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**Circulating genotypes of porcine respiratory and reproductive syndrome viruses in southern China: re-emerging lineage 3 and genomic recombination with vaccine variants**

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Porcine reproductive and respiratory syndrome virus (PRRSV) was first reported in China since the end of 1995 and several variants were further reported in subsequent years, causing huge economic losses to Chinese swine industry. In 2006, a country-wide outbreak of porcine high fever syndrome, caused by a highly pathogenic PRRSV (HP-PRRSV) emerged in China affecting more than 20 million pigs. To date, three lineages (lineage 3, lineage 5.1 and lineage 8.7) of PRRSV were reported in China based on our global genotyping for type 2 PRRSV. Among these three lineages, only lineage 8.7 was the most significant variant where infected pigs showing severe clinical symptoms. Much investigation to this economically important lineage (lineage 8.7) caused lesser attention on other lineages in China during recent years. Based on our viral isolation in Guangdong Province of Southern China during 2009 and 2011, the majority of isolates collected were grouped as HP-PRRSV cluster. Moreover, circulating vaccine-associated lineage (lineage 5.1) and re-emerging lineage 3 isolates were also found. Lineage 3 was previously reported in China, Hong Kong and Taiwan, but there were no reports for this lineage after 2005 in China. Here, we present the re-emerging of this lineage 3 viruses in southern China in 2010 and their evolutionary story. Additionally, we had identified inter-lineage genomic recombination between MLV vaccine strain and re-emerging lineage 3 virus in a farm practicing MLV vaccination. Although modified live virus (MLV) vaccines provide solid protection against PRRSV infection, the safety of MLV vaccines has been questioned since the detection of vaccine revertants which caused productive problems similar to those of wild-type PRRSV. Based on our experimental study, no differences in virulence between the recombinant variant and wild-type lineage 3 were observed. However, further investigations on genomic recombination among PRRSV variants in China are needed.