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GENOME ANNOUNCEMENT

Genome Sequences of Two Thermophilic *Bacillus licheniformis* Strains, Efficient Producers of Platform Chemical 2,3-Butanediol

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Both *Bacillus licheniformis* strains 10-1-A and 5-2-D are efficient producers of 2,3-butanediol. Here we present 4.3-Mb and 4.2-Mb assemblies of their genomes. The key genes for the regulation and metabolism of 2,3-butanediol production were annotated, which may provide further insights into the molecular mechanism for the production of 2,3-butanediol with high yield and productivity.

Microbial production of 2,3-butanediol (2,3-BD) has a long history, and various bacteria have been used to produce 2,3-BD (2, 3, 5, 6, 8, 9, 16). 2,3-BD is a crucial platform compound, which could be used to produce valuable derivatives such as methyl ethyl ketone and 1,3-butadiene (2, 3). However, the 2,3-BD yield and productivity of generally recognized as safe (GRAS) strains, such as *Bacillus* species, were very low (3). It was reported previously that *Bacillus licheniformis* could be used for the production of 2,3-BD from glucose, xylose, and other sugars (9, 10, 11). *B. licheniformis* strains can also be used in industry for the manufacturing of enzymes, antibiotics, and chemicals and have been identified as being important in nutrient cycling in the environment (12). The *B. licheniformis* strain 10-1-A (CGMCC 5461) strain that was isolated from soil samples is a potential industrial candidate for 2,3-BD production, which could produce 2,3-BD with high productivity (>3.8 g liter^{-1} h^{-1}) and high yield (>96%) from glucose at a temperature above 50°C (unpublished results). *B. licheniformis* strain 5-2-D (CCTCC M 2011371) was also isolated from soil samples by our group, and it could also produce 2,3-BD from glucose with a high yield (>96%); however, the productivity was lower than that of strain 10-1-A (unpublished results).

Here, we present high-quality draft genome sequences of strains 10-1-A and 5-2-D, which were obtained using the Illumina HiSeq 2000 system. A total of 16,212,242 filtered reads for 10-1-A were assembled into 31 contigs and 15,307,178 filtered reads for 5-2-D were assembled into 45 contigs using VELVET (15). The genome annotations were performed by the RAST server (1). The functional descriptions were determined using the COG database (14). The genes encoding tRNAs and rRNAs were identified by tRNAscan-SE (7) and RNAmmer (4), respectively.

The draft genome sequences of strains 10-1-A and 5-2-D consist of 4,317,010 and 4,161,078 bases with GC contents of 45.9% and 46.1%, respectively. There were 33 and 35 predicted tRNAs in strains 10-1-A and 5-2-D, respectively. A total of 4,650 protein-coding sequences (CDSs) for strain 10-1-A were identified with an average length of 799 bp; a total of 4,452 CDSs for strain 5-2-D were also identified with an average length of 805 bp. A total of 501 and 493 subsystems were determined using the RAST server for strains 10-1-A and 5-2-D, respectively. Each sequence contains two complete operons and key coding genes for 2,3-BD metabolism, which could provide further insights into the production of 2,3-BD. There are 607 and 611 CDSs for the utilization of carbohydrates in strains 10-1-A and 5-2-D, respectively, indicating that strains 10-1-A and 5-2-D may have a wide substrate spectrum. Each genome sequence contains a series of membrane transport systems, including 73 CDSs involved in ATP-binding cassette (ABC) transporters and 25 CDSs involved in phosphotransferase systems. They may play important roles in the production of 2,3-BD with high productivity.

Nucleotide sequence accession numbers. The whole-genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under the accession numbers AJLV00000000 and AJLW00000000 for strains 10-1-A and 5-2-D, respectively. The versions described in this paper are the first versions, AJLV01000000 and AJLW01000000.

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