



Genome Announcements

Draft genome sequence of *Paraburkholderia tropica* Ppe8 strain, a sugarcane endophytic diazotrophic bacterium



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ABSTRACT

Paraburkholderia tropica (syn *Burkholderia tropica*) are nitrogen-fixing bacteria commonly found in sugarcane. The *Paraburkholderia tropica* strain Ppe8 is part of the sugarcane inoculant consortium that has a beneficial effect on yield. Here, we report a draft genome sequence of this strain elucidating the mechanisms involved in its interaction mainly with Poaceae. A genome size of approximately 8.75 Mb containing 7844 protein coding genes distributed in 526 subsystems was *de novo* assembled with ABySS and annotated by RAST. Genes related to the nitrogen fixation process, the secretion systems (I, II, III, IV, and VI), and related to a variety of metabolic traits, such as metabolism of carbohydrates, amino acids, vitamins, and proteins, were detected, suggesting a broad metabolic capacity and possible adaptation to plant association.

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Genome announcement

The genus *Burkholderia* contains 96 species and was recently divided due to the creation of a new genus named *Paraburkholderia*.^{1,2} This new genus is composed of 46 species isolated mainly from rhizosphere soil and plant tissues^{1,2} and includes the older nitrogen-fixing species, *B. tropica*, *B. unamae*, and *B. silvatlantica*, which are all associated with non-legume plants.^{3–5}

Paraburkholderia tropica (basonym: *Burkholderia tropica*³) was first isolated from the sugarcane stem. In addition to nitrogen fixation, it is capable of promoting plant growth and acts as a biological control agent. *P. tropica* strain Ppe8 is part of the sugarcane consortium inoculant, developed by The Brazilian Agricultural Research Corporation (Embrapa), which promotes sugarcane yield increments in the field.^{6–9} Due to its agronomical importance and biotechnological potential, the genome of *P. tropica* strain Ppe8 was sequenced to identify genes potentially associated with these beneficial characteristics.

The *P. tropica* strain Ppe8 (BR11366) was provided by the Johanna Döbereiner Biological Resource Center (CRB-JD) at Embrapa Agrobiologia. Genomic DNA was prepared from an

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overnight (18 h) culture of *P. tropica* Ppe8 grown in JMV liquid medium using the Wizard[®] Genomic DNA Purification Kit (Promega, USA). The genome sequence of Ppe8 was performed by Macrogen Company (South Korea) using the 100 bp paired-end library in Illumina MiSeq platform. It generated 1,845,481,494 bases (1.8 Gb) of sequence data with an average genome coverage of 208X. The reads were trimmed using FASTX-Toolkit (<http://hannonlab.cshl.edu/fastx.toolkit>) and only bases with a quality above 20 (Q20) were used to assemble the genome. The ABySS software version 1.9.0¹⁰ was used for *de novo* assembly and contigs shorter than 200 bp were eliminated. Annotation and identification of metabolic pathways for the draft genome was performed using the RAST version 2.0 server.¹¹

The genome has approximately 8.75 Mb and contains 7844 Coding DNA Sequences (CDSs) distributed across 526 subsystems (functional metabolic pathway or cellular structure of a set of homologous genes in different genomes), G+C content of 64.7 (%) and 78 RNAs, including rRNAs, tRNAs and ncRNA. The most abundant subsystem was “amino acids and derivative” (789 genes), followed by “carbohydrates” (764 genes), “cofactors, vitamins, prosthetic groups, and pigments” (409 genes), “fatty acids, lipids, and isoprenoids” (334 genes), and “metabolism of proteins” (314 genes). The regulation of nitrogen metabolism is quite diverse with 56 genes involved in several processes, such as, allantoin utilization (6), nitrosative stress (3), amidase clustered with urea and nitrile hydratase functions (2), nitrate and nitrite ammonification (21), ammonia assimilation (18), nitrilase (2), and denitrification (4). In addition, the structural organization of 20 genes related to nitrogen fixation (*nif* genes) was very similar to other nitrogen-fixing *Paraburkholderia* species, such as *P. kururienensis*. Furthermore, 264 genes related to membrane transport, including different secretion systems such as type I (*hlyD* and *tolC* genes), II (ORFs *_638*, *_4162* and others genes), III (*epaP*, *epaO*, *hrpB2*, *sctV*, *sctS*, *sctL*, *sctU*, *stcC*, *sctD*, and others), IV (*virJ*), and VI (*lip2* and *hsij2* genes), which are involved in fiber secretion system, type IV pilus, and conjugative transfer, were identified. ABC transports, cation transporters, and uni-, sym-, and anti-protons systems were also detected, suggesting that the bacteria have a broad capacity to transport different molecules.

The assembled contigs were deposited in the DDBJ/ENA/GenBank and published with the accession number MSDZ000000000.1; BioSample: SAMN06166932. The version described in this paper is the first version of the genome sequence deposited.

Conflicts of interest

The authors declare no conflict of interest.

Acknowledgments

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