

A Field-Based Assessing the Role of PCV-2 and Other Swine Viruses in Postweaning Multisystemic Wasting Syndrome

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Summary and Implications

A case-control study was conducted to assess the association of major swine viral pathogens, including porcine circovirus type 2 (PCV2) with postweaning multisystemic wasting syndrome (PMWS). Cases were defined as individual pigs with a clinical history of progressive weight loss and respiratory signs and that were subsequently diagnosed with PMWS on the basis of characteristic histopathological lesions. Controls were pigs clinically unaffected and/or from herds in which PMWS had not been diagnosed and with no clinical signs compatible with PMWS. A total of 31 cases and 56 controls were identified from diagnostic submissions or farms within a 6-month period. Among viruses examined, PCV2 appeared to be the most strongly associated with PMWS ($P < .05$). Risk for PMWS was much higher if animal was coinfecting with porcine reproductive and respiratory syndrome virus (odds ratio = 31.2). However, PCV2 was found in 62.5% of the control animals and was not detected in 2 of the 31 PMWS pigs. Furthermore, no significant genetic difference was observed among PCV2 isolates from PMWS and clinically normal pigs. The role of PCV2 in PMWS remains to be reassessed.

Introduction

Postweaning multisystemic wasting syndrome (PMWS) is an emerging problem of growing pigs worldwide (3,5). The syndrome is characterized by progressive weight loss in pigs at 4-16 weeks of age. Other common clinical symptoms are respiratory signs such as tachypnea and dyspnea, icterus, and diarrhea (5). Pathological changes have been observed in lymphoid organs and lungs of affected pigs. A consistent histopathological finding is the depletion of lymphoid cells and replacement of macrophages in the B- and T-cell-dependent areas of all lymphoid tissues.

Type 2 PCV is demonstrated to be infectious to naïve swine (4,7). However, pathological changes compatible with lesions described in field cases have been reproduced only in pigs experimentally coinfecting with both PCV2 and porcine parvovirus (1,4,6). Colostrum-fed pig were inoculated with PCV2 and then vaccinated with commercial inactivated bacterial vaccines. Twenty-one

percent of them develop clinical disease and lesion associated with PMWS (2). Therefore, the causal role of PCV2 in PMWS has not been conclusively demonstrated. The following case-control study was conducted to evaluate the relative importance of PCV2 and some major swine viral agents in PMWS and determine whether genetic trait of PCV2 is associated with its pathogenicity.

Materials and Methods

The investigation was a field based case-control study. Cases were pigs at 4 to 16 weeks of age with clinical signs of PMWS and later diagnosed as PMWS based on the presence of characteristic microscopic lesions. Controls were pigs at 4 to 16 weeks of age that were submitted with clinical history completely unrelated to PMWS to Iowa State University Veterinary Diagnostic Laboratory for diagnostic evaluation. A total of 31 cases and 56 controls were identified within a six-month period and used for the study. Serum and various tissues were collected from all animals and assayed by virus isolation (VI), polymerase chain reaction (PCR) and/or immunohistochemistry (IHC) for PCV2, porcine reproductive and respiratory syndrome virus (PRRSV), parvovirus (PPV), enterovirus (PEV), swine influenza virus (SIV), porcine respiratory coronavirus (PRCV), transmissible gastroenteritis virus (TGEV), porcine endogenous retrovirus (PERV), porcine lymphotropic herpesvirus type 1 (PLHV-1), and bovine viral diarrhea virus (BVDV). Appropriate serologic assays were performed to determine the presence and absence of antibody against some of these viruses. The proportion of pigs virologically and/or serologically positive for each virus was determined for case and control groups and statistically compared to determine the strength of the association of each agent with PMWS individually or in combination. In addition, PCV2 isolates from six cases and four controls were selected. The entire genome of each isolate was sequenced and compared each other.

Results and Discussion

The significance of PCV2 and several other viral pathogens (i.e., PRRSV, PPV, PEV, SIV, TGEV, PRCV, PLHV-1, BVDV) relative to development of PMWS was assessed using a case-control study design. The proportion of animals in each group positive for individual virus is illustrated in Figure 1. Regardless of individual animal's clinical status, all 87 animals tested were positive by PCR for PERV, demonstrating that this virus is ubiquitous in swine.

Besides retrovirus, PCV2 was the next common viral agent detected in this study. Using various virological assays (VI, IHC, PCR), up to 29 of 31 PMWS pigs (93.5%) were positive for PCV2, while the virus was found in up to 35 of 56 control pigs (64%). Interestingly, PCV2 was not detected by any virological or serological means in 2 of the 31 pigs affected by PMWS. On the other hand, these two pigs were positive for PRRSV and PLHV-1. It is also worthwhile to

note that PCV type 1, nonpathogenic strain, was also detected but only in control pigs (2%).

