

Tippawan Juntafong 2009: Association between PCV2 and Occurrence of PMWS in Piglets in Thailand. Master of Science (Veterinary Microbiology), Major Field: Veterinary Microbiology, Department of Veterinary Microbiology and Immunology. Thesis Advisor: Associate Professor Porn Tippa Lekcharoensuk, Ph.D. 150 pages.

Porcine circovirus type 2 (PCV2) is recognized as a causative agent of postweaning multisystemic wasting syndrome (PMWS). However, PCV2 has been isolated from both healthy and PMWS affected swine herds. Reports on association between PCV2 and PMWS occurrence were controversial. Therefore, this study aims to elucidate whether PCV2 infection correlates with the occurrence of PMWS in swine farms with and without PMWS in Thailand. The ORF2 ELISA was performed to determine the presence of antibodies to PCV2. PCV2 specific antibodies was detected in both farm categories but with a greater percentage in pigs from farms without PMWS. The seroprevalence in PMWS-negative and affected farms were 94.29% and 81.43%, respectively. In addition, whole blood and fecal swabs were analyzed by PCR for the presence of PCV2 nucleic acid. PCV2 DNA was detected in pig from both farm categories. The total number of PCV2-positive samples was greater in the PMWS-affected farms (67.14%) than in the PMWS-negative farms (7.14%). Sequence analysis of the ORF2 region of 10 PCV2 isolates (9 PMWS-affected farms and a PMWS negative farm) revealed that nucleotide sequence identities among ORF2 of PCV2 isolates in this study are ranged from 92.4 to 99.5%. Phylogenetic analysis demonstrated that the 10 isolates were clustered in PCV2 group 1. Seven out of nine isolates from PMWS-affected farms were in cluster 1A/B. This is the first report of PCV2 cluster 1A/B in Thailand. Two isolates from farms with PMWS and an isolate from a PMWS-negative farm were separated into a new cluster closely related to cluster 1C. These results indicate that PCV2 infection associates with the occurrence of PMWS in Thai pigs. However, there is no conclusive correlation between PCV2 genotypes and virulence of PCV2 infection.

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