

Title: Occurrence and molecular epidemiology of Methicillin Resistant *Staphylococcus aureus* (MRSA) on-farm, at slaughter and pork. - NPB project #09-171 Revised

Investigator: Wondwossen A. Gebreyes

Institution: The Ohio State University

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Scientific Abstract:

The present serial cross-sectional study targeting ten cohorts of commercial swine farms was conducted to investigate the occurrence and prevalence of methicillin resistant *Staphylococcus aureus* (MRSA) in finishing pigs on-farm, at lairage and assess the potential of carriage at slaughter and retail levels. Paired nasal and peri-anal swab samples were collected from market-age pigs on-farm and the same batch of pigs were followed and sampled at the lairage before slaughter and carcass swabs at post evisceration stage before chilling. Pork samples from the same batch of pigs were collected at retail market. Samples were examined following conventional cultural methods using selective enrichment method. Isolates were tested for antimicrobial resistance by the broth microdilution method. PCR was used to detect the presence of species-specific gene (*nuc*) and methicillin resistance marker gene (*mecA*). The genotypic relatedness of isolates was determined using the pulsed-field gel electrophoresis (PFGE) and multi-locus sequence typing (MLST). One or more MRSA positive pigs were detected in five of the ten herds (50%). The prevalence of MRSA in pigs was higher at lairage and ranged from 0% to 54.2% per farm compared to the same batch of pigs sampled on-farm (0% to 12.5%). MRSA was detected in 1.7% (4/235) of the carcass swab and 3.7% (5/135%) of the retail pork samples. MRSA isolates recovered from various stages of sampling were multidrug resistant (MDR) and besides β -lactams, resistance to tetracycline (76.4%), clindamycin (72.7%) and erythromycin (62%) was detected. Genotypically related isolates were recovered across all stages of the pork production chain based on *cfr9I* PFGE. Genotyping using MLST of selected isolates revealed that ST398 was detected from pigs on-farm and at lairage and retail pork samples and in addition ST5, ST9, ST39 and ST72 were detected at different points of sampling. Results of the present study show that MRSA can be detected at all sampling points through out the pork production chain and suggests the need for further detailed epidemiological studies involving more representative farms and slaughterhouses and associated environments across major pig producing states in the US.

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.

For more information contact:

National Pork Board • PO Box 9114 • Des Moines, IA 50306 USA • 800-456-7675 • Fax: 515-223-2646 • pork.org
