

Genome Reports

Complete Genome Sequence of a Methicillin-Resistant *Staphylococcus aureus* Sequence Type 72 Strain SA520 Isolated from Korean Hospital

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Received: February 12, 2023 / Revised: May 15, 2023 / Accepted: May 16, 2023

Once known as a major community-genotype, sequence type (ST) 72 methicillin-resistant *Staphylococcus aureus* (MRSA) strains have been increasingly identified in hospital-associated infections in Korea. Here, we report the complete genome sequence of SA520 isolated from a patient in Korea.

Keywords: Methicillin-resistant *Staphylococcus aureus*, sequence type 72, SA520

Community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) usually carrying type IV or V staphylococcal cassette chromosome *mec* (SCC*mec*) has emerged in global communities [1]. Although distinctive lineages of CA-MRSA have been found in different countries [2], a unique sequence type (ST) 72 MRSA-SCC*mec* IV has become a major cause of infection in both community and hospital settings in Korea [3, 4]. We report here the complete genome sequence of a ST72 MRSA-SCC*mec* IV strain, SA520, isolated in Korea.

S. aureus SA520 was isolated from a blood sample from a patient with bacteremia hospitalized in Seoul National University Bundang Hospital in Korea [5], and identified using 16S ribosomal RNA gene sequencing (Bionics, Seoul, Korea). For whole genome sequencing, genomic DNA was extracted by using a Genmed DNA kit (Korea). Sequencing libraries were constructed by hybrid sequencing using an Oxford Nanopore MinION

(Oxford Nanopore Technologies, UK) and Illumina iSeq platforms (Illumina, USA). *De novo* assembly of Unicycler v0.4.8 was employed to generate high-quality complete genome. The assembled genome was annotated using both Prokka v1.14.6 and Rapid Annotation using Sub-system Technology (RAST) v.2.0.

The total length of the completed genome was 2,765,395 bp with 607× genome coverages, which comprised of one large circular chromosome of 2,762,063 bp (G+C content, 32.84%) and a plasmid (pSA520) of 3,332 bp (G+C content, 29.53%). The complete genome sequences of *S. aureus* SA520 and a 3-kb plasmid pSA520 have been deposited in the GenBank under the accession numbers CP101312 and CP101313, respectively. The sequence data were compared with a previously reported sequences of ST72 CA-MRSA CN1 strain resulting in a 99.93% average nucleotide identity (ANI) value [6].

In silico genotyping was performed using Center for Genomic Epidemiology (CGE) software for multilocus sequence typing, as well as SCC*mec*, *spa*, and *agr* typing. Antimicrobial resistance genes (ARGs) and virulence

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Table 1. Genetic characteristics of ST72 CA-MRSA SA520 and CN1 strains.

Strain	SA520	CN1 ^a
Genome size (bp)	2,765,395	2,757,070
G+C content (%)	32.8	32.79
Coverage	607	40-60
Plasmid	pSA520	pHL1 and pHL2
MLST	ST72	ST72
SCCmec	IV	IV
<i>spa</i> type	t13921	t324
<i>agr</i> type	I	I
ARGs	<i>mecA</i> , <i>blaZ</i>	<i>aadD</i> , <i>blaZ</i> , <i>bleO</i> , <i>mecA</i>
Virulence genes	Gamma-hemolysin (<i>hlgA</i> , <i>hlgB</i> , <i>hlgC</i>), Leukocidins (<i>lukD</i> , <i>lukE</i>), IEC (<i>sak</i> , <i>chp</i> , <i>scn</i>), SEs (<i>seg</i> , <i>sei</i> , <i>sem</i> , <i>sen</i> , <i>seo</i> , <i>seu</i>), Aureolysin (<i>aur</i>), Serine protease (<i>splA</i> , <i>splB</i>)	Gamma-hemolysin (<i>hlgA</i> , <i>hlgB</i> , <i>hlgC</i>), Leukocidins (<i>lukD</i> , <i>lukE</i>), IEC (<i>sak</i> , <i>chp</i>), SEs (<i>seg</i> , <i>sei</i> , <i>sem</i> , <i>sen</i> , <i>seo</i> , <i>seu</i>), Aureolysin (<i>aur</i>), Serine protease (<i>splA</i> , <i>splB</i> , <i>splC</i> , <i>splD</i>)

IEC, Immune evasion cluster; SE, Staphylococcal enterotoxin

^aGenBank accession number: CP003979.1

associated genes were identified by ResFinder (<https://cge.food.dtu.dk/services/ResFinder/>) of CGE. Standard antimicrobial susceptibility assay [7] revealed that SA520 strain displayed resistance to β -lactams (ampicillin, cefoxitin, and penicillin). SA520 MRSA strain was identified as ST72 clonal lineage carrying SCCmec IV with *spa* type t13921 and *agr* type I. ResFinder analysis indicated two ARGs corresponding to the resistance phenotypes: *mecA*, and *blaZ*. Moreover, virulence genes encoding gamma-hemolysin components, leukocidins, immune evasion clusters (IECs), staphylococcal enterotoxins (SEs), aureolysin, and serine protease were identified in SA520 (Table 1).

Acknowledgments

This study was supported by a grant (2021ER220100) from Research of Korea Centers for Disease Control and Prevention.

Conflict of Interest

The authors have no financial conflicts of interest to declare.

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