81 Genomic analysis of Staphylococcus aureus along a pork production chain and in the community, Shandong Province, China

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Background: Livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) is an increasingly important public health concern worldwide; however, data on LA-MRSA from Asian countries is scarce. Here, we performed a comprehensive molecular epidemiological survey of S. aureus along a representative pork production chain and in the community in Shandong Province, China.

Materials/methods: Selective cultures, spa-typing and whole-genome sequencing were used to survey the occurrence and potential transmission of S. aureus in various sectors, including 899 pig samples (snout or skin swabs, carcass swabs and pork portions), 845 human nasal samples and 239 environmental samples from commercial farms, a slaughterhouse, a pork market and the surrounding community.

Results: MRSA was detected in higher frequencies in samples from two commercial pig farms (pigs, 49%; farm workers, 64%; environmental samples, 16%), than in samples from the slaughterhouse (fatteners, 8.2%; carcasses, 1.1%; operation workers, 0%; environmental samples, 3.8%), the pork market (pork, 14%; sellers, 0%) or individuals in the community (6.8%). There were significant differences in population structures, antimicrobial susceptibility profiles, and the presence of resistance and virulence genes between human- and pig-associated isolates. Two separate MRSA populations were observed in this Chinese region, one connected to pigs with mainly MRSA CC9 carrying tet(L) but lacking  erm(B) and ICE genes, and one in humans with primarily MRSA ST59 carrying  erm(B) and ICE genes but lacking tet(L), also two different MSSA ST398 populations are circulating in humans and pigs differing in ICE genes. The phylogenetic analysis confirmed the dissemination of LA-MRSA between various segments along the production chain. However, MRSA of the same sequence type was not found to be disseminated between the commercial farms and the surrounding communities. Furthermore, we observed one MRSA ST398 and detected a novel CC9 variant ST3597 within the chain.

Conclusions: The current study provides the first “One Health” survey and comprehensive molecular epidemiology portrait of S. aureus along a pork production chain and in the community in Asian counties. To better understand the occurrence of LA-MRSA in pigs in China and to monitor its epidemiological changes, surveillance, as well as further research studies in pigs, humans and their environment, are needed.