

Genome Reports

Complete Genome of Methicillin-Resistant *Staphylococcus pseudintermedius* Z0118SP0130 Isolated from a Companion Dog

Haeseong Lee, Jae-Young Oh, and Jong-Chan Chae*

Division of Biotechnology, Jeonbuk National University, Iksan 54596, Republic of Korea

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Methicillin-resistant *Staphylococcus pseudintermedius* Z0118SP0130 was isolated from eye specimen of a companion dog in South Korea. The complete genome of Z0118SP0130 consisted of a 2,663,277 bp chromosome and there was no plasmid. The strain was identified as the sequence type 45 and contained a *mecA* gene which comprised of staphylococcal cassette chromosome *mec* type Vb (5C2&5). Antimicrobial resistance to erythromycin, clindamycin, quinupristin-dalfopristin, trimethoprim-sulfamethoxazole, mupirocin, oxacillin, streptomycin, and gentamicin was observed in the strain.

Keywords: *Staphylococcus pseudintermedius*, companion dog, complete genome

Staphylococci is a normal flora in the skin of humans and other mammals. Among them, *Staphylococcus pseudintermedius* is a bacterium found in mucous membranes and skin of many mammals including companion animals [1]. The potential of animal disease caused by *S. pseudintermedius* was recently recognized because it was identified as *S. intermedius* until taxonomic assignment of the name was proposed [2]. The species exhibits phenotypic features similar to coagulase-positive *S. intermedius* and cause opportunistic infections in body tissues such as pyoderma and wound infections [1]. Although *S. pseudintermedius* was generally reported to be sensitive against antibiotics belonging to beta-lactam class in the past, methicillin-resistant *S. pseudintermedius* (MRSP) has been emerged and contains a *mecA* gene responsible for production of an altered penicillin binding protein organizing staphylococcal chromosomal

cassette (SCC*mec*) [3]. MRSP infection has not only been increased in animals but also its animal-to-human transmission has been occurred causing public health problem [4, 5].

S. pseudintermedius Z0118SP0130 (KCTC 43165) was isolated from eye specimen of a companion dog and identified as sequence type 45. A sample swap was inoculated in CHROMagar Orientation (CHROMagar, France) and incubated at 30°C for 48 h under aerobic condition. A single colony was isolated and identified as *S. pseudintermedius* by 16S rRNA gene comparison which showed 100% similarity to one of *S. pseudintermedius* strain 21-3929 (GenBank accession No. CP128234.1).

Antibiotic susceptibility testing was performed according to the Kirby-Bauer method. Twelve antibiotic discs (oxacillin, erythromycin, clindamycin, quinupristin/dalfopristin, trimethoprim/sulfamethoxazole, streptomycin, gentamicin, mupirocin, vancomycin, teicoplanin, linezolid, tigecycline) (Oxoid, UK) were placed on the Mueller Hinton agar (BD Difco, USA) medium using the

***Corresponding author**

Phone: +82-63-850-0840, Fax: +82-63-850-0834
E-mail: chae@jbnu.ac.kr

Table 1. Genome features of *Staphylococcus pseudintermedius* Z0118SP0130.

Features	Value
GenBank accession No.	CP060700.1
No. of contigs	1
Length (bp)	2,663,277
G+C content (%)	37.50
No. of CDSs	2,454
No. of rRNA (5S, 16S, 23S) genes	7, 6, 6
No. of tRNA genes	60
No. of ncRNA genes	4

CDSs, protein coding sequences

disc dispenser (Oxoid) which was inoculated with the bacterial suspension diluted in saline solution. After incubating at 37°C for 18 h, the disc zone diameter was measured with the SCAN 4000 equipment (Interscience, USA). Antibiotic resistance was determined according to the criteria of the Clinical and Laboratory Standards Institute guidelines. The Z0118SP0130 strain was resistant to oxacillin, erythromycin, clindamycin,

quinupristin-dalfopristin, trimethoprim-sulfamethoxazole, streptomycin, gentamicin, and mupirocin.

