Draft genome sequence of Paraburkholderia sp. strain XV isolated from the rhizosphere of mango (Mangifera indica L.)

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A B S T R A C T

Here, we report the draft genome of Paraburkholderia sp. XV. This strain was isolated from the rhizosphere of mango (Mangifera indica L.). Its genome consists of 9,189 coding DNA sequences, 60 tRNAs, a single copy of the 16S rRNA, 5S rRNA, and 23S rRNA gene, and 1 tmRNA. The GC content is 62.6%.

Mango (Mangifera indica L.), native to South and Southeast Asia, has been described as one of the most economically important tropical fruits globally. Its annual production is approximately 42 million tons, making it the second most cultivated fruit. The largest mango-producing countries are India, China, Thailand, Indonesia, Pakistan, and Mexico (Kumar et al., 2021; Mirza et al., 2020). Sustainable agricultural practices to maintain or increase mango productivity, such as the use of plant growth-promoting microorganisms, are determinants for its global competitiveness (de los Santos Villalobos et al., 2015; Kuo et al., 2001).

The genus Paraburkholderia was recently recognized as a distinct taxon in the broader Burkholderia sensu lato group and contains a range of diverse species. The majority of Paraburkholderia is composed of plant beneficial species with modes of action that include: antibiotic production, biological nitrogen fixation, siderophore secretion, phytohormone biosynthesis, ACC deaminase activity, and phosphorus solubilization, among others (Mavima et al., 2020).

Strain XV was isolated from the rhizosphere of mango (Mangifera indica L.) variety Ataulfo in a commercial field located in Chahuites, Oaxaca, Mexico (de los Santos Villalobos et al., 2013). Baz agar medium was used, with the following composition (g L⁻¹): solution 1 (0.4 K₂HPO₄, 0.4 KH₂PO₄, 0.2 MgSO₄, 0.02 CaCl₂, 0.01 FeCl₃, 0.002 Na₂MoO₄, 0.075 bromothymol blue, and 15 agar) and solution 2 (5.0 arabinose, succinate, or sucrose). Both solutions were adjusted to pH 5.7 and autoclaved separately at 121 °C and 1 atm for 15 min, and then the two solutions were combined. A 10 g root sample was agitated for 1 h at 100 rpm (using a rotary shaker) in 90 ml of sterile 10 mM MgSO₄·7H₂O. The material liberated from the root surface was diluted in series, spread onto the surface of Petri dishes containing Baz agar medium, and incubated at 28 °C for 7 days (de los Santos Villalobos et al., 2012). Bacterial colonies were purified by sequential streaking on Petri dishes containing Baz agar medium, and a macroscopic and microscopic examination was carried out, in triplicate, to ensure axenicity. All obtained isolates were cryopreserved at -80 °C using Baz broth medium and 30% glycerol.

Strain XV was previously reported by Parra-Cota et al., (2014) to promote Amaranthus cruentus growth, where an increased grain yield and harvest index occurred when used in combination with chemical fertilization. Also, A. cruentus plants inoculated with strain XV showed a tissue-specific induction of several genes involved in photosynthesis, sugar- and N- metabolism, and transport. Additionally, de los Santos...
Villalobos et al., (2013) reported a mango growth-promoting effect by co-inoculation of strain XV and *Rhizobium* sp. strain XXV in mango, resulting in increased dry biomass, increased root, stem, and foliar areas, and an increased number of flowers.

