Genetic Analysis of Classical Swine Fever Viruses from Vietnam in 2010

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Introduction
Classical swine fever (CSF) has been endemic in Vietnam for decades, and is still a disease of major economic importance. Genetic analysis of CSF viruses isolated in the north of Vietnam in 2010 was done in order to have better understanding of epidemiology of CSF in the country and the region.

Materials and Methods

Viruses analyzed were from 44 CSF cases in the north of Vietnam detected at National Center for Veterinary Diagnosis in Hanoi between January and August 2010.

Sequencing and phylogenetic analysis:
Sequencing of 190nt of E2 gene was done as described by Paton, et al (1). Multiple alignments were generated by ClustalW with sequence data of 44 Vietnamese and 271 reference viruses from GenBank database, and phylogenetic analysis was performed by neighbor-joining method in MEGA 4.1 program.

Results and Discussions

Fig 1 shows the phylogenetic relationship of 44 Vietnamese and 271 reference CSF viruses. All Vietnamese viruses 2010 were clustered into sub-genotype 2.1, and formed a distinct group from genotype 2.1a and 2.1b. The classification of this group has never been described before, and was named as 2.1c. There were 4 out of 271 reference viruses found in this group 2.1c that included viruses of Laos 1999 and China 1998. In pairwise comparisons, the minimum similarity among Vietnamese viruses within 2.1c was 95.5%. These results indicate that the origin of 2.1c viruses in Vietnam was introduced years ago, and has been making evolution locally.

A single sub-genotype 2.1c of CSF virus was shown to be prevailing in the north of Vietnam in 2010, while Dung, et al reported the presence of both sub-genotype 2.1 (8 isolates) and 2.2 (10 isolates) in the same region in 2003. The viruses of 2.2 might have died out in the north of Vietnam during the last 7 years.

The recent study in southern China showed the predominance of sub-genotype 2.1b, and the absence of 2.1c-like viruses (3). The north of Vietnam is sharing the border with southern China, but the prevailing virus genotype is different. This implies that the cross-border exchange of CSF viruses is not a common incidence in contrast to the quick spread of PRRS virus across the border as observed in the recent epidemics in China, Vietnam, Lao PDR, and Cambodia. The further analysis on this different pattern of virus movement between these 2 viruses would be beneficial for understanding of epidemiology of both CSF and PRRS viruses in this region.

Acknowledgements
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References
2. NT Dung, et al. (2003); Proc of CSF WS Hanoi

Fig 1. Phylogenetic relationship of 44 CSF viruses of Vietnam 2010 and 271 reference viruses