

AN UPDATE ON THE STATUS OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV) ISOLATED IN MALAYSIA

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Introduction

Porcine reproductive and respiratory Syndrome (PRRSV) is an economically important viral disease and an infectious viral disease in swine farms worldwide. The virus is easily transmitted through direct contact to susceptible pigs and vertically to foetuses. PRRS is also known as Mystery Swine Disease, Blue Ear Disease, Porcine Endemic Abortion & Respiratory Syndrome (PEARS) and Swine Infertility Respiratory Syndrome (SIRS). It was first detected in North America in 1987, Europe in 1990 and has since been recorded in many other parts of Asia such as Vietnam and China.

The porcine reproductive & respiratory syndrome virus (PRRSV), the causative agent for the syndrome, is a positive-sense single stranded RNA virus, belonging to the family *Arteriviridae* of the order *Nidovirales*, and genus *Arterivirus*. Based on genetic differences, there exist two major genotypes the European (EU genotype, Type 1) and the North American (US genotype, Type 2) strains (Nelsen 1999). Most recently, a highly pathogenic strain of PRRSV, genetically characterized by a unique discontinuous deletion of 30 amino acids (aa) in the non structural protein (Nsp2) of the American strains was confirmed by the Office International Des Epizooties (OIE) and the Food and Agricultural Organization (FAO) as the causative agent for the “high fever” disease designated as the highly pathogenic strain of PRRSV.

This paper serves as an update on the status of PRRSV in Malaysia.

Materials and Methods

A total of 16 pooled organ (kidney, lungs, lymph nodes, tonsils, liver, and spleen) samples from 16 pig farms were collected from Selangor, Johor, Penang and Sarawak. The presence of PRRSV in the samples was assessed using a previously described reverse transcriptase nested PCR assay that amplifies a 241 bp nucleotide (European strain) and 337 bp nucleotide (North American strains) respectively (Pesch 2003). Three sets of primers were used. PLS: 5'-ATG GCC AGC CAG TCA ATC-3'; PLR: 5'-TCG CCC TAA TTG AAT AGG TG-3' (Mardassi et al. 1994) to reverse transcribe and amplify a common site in the ORF 7 region of both strains. The nested primer sets for the North American and European Strains were P-US-s: 5'-AGT CCA GAG GCA AGG GAC CG-3'; P-US-as: 5'-TCA ATC AGT GCC ATT CAC CAC-3' and P-

EU-s: 5'-ATG ATA AAG TCC CAG CGC CAG CGC CAG-3'; P-EU-as: 5'-CTG TAT GAG CAA CCG GCA GCA T-3', respectively.

Results

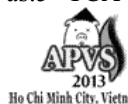
Preliminary findings showed that 81.25% (13/16) of the samples tested were positive for PRRSV. Out of the 16 farms tested, 68.75% were positive for the American strain while 25% were positive for the European strain, 12.5% were positive for both American and European strains while 18.75% were negative for both strains.

Discussion and Conclusions

A seroprevalence study done in 2008 showed that 94% of the farms and 82.4% of the pigs tested were seropositive for PRRS (Jasbir 2008). Subsequently, a genetic characterization study done in 2012 showed a seroprevalence of 89.2% with only American PRRS virus strains detected in selected pig farms in Malaysia (Vania 2012). As opposed to the two previous studies, current findings show that both American and European strains are found in Malaysia. To date, there has been no report of highly pathogenic PRRSV in Malaysia. Out of the 16 farms studied, only 1 farm showed typical clinical signs of highly pathogenic PRRSV with high mortality rates in the sow. Whether it is a true highly pathogenic PRRS strain, it can only be determined and confirmed based on subsequent genetic studies that need to be conducted on the nsp2 gene of the positive American strains detected in this preliminary study, virus isolation and pathogenicity studies.

Literature cited

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The 6th Asian Pig Veterinary Society Congress

Ho Chi Minh City, Vietnam

September 23-25, 2013