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Whole Genome Sequencing of a Methicillin-Resistant *Staphylococcus aureus* Sequence Type 5 Strain SA492 Isolated from a Patient in Korean

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Methicillin-resistant *Staphylococcus aureus* (MRSA) represents antimicrobial-resistant bacteria that can cause a wide range of illnesses both in humans and animals. Multidrug resistance phenotype is common, especially in healthcare-associated (HA) MRSA strains. Currently, one of the most prevalent HA-MRSA clonal lineages in Korean hospitals is sequence type (ST) 5 carrying staphylococcal cassette chromosome *mec* type II (ST5-SCC*mec* II). Here, we report the complete genome sequence of an ST5 HA-MRSA strain (SA492) originated from a patient in Korea.

Keywords: *Staphylococcus aureus*, HA-MRSA, sequence type 5

Staphylococcus aureus is an opportunistic human and animal pathogen capable of causing a wide spectrum of clinical and subclinical disease [1, 2]. One of the most significant healthcare-associated (HA) MRSA lineages in Korea is sequence type (ST) 5 carrying staphylococcal cassette chromosome *mec* type II (ST5-SCC*mec* II) [3]. Here, we report the complete genome sequence of an ST5-SCC*mec* II strain, SA492, isolated from a tertiary hospital in Korea.

HA-MRSA SA492, a clinical bloodstream isolate, was kindly provided from the Asian Bacterial Bank of Asia Foundation for Infectious Disease in Korea [4]. Genomic DNA was extracted using a Genenmed Kit (Seoul, Korea). Whole genome sequence data were generated by hybrid sequencing using Oxford Nanopore MinION (Oxford Nanopore Technologies, UK) and Illumina iSeq platforms (Illumina, USA). Basecalling of Nanopore data and removal of low-quality data were performed with Guppy v3.1.5. and NanoFilt v2.8.0 (remove Q score < 7 with minimum length 1,000), respectively. Adapters and low-quality reads for Illumina data were eliminated by Trimmomatic v0.39 (remove Q score < 20). *De novo* assembly of Nanopore and Illumina data was carried out with Unicycler v0.4.8. software. Rapid Annotation using Prokka v1.14.6 and Subsystem Technology (RAST) v.2.0 were used to annotate the complete sequence of SA492 strain.

The resulting genome was 2,856,680 bp in length with 90× genome coverages, which were comprised of one large circular chromosome (32.91% G+C content) with no plasmid. The complete genome sequence of SA492 was submitted to the GenBank sequence database and accession number of CP101314 has been assigned. The average nucleotide identity (ANI) value obtained by comparing the sequence data to previously published sequences of the ST5 HA-MRSA NCCP14562 strain was 99.80% [5].

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Table 1. Comparison of genetic characteristics of SA492 and NCCP14562 strains.

Strain	SA492	NCCP14562
Genome size (bp)	2,856,680	2,910,941
G+C content (%)	32.9	32.9
Coverage	90	21-22
MLST	ST5	ST5
SCC*mec* type	II	II
spa type	t2460	t002
agr type	II	II
ARGs	*ant(9)-la* , *erm*(A), *mecA, tet(M)*	ant(9)-la , erm(A), mecA, tet(M)
Virulence genes	gamma hemolysin (*hlgA, hlgB, hlgC*)	gamma hemolysin (*hlgA, hlgB, hlgC*)
	LukED (*lukD, lukE*)	LukED (*lukD, lukE*)
	aur	*aur*
	serine protease (*splA, splB*)	serine protease (*splA, splB*)
	SEs (*sec, seg, sei, sel, sem, sen, seo, seu*)	SEs (*sec, seg, sei, sel, sem, sen, seo, seu*)
	tst1	*tst1*
GenBank accession no.	CP101314	CP013953.1
Reference	in this study	[5]

In silico genotype analysis was conducted using Center for Genomic Epidemiology (CGE) software for SCC*mec*, multilocus sequence type (MLST), *agr*, and *spa* types. SA492 strain was identified as ST5-SCC*mec* II with *agr* II and *spa* type t2460 (Table 1). Genetic factors for antimicrobial resistance and pathogenicity were identified by integrative data from BLAST search and ResFinder (https://cge.food.dtu.dk/services/ResFinder/) of CGE. ResFinder analysis revealed three ARGs correspond to the resistance phenotypes to b-lactams, erythromycin, and tetracycline: *mecA*, *ant(9)-Ia*, *erm(A)*, and *tet(M)*. Moreover, virulence genes encoding aureolysin (*aur*), serine protease (*splA* and *splB*), gamma-hemolysin complements (*hlgABC*), leukocidin E and D (*lukED*), toxic shock syndrome toxin-1 (*tst1*), and staphylococcal enterotoxins (*sec, seg, sei, sel, sem, sen, seo,* and *seu*) were identified in the SA492 genome.

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Conflict of Interest

The authors have no financial conflicts of interest to declare.

References

1. Bartels MD, Boye K, Rhod Larsen A, Skov R, Westh H. 2007. Rapid increase of genetically diverse methicillin-resistant *Staphylococcus aureus*, Copenhagen, Denmark. *Emerg. Infect. Dis.* **13**: 1533-1540.
2. Kim ES, Song JS, Lee HJ, Choe PG, Park KH, Cho JH, *et al.* 2007. A survey of community-associated methicillin-resistant *Staphylococcus aureus* in Korea. *J. Antimicrob. Chemother.* **60**: 1108-1114.
3. Peck KR, Baek JY, Song J-H, Ko KS. 2009. Comparison of genotypes and enterotoxin genes between *Staphylococcus aureus* isolates from blood and nasal colonizers in a Korean hospital. *J. Korean Med. Sci.* **24**: 585-591.
4. Kang K-M, Park JH, Kim SH, Yang SJ. 2019. Potential role of host defense antimicrobial peptide resistance in increased virulence of health care-associated MRSA strains of sequence type (ST) 5 versus livestock-associated and community-associated MRSA strains of ST72. *Comp. Immunol. Microbiol. Infect. Dis.* **62**: 13-18.
5. Park C, Rho K, Shin J, Cho SY, Lee DG, Chung YJ. 2021. Genomic analysis of heterogeneous vancomycin-intermediate *Staphylococcus aureus* strains from different clonal lineages in South Korea. *Microb. Drug Resist.* **27**: 1271-1281.