

Genome Reports

Complete Genome Sequence of an *optrA*-positive Linezolid-resistant *Staphylococcus rostri* Strain PJFA-333 Isolated from a Pig in Korea

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Linezolid, the first oxazolidinone introduced into human clinical use, has become a last resort antibiotic in treatment of serious infections caused by Gram-positive pathogens, including methicillin-resistant staphylococci and vancomycin-resistant enterococci. Although oxazolidinones are strictly prohibited for use in food-producing animals, occurrence of linezolid-resistant staphylococci has recently been reported in livestock farms in Korea. Here, we report the complete genome sequence of an *optrA*-positive linezolid-resistant *Staphylococcus rostri* strain PJFA-333 isolated from a pig farm in Korea.

Keywords: *Staphylococcus rostri*, linezolid resistance, *optrA*

Emergence of linezolid resistance in *Staphylococcus* spp. isolated from livestock farms has become a significant threat to public health [1]. Linezolid resistance in staphylococci has frequently been associated with acquisition of the transferable oxazolidinone gene, *cfr* [2]. Recently, a novel oxazolidinone-phenicol resistance gene, *optrA*, has also been detected in enterococcal and staphylococcal isolates of humans and animals [3]. In the current report, we present the complete genome sequencing results of an *optrA*-positive linezolid-resistant *Staphylococcus rostri* PJFA-333 strain isolated from a pig in Korea.

A linezolid-resistant *S. rostri* PJFA-333 strain was isolated from a nasal swab sample obtained from a finishing pig in Jeolla-do, Korea. For whole-genome sequencing analysis, genomic DNA sample of the PJFA-333

strain was prepared using the Wizard Genomic DNA Kit (Promega, USA) according to the manufacturer's recommendation. Genome sequence libraries were constructed by a combination of Illumina iSeq (Illumina, USA) and Oxford Nanopore MinION (Oxford Nanopore Technologies, UK) sequencing platforms. Trimmed and filtered high-quality reads of Nanopore and Illumina sequence data were assembled *de novo* using the Unicycler v.0.5.0 software. The assembled PJFA-333 genome revealed a genome size of 2,390,967 bp (G+C content of 38.4%), which contained seven contigs. The seven contigs were comprised of a single large chromosome of 2,337,213 bp and six plasmids (Table 1). The complete sequence was annotated using Rapid Annotation using Subsystem Technology (RAST) v.2.0 [4] and Prokka v.1.14.6 [5]. The sequence of a 16S rRNA gene extracted from the genome showed 100% sequence similarity to a *S. rostri* strain ARI 262T (GenBank Accession No. FM242137). Genomic comparison with a previously published sequences of *S. rostri* strain DSM

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Table 1. Genetic characteristics of the linezolid-resistant *S. rostri* PJFA-333 strain.

Genetic features	PJFA-333
Source	Pig
Antimicrobial resistance ^a	CHL-CLI-LZD-TET
Genome size	2,390,967 bp
GC content	38.4%
No. of contigs (bp, G+C contet, and CDS)	7
Chromosome	2,337,213 bp; 38.5%; 2,239
Plasmids	pSR7-1 (36,227 bp; 32.8%; 40) pSR7-2 (8,025 bp; 32.4%; 9) pSR7-3 (4,047 bp; 29.1%; 4) pSR7-4 (2,706 bp; 27.2%; 3) pSR7-5 (1,491 bp; 32.9%; 2) pSR7-6 (1,258 bp; 33.8%; 2)
No. of RNAs	76 (tRNA, 57 ; and rRNA, 19)
Antimicrobial resistance genes (location)	<i>mecA</i> (chr ^b); <i>tet(M)</i> (chr); <i>vga(A)V</i> (chr); <i>cfr</i> (pSR7-1); <i>fexA</i> (pSR7-1); <i>bleO</i> (pSR7-2); <i>ant(9)-la</i> (pSR7-2); <i>optrA</i> (pSR7-2)
GenBank accession numbers	CP113107 (Chr) pSR7-1 (CP113108), pSR7-2 (CP113109), pSR7-3 (CP113110), pSR7-4 (CP113111), pSR7-5 (CP113112), pSR7-6 (CP113113)

^aCHL, chloramphenicol; CLI, clindamycin; LZD, linezolid; and TET, tetracycline
CDS, coding sequence; chr, chromosome

21968 (GenBank Accession No. GCA_002902145.1) resulted in 99.8% average nucleotide identity (ANI) value calculated by OrthoANiU algorithm [6]. Analysis of antimicrobial resistance genes in PJFA-333 strains was carried out using ResFinder (<https://cge.cbs.dtu.dk/services/ResFinder/>) of Center for Genomic Epidemiology and BLAST search. Standard antimicrobial susceptibility tests [7] of PJFA-333 strain revealed resistance phenotypes to chloramphenicol, clindamycin, linezolid, and tetracycline. BLAST analysis of the genome also identified various antimicrobial resistance genes [*mecA*, *vga(A)V*, *bleO*, *ant(9)-la*, *cfr*, *optrA*, *fexA*, and *tet(M)*]. The two oxazolidinone resistance genes, *cfr* and *optrA*, were located on a 36-kb plasmid pSR7-1 and 8 kb-plasmid pSR7-2, respectively. Moreover, the florfenicol resistance gene, *fexA*, was co-localized with *cfr* on the pSR7-1.

The complete genome sequences of the PJFA-333 strain (CP113107) and the six plasmids (CP113108 - CP113113) have been deposited in the GenBank sequence database.

Acknowledgments

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Conflict of Interest

The authors have no financial conflicts of interest to declare.

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