

SWINE HEALTH

Title: Evaluation of genetic diversity and dynamics of virus infection in a wean-to-finish pig population. Identification - **NPB # 12-068**

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Date Submitted: 04/30/14

Scientific Abstract:

Influenza A virus (IAV) can persist in populations for prolonged periods of time. The objectives of this study were to estimate the diversity of IAV in an infected growing pig population, and to determine the extent of which pig re-infection with resident viruses occurs.

A cohort of 132 out of 2200 commercial pigs were randomly selected at weaning and followed for 15 weeks in a wean-to-finish herd (WF). Pigs were individually identified and nasal swabs were collected weekly to test them by IAV real time RT-PCR. Serum samples were collected monthly to evaluate seroconversion by ELISA. A subset of 96 samples from pigs that tested positive more than once were selected for complete genome sequencing and subtyping using next generation sequencing technologies (NGS). Phylogenetic analysis was performed by gene segment to estimate the genetic relationship between viruses over time. The proportion of positive and negative samples was compared between weeks, and the weekly and period prevalence were estimated. Finally, the proportion of pig re-infection defined as two or more positive RT-PCR results in non-consecutive weeks, was estimated and the phylogenetic relationship of viruses within pigs evaluated.

Ninety nine percent of the pigs tested IAV positive at least once during the study, and 100% seroconverted by week 12. Based on sequencing there were three genetically distinct viruses, two H1 viruses and one H3. While the first IAV epidemic (week 2) was dominated by H1 viruses, the second one (week 7) was dominated by H3 viruses. However, using deep genome sequencing we were able to identify H1 viruses in all weeks and H3 in most of the weeks. Eighty three percent of the pigs became re-infected with IAV, with most of them becoming re-infected with a different subtype of IAV. However a few pigs were re-infected with IAV of the same subtype and some with IAV of the same genetic cluster.

Our study indicated that IAV was widespread, transmitted rapidly in pigs after weaning and that IAV genetic diversity was significant. Deep genome sequencing was helpful to determine co-infections in pigs and that viral populations change over time with the distribution of subtypes changing as well. Re-infection was common and it was more likely to happen with antigenically distinct viruses of a different subtype.

Our results provide a basic understanding on influenza virus diversity and transmission in pigs after weaning in a commercial herd. We identified conditions for IAV persistence and reassortment after weaning. This information is relevant in order to understand why IAV persists in populations and what risk endemically infected populations represent in the generation of new viruses. Our results should assist in the development of better vaccines and strategies to control and reduce the impact of IAV in pigs.

These research results were submitted in fulfillment of checkoff-funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer-reviewed.

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