

Genome Reports

Complete Genome of Methicillin-Resistant *Staphylococcus epidermidis* Z0118SE0272 Isolated from a Residential Environment

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Staphylococcus epidermidis is a normal flora of human skin and is occasionally associated with pathogenic infections. We report the complete genome sequence of methicillin-resistant *Staphylococcus epidermidis* strain Z0118SE0272 isolated from the residential environment sharing by a companion dog and dwellers. Resistance to cefoxitin was observed in the strain, whereas it was susceptible to erythromycin, clindamycin, quinupristin-dalfopristin, trimethoprim-sulfamethoxazole, mupirocin, vancomycin, teicoplanin, linezolid, and tigecycline. The strain Z0118SE0272 identified as sequence type 130 possessed the *mecA* gene responsible for methicillin resistance, which composed the new type of staphylococcal cassette chromosome *mec* elements lacking *mecRI*.

Keywords: *Staphylococcus epidermidis*, methicillin-resistant, complete genome

The genus *Staphylococcus* is a gram-positive bacterium that colonizes in skin surface of humans and animals [1, 2]. Among the *Staphylococcus* spp., *Staphylococcus epidermidis* is known as a coagulase-negative bacterium and a major pathogen of nosocomial infection forming biofilm. This species can infect patients through their wound or medical devices, which may increase the patient's mortality rate [3, 4]. Currently, as the antibiotic resistance rate of *S. epidermidis* increases, problems are arising in treating bacteremia by antibiotic therapy in hospitals. Among them, methicillin-resistant *S. epidermidis* (MRSE) has attracted the major concern [5]. Methicillin-resistance is mediated by the *mecA* gene

which comprises staphylococcal chromosome cassette *mec* (SCC*mec*) with *mecA*, *ccr*, *orfX*, and insertion sequences. And several different types have been identified in methicillin-resistant *Staphylococcus aureus* owing to the various genetic diversity [6]. However, the SCC*mec* structure of MRSE has not been classified. In this study, strain Z0118SE0272 was isolated from the surface of a sofa in a residential house where a veterinarian raised a companion dog and the complete genome was determined.

The swapped sample was inoculated into Chromagar Orientation (CHROMagar™) and incubated for 24 h at 30°C. The candidates of *Staphylococcus* species were separated through chromogenic selection. After purifying the colonies, identification of *S. epidermidis* was conducted by PCR and sequencing of the *mutS* gene [7]. An antibiotic susceptibility test was performed using the disk diffusion method against cefoxitin, erythromycin, clindamycin, quinupristin-dalfopristin, trimethoprim-sulfamethoxazole, mupirocin, vancomycin, teicoplanin,

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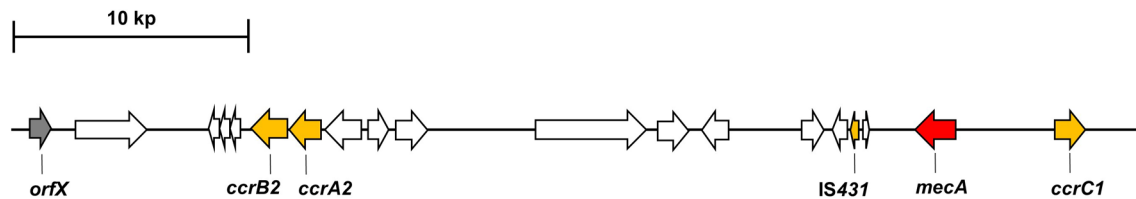


Fig. 1. Genetic structure of staphylococcal cassette chromosome *mec* (SCC*mec*) in *Staphylococcus epidermidis* Z0118SE0272. *mecA*, penicillin-binding protein; *ccr*, recombinase; *orfX*, unknown open reading frame; IS, insertion sequence.

linezolid, and tigecycline. As the results, the strain Z0118SE0272 showed resistance only to cefoxitin and susceptibility to all of other antibiotics.

For genome sequencing, total genomic DNA was extracted with a QIAamp DNA Mini Kit (Qiagen, Germany). The quantity and quality of the DNA were measured using a Qubit 4 fluorometer (Invitrogen, Singapore). The extracted DNA was sequenced using PacBio RSII (Pacific Biosciences, USA) and HiSeq X Ten (Illumina, USA) systems at the Macrogen (Republic of Korea). After sequencing, 271,066 and 11,673,674 reads were obtained from PacBio and HiSeq sequencers, respectively. The generated reads were hybrid assembled using Unicycler (v0.4.9) [8] with the default setting. Based on generated contigs, one chromosome (2,509,266 bp) and three plasmids (30,151 bp, 16,926 bp, and 2,563 bp) were determined (Table 1). Annotation was performed with NCBI prokaryotic genome annotation pipeline (PGAP) and found that strain Z0118SE0272 consisted of 2,369 coding sequences, 19 (7 of 5S, 6 of 16S, 6 of 23S) rRNA genes, and 61 tRNA genes (Table 1). The antimicrobial resistance genes were identified using

the comprehensive antibiotic resistance database (CARD) [9]. The chromosome (accession no. CP069219) included resistance genes for quinolone (*norA*, *norC*, and *sdrM*), trimethoprim (*dfrC*), and beta-lactam antibiotics (*mecA*). The 30,151 bp of plasmid (accession no. CP06220) contained resistance genes for beta-lactams (*blaZ*), aminoglycosides (*ant(4')-Ib*), and chlorhexidine gluconate (*qacB*).

A SCC*mec* structure was found using the SCC*mec* finder [10]. The *ccrA2* and *ccrB2* were located downstream of *mecA* and the *ccrC1* also existed adjacent to upstream as shown in Fig. 1. However, the structure lacked *mecRI* encoding the signal transducer and the repressor proteins which usually were detected in previously known SCC*mec* types [6].

Nucleotide Sequence Accession Number

The genome sequence of *Staphylococcus epidermidis* Z0118SE0272 has been deposited in GenBank/EMBL/DDBJ under accession CP069219-CP069222. The strain was deposited in KCTC under deposition number 43153.

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Conflict of Interest

The authors have no financial conflicts of interest to declare.

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Table 1. Genome features of *Staphylococcus epidermidis* Z0118SE0272.

Contig	Length (bp)	No of CDS	No of tRNA	No of rRNA	G+C ratio (%)
Contig 1 (Chromosome)	2,509,266	2,313	61	19	32.0
Contig 2 (plasmid)	30,151	34	0	0	29.0
Contig 3 (plasmid)	16,926	20	0	0	28.0
Contig 4 (plasmid)	2,563	2	0	0	29.0
Total	2,558,906	2,369	60	19	32.16

CDS, coding sequences

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