



The Genome Sequence of *Brucella intermedia* DF13, a 2,4-Dichlorophenoxyacetic Acid-Degrading Soil Bacterium Isolated in Brazil

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ABSTRACT *Brucella intermedia/Ochrobactrum intermedium* strain DF13 was isolated from Brazilian soil and is able to degrade 2,4-dichlorophenoxyacetic acid (2,4-D). Here, we report on its genome sequence, with 4,570,268 bp and a 57.8% G+C content.

KEYWORDS *Ochrobactrum intermedium*, *Brucella intermedia*, bioremediation, biodegradation, 2,4-dichlorophenoxyacetic acid (2,4-D), soil

Members of the genus *Brucella* are Gram-negative aerobic bacilli (1), belonging to the *Brucellaceae* family (2, 3), and are known as human and animal pathogens (2). Based on recent and thorough genome comparisons, the genus *Ochrobactrum* has been reclassified and its species included within the genus *Brucella* (4, 5). Consequently, strain DF13, originally classified as *Ochrobactrum intermedium*, is synonymous with *Brucella intermedia*. *Ochrobactrum intermedium* is known to biodegrade organic pollutants (6) as well as organophosphorus pesticides (7, 8). The genus *Ochrobactrum* was described as capable of degrading the pesticide 2,4-dichlorophenoxyacetic acid (2,4-D) (9). Based on our interests in biodegradation, we report on this strain's genome. The strain was isolated from topsoil, at a depth of 0 to 20 cm, from Fazendinha Agroecológica-SIPA, located at 43°40'00"W and 22°44'30"S. For isolation, a dilution (10^{-1}) of 10 g of the soil was performed with 0.1% NaCl (wt/vol), 0.1% (wt/vol) sodium pyrophosphate, and 0.1% (vol/vol) Tween 20 after incubation at 30°C and centrifuged at 180 rpm for 20 min. Then, serial dilution (10^{-2} to 10^{-7}) in 0.85% saline was performed. A total of 100 μ L of each dilution was plated on a 2,4-D, MEMB selective medium (10). The strain was maintained and grew in a minimal mineral medium with 2,4-D as the sole carbon source. A single colony grown on LB medium at 28°C was used for DNA extraction using the PureLink genomic DNA minikit (Invitrogen) and was quantified with a Qubit fluorometer.

The genomic paired-end library (2 \times 300 bp) with 550-bp medium-sized inserts was built using the Nextera XT DNA library preparation kit (Illumina, San Diego, CA) and sequenced on Illumina MiSeq (INQCS; Fiocruz, Manguinhos, RJ, Brazil) using the MiSeq reagent kit V3 (600 cycle). FastQC v0.11.9 (11) and Trim Galore v0.6.6 (12) tools were used to check and trim at a cutoff of >30 for quality Phred score. Genome assembly was performed combining *de novo* and mapping assembly techniques. SPAdes v3.15.0 (13) was used for the *de novo* assembly and the output was used for assembly with MeDuSa v1.6 (14) using 27 *Brucella intermedia* reference genomes available from the NCBI. CheckM v1.4.0 (15) and QUAST v5.0.2 (16) were used to check assembly quality and contamination. Genomic annotation was made with NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.3 (17–19). Taxonomic identification was

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based on the Average Nucleotide Identity (ANI) v3.8.3, Pairwise Tetra-correlation (TETRA) v3.8.3, and Tetra Correlation Search (TCS) v3.8.3 from JSpeciesWS (20). The sequencing resulted in 1,036,905 raw reads (602,099,110 bp). SPAdes resulted in 53 contigs, and the MeDuSa assembly resulted in a genome length of the 4,570,268 bp based on 6 scaffolds with 95.7× coverage; the N_{50} value was 4,552,750 bp, and the L_{50} had 1 scaffold with a 57.8% G+C content in the QUAST result. CheckM showed 100% completeness and 0% contamination. PGAP annotation resulted in 4,342 genes: 4,281 coding DNA sequences (CDS), 5 rRNA genes, and 52 tRNAs genes. The TCS, ANI, and TETRA results were 0.9994, 98.65, and 0.99949, respectively, for *Brucella intermedia* type strain NCTC12171 (NCBI assembly accession number [GCA_900454225.1](https://doi.org/10.1093/bioinformatics/btv171)). The results were 0.98984 (TCS), 82.37 (ANIb), and 0.98984 (TETRA) for *Brucella daejeonensis* type strain DSM 26944 (NCBI assembly accession number [GCA_014199265.1](https://doi.org/10.1093/bioinformatics/btv171)). Default parameters were used for all software tools.

Data availability. The genome sequence has been deposited at GenBank under accession number [JAIQVX000000000](https://doi.org/10.1093/bioinformatics/btv171). Raw read data are available at SRA accession number [SRR15853869](https://doi.org/10.1093/bioinformatics/btv171), BioProject number [PRJNA757421](https://doi.org/10.1093/bioinformatics/btv171), and BioSample number [SAMN20961033](https://doi.org/10.1093/bioinformatics/btv171).

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We claim that there are no conflicts of interest.

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