




Genome sequence of *Veillonella atypica* KHUD-V1 isolated from a human subgingival dental plaque of periodontitis lesion

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사람 치주염 병소의 치은 연하 치태에서 분리된 *Veillonella atypica* KHUD-V1의 유전체 염기서열 해독

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Here we report the genome sequence of *Veillonella atypica* strain KHUD-V1 isolated from subgingival dental plaque of Korean chronic periodontitis patients. Unlike other *V. atypica* strains, KHUD-V1 carries two prophage regions and prophage remnants, as well as several genes homologous to prophage-associated virulence factors, such as virulence-associated protein E, a Clp protease, and a toxin-antitoxin system. The isolate and its genome sequence obtained here will aid to understand the diversity of the genome architecture of *Veillonella* within an evolutionary framework and the role of prophages that contribute to the genetic diversity as well as the virulence of *V. atypica*.

Keywords: *Veillonella atypica*, genome, periodontitis, prophage

Anaerobic, Gram-negative cocci *Veillonella* species are a part of the normal microflora of the oral cavity, gastrointestinal

and urogenital tracts in humans (Pei *et al.*, 2004; Keijsers *et al.*, 2008; van den Bogert *et al.*, 2011). However, they can participate in mixed-species infections and have been isolated from patients with skin, dental, and respiratory infections. Rarely, *Veillonella* can cause serious infections like meningitis, endocarditis, and osteomyelitis (Saladi *et al.*, 2017).

Bacteriophages are viruses that infect bacteria. Once the bacteriophage genome is integrated into the host cell genome, it is called a prophage. Prophages play an intricate role in the evolution of bacterial genome, contribute to the genetic diversity even within the same species, and act as regulators of the microbiota composition (Roodt *et al.*, 2012; Lugli *et al.*, 2016). Prophages are also known to be closely related to the adaptation of existing pathogens to new hosts and the emergence of new pathogens or epidemic clones.

So far, very little is known about the occurrence and genetic variability of prophages within the *Veillonella*. Here, we report a genome sequence of *V. atypica* strain KHUD-V1 isolated from subgingival dental plaque of Korean chronic periodontitis

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patients. Interestingly, the genome of this strain contains two prophage regions, which are not found in the currently registered *V. atypica* genomes. Several virulence factors that may be associated with the prophages were also found. *V. atypica* strain KHUD-V1 has been deposited in the Korean Collection for Type Cultures (KCTC) for future reference and research. The new clinical isolate and its genome sequence obtained here will aid to understand the diversity of the genome architecture of *Veillonella* within an evolutionary framework, and the role of prophages that contribute to the genetic diversity as well as the virulence of *V. atypica*.

The bacterial genomic DNA was extracted, and the sequencing library was constructed following the paired-end sequencing on the Illumina Hi-Seq X platform. In total, 15,818,696 paired-

Table 1. Genome features of *Veillonella atypica* KHUD-V1

Attribute	Value
Genome size (bp)	2,189,293
GC content (%)	38.99
No. of scaffolds	54
Total genes	2,056
Protein-coding genes	1,969
tRNAs	42
Complete rRNAs (5S, 16S, 23S)	1, 1, 1
Partial rRNAs (16S, 23S)	1, 3
ncRNAs	4
Pseudogenes	34

end read pairs (2×151 bp) were obtained. After filtering out low quality raw reads, SPAdes (version 3.12.0) (Bankevich *et*