In addition to PCV2, other viruses except TGEV and BVDV were detected in varying proportions of animals examined (Figure 1). However, animals positive for these viruses except PRRSV were almost equally distributed between case and control groups, suggesting that infection of PPV, PEV, SIV, PRCV, or PLHV-1 is virtually insignificant relative to PMWS. In contrast, PRRSV was present in 42% and 20% of PMWS and control animals, respectively.

Because it was an observation study, the causality of PMWS could not be determined but the risk for PMWS development could be assessed. Statistically PCV2 as single entity was the most strongly associated with PMWS among viruses tested for (odd ratio = 9.3). That is, animals with PCV2 have nine times higher risk for PMWS compared with animals without PCV2. In comparison, pigs infected with PRRSV had odd ratio of 3.4 for developing PMWS as compared to pigs without PRRSV infection. However, the risk for PMWS was much higher in pigs infected with both PCV2 and PRRSV (odd ratio = 31.2). Such a significantly increased risk for PMWS was not observed in combination of PCV2 and other viruses or in combination of other viruses each other.

Genetic analysis of selected PCV2 from case and control pigs is summarized in Figure 2. Sequence homology among PCV2 from the same group was 98.9% for cases and 99.1% for controls, respectively. Comparison of linear nucleotide sequence did not reveal significant genetic difference between PCV2 from clinical cases of PMWS and ones from control pigs. Furthermore, no significant genetic difference was observed between PCV2 from control pigs in this study and PCV2 from clinical PMWS cases previously reported by other investigators. These observations indicate that apparent difference in pathogenicity is not attributed to genetic trait.

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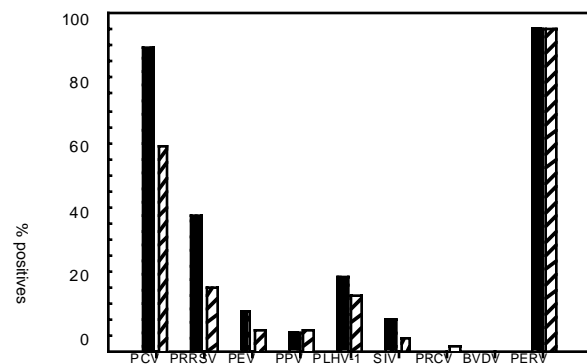


Figure 1. Proportion of animals positive for a given virus. For each virus solid and shaded bars represent PMWS and control pigs, respectively.

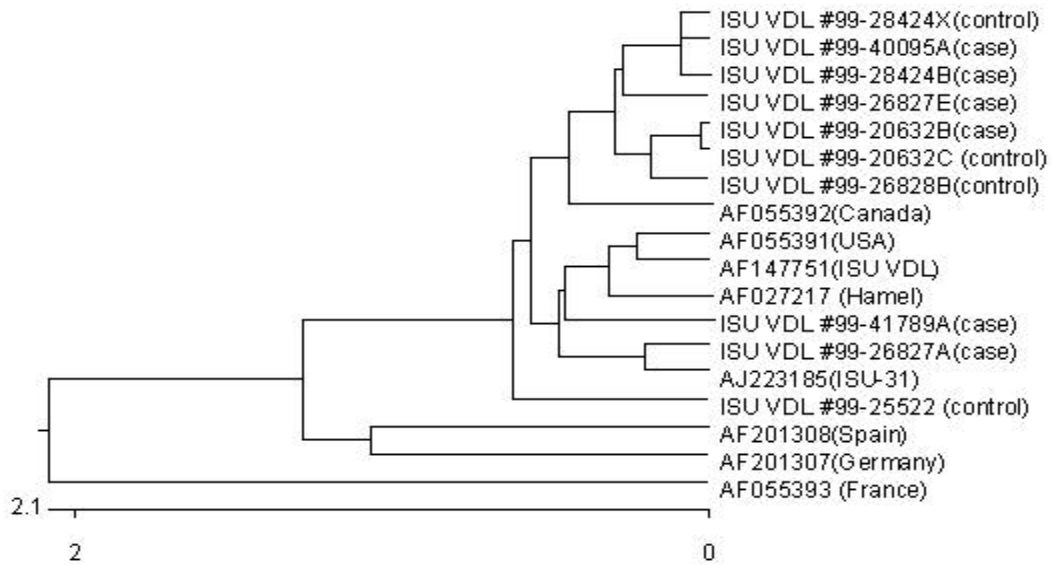


Figure 2. Phylogenetic diagram of PCV2 isolates from case and control groups. Ones with ISUVDL accession number are isolates used in the study. Others are field isolates from PMWS cases whose sequences were deposited to GenBank by other investigators.