Genomic DNA of strain Z0118SP0130 was extracted with QIAamp DNA mini kit (Qiagen, Germany) from cells which were grown aerobically at 37°C for 24 h in blood agar medium. Whole genome sequencing was conducted at Macrogen Inc. (Republic of Korea) using PacBio RSII (PacBio, USA) and HiSeq X ten (Illumina, USA) platforms. The determined subreads exhibited about 217-fold coverage and only one contig of 2,663,277 bp was generated from them by assembly using Unicycler v0.4.8 [6]. Prokka v1.11 [7] was used for gene annotation which subsequently found 2,454 protein coding sequences (CDSs), 60 tRNA genes, and 19 rRNA genes as described in Table 1. The GC content of the genome was 37.50%. The circular genomic map was generated with genome circular viewer in PATRIC server (Fig. 1) [8]. The genomic distances between strain Z0118SP0130 and the related strains were measured with the online Average Nucleotide Identity calculator (CJ Bioscience, Republic of Korea). The values were 99.24% with *S. pseudintermedius* strain 21-3929 (GenBank accession

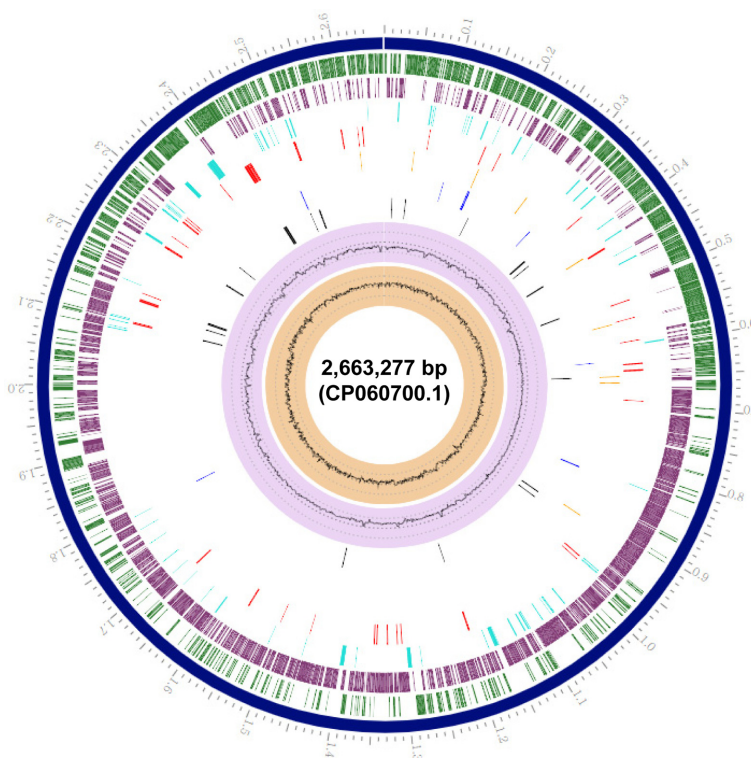


Fig. 1. The genome of strain Z0118SP0130 generated using genome circular viewer in PATRIC server. Each color represents CDS (green and purple), AMR genes (red), GC contents (pink), genome size (blue), and non-coding sequences (cyan).



Fig. 2. The genetic structure of staphylococcal cassette chromosome *mec* (SCC*mec*). *Staphylococcus pseudintermedius* Z0118SP0130 had a similar structure to SCC*mec* V(5C2&5)b.

No. CP128234.1) and 99.42% with *S. pseudintermedius* strain LMG 22219 (GenBank accession No. GCA_001792775.2).

Investigation on antibiotic resistant genes in the genome was performed using the Comprehensive Antibiotic Resistance Database (CARD) v3.2.8 [9] and found the β -lactam antibiotics resistance genes (*mecA*, *blaZ*), tetracycline resistance gene (*tetM*), trimethoprim resistance gene (*dfrG*), streptogramin resistance gene (*vatE*), lincosamide resistance gene (*lmrB*), mupirocin resistance gene (*ileS*), erythromycin resistance gene (*ermB*), and aminoglycoside resistance genes [*aad(6)* and *aac(6')-Ie-aph(2'')-Ia*]. This was consistent with the result of antimicrobial susceptibility test.

A SCC*mec* responsible for methicillin resistance was found in the genome. The structure was closely similar to the SCC*mec* type Vb (5C2&5) identified in *Staphylococcus aureus* which consisted of insertion sequences IS431 and two *ccrC1*, cassette chromosome recombinase genes, on both sides of *mecA* gene (Fig. 2) [10].

Nucleotide Sequence Accession Number

The genome sequence of *Staphylococcus pseudintermedius* Z0118SP0130 has been deposited in NCBI GenBank under accession CP060700.1. The strain was deposited in KCTC under deposition number 43165.

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Conflict of Interest

The authors have no financial conflicts of interest to declare.

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