

Genetic Characterization of ORF5 and ORF7 gene of Porcine Reproductive & Respiratory Syndrome Virus found in Malaysia.

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Introduction

Porcine reproductive and respiratory syndrome (PRRS) is one of the most important infectious diseases of swine [1] worldwide and has caused great economic losses in the swine industry. In this study we compare the ORF5 and ORF7 gene sequence from Malaysia with gene isolates from other Asian countries to study the diversity of PRRSV in Malaysia and its genetic relatedness to vaccine virus strains which may help shed some light on the potential origin of PRRSVs in Malaysia.

Materials and methods

Sampling

Pooled organs (brains and lymph nodes) were collected from an atypical PRRSV outbreak in Malaysia for diagnosis and genetic characterization.

Phylogenetic analysis of the ORF7 and ORF5

Sequencing of the ORF5 and ORF7 gene of PRRSV was done using the BigDye Terminator v3.1 cycle sequencing kit chemistry. The phylogenetic tree was constructed by using the distance-based neighbor joining method and generated by using Mega 5[®] (Biodesign Institute, Tempe, Arizona).

Result

The nucleotide sequence identity matrix of the ORF5 gene derived from this study showed 100% nucleotide sequence identity match with JN-HS from Shandong, China, BH58/10 from Laos, 112HCM from Ho Chi Minh, Vietnam, HCMC-3867 from Tay Ninh, South Vietnam, Hau Giang from Vietnam and JilinTNI from China. The nucleotide sequence identity matrix of the ORF7 gene derived

from this study showed that the nucleotide sequence of ORF7 gene derived from this study is 99.4% similar to JN-HS from Shandong, China, JX-A1 from China, BH58/10 from Laos, XL from China, YD from China, DC from China, BB0907-F44 from China, BB0907-S34 from China, DT7 from Dong Thap, Vietnam, DN1107 from Dong Nai, Vietnam, DN694 from Dong Nai, Vietnam, DN 444 from Dong Nai, Vietnam and HCM.CC3 from Ho Chi Minh, Vietnam.

Discussion

The genes characterized in this study and the neighboring countries; Vietnam, Cambodia, Laos, and Thailand share the same ancestor from Shandong, China; a US-type PRRSV strain whose common ancestors are VR-2332-USA and RespRRS-USA. It has been documented that PRRSV strains differ in virulence and vary genetically. Concerns that vaccine strains or derivatives of the vaccine strains may induce disease continue to be discussed [2] because vaccine viruses have been demonstrated to persist in vaccinated pigs and to spread to non-vaccinated pigs, indicating their ability to circulate in the field [3]. Our study suggests that recombination events between vaccine strains and field isolates may contribute to PRRSV virulence in the field.

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Reference

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