

Title: Prevalence and characterization of *Staphylococcus aureus* in pigs in the USA – NPB #13-056 Revised

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Date Submitted: 08/03/15

Scientific Abstract

A cross-sectional study of 36 herds of growing pigs across 11 states was conducted to estimate the prevalence of *S. aureus* (including MRSA), and characterize the isolates with respect to spa type, MLST type, presence of enterotoxin genes, and antimicrobial and zinc resistance. A positive control herd known to harbor MRSA was also included in the study. On each farm, nasal swabs were collected from 20 growing pigs older than 4 weeks of age. Overall, 739 pig nasal swabs were collected, of which 558 (76%) were culture positive for *S. aureus* from 35 of the 36 farms (97%). Except the positive control farm, on which all 20 pigs tested MRSA positive, no MRSA were detected in any of the pigs. Among the 35 *S. aureus* positive farms there was considerable diversity found with 33 spa types detected within 4 MLST sequence types. The most prevalent spa types (sequence type) were t337 (ST9), t034 (ST398) and t002 (ST5) which together accounted for 59% (627/1070) of isolates typed. No isolates carried any of the major enterotoxin genes implicated in foodborne staphylococcal enterotoxigenesis. Antimicrobial resistance testing showed resistance was most common to spectinomycin (100%), tetracycline (94%), clindamycin (75%) and penicillin (72%), and 89% (116/130) of isolates were resistant to 5 or more antibiotics (multidrug resistance *S. aureus*, MDRSA). ST398 (t034) MRSA isolates from the positive control farm were positive for the *czrC* gene, but no other isolates tested were positive. However, 14% of SA (18/130) tested were phenotypically zinc resistance based on a break point of 4mM zinc. The absence of MRSA from all 36 study herds supports accumulating data suggesting the MRSA is less prevalent in US swine farms than in many European countries such as Holland and Denmark. It appears 3 lineages (ST9, ST398, and ST5) predominate among *S. aureus* carried by healthy growing pigs in the USA. Although all isolates were methicillin susceptible, these 3 lineages have to date been those most commonly reported for MRSA isolates from pigs. The absence of major enterotoxin genes suggests that staphylococcal enterotoxigenesis associated with pork products is more likely the result of contamination in the harvest and post-harvest segments of the pork supply rather than originating on the farm. Multiple antimicrobial resistance was common, in line with some other recent studies in farm workers and rural residents in the USA. However, current evidence suggests that pig adapted *S. aureus* rarely harbor major virulence factors associated with human disease. Hence the human health significance, if any, of multiple resistance in this group of organisms is yet to be established.

These research results were submitted in fulfillment of checkoff-funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer-reviewed.

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