Examination for a viral co-factor in postweaning multisystemic wasting syndrome (PMWS)

In order to test the hypothesis that a putative co-factor for the development of postweaning multisystemic wasting syndrome (PMWS) in pigs could be of viral origin, we performed extensive virological examinations on organ material from pigs diagnosed with PMWS originating from within a Danish PMWS-transmission study. Virus isolation attempts were carried out on a large panel of different cell types including primary pig kidney cells and lung macrophages, primary rabbit kidney cells and seven established cell lines (MARC-145, ST117, PK15, BHK21, HeLa, Vero, and MDCK). Although these represent cells with susceptibility to a wide range of known viruses, the results did not provide evidence for a specific virus other than PCV2 contributing to the development of PMWS. Furthermore, in order to test whether specific genotypes of PCV2 may trigger the switch from PCV2 infection to clinical disease, we compared complete DNA genome sequences of PCV2 derived from PMWS-positive as well as PMWS-negative pigs. On the basis of the DNA sequences, the PCV2 isolates were divided into two groups. Group 1 consisting of one isolate originating from a herd unaffected by PMWS, with group 2 consisting of nine isolates originating from four PMWS-affected herds, four PMWS-positive pigs plus one unaffected herd. The PCV2 genomes from the two groups showed 95.5% identity. Alignment analyses of the sequences encoding the replicase and capsid protein from group 1 and group 2 PCV2 isolates showed two amino acid differences encoded in the replicase protein, while 19 amino acid differences were predicted among the capsid protein sequences. The PCV2 DNA sequence analysis supports recent observations from studies in USA as well as Europe, which suggest that strain variations may influence the clinical outcome of PCV2 infection.