

PORK SAFETY

Title: Evaluation of the nasal microbiome and its potential role in MRSA colonization in pigs – NPB #11-096

Investigator: J Scott Weese

Institution: University of Guelph

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Scientific Abstract: Since first recognition of livestock-associated MRSA in Europe, significant concern has been raised about the potential impacts on pig farmers and veterinarians, rural residents and the broader population. A better understanding of factors that affect MRSA carriage by pigs is needed to develop effective control programs. While not adequately studied, it has been assumed that the pig has a complex and abundant bacterial population in its nasal passages, and that may play a critical role in determining the fate of bacteria to which it becomes exposed. The objective of this study was to describe the nasal microbiome of slaughter-age pigs and to evaluate the influence of the microbiome on MRSA colonization.

The nasal microbiome of age- and farm-matched MRSA carriers and non-carriers was evaluated and compared. To further evaluate the influence of management on the nasal microbiome, swabs were collected from a set of age-matched pigs on a farm that fed a liquid diet.

The swine nasal microbiome is complex and highly variable between individuals. Species richness is high, with between 25 and 277 species identifications per animal (mean 120, median 98). There was no difference in richness between MRSA carriers and non-carriers ($P=0.94$).

Overall, the Proteobacteria Phylum was most abundant. Firmicutes was the second most common Phylum overall and was predominant in some individuals (largely based on high abundances of *Staphylococcus*, *Bacillus* and *Paenibacillus* spp). The following other phyla were identified in decreasing relative abundances: Bacteroidetes, Spirochaetes, Actinobacteria, Cyanobacteria, Thermotogae, Tenericutes, Synergistes, Fibrobacteres, Fusobacteria, Elusimicrobia, Lentisphaerae and Deferribacteres. The microbial population structure did not differ between groups (Parsimony test $P>0.05$). Using principal component analysis, there was no apparent clustering of the MRSA carriers. There were few differences between groups at lower taxonomic levels, with no differences at the Phylum or Class level.

While there was no difference between farm-matched MRSA positive and negative pigs, there was a significant difference between those pigs and pigs from a different farm that were liquid diet-fed. Liquid-fed pigs had significantly fewer Bacteroidetes and Proteobacteria, and more Firmicutes. There were numerous differences between groups at lower taxonomic levels. This indicates that management factors can influence the nasal microbiome, so further comparison of factors that modify the nasal microbiome and the corresponding influence on MRSA (as well as other swine or zoonotic pathogens) is indicated.

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

This has been the first comprehensive study of the porcine nasal microbiome and it has demonstrated a highly complex microbial population. There was no evidence that the endogenous nasal microbiota is a key factor in determining whether MRSA will be able to colonize an individual pig. Therefore, other measures to control this concerning bacterium are indicated. However, this study has provided the first insight into the normal composition of the nasal microbiome and identified that management factors (diet) can influence it. It is possible that differences in the nasal microbiome could influence various aspects, such as the immune response and carriage of various bacterial and viral swine and zoonotic pathogens. This study has provided critical baseline information about the composition of the nasal microbiome and future study of the role of this microbiome (as well as the microbiomes of other body sites) is indicated.