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Complete Genome Sequences of Two Quinolone-Resistant Methicillin-Resistant *Staphylococcus aureus* Strains Isolated from Broilers in Korea

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Fluoroquinolones have been extensively used in treatment or prevention of serious infections in humans and food-producing animals, especially in poultry, due to their broad-spectrum activity to both Gram-positive and -negative pathogens. However, the use of fluoroquinolones in poultry production selects for bacteria carrying genetic determinants for quinolone resistance. Here, we present the complete genome sequences of two methicillin-resistant *Staphylococcus aureus* (MRSA) strains displaying quinolone resistance, which were isolated from healthy broilers in Korea.

Keywords: **Methicillin-resistant *Staphylococcus aureus* (MRSA), quinolone resistance, broilers**

Fluoroquinolones are classified as the highest priority and critically important antimicrobials in human and veterinary medicine, respectively [1, 2]. However, emergence of quinolone resistance, especially in methicillin-resistant *Staphylococcus aureus* (MRSA), as a result of extensive use of fluoroquinolones in food-producing animals has become a significant threat to public health. The occurrence of quinolone-resistant *S. aureus* possessing mutations in the quinolone resistance-determining regions (QRDRs) of *gyrA* and *parC* has previously been reported in chicken meat production systems in Korea [3, 4]. In the current study, we present the complete genome sequences of two quinolone-resistant MRSA strains, CJFA-182 and CKFA-361, isolated from healthy broiler chickens.

The two quinolone-resistant MRSA strains, CJFA-182 and CKFA-361, were isolated from healthy broilers (oropharyngeal and skin swabs, respectively) in Jeolla and Kyeongsang in Korea, respectively [3]. For genome sequencing analysis, total genomic DNA of the CJFA-182 and CKFA-361 strains were extracted using the Wizard Genomic DNA Kit (Promega, USA) according to the manufacture's recommendation. Genome sequence libraries were constructed by the Oxford Nanopore MinION system (Oxford Nanopore Technologies, UK) with the Illumina iSeq (Illumina, USA) sequencing platform for an error correction. *De novo* assembly of trimmed and filtered high-quality reads was conducted using the Unicycler v.0.5.0 software. The assembled genomes of CJFA-182 and CKFA-361 strains yielded three and two contigs with 2,985,125 bp (G+C content of 32.8%, and 57× and 313× of genome coverages on MinION and iSeq) and 2,834,769 bp (G+C content of 32.9%, and 84× and 427× of genome coverages on MinION and iSeq), respectively. The three contings of CJFA-182 strain represent a single chromosome of 2,799,475 bp and two plasmids (pCJFA-182_1 and pCJFA-182_2). The two contigs of CKFA-361 strain

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Table 1. Genetic characteristics of quinolone-resistant MRSA CJFA-182 and CKFA-361 strains.

Genetic features	CJFA-182	CKFA-361
Source	Broiler	Broiler
MLST-SCC*mec-agr-spa*	ST692-SCC*mec* V-I-t2247	ST188-SCC*mec* IVa-I-t189
Antimicrobial resistance[a]	AMP-CEF-CIP-CLI-ERY-PEN-TET	AMP-CEF-CIP-CLI-ERY-GEN-PEN-SXT
Genome size	2,958,125 bp	2,834,769 bp
GC content	32.8%	32.9%
CDS	2821	2680
No. of contigs	3	2
Chromosome	chr (2,927,067 bp)	chr (2,799,475 bp)
Plasmids	pCJFA-182_1 (29,583 bp) pCJFA-182_2 (1,475 bp)	pCKFA-361 (35,294 bp)
No. of RNAs	80	79
Antimicrobial resistance genes (location)	*mecA* (chr) *blaZ* (chr) *ermB* (chr) *tet*(S) (chr) *blaZ* (pCJFA-182_1) *tet*(L) (pCJFA-182_1)	*mecA* (chr); *aph(2")-Ia* (pCKFA-361) *blaZ* (pCKFA-361) *ermB* (pCKFA-361) *dfrE* (pCKFA-361)
GenBank accession numbers	CP085320 (chr) CP085321 (pCJFA-182_1) CP085321 (pCJFA-182_2)	CP085318 (chr) CP085319 (pCKFA-361)

[a]AMP, ampicillin; CEF, cefoxitin; CIP, ciprofloxacin; CLI, clindamycin; ERY, erythromycin; GEN, gentamicin; PEN, penicillin; SXT, sulfamethoxazole-trimethoprim; and TET, tetracycline.
CDS, coding sequence; chr, chromosome.

were comprised of a chromosome of 2,799,475 bp and a 35-kb plasmid (pCKFA-361) (Table 1).

The complete sequences were annotated using Prokka v.1.14.6 [5] and Rapid Annotation using Subsystem Technology (RAST) v.2.0 [6]. Comparative genomic analysis with previsouly published sequences of ST692-MRSA strain K12S0375 (GenBank Accession No. JYGF000000) [7] and ST188-MRSA strain CUHK_188 (GenBank Accession No. JFFV000000) [8] showed 99.93% and 99.7% average nucleotide identity (ANI) values calculated by OrthoANIu algorithm [9]. Analysis of the presence of antimicrobial resistance genes in the two MRSA strains was carried out using ResFinder v.4.4.2 (https://genepi.food.dtu.dk/resfinder) of Center for Genomic Epidemiology and BLAST search. BLAST and ResFinder anaylsis confirmed double point mutations in *gyrA* (S84L) and *parC* (S80F) in both CJFA-182 and CKFA-361 strains and also identified various antimicrobial resistance genes associated with the observed resistance phenotypes (Table 1).

The complete genome sequences of two quinonle-resistant MRSA strains CJFA-182 (CP085320-CP085322) and CKFA-361 (CP085318-CP085319) 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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