

Actinobacillus suis molecular epidemiology

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Introduction. *Actinobacillus suis* is an early colonizer of the upper respiratory tract of swine. This pathogen has recently emerged as an important cause of mortality in swine herds. Currently, there are no commercial vaccines available for the control of *A. suis*, and most field veterinarians rely on autogenous vaccines and antimicrobial treatments to control disease. The present study describes the molecular epidemiology of *A. suis* field isolates that were recovered from tissues submitted to the University of Minnesota Veterinary Diagnostic Laboratory. We identified important trends regarding the genetic variability, prevalence of strains, geographic distribution, age of affected animals, association with lesions, and antimicrobial resistance profiles of *A. suis* isolates recovered from North American swine herds.

Materials and methods. We genotyped 56 *A. suis* isolates recovered from swine tissues submitted to the University of Minnesota Veterinary Diagnostic Laboratory using the repetitive element-based PCR (1). We compared the genomic fingerprints obtained using primers targeting the enterobacterial repetitive intergenic consensus (ERIC) and boxA sequences and calculated the discriminatory power of each set of primers using the Simpson's index of diversity (2). Genotyping results were analyzed using the GelCompare software, and dendrograms based on genomic fingerprints were constructed using the Pearson's Product Moment Correlation and the unweighted pair group method with arithmetic mean (UPGMA) methods. We also evaluated the date of isolation, location of affected herd, age of affected animals, tissues that yielded *A. suis* isolation, lesions associated with isolation, and antimicrobial resistance profiles for each isolate that was genotyped.

Results. Using the ERIC-PCR technique, we identified 2 main clusters of strains among the 56 *A. suis* isolates. The ERIC-PCR strain group 1 contained 51 isolates, and strain group 2 contained 5 isolates. The Simpson's index of diversity for the ERIC-PCR was 0.166, therefore a random isolate has a 16.6% chance of being classified as a new strain. Using the box-PCR technique, we identified 6 clusters of strains: groups 2, 3, and 4 each had 1 isolate each; groups 1 and 5 had 8 isolates; and group six had 37 isolates. The Simpson's index of diversity for the box-PCR was 0.531, therefore a random isolate has a 53.1% chance of being classified as a different strain. The 56 isolates analyzed in this study were obtained from 25 different swine herds from 9 different states. Finishing pigs (between 10 and 20 weeks of age) were the main affected population (n=29), followed by 6-month to 2-year-old pigs (n=8), 0 to 3 week-old piglets (n=6), and nursery pigs (n=4). Age was not available for 9 pigs. *Actinobacillus suis* was isolated from 26 lung/pleura samples, 18 systemic sites (liver, pericardium, lymph node, spleen, and skin), and 4 tonsil samples. The isolation site was not available for 8 isolates. Forty isolates were recovered from tissues with lesions, whereas 6 isolates were from animals with no apparent lesions. Lesion information was not available for 10 animals. Thirty-two different antimicrobial resistance profiles were identified among the 56 *A. suis* isolates genotyped, with no clear predominance of a single profile. Isolates from the same genotype group had different antimicrobial resistance profiles.

Discussion. Although 6 different strains of *A. suis* were identified among 56 field isolates using the box-PCR, this organism is still highly clonal compared with *Haemophilus parasuis*, for example, for which more than 40 different strains were identified from 120 field isolates. Although *A. suis* can affect pigs of any age, finishing pigs are the main affected population in North American swine herds. The fact that isolates sharing similar genomic fingerprints have different antimicrobial resistance profiles indicates that resistance genes may be harbored in plasmids. We have recently confirmed this hypothesis by detecting tetracycline and beta-lactam resistance genes in plasmids isolated from *A. suis* (data not shown).

Conclusions/relevance. *Actinobacillus suis* affecting North American swine herds are highly clonal. Further studies are needed to evaluate if isolates sharing similar genomic fingerprints also share similar protective antigens. This information may be important for the selection of vaccine strains to be used in the control of this emergent swine pathogen.

References 1. Versalovic et al. Nucleic Acids Res 1991;19:6823-31. 2. Simpson. Nature. 1949;163:688.