

Genetic characterisation of porcine circovirus 2 found in Malaysia

ABSTRACT

Background: Porcine circovirus type 2 is the primary etiological agent associated with a group of complex multi-factorial diseases classified as Porcine Circovirus Associated Diseases (PCVAD). Sporadic cases reported in Malaysia in 2007 caused major economic losses to the 2.2 billion Malaysian ringgit (MYR) (approximately 0.7 billion US dollar) swine industry. The objective of the present study was to determine the association between the presence of PCV2 and occurrences of PCVAD. Results: This study showed that 37 out of 42 farms sampled were positive for PCV2 using PCR screening. Thirteen whole genome of PCV2 isolates from pigs with typical PCVAD symptoms were successfully sequenced. These isolates shared 98.3-99.2% similarities with sequences of isolates from the Netherlands. All thirteen isolates fell into the same clade as PCV2b isolates from other countries. Amino acid sequence analysis of the putative capsid protein (ORF2) of the PCV2 revealed that there are three clusters found in Malaysia, namely cluster 1C and 1A/1B. Of interest, three of the isolates (isolates Mal 005, Mal 006 and Mal 010) had a proline substitution for arginine or isoleucine encoded at nt. position 88-89. Eight of the isolates had mutations at the C terminus of the putative capsid protein suggestive of higher pathogenicity which may account for the high reports of PCVAD clinical symptoms in 2007. Conclusion: Phylogenetic study suggests that there may be a link between movements of animals by import of breeders into the country being the route of entry of the virus. While it is not possible to eradicate the virus from commercial pigs, the swine industry in Malaysia can be safeguarded by control measures implemented throughout the country. These measures should include improved biosecurity, disease surveillance; vaccination as well as enforcement of regulations formulated to control and prevent the spread of this disease on a national scale.

Keyword: PCV2; PCVAD; Phylogenetic