

Draft genome sequence of lytic bacteriophage SA7 infecting *Staphylococcus aureus* isolates

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Staphylococcus aureus 분리주를 감염시키는 용균 박테리오파지 SA7의 유전체 염기서열 초안

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Staphylococcus aureus is a Gram-positive and a round-shaped bacterium of *Firmicutes* phylum, and is a common cause of skin infections, respiratory infections, and food poisoning. Bacteriophages infecting *S. aureus* can be an effective treatment for *S. aureus* infections. Here, the draft genomic sequence is announced for a lytic bacteriophage SA7 infecting *S. aureus* isolates. The bacteriophage SA7 was isolated from a sewage water sample near a livestock farm in Chungcheongnam-do, South Korea. SA7 has a genome of 34,730 bp and 34.1% G + C content. The genome has 53 protein-coding genes, 23 of which have predicted functions from BLASTp analysis, leaving the others conserved proteins with unknown function.

Keywords: *Staphylococcus aureus*, draft genome sequence, PacBio SMRT, SA7, sewage water

Staphylococcus aureus is a Gram-positive opportunistic pathogenic bacteria, many strains of which are resistant to one or more antibiotics (Chambers and DeLeo, 2009). *S. aureus* strains has shown an increasing resistance to antibiotics (Lowy,

2003), thus bacteriophages have been considered as an alternative treatment against *S. aureus* infection. Here, the draft genomic sequence of a bacteriophage *S. aureus* SA7 and the genomic features are presented.

Bacteriophage SA7 infecting *S. aureus* was isolated from a sewage water sample near a livestock farm in Chungcheongnam-do, South Korea. 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), and the phage DNA was sequenced using a PacBio SMRT system (Macrogen). Quality-controlled trimmed sequence reads were assembled to a single contig at 249-fold coverage using HGAP v2.0. 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>).

The bacteriophage SA7 has a 34,730 bp double-stranded DNA (dsDNA) genome with 53 predicted coding genes (Table 1). No tRNA was detected from the SA7 genome. The coding density of the genome is 95.2% and the G + C content of SA7

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Table 1. Genome features of the bacteriophage SA7

Feature type	Genomic feature
Contig	1
Genome size (bp)	34,730
G + C content (%)	34.1
Total genes	53
Protein-coding genes	53

is 34.1%. This is slightly higher than the G + C content (32.9%) of the genome of the representative *S. aureus* strain MS4, however it is similar to that of other bacteriophages infecting *S. aureus* (Gill, 2014). The bacteriophages infecting Gram-negative host bacteria tend to have a lower G + C content than that of their hosts (Whichard *et al.*, 2010; Kumar *et al.*, 2013). Of the 53 predicted coding genes, 23 genes (43.4%) had putative function from BLASTp analysis (Camacho *et al.*, 2009), and the rest were hypothetical or conserved proteins. Analysis of orthologous genes between *S. aureus* SA7 and another representative bacteriophage *Staphylococcus* phage K (Gill, 2014) resulted in no shared coding gene between two bacteriophages. The unexpected mere overlap between two bacteriophages infecting the same host represents the diversity of genomic organization of bacteriophages.

Nucleotide sequence accession number

The genome sequence of bacteriophage SA7 was deposited into GenBank under accession number KY695153.

적 요

포도상구균(*Staphylococcus aureus*)은 그람양성이고 구형의 박테리아로 *Firmicutes* 문에 속하며, 피부나 호흡기 감염 그리고 식중독의 주요 감염원 중에 하나이다. 포도상구균을 감

염시키는 박테리오파지는 포도상구균 감염에 효과적인 처방으로 쓰일 수 있다. 본 연구에서는 충청남도 에 위치한 가축농장의 오수에서 분리된 포도상구균 박테리오파지 SA7 균주의 유전체 초안을 분석하였다. 본 균주는 G + C 비율이 34.1%이며, 34,730 bp 로 구성된 dsDNA 를 지니고 있었다. 염색체에서 53 개의 단백질 코딩 유전자가 확인되었으며, 이 중 23 개의 유전자는 BLASTp 분석으로부터 기능을 가지고 있다고 추정되었다. 나머지는 가설 단백질 혹은 보존 단백질이었다.

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