

PUBLIC HEALTHWORKER SAFETY

Title: Evaluation of methodologies for qualitative and quantitative detection of methicillin-resistant *Staphylococcus aureus* (MRSA) in retail pork -NPB #08-219

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Scientific Abstract:

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a critically important human pathogen and has emerged as an important cause of infections of people in the community. MRSA can also be found in various animal species, including pigs. Studies have identified MRSA colonization in pigs in various countries internationally, including the United States and Canada. In Europe, numerous studies have reported an associated between contact with pigs and MRSA infections, specifically infections caused by sequence type 398 (ST398), an MRSA clone that appears to have originated in pigs. The widespread presence of MRSA in pigs has raised concern about the potential for contamination of meat, and meat as a vehicle for MRSA dissemination to people in the community. Recent studies have identified MRSA in retail meat in Europe and North America, yet the relevance of this is currently unclear. One aspect that needs investigation is the level of contamination of pork, since available studies have relied on enrichment culture methods that could potentially detect very low levels of contamination. Further, studies using proper sampling schemes are needed to avoid sampling bias. This study involved evaluation of various methods for qualitative and quantitative detection of MRSA in retail pork, through the use of experimentally inoculated samples. Optimal methods were then used to test evaluate retail pork collected through the systematic sampling methods of the Canadian Integrated Program for Antimicrobial Resistance Surveillance.

There was some variability in the consistency and detection threshold of qualitative methods, with methods using larger samples of meat and selective agar being more consistent and with a lower detection threshold. Rinse methods were equivalent to more labor-intensive homogenization methods. Optimal methods are able to detect 10 CFU/g, or lower. Similarly, quantitative methods varied, with methods using larger samples and selective agar being superior.

MRSA was isolated from 8/127 (6.3%) ground pork samples and 14/89 (14%) pork chops, for an overall rate of 9%. Seven of 22 positive samples were only positive using the enrichment culture method, mean the level of contamination was likely less than 20 bacteria per gram of meat. Of the samples where enough MRSA was present to determine a number, only 20 bacteria per gram were present in 9/15 (60%), while the remaining 6 samples had 30, 90, 100, 110, 340 and 3590 CFU/g. All isolates were spa type t002, negative for Panton Valentine leukocidin genes and classified as USA100 by PFGE. Two different USA100 subtypes were present.

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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