

## SWINE HEALTH

**Title:** Comparing the whole genome sequences of historical and recent *Streptococcus suis* strains to identify virulence factors, genes or markers responsible for pathogenesis, NPB#17-129

**Investigator:** Douglas Marthaler

**Institution:** Kansas State University

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### Scientific Abstract:

*Streptococcus suis* has become a reemerging bacterium causing significant economic losses for the swine industry. As both commensal and pathogenic strains of *S. suis* exist, numerous serotypes (n=35) and multilocus sequence types (ST, n=1161) have been identified and are used to differentiate *S. suis* strains. The goal of our study was to characterize 114 historical isolates of *S. suis* from clinical diagnostic cases between 1999 and 2013 to identify any shift in the historical isolates of *S. suis*. The predominant serotypes were 1/2 (n=21), 2 (n=20), and 7 (n=20). Serotype 2 slightly decreased while serotype 7 remained relatively constant within the 3 time periods. Serotype 1/2 nearly doubled between the first and last time period. The predominant sequence type was ST28 (24%) while 25% of the isolates had novel ST profiles. Interestingly, only a single ST1 isolate was identified within the first 10 years while five isolates were identified within the last five years of the study.

The virulence genes MRP, EF, and SLY have been associated with some pathogenic strains of *S. suis*, and only five and six isolates contained the MRP and EF gene, respectively. The gene SLY was identified in 61% of the isolates. Three genes were recently identified as indicators of pathogenicity in a contemporary set of *S. suis* strains from the United States, and 95-100% of the isolates contained these three genes, indicating the new virulence genes have not changed over time. AMR genes were investigated in the historical *S. suis* isolates. A majority (93%) of the *S. suis* isolates contain an AMR profile of ErmB, tet32, and tetO (69.3%) or tet32 and tetO (23.7%). The reduction of the ErmB gene occurred, which contributed to an increase of the tet32 and tetO profile over time. AMR genes to beta-lactams were not identified in the isolates. This historical study suggests an increase in serotype 1 and decrease in serotype 7, indicating a shift in *S. suis* isolates. While this finding may be an artifact of the study, the comparison between historical and contemporary *S. suis* isolates provides reference and highlights other factors may be contributing to the reemergence of *S. suis* in the United States.

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For more information contact:

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

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