

Complete genome sequence of *Streptococcus hyointestinalis* B19, a strain producing bacteriocin, isolated from chicken feces

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Competing interests

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Availability of data and material

Upon reasonable request, the datasets of this study can be available from the corresponding author.

Abstract

Streptococcus hyointestinalis B19 was isolated from chicken feces collected from local farm in Anseong, Korea. *S. hyointestinalis* B19 was shown to produce bacteriocin-like compounds exhibiting inhibitory activities against several pathogens including strains of *Clostridium perfringens* and *Listeria monocytogenes*. The whole genome of *S. hyointestinalis* B19 strain was sequenced using PacBio RS II platform. The genome comprised four contigs with a size of 2,217,061 bp. The DNA G + C content was found to be 42.95 mol%. Annotation results revealed 2,266 coding sequences (CDSs), 18 rRNAs, and 61 tRNA genes. Based on genome analysis, we found that the strain B19 possessed various genes associated with bacteriocin synthesis, modification, and transport.

Keywords: *Streptococcus hyointestinalis* B19, Whole genome, Chicken feces, Bacteriocin

In recent years, there have been increasing studies to find alternatives to antibiotics, such as antibodies, probiotics, bacteriophages, and bacteriocins because of the increase in antibiotic resistance [1,2]. In our previous study, we reported that *S. hyointestinalis* B19 has potential to be used in similar applications [3]. *S. hyointestinalis* B19 strain was found to produce antimicrobial protein molecules, which possess characteristics similar to those of bacteriocin (heat stability). The selected strains of *Clostridium perfringens* and *Listeria monocytogenes* were strongly inhibited by the strain B19. To confirm whether the antimicrobial substance is bacteriocin and to better understand the characteristics of the molecule, we carried out whole genome sequencing of the strain B19.

S. hyointestinalis B19 was isolated from chicken fecal samples collected from local farm in Anseong, Korea. The genomic DNA was extracted from the strain B19 cultured to stationary phase in M17 medium supplemented with 0.5% (w/v) glucose using QIAamp PowerFecal DNA Kit (Qiagen) according to the manufacturer's instructions. The whole genome of strain B19 was sequenced using Pacific Biosciences (PacBio) RS II Single Molecule Real Time (SMRT) platform with a 20 kb SMRTbell™ template library at ChunLab. The reads were assembled on PacBio SMAR Analysis 2.3.0. Genome analysis and annotation were performed by CLGenomics™ v. 1.55 software. Transfer RNAs (tRNAs) were identified using tRNAscan-SE v. 1.3.1. Ribosomal RNAs (rRNAs) and non-coding RNAs (ncRNAs) were identified using INFERNAL v. 1.0.2 with Rfam 12.0 database. For CRISPR, PilerCR v. 1.06 and CRT v. 1.2 were used. Protein-coding sequences (CDSs) were identified by using PRODIGAL v. 2.6.2 [4] and compared to protein databases (SwissProt, KEGG, SEED, EggNOG) using USEARCH v. 8.1

Authors' contributions

Conceptualization: Kim GB.
 Data curation: Lee JE.
 Formal analysis: Heo S.
 Investigation: Lee JE, Heo S, Kim GB.
 Writing - original draft: Lee JE.
 Writing - review & editing: Lee JE, Kim GB.

Ethics approval and consent to participate

This manuscript does not require IRB/IACUC approval because there are no human and animal participants.

[5] for functional annotation. The draft genome of *S. hyointestinalis* B19 consisted of a 2,217,061 bp chromosome with a G + C content of 42.95% (Table 1). The genome contained 2,266 coding sequences (CDSs), 18 rRNAs, and 61 tRNA genes (Fig. 1).

The mining of the bacteriocinogenic gene clusters was performed by using the BAGEL4 platform [6]. The genome possessed *thmA*-, *thmB*-like genes, and bovicin 255-like genes. The former genes encode peptides ThmA and ThmB, respectively, that form Thermophilin 13, the bacteriocin

Table 1. Genome features of *Streptococcus hyointestinalis* B19

Property	Value
Genome assembly	
Assemble method	SMAR analysis version 2.3.0
Genome coverage	438.91x
Genome features	
Genome size (bp)	2,217,061
No. of contigs	4
G + C content (%)	42.95
Protein-coding genes (CDSs)	2,266
rRNA genes	18
tRNA genes	61
Plasmids	0
Genbank accession No.	JAAKGB000000000

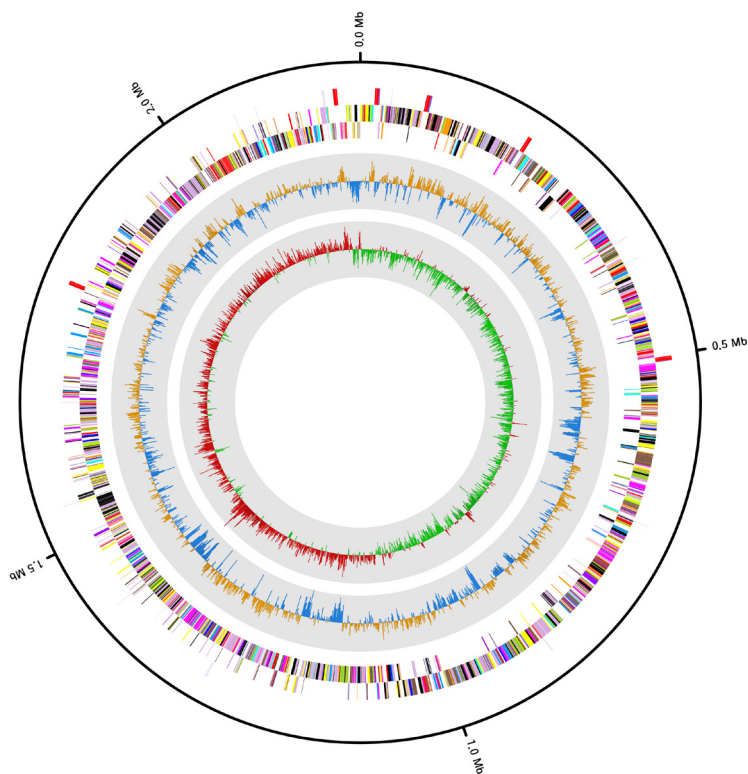


Fig. 1. Circular genome map of *Streptococcus hyointestinalis* B19. From the outermost circle to the center, each circle indicates information about tRNA/rRNA, forward and reverse coding sequences (CDSs), GC ratio, and GC skew.

first isolated from *S. thermophilus* [7]. Strain 19 also contains the genes associated with ABC-transporter and bacteriocin immunity for bacteriocin export and self-immunity to bacteriocin, respectively. These two genes are common members of the lantibiotic gene clusters [8].

Nucleotide sequence accession number

The GenBank/EMBL/DDBJ accession number for the genome sequence of *S. hyointestinalis* B19 is JAAKGB000000000.

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