

Complete genome sequence of *Staphylococcus aureus* MFDS1022333 isolated from chicken mayo rice

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치킨마요덮밥에서 분리된 *Staphylococcus aureus* MFDS1022333의 유전체 서열 분석

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Staphylococcus aureus is a foodborne pathogen that affects humans. This study analyzed the complete genome of *Staphylococcus* strains (MFDS1022333) suspected to be the cause of food poisoning found in chicken mayo rice distributed at schools located in Busan, South Korea in 2022. The complete genome sequence of *Staphylococcus aureus* MFDS1022333 consisted of a chromosomal DNA which was 2,735,468 bp in length with 32.9% G + C content. Gene analysis confirmed that this genome identified 2,529 CDSs, 60 tRNAs, and 19 rRNAs.

Keywords: *Staphylococcus aureus*, chicken, complete genome

Staphylococcus aureus is a food-poisoning bacterium that causes illness in humans who consumed contaminated foods (Kadariya *et al.*, 2014; Paiva *et al.*, 2021). It is detected in commonly consumed foods, such as chicken and eggs, and can cause diarrhea, vomiting, and other related symptoms (Liang *et al.*, 2023). Most cases are caused by enterotoxins produced when infected with *Staphylococcus aureus* (Gajewska *et al.*, 2023). Global foodborne poisoning by *Staphylococcus* are reported annually (Hennekinne *et al.*, 2012; Savini *et al.*, 2023), and epidemiological study is required to reveal the causes.

In this study, we analyzed the complete genome sequence of *S. aureus* isolated from Busan, South Korea in 2022.

Staphylococcus aureus MFDS1022333 was isolated by the Ministry of Food and Drug Administration (MFDS, South Korea) after a food poisoning event at a school. The pathogen was isolated from chicken mayo rice and also detected from cookers and patients who consumed food.

For high-quality genomic DNA, the pathogen was incubated in tryptic soy agar at 37°C and extracted using a Genomic DNA prep kit for the bacterium (Bioneer). After measuring the quantity and quality of the genomic DNA using NanoDrop 2000 UV-visible spectrophotometer (Thermo Fisher Scientific), a sequencing library for single-molecule real-time (SMRT) bell templates was prepared. The genomic DNA was sheared into approximately 10 kb fragments using a G-tube (Covaris), and a library was constructed using the SMRTbell Express Template Prep kit 2.0 (Pacific Biosciences). The final library was diluted using the Qubit™ dsDNA HS Assay Kit (Thermo Fisher Scientific) and an Agilent 2100 Bioanalyzer (Agilent Technologies). Sequencing was performed using the PacBio sequel system, a long-read sequencing platform.

Sequencing data were obtained, and the SMRT Link was used for demultiplexing and assembly. A total of 298,248 reads were assembled using Microbial Assembly with the default

