

# Draft Genome Sequence of *Pseudomonas* sp. Strain CMAA 1215, a Plant Growth-Promoting Bacterium Isolated from a Brazilian Mangrove

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The aim of this study was to sequence the genome of the plant growth-promoting *Pseudomonas* sp. strain CMAA 1215, an osmotolerant bacterium isolated from mangrove soil.

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Mangroves are remarkable environments found in tropical regions worldwide and have been considered a biodiversity hot spot (1). Brazil has one of the largest areas of mangroves in the world, and although it has been extensively studied for the ecological traits of its fauna and flora, there is still a lack of knowledge on its microbial communities. In our survey on the bacterial ecology of Brazilian mangroves, we recovered an osmotolerant bacterium, strain CMAA 1215, from the soil of the Cananéia Island mangrove (25°05' 12.61" S, 47°57' 41.21" W). This strain, classified as a *Pseudomonas* sp., has proven to be a potential plant growth promoter through its ability to produce 1-aminocyclopropane-1-carboxylate (ACC) deaminase and indolacetic acid (IAA) and solubilize inorganic phosphate.

Many members of the genus *Pseudomonas* have been described as plant growth promoters. However, new evidence has shown that *Pseudomonas* strains exhibit highly heterogenic genomes in which only 25 to 35% of the genes are shared by all members of the genus and about a third of the genes are unique to each strain (2). Hence, the discovery of new plant growth promoter genes may be advocated and exploited for the development of improvements regarding agricultural crop management.

Thus, to extend knowledge of the genes related to plant growth promotion in strain CMAA 1215, whole-genome sequencing was performed using the Ion Torrent (PGM) platform. Genomic DNA was extracted from a pure culture grown overnight on LB medium using the PureLink genomic DNA kit (Life Technologies). Sequencing was carried out on the Ion 316 chip sequencer provided in the Ion sequencing kit 200 bp version 2.0, according to the manufacturer's protocol. The genome sequence was *de novo* assembled using the MIRA version 3.4, CLC Genomics Workbench version 5.5.1, and SeqMan NGen version 4.0.0 packages, and the contigs obtained from the assembly were integrated using CISA (3, 4). The taxonomic position of strain CMAA 1215 was further evaluated by using the JSpecies package (5).

A total of 2,717,642 assembled reads ( $Q > 20$ ) with a mean length of 183 bp were obtained using a reference-based approach and allocated into 224 contigs ranging from 2,827 to 183,862 bp in size (50× coverage). The assembled data were analyzed by RAST (6), and the draft genome size was found to be 6,658,235 bp, comprising 6,644 open reading frames (ORFs), 64 tRNA genes, 6

rRNA genes, and a G+C content of 62.95 mol%. The genome contains 11 copies of genes usually related to plant growth promotion (6). The 16S rRNA gene analysis revealed that strain CMAA 1215 has high identity (99.9%) to the type strain of *Pseudomonas putida* (GenBank accession no. D84020). However, the average nucleotide identity (ANI) of CMAA 1215 and its phylogenetically closely related neighbor is 88.2%, which suggests that CMAA 1215 may be the nucleus of a new taxon.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [AVOY00000000](https://www.ncbi.nlm.nih.gov/nuclink/AVOY01000000). The version described in this paper is version AVOY01000000.

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