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Genomic analysis of *Staphylococcus aureus* from a Chinese pig farm reveals SCCmec V/VII co-existence and dual-copy of *blaZ-blaR1-blaI* in a highly oxacillin- resistant isolate

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Background

From a One Health perspective, methicillin-resistant Staphylococcus aureus (MRSA) in pigs may serve as a reservoir of resistance for humans MRSA.

Objective

To characterize the antimicrobial resistance phenotypes and genomic features of MRSA circulating in a Chinese pig farm.

Methods

Skin and nasal swabs (n=160) from sows and piglets were collected from a pig farm in Jiangxi Province, China. Staphylococci were isolated on high-salt selective media, and single colonies were confirmed by MALDI-TOF. Methicillin resistance was assessed by cefoxitin disk diffusion and microbroth oxacillin tests. Whole-genome sequencing (WGS) via short read sequencing was performed followed by genome analysis.

Results

1. A total of 67 S. aureus isolates were recovered; 17 (25.4%) were cefoxitin-susceptible and 50 (74.6%) were methicillin resistant. Notably, isolate JX1PS1 exhibited no cefoxitin inhibition zone and an oxacillin MIC of 128 ug/ml, indicating high-level resistance. Genomic analysis showed that JX1PS1 carried SCCmec IVb and contained duplicated *bla* regulatory/structural modules (*blaZ-blaR1-blaI*), which may have contribute to its high-level β-lactam resistance phenotype (Figure 1).

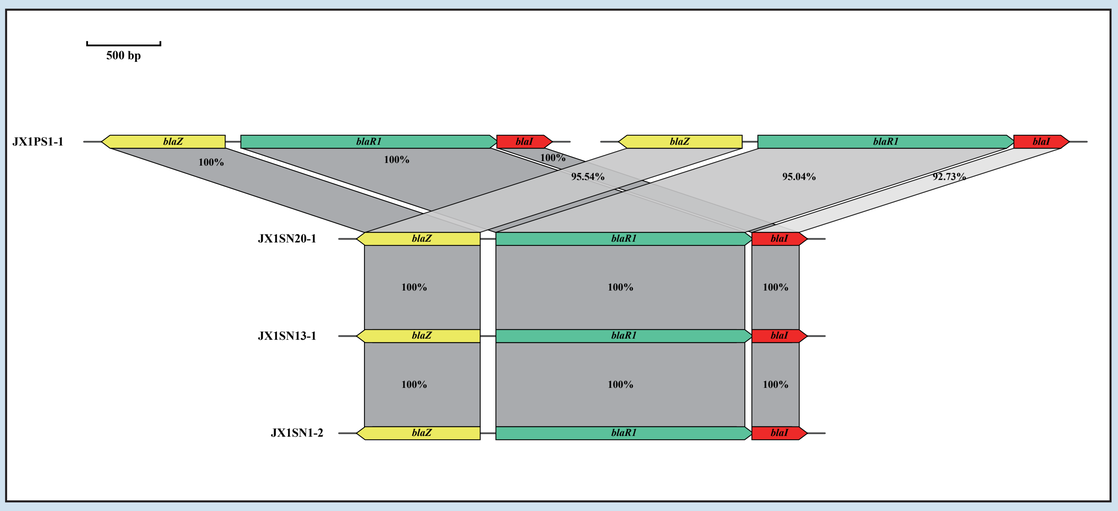

Figure 1. Duplication of *bla* regulatory/structural modules in isolate JX1PS1.

2. 57 strains passed quality control and were predominantly of ST398 or SLV398, a livestock-associated MRSA lineage. SCCmec analysis revealed, with the exception of JX1PS1, all isolates co-harbored SCCmec V and SCCmec VII elements—an uncommon configuration in pigs and, to our knowledge, the first report of widespread SCCmec V/VII co-existence in Chinese swine *S. aureus* (Figure 2).

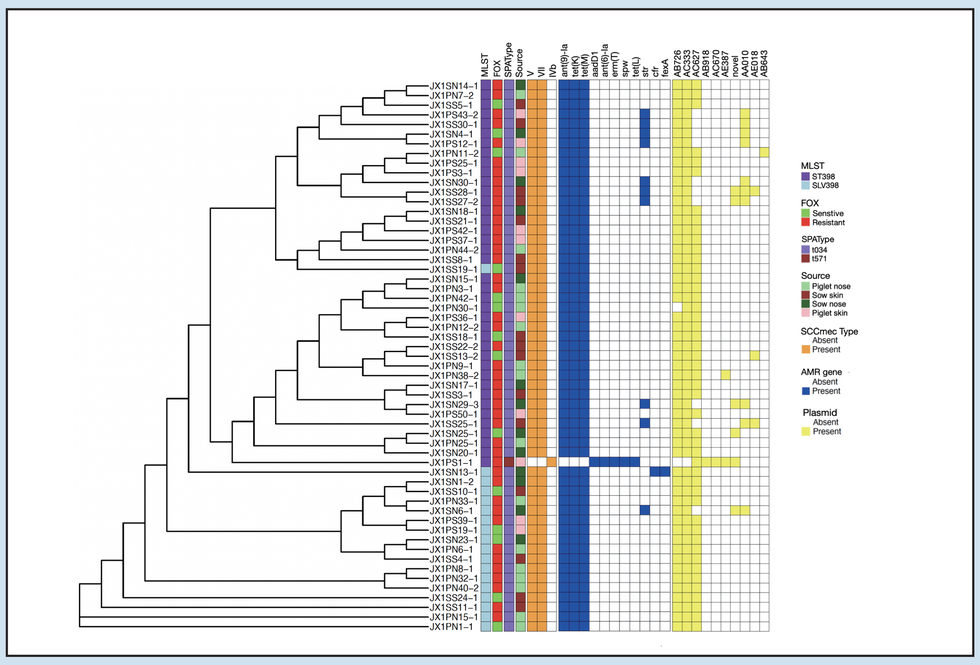

Figure 2. Phylogeny and genomic features of 57 *S. aureus* isolates.

Conclusions

MRSA ST398 in a Chinese pig farm carried both SCCmec V and VII types, with one strain carrying dual-copy of blaZ-blaR1-blaI. Continued genomic surveillance across the livestock–human interface is warranted to prevent potential zoonosis.

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