Characterization of methicillin-resistant Staphylococcus aureus Sequence Type 398 - DTU
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Staphylococcus aureus is an opportunistic pathogen that colonizes the nares and skin surfaces of several animal species, including man. S. aureus can cause a wide variety of infections ranging from superficial soft tissue and skin infections to severe and deadly systemic infections. Traditionally S. aureus and methicillin-resistant Staphylococcus aureus (MRSA) have been associated with hospitals, but during the past decades MRSA has emerged in the community and now a new branch of MRSA has been found in association with livestock (LA-MRSA). A specific lineage (multilocus sequence type 398 (ST398)) has been particularly successful in colonization of pigs and ST398 has become the most frequently reported MRSA strain found in association with livestock.

Currently the understanding of the successful colonization and transmission of LA-MRSA ST398 in pigs are limited and mainly based on observational field surveys. The aim of this work was to develop a high-throughput approach for genotypic and phenotypic characterization of LA-MRSA ST398 in the porcine reservoir.

The thesis represents three studies (manuscript I-III). In manuscript I a genome-saturated transposon mutant library was generated and Transposon Directed Inserted site Sequencing (TraDIS) was for the first time assessed in an LA-MRSA ST398 strain. Using this high-throughput approach, genes essential for LA-MRSA ST398 survival under laboratory conditions and in whole porcine blood in vitro were identified. In manuscript II, genes important for LA-MRSA ST398 survival on porcine skin and nasal epithelium ex vivo were identified. These genes could represent targets for de-colonization, which could help prevent further spread and adaption of LA-MRSA ST398. Manuscript III describes the construction of the S. aureus VirulenceFinder database. The database can be applied for identification of virulence genes in S. aureus using whole genome 5 sequence data. The S. aureus VirulenceFinder will be part of the tool package generated for the Centre for Genomic Epidemiology (CGE) (www.genomicepidemiology.org).

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