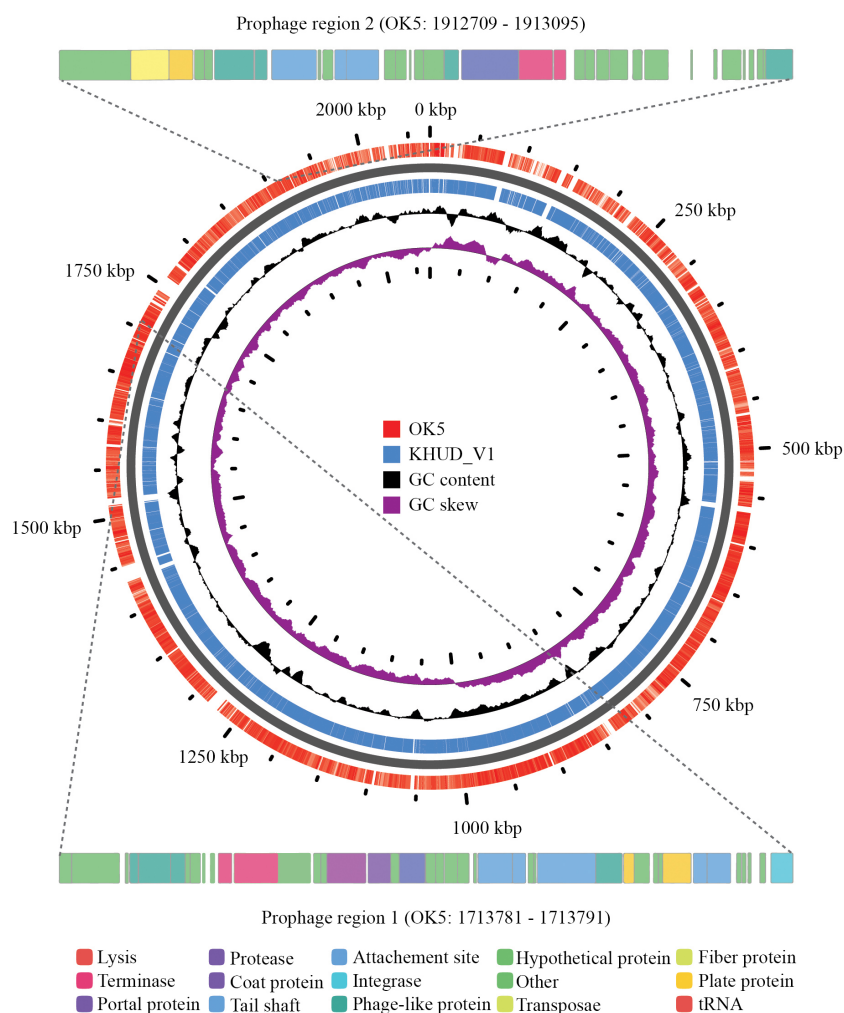


Fig. 1. Prophages present in *Veillonella atypica* KHUD-V1. Location of the prophages on the host chromosome and characterization of the genes were imaged using PHASTER.

al., 2012) with default parameters was used to construct the genome, creating 54 scaffolds (> 500-bp length). Gene annotation of the genome was performed by the NCBI Prokaryotic Genome Annotation Pipeline (Tatusova *et al.*, 2016). The genome of *V. atypica* KHUD-V1 was found to contain 2,189,293 bp with a G+C content of 38.99% (Table 1). A total of 1,969 protein-coding genes, 7 rRNAs, and 42 tRNAs were annotated (Table 1). Two clustered regularly interspaced short palindromic repeats (CRISPRs) arrays were also identified.

Pan genome analysis was performed using the currently registered *V. atypica* genomes in NCBI GenBank by Pan Genome Analysis Pipeline (PGAP) tools (Zhao *et al.*, 2012). PHASTER (PHAge Search Tool Enhanced Release) (Arndt *et al.*, 2016) was used to identify and annotate prophage sequence regions (Fig. 1). We identified 247 KHUD-V1 strain-specific genes, including two prophage regions and prophage remnants, as well as several genes homologous to prophage-associated virulence factors, such as virulence associated protein E, a Clp protease, and a toxin-antitoxin system.

Nucleotide sequence accession number

This Whole Genome Shotgun sequencing project for *V. atypica* KHUD-V1 is available at GenBank under the accession no. QXZZ00000000. The version described in this paper is Version QXZZ01000000.

적 요

본 논문에서는 한국인 만성 치주염 환자의 치은연하치태에서 분리된 *Veillonella atypica* KHUD-V1의 유전체 서열을 보고한다. 다른 *V. atypica* 균주와 달리, KHUD-V1에서는 프로파지 및 이와 관련된 것으로 추정되는 여러 병독성 인자가 확인되었다. *V. atypica* KHUD-V1 균주 및 이 균주의 유전체 서열정보는 *Veillonella*의 유전체 다양성을 진화론적 관점에서 이해하고, *V. atypica*의 병독성 및 유전적 다양성에 기여하는 프로파지의 역할을 연구하는데 유용할 것이다.

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