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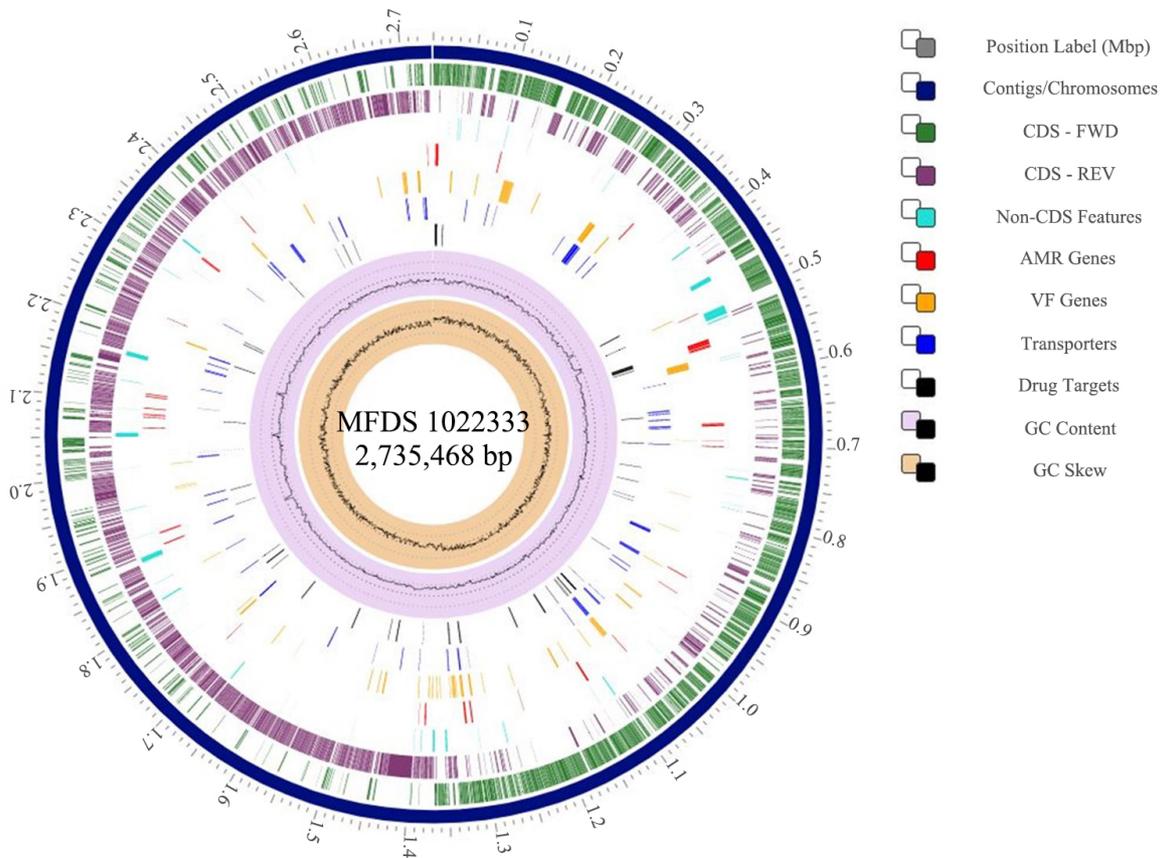


Fig. 1. Complete genome map of *Staphylococcus aureus* MFDS1022333. Genome map of MFDS1022333 produced in Bacterial and Viral Bioinformatics Resource Center server. Each piece of information is shown as follows: Forward CDS, Reverse CDS, Non-CDS Features, GC content, GC Skew, AMR genes, VF genes, transporters, and drug targets.

Table 1. Genome features of *Staphylococcus aureus* MFDS1022333

Feature	Chromosome
Size (bp)	2,735,468
G + C contents (%)	32.9%
Total number of CDSs	2,529
rRNA genes	19
tRNA genes	60
GenBank Accession No.	CP138576

parameters in SMRT tools version 10.2. The assembled data had a coverage of 411X. The MFDS1022333 genome consisted of a circular chromosome of 2,735,468 bp (Fig. 1) with 32.9% G + C content and 2,529 coding sequences (Table 1).

The complete genome of the *S. aureus* strain MFDS1022333 was analyzed using multi-locus sequence typing (MLST) version 2.0.9, available through the Center for Genomic Epidemiology (CGE) (Larsen *et al.*, 2012). This strain belonged to the

sequence type 6. Gene annotation was performed using the BV-BRC version 3.32.13a (Wattam *et al.*, 2017). The Virulence Factor Database (VFDB) detected a total of 63 virulence genes, including *sea*, *hlgA* and *aur* genes (Hennekinne *et al.*, 2012). The *sea* is a gene encoding enterotoxin (SEs) that is most frequently reported in foodborne pathogens (Le *et al.*, 2021). This genomic information can be used to understand food-poisoning pathogens and foodborne illnesses.

Nucleotide sequence accession number(s)

The complete genome sequence of *Staphylococcus aureus* MFDS1022333 has been deposited in the NCBI GenBank database under accession number CP138576 (chromosome, MFDS1022333), and the strain has been deposited in the Korean Culture Collection for foodborne pathogens under strain number MFDS1022333.

적 요

황색포도상구균은 인간에게 영향을 미치는 식품매개 병원체이다. 본 연구에서는 2022년 부산 학교에서 식중독 사고의 원인 식품으로 추정되는 치킨마요덮밥에서 분리된 *Staphylococcus aureus* MFDS1022333의 유전체 분석을 진행하였다. *Staphylococcus aureus* MFDS1022333는 2,735,468 bp의 Chromosome 과 32.9%의 G + C contents로 구성되었다. 또한, 유전체에서 예측된 유전자의 총 수는 2,529개의 단백질 코딩유전자, 60개 tRNA, 그리고 19개의 rRNA로 확인되었다.

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Conflict of Interest

The authors have no conflict of interest to report.

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