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Complete Genome Sequence of *Bifidobacterium longum* subsp. *longum* DS0950 Isolated from Infant Feces with Obesity-Ameliorating Effects

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***Bifidobacterium longum* subsp. *longum* DS0950 (*B. longum* DS0950) was isolated from infant feces and has been reported to be effective in preventing obesity. The whole-genome sequence of *B. longum* DS0950 was obtained using the PacBio RS II platform, and it was consists of a single chromosome of 2,433,092 bp. The *B. longum* DS0950 contains genes associated with the synthesis of bacteriocins and a series of genes capable of producing xylitol from ribulose-5-phosphate.**

Keywords: **Probiotics, *Bifidobacterium longum* subsp. *longum*, anti-obesity, whole-genome sequencing**

Bifidobacterium longum subsp. *longum* is a representative colonizer of the early intestinal microbiota of newborn and is commonly found in the human gastrointestinal tract [1]. *Bifidobacterium longum* subsp. *longum* DS0950 (*B. longum* DS0950) was isolated from infant feces and has been demonstrated as a potential probiotic that can alleviate obesity through mechanisms involving weight loss and reduced fat accumulation [2].

The bacterial genomic DNA was extracted using bead beating and phenol-chloroform method [3]. Subsequently, the purity of DNA was accessed using the NanoDrop Spectrophotometer (Thermo Fisher Scientific, USA). Genomic DNA library construction and sequencing on the PacBio RSII platform were carried out by Macrogen Inc. (Republic of Korea). De novo assembly was performed with HGAP (v3.0) [4] and annotated using Prokka (v1.12b) [5].

To assess the genetic safety of *B. longum* DS0950 and identify acquired antibiotic resistance genes, ResFinder v4.1 and VirulenceFinder v2.0 [6] were employed for the detection of antibiotic resistance and toxicity genes. Resistance genes were identified using the Comprehensive Antibiotic Resistance Database (CARD) and Resistance Gene Identifier (RGI) web server v5.2.0 [7]. Mobile genetic elements of the bacterial strains were determined using Mobile Genetic Elements (MGE) version 1.0.3 (database version 1.0.2) [8]. Bacteriocin production was investigated using BAGEL4 [9]. Pathway analysis was performed using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database to identify functional metabolic genes in *B. longum* DS0950.

The total genome length of *B. longum* DS0950 was 2,433,092 bp consisting of a single contig. The overall G+C content was 60.14%. The genome comprises 2,002 coding sequences, 12 rRNA genes, and 57 tRNA genes (Table 1). According to the results of the KEGG pathway

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Table 1. General genomic features of the *B. longum* DS0950.

Strain	*B. longum* DS0950
Genome size (bp)	2,433,093
G+C content (%)	60.14
Total number of genes	2,055
Total coding genes (CDS)	2,002
tRNA	57
rRNA	12
ncRNAs	3

analysis, key genes related to metabolism were identified: 165 genes involved in carbohydrate metabolism, 145 genes related to amino acid metabolism, 57 genes related to energy metabolism, 54 genes related to nucleotide metabolism, and 26 genes related to lipid metabolism (Fig. 1). Genes associated with carbohydrate metabolism, particularly those involved in glycolysis and the pentose phosphate pathway, facilitate the production of ribulose-5-phosphate. This strain was predicted to produce xylitol through genes encoding ribulose phosphate 3-epimerase (EC:5.1.3.1), D-xylulokinase (EC:2.7.1.17), and D-xylulose reductase (EC:1.1.1.9). These characteristics differ from typical features of *B. longum*, which produces only xylose by encoding xylose isomerase. Additionally, BAGEL4 genome mining detected one bacteriocin operon in *B. longum* DS0950 that exhibited homology with BLD 1648 of *Bifidobacterium longum* subsp. *longum* DJO10A (Fig. 2).

ResFinder, VirulenceFinder, and the CARD database were utilized to screen strains for antibiotic resistance and toxicity genes and evaluate their safety. The results indicated the absence of antibiotic resistance and toxicity genes in the *B. longum* DS0950 genome. However, a mutation (rpoB) was identified in chromosomal DNA.

Furthermore, no transposable or mobile elements that could facilitate the transfer of antibiotic resistance or toxicity genes were found, as there was an absence of mobility genes associated with horizontal gene transfer. Therefore, it has been deemed suitable for probiotic use. The genome sequence of *B. longum* DS0950, recognized

