



## Genome sequence of *Bifidobacterium dentium* strain ATCC 15424 originally isolated from pleural fluid of an empyema patient



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## 농흉 환자의 흉막액에서 분리된 *Bifidobacterium dentium* strain ATCC 15424의 유전체 염기서열 해독

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We present here a draft genome sequence of *Bifidobacterium dentium* strain ATCC 15424, originally isolated from pleural fluid of an empyema patient. The genome is 2,625,535 bp in length and has a GC content of 58.5%. The genome includes 2,154 protein-coding genes, 4 rRNAs, and 55 tRNAs. Unlike other *B. dentium* strains isolated from human dental caries, ATCC 15424 carries 247 strain-specific genes, including prophage remnants and type III/IV secretion system proteins, N-acetylmuramoyl-L-alanine amidase, and PRTRC system protein E. The sequence information will contribute to understanding of the natural variation of *B. dentium* as well as the genome diversity within the bacterial species.

**Keywords:** *Bifidobacterium dentium*, genome, pleural fluid isolate

The genus *Bifidobacterium* is mainly found in the gastrointestinal tract of human and known to have beneficial effects, such as reducing the number of harmful bacteria *via* the host and enhancing intestinal immunity (Gibson and Wang,

1994; Gill *et al.*, 2001; Manome *et al.*, 2019). *Bifidobacterium dentium* is predominant among *Bifidobacterium* species that are found in the intestine as well as in the mouth, and it has been recognized to be related to dental caries (Munson *et al.*, 2004; Manome *et al.*, 2019). The type strain of *B. dentium* (JCM 1195<sup>T</sup>) isolated from human dental caries was first reported by Scardovi and Crociani (1974) and the complete genome of this organism has recently been sequenced (Toh *et al.*, 2015). Currently, the genome sequences of *B. dentium* strains, which were isolated from the human mouth, vagina, and infant and adult feces, are available in GenBank. Meanwhile, *B. dentium* ATCC 15424 was isolated from an empyema patient (Geroge *et al.*, 1965) and initially described as “*Actinomyces eriksonii*”, but later found to be *B. dentium* (Biavati *et al.*, 1982). As bacterial strains isolated from different environments can exhibit different phenotypic and genomic features, strain ATCC 15424 originated from pleural fluid drew our attention. Here we first report a draft genome sequence of *B. dentium* ATCC 15424. The sequence information will contribute to understanding of

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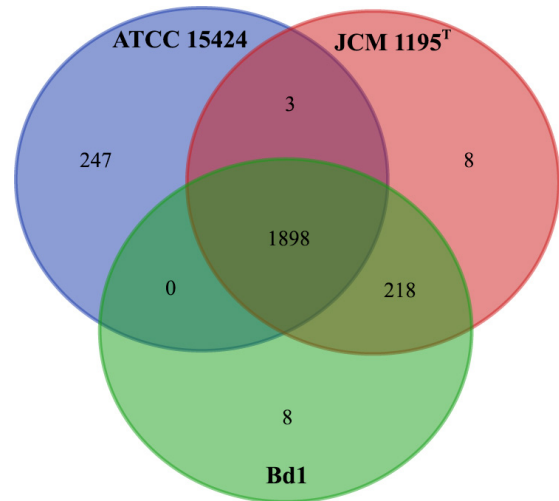
**Table 1.** Genome features of *Bifidobacterium dentium* ATCC 15424

Attribute	Value
Genome size (Mb)	2.62554
GC content (%)	58.5
No. of scaffolds	21
Total genes	2,258
Protein-coding genes	2,154
tRNAs	55
Complete rRNAs (5S, 16S, 23S)	2, 1, 1
Partial rRNAs	0
ncRNAs	3
Pseudogenes	42
N50	383,661
Overall estimated genome coverage	782.3x

the natural variation of *B. dentium* as well as the genome diversity within the bacterial species.

*B. dentium* ATCC 15424 was grown at 37°C in tryptone-yeast extract-glucose (TYG) anaerobically (85% N<sub>2</sub>, 10% H<sub>2</sub>, and 5% CO<sub>2</sub>). The bacterial genomic DNA was extracted, and the sequencing library was constructed as described previously (Moon *et al.*, 2019). In total, 6,923,297 paired-end read pairs (2 × 151 bp) were obtained. After filtering out low quality raw reads, SPAdes (version 3.12.0) (Bankevich *et al.*, 2012) with default parameters was used to construct the genome, resulting in 21 scaffolds (> 500-bp length). Gene annotation of the draft genome was performed by the NCBI Prokaryotic Genome Annotation Pipeline (Tatusova *et al.*, 2016).

The genome of *B. dentium* ATCC 15424 is 2,625,535 bp long and has a GC content of 58.5%. A total of 2,154 protein-coding genes, 4 rRNAs, and 55 tRNAs were annotated (Table 1). We calculated Average Amino acid Identity (AAI) and Average Nucleotide Identity (ANI) between ATCC 15424 and other two strains isolated from dental caries (JCM 1195<sup>T</sup> and Bd1) using Enveomics collection (<http://enve-omics.ce.gatech.edu/enveomics/>). The sequence data of *B. dentium* strains were obtained from NCBI *B. dentium* genome site (<https://www.ncbi.nlm.nih.gov/genome/?term=Bifidobacterium+dentium>). The results showed that ATCC 15424 shares 98.29% AAI (two-way) and 98.88% ANI (two-way) with the other strains JCM and Bd1, respectively. Meanwhile, 247 genes specific for

**Fig. 1.** Genomic comparison of *B. dentium* ATCC 15424 with other strains from dental caries. Venn diagram illustrates the number of shared and strain-specific genes found in the genome of each *B. dentium* strain.

strain ATCC 15424 were identified, such as prophage remnants, and genes encoding type III and IV secretion system proteins, N-acetylmuramoyl-L-alanine amidase and PRTRC (ParB-Related, ThiF-Related Cassette) system protein E (Fig. 1).

#### Nucleotide sequence accession number

This Whole Genome Shotgun sequencing project for *B. dentium* ATCC 15424 is available at GenBank under the accession SQKK00000000.1. The BioProject ID in GenBank is PRJNA529663.

## 적 요

본 논문에서는 농흉 환자의 흉막액에서 분리된 *Bifidobacterium dentium* ATCC 15424 균주의 유전체 염기서열을 분석하여 보고한다. 이 균주의 유전체는 구강에서 분리된 다른 *B. dentium* 균주에 존재하지 않는 type III 및 IV secretion system proteins, N-acetylmuramoyl-L-alanine amidase 그리고 PRTRC system protein E를 암호화하는 유전자 등 247개의 ATCC 15424 균주 특이적인 유전자들을 포함한다. 이 유전체의 서열 정보는 *B. dentium*의 자연적 변이와 세균 종 내의 유전체 다양성을 이해하는 데 유용할 것이다.

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