Thus, high-quality genomic DNA was extracted from a fresh culture strain of XV grown in Baz Broth medium [24 h at 32 °C, using an orbital shaker at 121 rpm, obtaining $1 \times 10^6$ Colony Forming Units (CFU)/mL], following the protocol described by Valenzuela-Aragon et al., (2018). Bacterial DNA (OD$_{260/280} = 1.8–2.0$, total amount of DNA $\geq 1 \mu g$, concentration $\geq 25$ ng/µL) was sequenced on an Illumina MiSeq platform, yielding a total of 1,801,920 reads [2 × 300 base pairs (bp)]. The quality of the obtained raw reads was analyzed by FastQC version 0.11.5 Andrews (2010). Trimmomatic version 0.32 (Bolger et al., 2014) was used to remove adapter sequences and low-quality bases, which represents only 1.89% of the total reads. Subsequently, a *de novo* assembly was generated by SPAdes version 3.10.1 (Bankevich et al., 2012), using the parameter –careful for error correction in reads and -cov-cutoff auto (in which SPAdes automatically computes the coverage threshold using a conservative strategy). The draft genome of strain XV contained 9,120,057 bp and an average GC content of 62.6%, N50: 60,799 bp, and L50: 44. The assembled contigs were ordered by Mauve Contig Mover version 2.4.0 (Rissman et al., 2009), using the reference genome *Paraburkholderia caribensis* MWAP64T (GenBank accession no. CP013102), due to the greatest 16S rRNA gene homology (99.93%). A circular chromosome map was generated using the CGView Server (Fig. 1) (Grant and Stothard, 2008).

Genome annotation was performed by Prokka v 1.11.0 Seeman (2014). The GC content of the genome was calculated as 62.6% (Fig. 1). Plasmid detection was carried out by PlasmidFinder 2.0 (Carattoli et al., 2014), and no plasmids were detected. Subsequently, genome annotation was also carried out through Rapid Annotation Using Subsystem Technology (RAST) server version 2.0 (http://rast.nmpdr.org) (Overbeck et al., 2013), by the default RASTtk pipeline (Fig. 2). Default parameters were used for all software unless otherwise noted.

The genome is predicted to contain 60 tRNAs, a single copy of the 16S rRNA, 5S rRNA, and 23S rRNA genes, 1 tmRNA, and 9,189 coding DNA sequences (CDS). The most abundant subsystem was Carbohydrates (499 CDS); followed by Amino acids and derivatives (490 CDS); Cofactors, Vitamins, Prosthetic Groups, Pigments (222 CDS); protein metabolism (219 CDS); and Respiration (202 genes). Besides, genes of agricultural importance include 43 CDS related to the resistance to antibiotics and toxic compounds and the tolerance to colicin E2, and 5 CDS related to secondary metabolism such as plant hormones (auxin biosynthesis), and plant alkaloid segregation (alkaloid biosynthesis from L-lysine). In addition, strain XV presented 140 CDS associated with stress response, including osmotic stress (16 CDS) and oxidative stress (86 CDS). Finally, the genome of this strain contains CDS related to iron (8), potassium (14), nitrogen (20), sulfur (43), and phosphorus (35) acquisition and metabolism (Fig 2, and Table S1).

In this manner, the genome of *Paraburkholderia* sp. strain XV includes genes associated with plant growth promotion. Currently, scientific evidence has shown this effect in mango and amaranth crops (de los

**Fig. 1.** Circular chromosome map of *Paraburkholderia* sp. strain XV showing the distribution of coding sequences (CDS), tRNAs, rRNAs, and GC content skew (50% of the total base-pair window). The map was generated using the CGView Server beta online tool.
Therefore, due to the genomic and functional features, this strain is a promising active ingredient for biofertilizers formulations for contributing to food security.

Data availability

This draft genome sequence has been deposited in DDBJ/ENA/GenBank under accession number JAGUUD000000000. The version described in this paper is the first version, JAGUUD010000000, under BioProject number PRJNA725878 and BioSample number SAMN18912763. Raw data have been deposited in the NCBI SRA under accession number SRR14372668.

Author contributions

Conceptualization, S.d.l.S.-V., and J.M.K.; writing—original draft preparation and visualization, all authors; writing—review and editing were developed by all authors; supervision, project administration, funding acquisition, S.d.l.S.-V., J.M.T., S.Y.H., and J.J.P.C. All authors have read and agreed to the published version of the manuscript.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.crmicr.2021.100055.

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