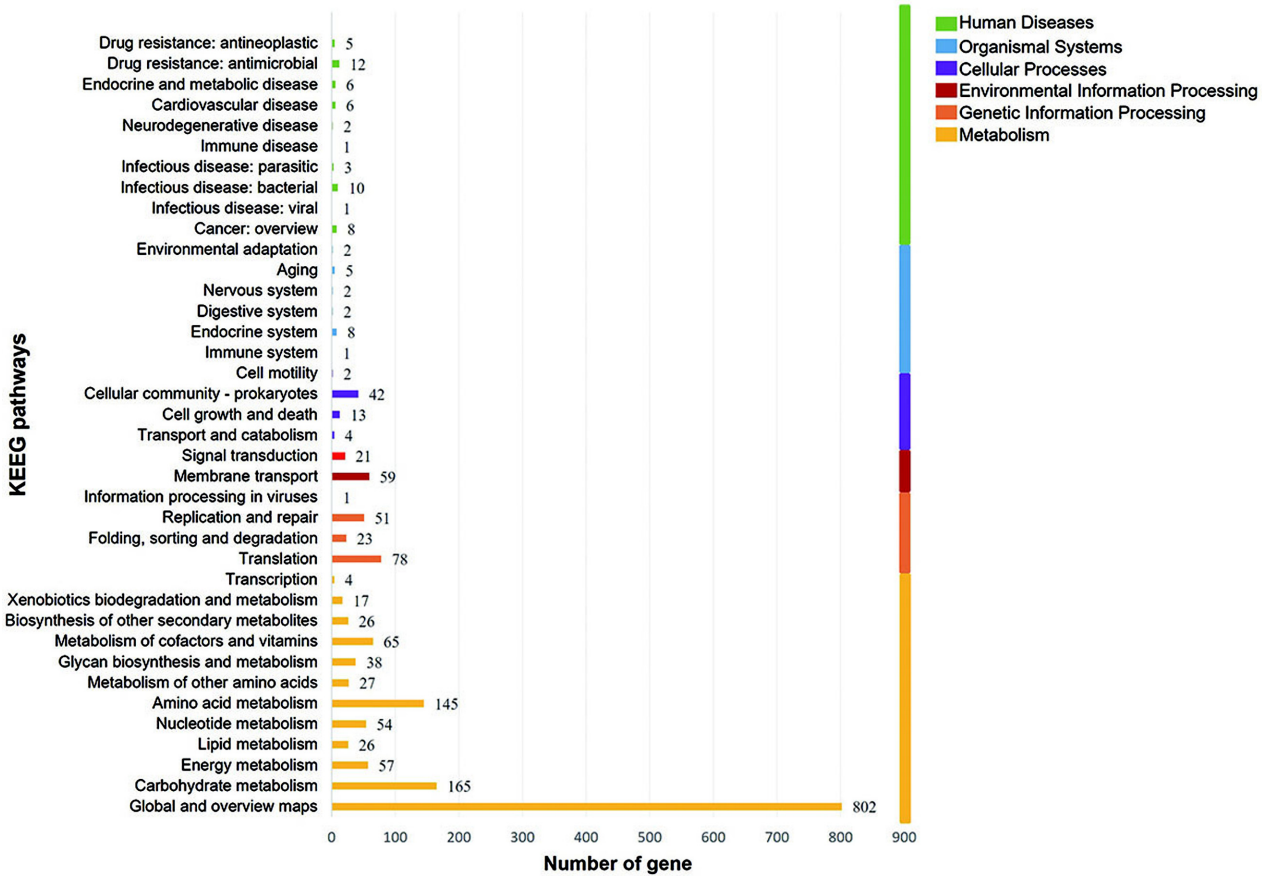

Fig. 1. Functional annotation by KEGG metabolic pathway of *Bifidobacterium longum* subsp. *longum* DS0950.

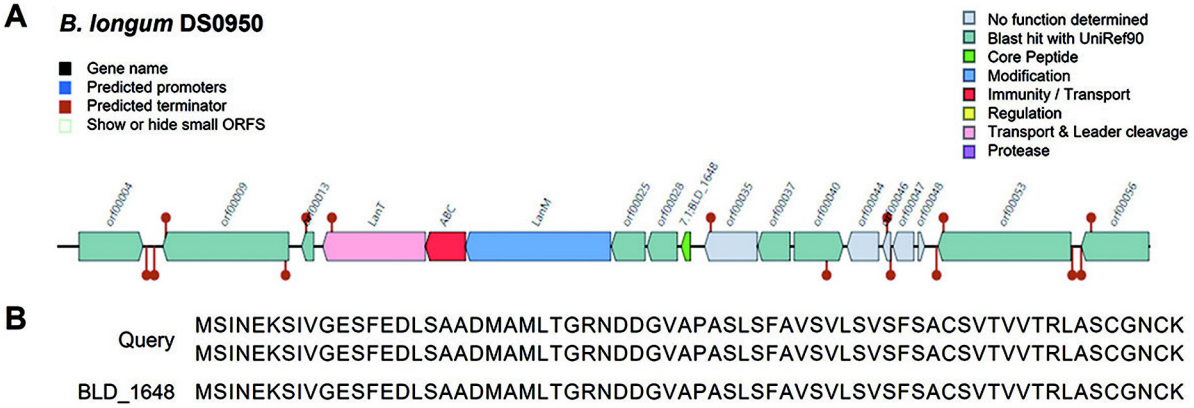

Fig. 2. Illustrations of the BGC mining results for *B. longum* DS0950. (**A**) Bacteriocin biosynthetic gene cluster. (**B**) multiple sequence alignment results of putative lantibiotic peptide with BLD 1648 in *Bifidobacterium longum* subsp. *longum* DJO10A.

for its efficacy in preventing obesity, offers valuable insights into the health-promoting characteristics of this strain and the mechanisms involved in its interaction with the host.

요 약

Bifidobacterium longum subsp. *longum* DS0950 (*B. longum* DS0950)은 신생아 분변에서 분리되었으며 비만 개선 효능이 보고되었다. *B. longum* DS0950 전장유전체 서열은 PacBio RS II platforms을 이용하여 확보하였으며, 유전체의 크기는 2,433,092 bp의 단일 contig로 분석이 되었다. *B. longum* DS0950 균주는 박테리오신의 합성에 관련된 유전자와, ribulose-5-phosphate로부터 xylitol 생산할 수 있는 일련의 유전자를 보유하고 있다.

Nucleotide Sequence Accession Number

The genome sequences are available at GenBank under the accession number CP069278.

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Conflict of Interest

The authors have no financial conflicts of interest to declare.

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