

Draft Genome Sequence of *Burkholderia* sp. Strain PML1(12), an Ectomycorrhizosphere-Inhabiting Bacterium with Effective Mineral-Weathering Ability

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We report the draft genome sequence of *Burkholderia* sp. PML1(12), a soil bacterium isolated from the Oak-*Scleroderma citrinum* ectomycorrhizosphere in the experimental forest site of Breuil-Chenué (France).

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Minerals represent the main source of nutritive cations in acidic and nutrient-poor forest soils in temperate regions (1). However, the nutrients entrapped in their structure are not directly accessible to the tree roots, which rely on soil microorganisms to weather the minerals (2, 3). Functional screening of bacterial strains isolated from the *Scleroderma citrinum* ectomycorrhizosphere and the surrounding bulk soil revealed an enrichment of effective mineral-weathering bacteria in the tree root vicinity (4–7). Notably, cultivation-dependent and -independent approaches revealed that the *Burkholderia* genus was the most abundant and the most effective mineral-weathering genus (6–9). A significant positive correlation was observed between the abundance of *Burkholderia* on minerals incubated in forest soils and the weathering level of these minerals (9, 10). Among *Burkholderia* strains tested, strain PML1(12) appeared the most effective and capable of improving tree growth in nutrient-poor condition microcoms (11). With the goal of characterizing this strain and of identifying the molecular mechanisms involved in its mineral-weathering ability, we determined the complete sequence of its genome.

Genomic DNA was obtained using the protocol of Pospiech and Neumann (12). The genomic DNA was sequenced on a genome sequencer (GS) FLX 454 System (Roche) at Cogenics (Meylan, France). A half-run was used to perform 3-kb paired-end tags (L-PET) yielding 1,452,141 reads that were 385 bp long on average. A *de novo* assembly was performed using Newbler 2.6. The draft genome has 293 contigs larger than 500 bp, which were assembled in 8 scaffolds, with a calculated total length of 9,340,894 bp (35× average depth of coverage), a G+C content of 60.83%, and an N_{50} contig size of 70,828 bp. The largest contig generated was 272,460 bp long. We aligned the draft genome with the 10 closest neighboring complete genomes (chromosomes and plasmids) of the *Burkholderia* genus using average nucleotide identity (ANI) tools (<http://enve-omics.ce.gatech.edu/ani/>) (13). The best ANI score (80.83% average nucleotide identity) was obtained with *Burkholderia glathei* strain LMG14190T, indicating

that strain PML1(12) could represent a novel species within the *Burkholderia* genus.

According to the automated annotation done using RAST, the genome contains a total of 8,761 predicted protein-coding genes, from which 2,241 (25.6%) were annotated as encoding hypothetical proteins. The genome contains a total of 46 tRNA coding genes. In addition, the genome of strain PML1(12) contains at least 4 complete copies of ribosomal operons of the following structure: 5S/23S/tRNA-ala-TGC/tRNAⁱ-GAT/16S. The genome of strain PML1(12) presents genes related to plant growth promotion, including the genes for the production of indole-3-acetic acid (*accD*). The genome presents one *N*-acylhomoserine lactone quorum-sensing system. Interestingly, the PML1(12) genome shows a large number of genes (690) for the metabolism of sugars and carbohydrates, including genes for the synthesis and transport of gluconate, an organic acid for which production has been previously linked with the ability of bacteria to weather minerals. The genome possesses 15 genes annotated as siderophore transporters, which indicates the ability of the strain to scavenge Fe-loaded siderophores synthesized by other bacteria.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [AEJF00000000](https://www.ncbi.nlm.nih.gov/nuclink/AEJF00000000) (project ID PRJNA53985; sample ID 53985).

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