

PUBLIC HEALTHWORKER SAFETY

Title: Investigation and Characterization of *Staphylococcus aureus* Bacteriophages that Inhabit Swine Production Environments – NPB #16-143

Investigator: Jason J. Gill

Institution: Texas A&M AgriLife Research

Date Submitted: January 12, 2018

SCIENTIFIC ABSTRACT

Staphylococcus aureus is a pathogen of significant concern in both humans and livestock. Asymptomatic carriage of *S. aureus* by swine, particularly multidrug-resistant (MDR) strains, poses a potential risk to workers involved with livestock production and to the larger community.

Bacteriophages are the most abundant form of life in the biosphere and are major predators of bacteria in natural environments. Recent interest in phages as novel antimicrobials has raised the possibility that phages infecting *S. aureus* may provide an alternative means for modulating this pathogen in the livestock environment and reducing the risk of transmission to humans. In this study, an environmental survey of 20 swine production facilities across the United States was conducted to determine the prevalence of *S. aureus* phages. Swab samples were collected and enriched against 10 *S. aureus* strains representing seven common lineages (USA300, USA800, ST5, ST9, ST80 and ST398) in two mixed-enrichment panels. Twelve of the 20 sample sites contained detectable phage. Host lineage or host source (human or animal) were not strong predictors of phage sensitivity. A collection of 51 phages was isolated from the environmental samples. These phages were placed into five molecular groups by restriction digestion of phage genomic DNA by the enzyme *DraI*, indicating overall phage diversity is low in these samples. Initial analysis of the collection by transmission electron microscopy and genome sequencing indicates the presence of three major phage types in the collection: temperate siphophages related to phiETA, virulent phi29-like podophages, and large myophages which are morphologically similar to *S. aureus* phage K but have been refractory to DNA sequencing. This last group may represent a novel class of *S. aureus* myophage with genomic DNA containing hypermodified bases.

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 This report has not been peer-reviewed.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
