

***Streptococcus suis* strains circulating in the U.S. and their association with pathogenicity**

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Key Points:

- *Streptococcus suis* isolates were classified into 20 different serotypes and 58 different Sequence types (ST)s.
- Serotypes 1 and 1/2 were associated with higher pathogenic frequency, while ST profiles 1 and 28 were associated with higher frequency of pathogenic isolates.
- The analysis of the association between pathotype, serotype, and ST showed that overall, STs were a better predictor of pathogenicity than serotypes.

Streptococcus suis (*S. suis*) is a bacterium that may be classified into pathogenic, opportunistic or commensal strains. Pathogenic strains cause disease of importance to the swine industry, with clinical manifestations such as meningitis, arthritis, and septicemia. *S. suis* can be further classified into serotypes or sequence type (ST). ST classification is primarily based on multilocus sequence typing (MLST), a nucleotide sequence-based technique for subtyping bacteria, while serotype classification is traditionally done by coagulation test, although serotyping with PCR-based and whole-genome sequencing techniques is also possible.

The study by Estrada et al. (2019) aimed to describe current strains circulating in the U.S. and to evaluate if specific serotypes or STs are associated with pathogenicity. Briefly, a total of 203 *S. suis* isolates from over 20 U.S. states sent for routine diagnosis were obtained from the University of Minnesota Veterinary Diagnostic Laboratory (UMNVDL) and the Kansas State Veterinary Diagnostic Lab (KSVDL) and classified into serotypes and STs. An additional 4 isolates from Canada and 1 from Mexico were included in the analysis. Isolates were also classified into pathogenic (obtained from brain/meninges, joint, heart, or liver and reported as the primary cause of meningitis, arthritis, epicarditis, or septicemia), possibly opportunistic (from lung of pigs without signs of neurological or systemic disease), and commensal (from laryngeal, tonsil, or nasal samples from farms with no known history or current control methods for *S. suis*).

Most isolates (94.2%) were classified into 20 different serotypes. The most predominant were serotypes 1/2 (n=54) and 7 (n=23). Of those 20 serotypes, the frequency of pathogenic isolates varied from 56-100% for 14 serotypes and was 0% for 6 serotypes. Serotypes 1 and 1/2 were associated with higher pathogenic frequency, while serotype 21 was associated with higher frequency of commensal isolates. Isolates were also classified into 58 different STs (20 previously reported and 38 new), the most predominant being ST28 (n=52) and ST94 (n=18). The frequency of pathogenic isolates was 0% in 33 out of the 58 STs and ranged from 44-100% for the remaining STs. ST profiles 1 and 28 were associated with higher frequency of pathogenic isolates, while profiles 750 and 821 were associated with higher frequency of commensal isolates.

The authors discuss that the large number of new ST profiles might be due to the addition of possibly opportunistic and commensal isolates, which are not usually subjected to typing. They also conclude that ST appears to be a stronger predictor of pathogenicity than serotypes. The full article is published and publicly available at <https://jcm.asm.org/content/57/9/e00377-19.long>