JOURNAL OF BACTERIOLOGY, Dec. 2011, p. 6799–6800 Vol. 193, No. 23
0021-9193/11/$12.00 doi:10.1128/JB.06196-11

Genome Sequence of *Bifidobacterium breve* DPC 6330, a Strain Isolated from the Human Intestine

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Received 15 September 2011/Accepted 21 September 2011

The draft genome of *Bifidobacterium breve* DPC 6330, isolated from an elderly patient, was determined. *B. breve* DPC 6330 was previously identified to synthesize the beneficial metabolite conjugated linoleic acid from free linoleic acid. The sequence will allow identification and characterization of the genetic determinants of its putative beneficial properties.

Bifidobacteria are common inhabitants of the human intestinal tract and are well studied for their health-promoting properties in the prevention and treatment of gastrointestinal disorders. In recent years, whole-genome sequencing has been employed to help determine the genetic bases for potential probiotic traits of bifidobacteria (13, 14), although so far the molecular bases for many of their beneficial activities remain unresolved.

Previous work identified a number of bifidobacterial isolates with the ability to convert linoleic acid to conjugated linoleic acid (CLA) in synthetic broth (3). The interest in the health-promoting properties of the CLA isomers has increased in recent years due to their potential immune modulation, anticarcinogenic, and antiobesity activities (4, 9, 12, 15). *Bifidobacterium breve* DPC 6330, an isolate from a fecal sample from an elderly patient, showed high CLA-producing ability among the isolates tested (3). Here, we present the draft genome sequence of *B. breve* DPC 6330, which will allow full characterization of its potential probiotic traits.

The genome of *B. breve* DPC 6330 was sequenced by 454 pyrosequencing on a GS-FLX sequencer to a coverage of 25-fold by Beckman Coulter Genomics, and the data were assembled into 47 contigs using the Newbler program (Roche Applied Science). Coding regions were predicted using Glimmer 3.0 (7, 8), and annotation was subsequently performed using GAMOLA (1). Complementary annotation data were provided by the SEED viewer (11) and the RAST annotation server (2). Comparative genomics analysis was performed using the Artemis comparison tool (5, 6) and Mauve software (6).

The uncompleted draft genome includes 2,385,951 bases with a G+C content of 58.6%. A total of 1,881 protein-encoding genes, 53 tRNA-encoding genes, and 2 rRNA operons were predicted in the draft genome. Order and orientation of the assembled contigs were determined by mapping against the recently available *B. breve* UCC2003 genome (10). Overall, the genome of *B. breve* DPC 6330 is highly similar to the *B. breve* UCC2003 genome in size, G+C content, and gene synteny. However, comparative genomic analysis revealed that DPC 6330 differs from the UCC2003 strain in certain functional categories, including regulatory proteins, putative mobile elements, and cell defense systems. The strains also differ in prophage-like elements that are located within both genomes. A cluster of genes encoding 19 putative phage-related proteins are identified within the *B. breve* DPC 6330 genome that are absent from UCC2003 and the completed *B. breve* ACS-071-V-Sch8b genome (GenBank accession no. CP002743). There are also significant differences in putative cell defense mechanisms, as there is variation in the restriction-modification systems and CRISPR-related elements present.

The availability of the genome sequence of DPC 6330 will allow further analysis and understanding of the health-promoting characteristics of the *B. breve* species.

Nucleotide sequence accession numbers. The draft genome sequence of *B. breve* DPC 6330 has been deposited in DDBJ/EMBL/GenBank under the accession number AFXX00000000. The version described in this paper is the first version, accession number AFXX01000000.

This work was supported by Science Foundation Ireland and funded by the Centres for Science, Engineering and Technology (SFI-CSET), Alimentary Pharmabiotic Centre (APC).

We acknowledge Orla O'Sullivan for bioinformatics assistance.

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