

Title: MRSA of Pigs and Genetic Analysis of Resistance Linked with *mecA* and *mecC*. - NPB #14-232

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Investigator: Catherine M. Logue Ph.D., MIFST

Institution: Iowa State University

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Scientific Abstract

Background: Methicillin-associated resistance in *S. aureus* is encoded by the *mecA* gene, carried on the staphylococcal cassette chromosome *mec* (*SCCmec*) resulting in an altered penicillin binding protein (PBP) () and reduced susceptibility to the β -lactam antibiotics including penicillin. Until now, detection of *mecA* or PBP was considered an indicator of methicillin resistance and confirmation of MRSA. Recently, new strains of MRSA resistant to methicillin but negative for *mecA* and PBP have been recognized.

Materials and Methods: This study examined the prevalence of *mecA* and *mec* variants in a collection of MRSA and non MRSA from swine, pork meat, other production animals, meat and humans for detection of resistance genes associated with methicillin resistance. Isolates examined were identified as methicillin resistant on media containing oxacillin. A total of 717 *S. aureus* and 188 non-*S. aureus* strains from production swine, other production animals, meat and human strains (n=150) were examined for *mec* genes including *mecA*, *mecA_{LGA251}*, *mecA1* and *mecC1* using PCR. Swine isolates were also subtyped for *SCCmec* using a multiplex PCR.

Results: Overall most isolates identified as methicillin resistant were positive for the *mecA* gene (n = 521) however, a small collection (n=35) were identified as *mecA_{LGA251}* positive, but they could not be confirmed as *mecC* using standard primers. Further typing using *mecA1* and *mecC1* primers detected the *mecA1* variant in nine isolates of both *S. aureus* and non-*aureus* species and one isolate from ovine was positive for the *mecC1* variant. Subtyping *mecA* positive isolates of swine (n = 519) using the *SCCmec* typing scheme found the most common subtypes detected included II, IV and VI. A significant number of isolates however could not be assigned to a subtype using the current scheme and will require further analysis to determine if there are more emerging subtypes not currently identified.

Conclusion: While the emerging *mecC* variant has not been detected in MRSA and non-MRSA of swine to date, our data suggests that there are other emerging novel variants of *mecA* and *mecA1* that would appear to be occurring. These novel variants may also be a source of, or recipient of resistance and could potentially pose a threat to animal or human health.

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
