

Complete genome of methicillin resistant *Staphylococcus epidermidis* Z0117SE0042 isolated from human nasal mucosa

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사람 코점막에서 분리된 메티실린 내성 *Staphylococcus epidermidis* Z0117SE0042의 유전체 염기서열

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Methicillin resistant *Staphylococcus epidermidis* Z0117SE0042 was isolated from nasal mucosa of veterinarian. The complete genome of strain Z0117SE0042 contains a 2.5 Mb chromosome and two circular plasmids of about 24 kb and 23 kb. Analysis of the genome determined in this study may contribute to evaluate the presence and prevalence of antibiotic resistant genes in normal flora of human.

Keywords: *Staphylococcus epidermidis*, genome, nasal mucosa

Staphylococcus epidermidis is a commensal bacterium that colonizes human skin and mucous membranes (Conlan *et al.*, 2012). Due to its proximity to the insertion sites of catheters or other medical devices, *S. epidermidis* frequently colonizes these devices and forms biofilms that are inherently resistant to the host defense system and antibiotics (Galac *et al.*, 2017). Staphylococcal species are frequently resistant to antibiotics, particularly belonging to penicillinase-resistant penicillin family (e.g. methicillin, oxacillin, and nafcillin), constraining treatment

options especially in clinical environment (Diep *et al.*, 2006). The *mecA* gene generally located on staphylococcal cassette chromosome *mec* (SCC*mec*) plays a key role in inactivation of β -lactam in Staphylococci. Currently, SCC*mec* is divided into 13 types (I–XIII) by *mec* gene complex and *ccr* gene complex (Baig *et al.*, 2018).

S. epidermidis Z0117SE0042 (CDC121, the other strain name) was isolated from nasal mucosa of veterinarian. The enrichment was performed on CHROMagar MRSA (CHROMagar) at 30°C for 2 days. The strain was identified based on *cpn60* gene sequences. The strain was deposited in Nakdonggang National Institute of Biological Resources (Sangju, Korea) under FBCC502765D of deposit number.

Genomic DNA of strain Z0117SE0042 was used to construct 20 kb SMRTbell™ template libraries. The whole genome sequencing was conducted with PacBio RSII and Illumina HiSeq sequencing platforms by Macrogen. The determined filtered subreads with about 263-fold coverage were assembled using hierarchical genome assembly process (HGAP, v3.0) including assembly polishing with Quiver (Chin *et al.*, 2013). As a result of *de novo* assembly, three circularized contigs of

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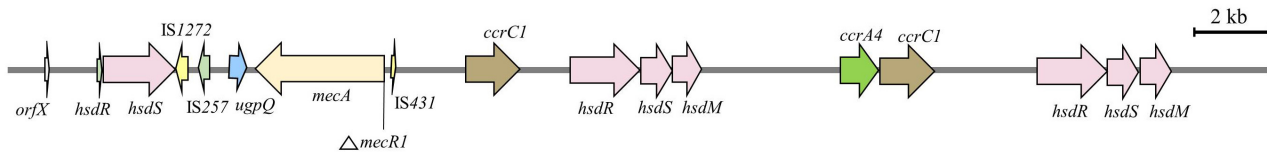


Fig. 1. SCCmec gene organization in Z0117SE0042 strain.

Table 1. Genome features of *Staphylococcus epidermidis* Z0117SE0042

Contig	Length (bp)	CDS	tRNA	rRNA	G + C ratio
Contig 1 (Chromosome)	2,524,648	2,306	60	19	32.2
Contig 2 (plasmid)	23,943	24	0	0	27.2
Contig 3 (plasmid)	23,348	28	0	0	29.0
Total	2,571,939	2,358	60	19	32.1

2,524,648 bp, 23,943 and 23,348 bp were generated. Automatic annotation for the genome was conducted with Prokka (v1.11, Victorian Bioinformatics Consortium) and found a total of 2,358 coding sequences (CDSs), 60 tRNA genes, and 19 rRNA genes (Table 1).

Genome sequence of strain Z0117SE0042 contained staphylococcal chromosomal cassette *mec* (SCCmec) similar to type V consisting of class C2 *mec* and type 5 *ccr* gene complexes. As shown in Fig. 1, its structure contained two kinds of *ccr* genes (duplicated *ccrC1* and *ccrA4*) which corresponded to excision and integration of SCCmec. The class C2 *mec* gene complex was composed of insertion sequence IS431 located on upstream of *mecA* and *mecR1* genes but the other IS431 usually located on downstream of *mecA* was absent. The *hsdR* gene and two other ORFs (*hsdS* and *hsdM*) were also detected in the *mec* gene complex which encoded for restriction-modification system. Unexpectedly, *ccrA4* was not only found with duplicated *ccrC1*, but duplicated *hsdR*, *hsdS*, and *hsdM* genes were also detected (Fig. 1). The SCCmec structure is unknown up to date. This might be caused by different bacterial origin since available SCCmec structure was generally reported from *S. aureus*.

In addition, chromosome contained several genes for β -lactam antibiotics resistance such as *pbp2a*, *pbpH*, *pbpB*, *blaZ*, *blaR1*, and *blaI*. And *tetA*, *msrA*, *msrB*, *isaB*, and *tcaA* genes conferring resistance to tetracycline, macrolides, lincosamides (clindamycin), and glycopeptide (teicoplanin) were located in the chromosome.

Nucleotide sequence accession number

The genome sequence of *Staphylococcus epidermidis* Z0117SE0042 has been deposited in NCBI GenBank under accession nos. CP034115-CP034117.

적 요

메티실린 내성 *Staphylococcus epidermidis* Z0117SE0042을 수의사의 코점막으로부터 분리하였다. 완전 해독된 Z0117SE0042 균주의 게놈은 약 2.5 Mb의 염색체와 24 kb, 23 kb 크기의 2개 플라스미드로 구성되어 있었다. 본 연구에서 해독된 유전체 정보는 인간의 정상미생물상에 존재하는 항생제 내성유전자의 분포를 추적하는데 유용한 기반이 될 것으로 기대된다.

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