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Complete Genome Sequences of Two Clonal Complex 398 Methicillin-Resistant *Staphylococcus aureus* Strains Isolated from Patients in Korea

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Clonal complex (CC) 398 community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) has emerged worldwide in a variety of livestock animals and humans. We report complete genome sequences of Panton-Valentine leucocidin (PVL) and immune evasion cluster (IEC) gene-positive CC398 MRSA strains isolated from patients in Korea.

Keywords: ***Staphylococcus aureus*, MRSA, clonal complex 398**

Methicillin-resistant *Staphylococcus aureus* (MRSA) belonging to clonal complex (CC) 398 has been increasingly found in livestock, becoming a major occupational hazard for people working in livestock farms [1]. CC398 MRSA strains usually exhibit decreased virulence compared with other MRSA lineages due to a limited number of virulence-associated determinants. However, highly virulent CC398 MRSA strains carrying risk factors such as Panton-Valentine leucocidin (PVL) and immune evasion cluster (IEC) genes have recently emerged in hospital and community settings [2, 3]. Here, we report the genomic information of two CC398 MRSA clinical isolates (SA489 and SA497).

Two *S. aureus* strains, SA489 and SA497, were obtained from open pus samples of two elderly female patients at Anseong hospital in Korea. Purified genomic DNA prepared using the Wizard Genomic DNA Kit (Promega, USA) was subjected to whole-genome sequencing (WGS) analysis. Genome sequence data were produced by a combination of Oxford Nanopore MinION (Oxford Nanopore Technologies, UK) and Illumina iSeq platforms (Illumina, USA). *De novo* genome assembly based on high-quality reads of Nanopore and Illumina data was performed using the Unicycler v.0.4.8 software. The assembled genomes of SA489 and SA497 strains yielded two circular contigs of 2,807,258 bp and 2,856,631 bp with 200× and 30× of genome coverages, respectively. Each contig comprised a single chromosome with a length of 2,786,528 and 2,835,900 bp, and a plasmid (pSA489 or pSA497) with lengths of 20,730 bp, and 20,731 bp, respectively. The complete sequences of SA489 and SA497 were annotated using Rapid Annotation using Subsystem Technology (RAST) v.2.0 [4] and Prokka v.1.14.6 [5]. Multilocus sequence typing (MLST) along with SCC*mec*, *agr* and *spa* typings were conducted using *in silico* genotyping software from the Center for Genomic Epidemiology. The presence of antimicrobial resistance genes (ARGs) and virulence-associated genes was confirmed by integrative data from BLAST search

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Table 1. Phenotypic and genotypic characteristics of CC398 MRSA SA489 and SA497 strains.

	SA489	SA497
Source	Patient	Patient
MLST	ST1232	ST1232
SCC*mec*	V	V
spa type	t034	t034
agr type	I	I
Antimicrobial resistance[a]	AMP-CEF-CLI-ERY-TET	AMP-CEF-CLI-ERY-TET
Antimicrobial resistance genes	*mecA*, *blaZ*, ant(9)-la, *erm*(A), *tet*(K), *tet38*	*mecA*, *blaZ*, ant(9)-la, *erm*(A), *tet*(K), *tet38*
Virulence genes[b]	PVL, IEC (*sak*, *chp*, *scn*)	PVL, IEC (*sak*, *chp*, *scn*),
Genome size (bp)	2807258	2856631
No. of contigs	2	2
GC content (%)	32.9	32.9
Plasmid	pSA489	pSA497
CDSs	2640	2718
GenBank accession numbers	CP115847, CP115848	CP115849, CP115850

[a]Amp, ampicillin; CEF, cefoxitin; CLI, clindamycin; ERY, erythromycin; and TET, tetracycline
[b]PVL, Panton-Valentine leucocidin; IEC, immune evasion cluster

and ResFinder (https://cge.cbs.dtu.dk/services/ResFinder/) of CGE. To determine antimicrobial resistance profiles, antimicrobial susceptibility tests were performed [6], and both SA489 and SA497 strains showed resistance to ampicillin, cefoxitin, clindamycin, erythromycin, and tetracycline.

Both MRSA strains were identified as sequence type (ST) 1232 belonging to CC398 with SCC*mec* V-*spa* t034-*agr* I types (Table 1). Nucleotide BLAST anaylsis revealed that the genomes of SA489 and SA497 strains harbored a variety of ARGs [*mecA*, *blaZ*, *ant(9)-la*, *erm*(A), *tet*(K), *tet*38] corresponding to their resistance phenotypes. In addition, chromosomally integrated prophages containing PVL, IECs, and staphylococcal exotoxin genes were identified in the two MRSA strains.

The complete genome sequences of SA489 and SA497 strains (CP115847 and CP115849) and their plasmids (CP115848 and CP115850) have been deposited in the GenBank sequence database.

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Conflict of Interest

The authors have no financial conflicts of interest to declare.

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