RESEARCH ABSTRACT

SWINE HEALTH

Title: Porcine circoviral associated disease: Lesions, concurrent infectious agents, efficacy of diagnostic tests in clinical samples and tissues and comparison of genomic homology. – **NPB #98-230**

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Abstract:

Thirty-four pigs, 2 each from 17 farms with clinical PMWS, were selected for study. No management practices common to all farms were discovered as potential predispositions to PMWS. PCV2 was demonstrated in all 34 pigs in association with lesions previously described for PMWS. In addition, enzootic pneumonia was confirmed in 24 pigs, PRRS in 2 pigs and septicemic salmonellosis in 2 pigs. The most consistent tissues with microscopic lesions suggestive of PMWS were lungs (100% of pigs), livers (88%), ileums (82%), enlarged lymph nodes (82%), stomachs (79%) and kidneys (68%). The prevalence of lesions in other tissues ranged from 50 to 6%. Viral inclusion bodies typical of PCV2 were observed in only 21% of PCV2-positive pigs. PCR was the most sensitive test to detect PCV2 (65% of tissues were positive), followed by in-situ hybridization (43% were positive) and virus isolation (22% were positive). The tissues from which PCV2 was most consistently demonstrated included enlarged lymph nodes (100% of pigs), ileum (100%), spleen (88%) and tonsil (68%). Lesions typical of PMWS were most commonly demonstrated concurrently with PCV2 in enlarged lymph nodes (82% of pigs) and ileum (82% of pigs), suggesting that these tissues would be the most useful for diagnostic testing. Virus isolation, PCR and IFA tests for other viruses identified porcine adenovirus in 74% of pigs and PRRS virus in 6% of pigs. No pigs tested positive for porcine parvovirus, pseudorabies virus, swine influenza virus, TGE virus or rotavirus. Twelve of the 34 pigs originated from 7 farms where the primary observed clinical manifestation of PMWS was wasting disease in association with diarrhea. Although no other infectious causes of diarrhea were demonstrated in affected pigs, lesions typical of PMWS were no more severe in the digestive tract of pigs with diarrhea compared to those with normal stools.

The entire genomes were cloned and sequenced from 4 isolates of PCV2 from 4 of the 17 farms in this study, 2 recent PCV2 isolates from neonatal pigs from 2 farms with congenital tremors (CT) and 1 isolate of an unknown type of PCV obtained in the late 1960's from a pig with CT. The 4 PMWS-PCV2s shared 99% nucleotide (nt) sequence identity with each other, and over 96% with all previously reported sequences of PMWS-PCV2s. The 2 recent CT-PCV2s shared 99% nt sequence identity with each other and also with our PMWS-PCV2 isolates. There were no consistent genomic differences between our recent PMWS and CT PCV2 isolates. The old CT-PCV shared 98% nt sequence identity with PK-15 PCV1 and only 72% with our new CT-PCV2s, indicating that it is the first sequenced field strain of PCV1 and the first PCV1 associated with disease.