

Draft genome sequence of lytic bacteriophage CF1 infecting *Citrobacter freundii* isolates

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Citrobacter freundii 분리주를 감염시키는 용균 박테리오파지 CF1의 유전체 염기서열 초안

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Citrobacter freundii is a facultative anaerobic and a Gram-negative bacterium of *Enterobacteriaceae* family, and is an opportunistic pathogen. Bacteriophages infecting *C. freundii* can be an effective treatment for *C. freundii* infections. Here, the complete genomic sequence is announced for a lytic bacteriophage CF1 infecting *C. freundii* isolates.

Keywords: *Citrobacter freundii*, bacteriophage, bacteriophage CF1, complete genome sequence, PacBio

Citrobacter freundii is an opportunistic pathogenic bacteria of the family *Enterobacteriaceae* (Wang *et al.*, 2000). Since *C. freundii* strains have exhibited an increasing resistance to antibiotics (Lockhart *et al.*, 2007). Bacteriophage that kill such pathogens may be useful in the control and containment of these infection. Therefore, bacteriophages have been considered as an alternative treatment against *C. freundii* infection. Here, the complete genomic sequence and the genomic features of a

bacteriophage *C. freundii* CF1 is presented.

Bacteriophage CF1 infecting *C. freundii* was isolated from a sewage water sample near a livestock farm in Chungcheongnam-do, South Korea. Bacteriophage CF1 infecting *C. freundii* in the family *Myoviridae* with Icosahedron head and Contractile tail. And phage DNA was extracted by incubating the bacteriophage culture with 20 mM EDTA, 50 µg/ml Proteinase K, and 0.5% (w/v) SDS at 50°C for 1 h, followed by Phenol-Chloroform extraction and ethanol precipitation (Sambrook and Russell, 2001). Phage DNA was then sequenced using a PacBio SMRT system (Macrogen). Quality-controlled trimmed sequence reads were assembled to a single contig at 3845-fold coverage using Canu v1.4. Genes were predicted with RASTtk (Brettin *et al.*, 2015), and the functions of predicted coding-genes were calculated with BLASTp searches (<https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Proteins>).

CF1 has a 50,339 bp double-stranded DNA (dsDNA) genome with 89 predicted coding genes and tRNA is not detected. The coding density of the genome is 92.3% and the G + C content of CF1 is 42.7%. This is significantly lower than the G + C content

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of *C. freundii* CFNIH1 (51.6%), which is the representative genome of *C. freundii*. A lower G + C content of a bacteriophage than a G + C content of a host seems to be a commonly represented feature. The *Salmonella* Felix O1 phage have a G + C content (39.0%), which is much lower than that of the host *Salmonella* (approximately 52%) (Moreno Switt *et al.*, 2013), and the similar pattern was found between a Felix O1-like phage (Guan *et al.*, 2015) and its host *C. freundii* (51.6%) (Kumar *et al.*, 2013). Of the 89 predicted coding genes, 34 are hypothetical or conserved genes, leaving 55 coding genes given a putative functions based on BLASTp analysis (Camacho *et al.*, 2009). Analysis of orthologous genes between *C. freundii* CF1 and another lytic bacteriophage *C. freundii* Mordin (Guan *et al.*, 2015) having 138 coding genes resulted in only one shared coding gene, which is an endolysin. Endolysin is a lethal bacteriocidal enzyme with an antibiotic capacity by destroying bacterial cell walls (Schmelcher *et al.*, 2012). The genomic location of this endolysin in *C. freundii* CF1 is from 23754 to 24248, and the gene name of its ortholog in *C. freundii* Mordin is Mordin_93. The unexpected bare overlap between two bacteriophages infecting the same host led to a comparison to the representative *Citrobacter* phage Stevie (NC_027350.1) which has about 50 kb double-stranded DNA genome and 90 coding genes (Shaw *et al.*, 2015). Unlike *C. freundii* Mordin, *Citrobacter* phage Stevie is similar to *C. freundii* CF1 in terms of the genome size and the number of genes. Moreover, the ortholog analysis showed that *C. freundii* CF1 and *Citrobacter* phage Stevie share 86 orthologous genes which cover 96.63% of genes in *C. freundii* CF1 genome, indicating that the genome of CF1 is quite close to that of Stevie.

Nucleotide sequence accession number

The genome sequence of bacteriophage CF1 was deposited in GenBank with the accession number KY694971.

Table 1. Genome features of *Citrobacter freundii* CF1

Feature type	Genomic feature
Contig	1
Genome size (bp)	50,339
G + C content (%)	42.65
Genes	89
Protein-coding genes	89

적 요

본 연구에서는 돼지 축사 근처 하수 오물에서 분리된 그람 음성균이자 항생제 내성을 쉽게 획득하여 병원성을 띠는 균주인 *Citrobacter freundii*를 host로 하는 박테리오파지의 유전체 분석을 수행하였다. 본 박테리오파지는 G + C 비율이 42.65%이며, 50,339 bp로 구성된 유전체 DNA를 지니고 있었다. 이러한 유전체 DNA에서 89개의 단백질 코딩 유전자가 확인 되었으며, 이 중 55개의 유전자는 BLASTP 분석으로부터 기능을 가지고 있다고 추정되었다. 또한 RNA는 확인되지 않았다.

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