

SWINE HEALTH

Title: Identification of a putative viral co-factor different from PCV2, in animals with PMWS.
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Scientific Abstract:

Despite the lack of correlation between PCV-2 infection and PMWS, PCV-2 is recognized as an important agent. In pursuit of identifying novel viral co-factor we analyzed well characterized PMWS associated tissue samples which may be responsible for disease progression. To this end, different tissues samples (Lymph node, tonsil, liver, lungs etc) from affected animals derived from three independent farms were collected for our study. The results obtained from Subtractive PCR hybridization indicate presence of activated host mitochondrial genes. Also in few cases the bacterial ribosome sequences have been noticed. The activation of mitochondrial genes indicate that the animals associated with PMWS undergo severe stress. However the complete genome sequencing analysis data indicated possible link between mutations within PCV2 capsid region and disease outcome, therefore supporting the hypothesis of strain variation that may constitute the factor that trigger switch from PCV2 infection to PMWS disease. Furthermore the virus isolation attempts were carried out using various cell lines. Although the cell lines used in our study represent susceptibility to wide range of known viruses failed to provide any evidence of a novel viral co-factor.

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