

Title: Survey of the Molecular Epidemiology of *Haemophilus parasuis* – NPB #02-079

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Abstract: The objective of the present study was to characterize the genetic diversity of *Haemophilus parasuis* field isolates with regard to serovar, herd of origin, and site of isolation. Isolates of *H. parasuis* obtained from pigs in 15 North American herds and multi-farms systems were evaluated. Ninety-eight *H. parasuis* isolates were genotyped with the Enterobacterial Repetitive Intergenic Consensus (ERIC)-based polymerase chain reaction (ERIC) technique and serotyped via agar gel precipitation test. Genomic fingerprints were analyzed and dendrograms were constructed to identify strains from the same serovar group, herd of origin, or isolation site and to evaluate the genetic variability within these categories. Results showed that serovar 4 (39%) and non-typeable (NT) isolates (27%) were most prevalent. Thirty-four distinct strains were identified among the 98 isolates using a 90% similarity cutoff. Strains from serovar 4 and non-typeable isolates had high genetic diversity (12 and 18 strains, respectively). One to 3 major clusters of prevalent strains could be identified in most of the evaluated herds. *Haemophilus parasuis* strains isolated from the upper respiratory tract were either serovar 3 or NT isolates. Potentially virulent strains (isolated from systemic sites) were either serovars 1, 2, 4, 5, 12, 13, or 14, or NT isolates. Although *H. parasuis* had high genetic diversity overall, only a few strains caused disease in the studied herds. The ERIC-PCR technique was more discriminative than serotyping, and a broad genetic variety was observed within particular serovar groups.

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