from cryotubes used for collecting air from the upper atmosphere. *Int J Syst Evol Microbiol* 59:2977–2986. <https://doi.org/10.1099/ijs.0.002527-0>.
3. Santos SN, Kavamura VN, Taketani RG, Vasconcellos RLF, Zucchi TD, Melo IS. 2015. Draft genome sequence of *Bacillus* sp. strain CMAA 1185, a cellulolytic bacterium isolated from Stain House Lake, Antarctic Peninsula. *Genome Announc* 3(3):e00436-15. <https://doi.org/10.1128/genomeA.00436-15>.
4. Yan Y, Zhang L, Yu MY, Wang J, Tang H, Yang ZW, Wan P. 2016. The genome of *Bacillus aryabhatai* T61 reveals its adaptation to Tibetan Plateau environment. *Genes Genom* 38:293–301. <https://doi.org/10.1007/s13258-015-0366-2>.
5. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: rapid annotations using subsystems technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.
6. Verma P, Yadav AN, Khannam KS, Kumar S, Saxena AK, Suman A. 2016. Molecular diversity and multifarious plant growth promoting attributes of bacilli associated with wheat (*Triticum aestivum* L.) rhizosphere from six diverse agro-ecological zones of India. *J Basic Microbiol* 56:44–58. <https://doi.org/10.1002/jobm.201500459>.