



# Draft Genome Sequence of *Bacillus* sp. HMA207, a Strain That Exhibits $\beta$ -D-Galactosidase Activity To Release Pyruvylated Galactose

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**ABSTRACT** The genome sequence of the *Bacillus* sp. strain HMA207, the culture supernatant of which exhibited  $\beta$ -D-galactosidase activity to release pyruvylated galactose (PvGal), was examined to identify a PvGal-ase-encoding gene. We report here the result of whole-genome shotgun sequencing, which revealed putative PvGal-ase genes.

In a wide range of organisms, pyruvic acid (Pv) is attached to the terminus of *N*-linked glycans (1, 2). This pyruvylation confers a negative charge and has versatile physiological roles, for example, in intercellular interactions (3). Although several enzymes involved in the biosynthesis of Pv-containing sugar chains have been reported, enzymes that metabolize Pv-attached oligosaccharides are not well understood (4–6). We previously screened soil samples and found a strain that exhibits  $\beta$ -D-galactosidase activity to release Pv-attached galactose (PvGal) (7). We further identified the strain to be a *Bacillus* species by 16S rRNA gene analysis and named the strain HMA207 (7). Here, we conducted whole-genome sequencing of *Bacillus* sp. strain HMA207 to identify the putative PvGal-ase genes.

The HMA207 strain was cultured in LB medium (0.5% yeast extract, 1% tryptone, 1% NaCl, and 3% agar; pH 7.0) at 30°C, with shaking at 200 rpm. For genomic DNA preparation, the ISOPANT extraction kit (Nippon Gene, Japan) was used according to the manufacturer's instructions. The draft genome sequence of strain HMA207 was acquired by a whole-genome shotgun-sequencing strategy using a MiSeq sequencer (Illumina, UK). With an average of 230-bp paired-end reads, a 7.78-Gbp sequence was generated from  $3.38 \times 10^7$  sequencing reads (1,470-fold coverage). As a quality control, we conducted trimming and filtering using Trimmomatic version 0.32 with the settings of paired-end mode (<http://www.usadellab.org/cms/?page=trimmomatic>). Platano version 1.2.1 was used to assemble these sequence reads, and 18 contigs were obtained, the longest of which contained 3,953,797 bp. Genome annotation was carried out using the BLAST version 2.2.26 (blastp) nonredundant protein sequence database with an E value of  $<1e^{-4}$  and Glimmer version 3.02b with the script g3-iterated.csh. The draft genome of *Bacillus* sp. strain HMA207 was 5.29 Mbp, with an overall GC content of 35.1%, putatively encoding 5,416 genes with a gene density of 977 bp/gene. The mean and median gene lengths were 827 bp and 714 bp, respectively. Based on annotation of the whole-genome sequence of *Bacillus* sp. strain HMA207, we found three putative glycosidase genes that potentially encode PvGal-ase, named ORF1119 (GenBank accession number [BEZT01000001](#)), ORF4395 (GenBank accession number [BEZT01000002](#)), and ORF4971 (GenBank accession number [BEZT01000004](#)), located in contig01, contig02, and contig04, respectively. Further elucidation based on such gene annotation would reveal how strain HMA207 degrades PvGal-containing oligosaccharides.

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**Data availability.** The contig sequences of *Bacillus* sp. strain HMA207 have been deposited at the DDBJ/EMBL/GenBank database under the accession numbers [BEZT01000001](#) to [BEZT01000018](#).

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