GENOMIC CHARACTERIZATION OF STAPHYLOCOCCUS AUREUS AT THE SWINE-HUMAN INTERFACE

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Background

The epidemiology of S. aureus in swine held little interest until the ST398 lineage of MRSA was found to be prevalent in pigs and pig farmers in the Netherlands in 2004 (Voss et al. 2005). ST398 MRSA have since been detected in multiple livestock species and in many countries (EFSA, 2009; Smith and Pearson, 2011), while genetically distinct variants of ST398 S. aureus occur in some human populations independent of livestock reservoirs (Carrel et al., 2017). Furthermore, other genotypes of MRSA can occur in pigs, particularly ST9 MRSA in Asia, and ST5 MRSA in North America (Chuang and Huang, 2015; Frana et al. 2013). In the USA, methicillin susceptible variants of the ST398, ST9 and ST5 lineages are widespread in commercial swine, yet MRSA variants appear to occur at relatively low prevalence (Sun, et al., 2015). Despite common exposure to, and colonization of, swine workers by livestock associated S. aureus, significant clinical infections appear to be uncommon in occupationally exposed people. However, invasive and even fatal infections are reported at relatively low incidence in some countries, and medically compromised people appear to be at particular risk, even in the absence of animal contact (Larsen et al., 2017). There is evidence that ST398 MRSA of livestock origin are less transmissible among humans than MRSA of human origin. Also, genomic studies typically have indicated that livestock associated MRSA (both ST398 and ST5) lack most virulence factors that occur in human clinical isolates (Schijffelen et al. 2010; Price et al. 2012; Hau et al, 2015). However, to date there has been little genomic characterization of methicillin susceptible S. aureus (MSSA) that are prevalent in swine populations. The purpose of this study was to describe the occurrence of virulence factors and antibiotic resistance genes in S. aureus isolates from pigs and swine veterinarians in the USA.

Material and methods

S. aureus isolates from growing pigs (n=30) or swine veterinarians (46) included ST9 (n=47), ST398 (19), ST5 (9), and ST72 (1). Isolates were analyzed using next generation sequencing and completed chromosome and plasmid sequences were annotated with gene and protein information using Prokka. Genes encoding virulence factors and antibiotic resistance were detected using only the filtered read-set and SRST2 (0.1.8) software based on published databases for sequence typing, virulence factors and antibiotic resistance genes, and genes detected were visualized using heat maps (presence/absence).
Results and discussion

No systematic differences were evident between the isolates from pigs and veterinarians, consistent with interspecies transmission without host adaptation. Among 173 putative virulence genes examined, 42 genes (including enterotoxins, Panton-Valentine leukocidin or toxic shock syndrome toxin genes) were not detected in any of the isolates. All isolates harbored 77 genes belonging to 6 functional groups with roles in cell attachment, iron regulation and cytotoxin production. The remaining 54 virulence genes were variably distributed and clustered by sequence type, with ST398 isolates having fewer virulence genes than ST9 and ST5 isolates. Twenty-four resistance genes were detected, also associated with sequence type. Overall, each MLST lineage carried distinct sets of putative virulence factors, and profiles of antibiotic resistance genes also differed among sequence types. However, apart from SCCmec elements including mecA, MRSA and MSSA isolates displayed similar profiles within MLST lineages.

Conclusions

The findings indicate that these 3 lineages that are prevalent in swine in the USA have evolved somewhat independently in this species, suggesting a limited effect of horizontal gene transfer of virulence genes and antibiotic resistance among different sequence types.

References


