Title: Characterization of emerging porcine parvovirus types in the U.S. pig population-NPB #11-065

Investigator: Tanja Opriessnig, Dr med vet, PhD

Institution: Iowa State University

DateSubmitted: August 9, 2012

Scientific Abstract

Recent evidence suggests that changes are occurring with porcine parvovirus (PPV). New strains of paroviruses have been identified in pigs in some parts of the world and questions are being asked about the association of these emerging viruses with reproductive or respiratory diseases in herds where these isolates have been identified. While the emerging paroviruses have been detected in pig herds in Europe and Asia, the prevalence of these subtypes in the U.S. has not been investigated prior to this study. The objective was to investigate the prevalence of members of the subfamily Parvovirinae in the U.S. pig population with emphasis on PPV1 (also known as classical PPV), PPV2 (also known as cvirus), PPV3 (also known as porcine PARV4, porcine Hokovirus, or porcine partetravirus) and PPV4 (also known as porcine bocavirus type 2). Lung tissues obtained from 483 pigs across five different age groups with varying disease manifestations (reproductive failure/abortion, enteritis, respiratory disease, systemic/central nervous disease) were tested by newly developed real-time PCR assays. While none of the emerging paroviruses (PPV2, PPV3 or PPV4) were detected in fetuses, PPV1 was identified in this age group as expected. The overall prevalence rates for PPV1, PPV2, PPV3 and PPV4 were found to be 11.7%, 20.7%, 12.4% and 9.5% in lung tissues, respectively. In addition to lung samples, 185 fecal samples were also tested and the overall prevalence rate for PPV1 was 2.7%, 7.6% for PPV2, 4.3% for PPV3 and 3.8% for PPV4. Genome sequence comparison and phylogenetic analysis of U.S. PPV2, PPV3, and PPV4 confirmed that they have similar genomic characteristics and sequence identities to available sequences from Asia and Europe. As strict non-diseased controls were not included in this study, a possible role of emerging PPVs in disease manifestations remains inconclusive. The clinical and pathological significance of essentially all emerging PPVs are both still poorly understood and serological investigation and biological assessment of these viruses by experimentally infecting pigs is needed.