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ORF1a of RVRp22, a ribavirin-resistant attenuated phenotype of PRRSV, plays an important role on viral virulence and genetic stability assessed in pigs

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Low genetic fidelity and limited cross-protection are two major hurdles faced in porcine reproductive and respiratory syndrome virus (PRRSV) vaccinology, which is the most challenging threat to the swine industries worldwide. MLV vaccines are commonly used for homologous protection though there have been safety concerns as vaccine viruses reverted to virulence reported in fields. RVRp22, a ribavirin-resistant attenuated phenotype of PRRSV had high genetic stability during sequential replication in pigs reported in previous study. Wherein, ORF1a of RVRp22 genome was assumed to be involved in enhanced genetic stability and viral virulence. Therefore, the present study constructed four chimeric viruses based on ORF1a, 1b, 1ab and nsp2 regions of RVRp22 genome named as RVRp22-1a, 1b, 1ab and nsp2, respectively into VR2332 backbone to see the potential role of ORF1a in viral virulence and genome stability during serial passages in pigs following *in vitro* evaluation in MARC-145 cells and PAMs. In results, the replication of RVRp22-1a, 1ab and nsp2 was significantly suppressed in PAMs but replicated efficiently in MARC-145 like RVRp22 (attenuated strain). RVRp22-1b replicated in both of PAMs and MARC-145 cells with the similar trend as found in VR2332 (prototype strain). Consistently, RVRp22-1a, 1ab and nsp2 challenged pigs had lower viral loads in sera and lungs than RVRp22-1b, which was maintained even after third passage. Furthermore, RVRp22-1a, 1ab and nsp2 showed significantly a lower mutation frequency in nsp2 (most variable region in PRRSV genome) compared to RVRp22-1b. In conclusion, the present study indicated that ORF1a of RVRp22 genome might be critically involved in PRRSV virulence and the attenuated replication was maintained during serial passages in pigs which were enhanced with high genetic stability.

Biography

Amina Khatun has completed her PhD in Veterinary Medicine (Microbiology) from Chonbuk National University (CBNU), South Korea. Currently, she is working as a Postdoctoral Researcher in the Department of Veterinary Immunology, College of Veterinary Medicine, CBNU. Her major research mostly focuses on functional genomics of PRRSV largely prospecting of viral pathogenesis to address two major hurdles in PRRSV vaccinology i.e. low genetic fidelity and limited cross-protection. Previously, she has completed her DVM and MS (Veterinary Pathology) from SAU, Sylhet, Bangladesh. She has published more than 10 papers in reputed journals. She has also been serving as a Reviewer of Ecology and Evolution Journal.

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