Genome Announcements

Complete Genome Sequence of Bacillus methylotrophicus Strain B25, a Potential Plant Growth-Promoting Rhizobacterium

Jonathan Gerbore, Aline Brutel, Arnaud Lemainque, Barbara Mairey, Claudine Médigue, David Vallenet, Francois Lefort, Damien Grizard

Bacillus methylotrophicus strain B25 (formerly Bacillus amyloliquefaciens subsp. plantarum) (1) is a Gram-positive bacterium isolated in Switzerland from the inner wood tissues of a decaying Platanus x acerifolia tree. Bacterial strains belonging to this clade are plant-associated microorganisms known to have beneficial effects on their hosts, such as growth promotion and health enhancement (2–4). The complete genome sequence of B. methylotrophicus strain B25 is reported here and will provide genomic information on the specific properties of this strain.

DNA was extracted with the GenElute bacterial genomic DNA kit (Sigma-Aldrich), according to the manufacturer’s instructions. Two libraries were constructed for sequencing at Genoscope. First, genomic DNA was fragmented, and inserts between 300 and 600 nucleotides (nt) were selected to construct a paired-end indexed library. Second, genomic DNA was fragmented, and inserts of around 8 kb were selected to construct a mate-paired indexed library. These libraries were loaded on an Illumina MiSeq sequencing device flowcell and sequenced on paired-ends, at 300 nt in length.

The reads from the paired-end library were merged with a homemade program and were assembled with mate-paired data using Newbler (overlap layout consensus [OLC]) (Roche). To reduce the number of undetermined bases, GapCloser was used.

The remaining gaps were then covered using PCRs and specific primers for gap edges. The PCR fragments were sequenced by primer walking. The whole-assembly data were integrated into the MicroScope platform (http://www.genoscope.cns.fr/agc/microscope) for automatic annotation (5).

The complete genome of B. methylotrophicus strain B25 contains a 3,854,619-bp circular chromosome and an 8,138-bp plasmid. The genome contains 3,679 coding sequences (CDS), with an average length of 934 bp, 21 tRNAs, and 68 tRNAs, and has a G+C content of 46.7%. The annotation predicted gene clusters coding for nonribosomal peptide synthetases (NRPS) and polyketide synthases (PKS). Among all predicted protein-coding genes, the strain B25 genome includes interesting genes involved in bacterium-plant interactions and plant growth promotion activities, i.e., the bacillilabactin siderophore, an operon required for biofilm formation (epsA-0), and a phytate-degrading enzyme (phytase) (6). Gene resistance analysis was conducted with the CARD system (http://arpcard.mcmaster.ca/) (7). The B25 genome contains only natural resistance genes conserved at the species level. Gene content comparisons and synteny conservations indicate that the closest neighbors of B25 are B. methylotrophicus strains FZB42 (6), IT-45 (6), LBFI12 (8), and Y2 (9). Further studies and genome comparisons of B. methylotrophicus strain B25 will enable the elucidation of the mechanisms supporting its plant-benefiting properties.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession numbers LN999829 and LN999830.

ACKNOWLEDGMENTS

The LABGeM (CEA/IG/Genoscope & CNRS UMR8030) and the France Génomique National infrastructure (funded as part of Investissement d’Avenir Program managed by Agence Nationale pour la Recherche, contract ANR-10-INBS-09) are acknowledged for support within the MicroScope annotation platform.

REFERENCES


Received 20 January 2016 Accepted 28 January 2016 Published 10 March 2016


