

Complete genome of methicillin resistant *Staphylococcus epidermidis* Z0117SE0041 isolated from human nasal mucosa

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사람 코점막에서 분리된 메티실린 내성 *Staphylococcus epidermidis* Z0117SE0041의 유전체 염기서열

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Methicillin resistant *Staphylococcus epidermidis* Z0117SE0041 was isolated from nasal mucosa of human who raised companion dog. The complete genome of strain Z0117SE0041 consists of a 2.5 Mb chromosome and three circular plasmids with about 47, 36, and 11 kb in size, respectively. Since strain Z0117SE0041 raises concerns due to its potential to cause a disease and disseminate antibiotic resistance, further genome analysis is required in detail.

Keywords: *Staphylococcus epidermidis*, genome, human

Staphylococci are common bacterial colonizers of the skin and mucous membranes of humans and other mammals. *Staphylococcus epidermidis* in particular is the most frequently isolated species from human epithelia (Otto, 2009). If *S. epidermidis*, a commensal on the skin, ruptures the skin surface and enters the bloodstream, it is considered as pathogen. *Staphylococcus aureus* and coagulase-negative Staphylococci (CoNS) cause 30% of hospital-acquired infections (Conlan *et*

al., 2012). *S. epidermidis* belongs to the group of CoNS, which is distinguished from coagulase-positive staphylococci such as highly pathogenic *S. aureus* by lacking coagulase. CoNS infections are associated with increasing use of catheters and medical devices inserted through the skin (Watanabe *et al.*, 2016). The increasing antibiotic resistance of nosocomial isolates of *S. epidermidis* poses a great challenge for the management of hospital-acquired infections in general (Du *et al.*, 2013).

S. epidermidis Z0117SE0041 (CDC120, the other strain name) was isolated from nasal mucosa of human who raised companion dog after enrichment on CHROMagar MRSA (CHROMagar) at 30°C for 2 days under aerobic condition. A purified isolate was identified as *S. epidermidis* by *cpn60* gene sequencing and deposited in Nakdonggang National Institute of Biological Resources under FBCC502764D of deposit number.

Genomic DNA of strain Z0117SE0041 was extracted from cells which were grown aerobically at 30°C for 20 h in blood agar medium and used to construct 20 kb SMRTbell™ template libraries. The whole genome sequencing was performed at Macrogen, Inc. using PacBio RSII and Illumina platforms. The

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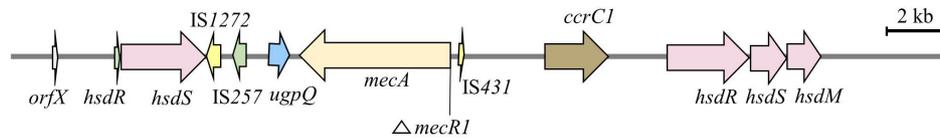


Fig. 1. SCCmec gene organization in Z0117SE0041 strain.

Table 1. Genome features of *Staphylococcus epidermidis* Z0117SE0041

Contig	Length (bp)	CDS	tRNA	rRNA	G + C ratio
Contig 1 (Chromosome)	2,477,784	2,249	60	19	32.3
Contig 2 (plasmid)	46,728	56	0	0	29.8
Contig 3 (plasmid)	36,008	36	0	0	28.3
Contig 4 (plasmid)	11,218	11	0	0	29.6
Total	2,571,738	2,352	60	19	32.16

determined filtered subreads with about 281-fold coverage were assembled as described previously (Patil *et al.*, 2017) generating four circularized contigs of 2,477,784, 46,728, 36,008, and 11,218 bp. This indicated that the assembled contigs were completed. Automatic annotation for the genome with Prokka (v1.11, Victorian Bioinformatics Consortium) determined a total of 2,352 coding sequences (CDSs), 60 tRNA genes, and 19 rRNA genes as described in Table 1.

Sequence analysis found that the β -lactam antibiotics resistant genes (*mecA*, *blaZ*, *blaR1*, and *blaI*) were located in the chromosome of Z0117SE0041. The staphylococcal chromosomal cassette *mec* (SCCmec) was detected in the genome which consisted of similar class C2 *mec* and type 5 *ccr* gene complexes including methicillin resistance regulatory sensor transducer (*mecR1*), methicillin resistance determinant (*mecA*), and cassette chromosome recombinase (*ccrCI*) genes with insertion sequence IS431 (Fig. 1). The structure of *mecA-mecR1-IS431* in *mec* gene complex of Z0117SE0041 strain was highly similar to class C2 *mec* gene complex of type V SCCmec but IS431 on downstream of *mecA* is missing in this *mec* gene complex (Fig. 1). Two other ORFs (*hsdS* and *hsdM*) on downstream of *hsdR* were detected which encoded for restriction-modification system.

Also, Z0117SE0041 chromosome harbored other antibiotic resistant genes such as *tetA*, *msrA*, *msrB*, *isaB*, and *tcaA* responsible for resistance to tetracycline, macrolides, lincosamides (clindamycin), glycopeptide (teicoplanin).

Nucleotide sequence accession number

The genome sequence of *Staphylococcus epidermidis* Z0117SE0041 has been deposited in NCBI GenBank under accession nos. CP034111-CP034114.

적 요

메티실린 내성 *Staphylococcus epidermidis* Z0117SE0041 을 반려견 주인의 코점막으로부터 분리하였다. 완전 해독된 Z0117SE0041 균주의 게놈은 약 2.5 Mb의 염색체와 47 kb, 36 kb, 11 kb 크기의 3개 플라스미드로 구성되어 있었다. Z0117SE0041 균주는 병을 유발하거나 항생제 내성을 전파할 수 있는 가능성이 있으므로 보다 깊이 있는 유전체 분석이 요구된다.

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