

Genome Reports

Complete Genome Sequence of *Bifidobacterium bifidum* DS0908, Isolated from Human Fecal Sample

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In this report, we present the whole-genome sequence of *Bifidobacterium bifidum* DS0908 isolated from the human fecal sample. The genome composed of a single circular chromosome is 2,223,317 bp long and the DNA G+C content is 62.65%. No virulence genes were detected in the genomic sequences of *B. bifidum* DS0908.

Keywords: *Bifidobacterium bifidum*, whole genome sequencing, fecal sample

Bifidobacterium, an anaerobic gram-positive bacterium, is one of the commonly studied genera that receive attention as probiotics, along with *Lactobacillus* [1]. Previous research has demonstrated the anti-obesity effects of *Bifidobacterium bifidum* DS0908, confirming its potential as a probiotic that can assist in obesity treatment by improving glucose metabolism, insulin sensitivity, and plasma lipid profiles [2]. In this report, genomic analysis was conducted on *B. bifidum* strain DS0908 and analysis of virulence factor-related genes was performed because it is one of the factors used to assess the safety of probiotics [3].

B. bifidum strain DS0908 was isolated from human fecal microbiota screening using De Man, Rogosa and Sharpe (MRS) agar. The genomic DNA of *B. bifidum* strain DS0908 was extracted using phenol: chloroform: isoamyl alcohol method [4]. Whole-genome sequencing was carried out using a PacBio RS II (Macrogen, Seoul,

South Korea). The total number of subreads was 1,000,097, with a total of 951,472,998 subread bases, and HGAP3 was used to assemble the long-reads. The entire assembled genome was visualized using Proksee [5]. Genome annotation was performed using Prokka (v1.14.6) [6]. In addition, the investigation of virulence genes was conducted using the VirulenceFinder 2.0 Server provided by the Center for Genomic Epidemiology (CGE) (<http://www.genomicepidemiology.org/>), analyzing genes belonging to 16 different classes. The percentage of identity was established with a 5% threshold [7].

One circular contig formed as result of assembly comprised a single chromosome (Fig. 1). The length of the contig was 2,223,317 bp; the N_{50} value was also 2,223,317 bp, and the DNA G+C content was 62.65%. A total of 1,793 protein-coding genes, 53 transfer RNA genes, and 9 ribosomal RNA genes were identified through genome annotation (Table 1). In the analysis of virulence factor-related genes, it was confirmed that *B. bifidum* strain DS0908 lacks any virulence genes as summarized in Table 2, indicating its safety with regard to toxicity.

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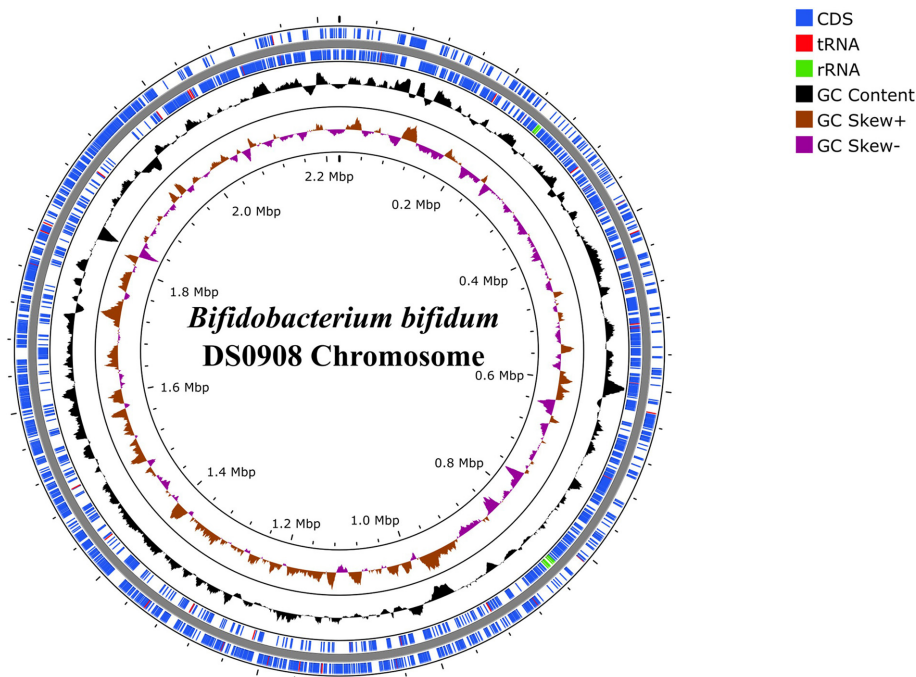


Fig. 1. Genome map of *Bifidobacterium bifidum* DS0908, generated using the Proksee tool.

Table 1. Genome features of *Bifidobacterium bifidum* DS0908.

Genome features	Value
Number of contigs	1
Chromosome size (bp)	2,223,317
GC contents (%)	62.65
Coding genes (CDSs)	1,793
Transfer RNAs (tRNAs)	53
Ribosomal RNAs (rRNAs)	9

The complete genome sequence data of *B. bifidum* strain DS0908 was submitted to the GenBank database with the accession number CP069279.1. The BioProject accession number is PRJNA698755 and the Bio-Sample accession number is SAMN17735950.

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Table 2. Analysis for the existence of potential genes associated with virulence factors in the genome of *Bifidobacterium bifidum* DS0908.

Class	Gene	<i>Bifidobacterium bifidum</i> DS0908 Contig1
Enterotoxin	<i>selk, selq, set</i>	–
Leucotoxin	<i>lukD</i>	–
Cytolysin	<i>cylA</i>	–
Cytotoxin K	<i>cytK</i>	–
Hemolysin	<i>hbl</i>	–
Gelatinase	<i>gelE</i>	–
Amino acid decarboxylase	<i>hdc1, hdc2</i>	–
	<i>tdc</i>	–
	<i>odc</i>	–
	<i>ldc</i>	–
Hyaluronidase	<i>hyl</i>	–
Endocarditis antigen	<i>efaA</i>	–
Enterococcal surface protein	<i>esp</i>	–
Aggregation substance	<i>asa1</i>	–
Adhesion of collagen	<i>ace</i>	–
Cereulide	<i>cesA</i>	–
Serine protease	<i>sprE</i>	–
Sex pheromones	<i>ccf, cob, cpd</i>	–
Transposon-related genes	<i>int, intTN</i>	–

–: not detected

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