RESEARCH ABSTRACT
SWINE HEALTH

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Title: Efficacy of Multiplex SIV TaqMan® RT-PCR and PRDC Microarray Hybridization in Predicting Swine Influenza Virus Genotype – **NPB#03-096**

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Abstract: Multiplex SIV TaqMan® RT-PCR end-point analyses to rapidly diagnose both the hemagglutinin (HA) and neuraminidase (NA) genes of swine influenza virus (SIV) were developed and analyzed for sensitivity and specificity using viral field isolates. The TaqMan® results were compared to those obtained by traditional diagnostic assays as well as HA nucleotide sequence analysis, and found to be accurate and rapid. Microarray hybridization data showed that this relatively new technique was not very sensitive and produced uninformative data. As a result, the hybridization experiments were not included in our diagnostic test comparison. Nucleotide sequence analysis of the SIV HA gene revealed that there are now three major H1 and five H3 genotypes circulating in U.S. swine herds.