

Draft Genome Sequence of *Bacillus licheniformis* Strain GB2, a Hydrocarbon-Degrading and Plant Growth-Promoting Soil Bacterium

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We report the 4.39 Mb draft genome of *Bacillus licheniformis* GB2, a hydrocarbonoclastic Gram-positive bacterium of the family *Bacillaceae*, isolated from diesel-contaminated soil at the Ford Motor Company site in Genk, Belgium. Strain GB2 is an effective plant-growth promoter useful for diesel fuel remediation applications based on plant-bacterium associations.

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Members of the genus *Bacillus*, and more specifically various species of *Bacillus licheniformis*, have been associated with diesel oil degradation in both pure and mixed bacterial cultures (1). It has been reported that *Bacillus licheniformis* strains can directly and indirectly enhance the growth of plant species such as *Arachis hypogea* (2), *Brassica campestris* (3), and *Vitis vinifera* cv. Malbec (4).

Using gas chromatography (GC) (model 450, Agilent Technologies) coupled to mass spectrometry (MS) (model 220, Agilent Technologies), *B. licheniformis* GB2 was found to degrade up to 41% of diesel range organics over 14 days. Under greenhouse conditions *B. licheniformis* GB2 promoted the growth of hybrid poplar cuttings (*Populus deltoides* × [*trichocarpa* × *deltoides*] cv. Grimminge), as well as *Cytisus striatus* and *Lupinus luteus*, indicating that this bacterial strain has a broad plant host specificity.

For sequencing, an Ion Torrent PGM (Life Technologies, Inc., Carlsbad, CA) was used after extracting DNA from stationary-phase cells of GB2 using techniques as described by Thijs et al. (5).

In total, 718,104 reads (mean length 241 bases) generated 174 Mb of data (>145 M Q20 bases) in Torrent Suite 4.2.1. These were assembled using SPAdes 3.1.0 (6, 7) (uniform coverage mode; k-mers 21, 33, 55, 77, 99) into 24 contigs greater than 500 bp, giving a consensus length of 4,392,282 bp at 20.0× coverage (largest contig 1,288,409 bp; N_{50} = 507,764 bp). To identify closely related organisms with complete genomes in NCBI RefSeq, the Rapid Annotations Subsystems Technology (RAST) server (8) was used.

Bacillus licheniformis ATCC 14580 (GenBank accession no. CP000002) was used as a reference to reorder the GB2 contigs in Mauve (9). Open reading frame (ORF) prediction and gene annotation was completed out using the PGAP (NCBI) pipeline (10). The genome of *Bacillus licheniformis* GB2 consists of a single circular chromosome (46.1% G+C content), including 4,586 coding genes that were arranged into pathways using Pathway Tools

(11, 12), 420 pseudogenes, 22 rRNAs (5S, 16S, 23S), 77 tRNAs, and 1 noncoding RNA (ncRNA).

Homologues of genes related to plant growth-promoting traits such as nitrogen fixation, inorganic phosphorus solubilization, auxin biosynthesis, as well as acetoin and siderophore production were found, along with copies of genes for alkane utilization including alkane monooxygenase (*alkB*), and aldehyde dehydrogenase (*alkH*). The lower naphthalene pathway is partially present in GB2.

The use of *B. licheniformis* GB2 as a plant growth-promoting inoculant for enhancing remediation of diesel-contaminated sites based on plant-bacteria partnerships is being investigated.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [JYGX000000000](https://www.ncbi.nlm.nih.gov/nuccore/JYGX000000000). The version described in this paper is version [JYGX010000000](https://www.ncbi.nlm.nih.gov/nuccore/JYGX010000000).

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