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Short communication

Porcine epidemic diarrhea virus in Asia: An alarming threat to the global pig industry

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To the editor,

In 2013, the emergence of highly contagious porcine epidemic diarrhea, causing serious economic losses in the United States (U.S.) pork industry due to high morbidity and mortality rates in piglets with severe vomiting and watery yellowish diarrhea(Paarlberg, 2014). Subsequently, the disease outbroke in European pig farms with worrying economic losses in 2014(Hanke et al., 2015; Dastjerdi et al., 2015).The causative agent was the porcine epidemic diarrhea virus (PEDV), an enveloped single-stranded positive-sense RNA virus belonging to the order Nidovirales, family Coronaviridae, and genus Alphacoronavirus (Saif et al., 2012). Dedicated efforts, involving extensive labor and cost, have been taken to control this disease every year; however, several outbreaks continue to occur around the world. This study aimed to perform a phylogenetic analysis of PEDV based on large datasets. Results demonstrated a variable epidemic trend of PEDV and indicated that Asia had a high risk of PEDV, posing a threat to the global porcine industry.

Genomic surveillance programs are essential for virus prevention and control. The S gene encodes the spike protein, which is the major antigen of PEDV. This protein is vital for understanding the spread and evolution of viruses owing to its high variability (Duarte and Laude, 1994). The huge dataset for bioinformatic analysis was built based on the nucleotide sequences of complete S gene, including the sequences identified in our lab ($n = 34$) and the sequences submitted to GenBank by other laboratories around the world by 2018 ($n = 1041$)(Table 1). Phylogenetic analysis was implemented by using the maximum likelihood method implemented in package 1.6.1 IQ-TREE (Nguyen et al., 2014). The robustness of the maximum likelihood trees was obtained by bootstrap resampling (1000 samples).

Since its first report in Britain in the 1970s (Oldham, 1972), PEDV outbreaks were subsequently discovered in Europe and Asia (Pensaert et al., 1986; Puranaveja et al., 2009). Phylogenetic analysis showed that the epidemic of PEDV in Europe and Asia displayed highly variable trends in recent decades; the viral strains identified in these regions had evolved to an S INDEL and recombinant cluster in the recent years, while the isolates in these regions were clustered in the classical PEDV group (G1a, G1b) previously. Additionally, results indicated that Asia was the root source of group G2, which was divided into two large subgroups (G2a and G2b). Group G2a mainly developed in Asia, while G2b primarily appeared in Asia and North America (Fig. 1).

The epidemic of PEDV in North America displayed an attenuated trend in recent years, and the few numbers of outbreaks reported in the U.S. during 2016–2017 was mainly attributed to strict biosecurity measures and feeding infected intestinal tracts (Scherba et al., 2016). Compared with that in North America, the epidemic situation of PEDV in Asia presents a highly complicated variability owing to the continuous outbreak and emergence of recombinant or new isolates. This suggested that the vaccination of pigs by using the current attenuated live or inactivated vaccines that were adopted by many Asian countries could not confer enough protection against PEDV. Moreover, the recycled spreading of the virus might increase the mutation rate and isolate population steadily in the regions where effective preventive and control measures were poorly implemented. Thus, it is necessary to

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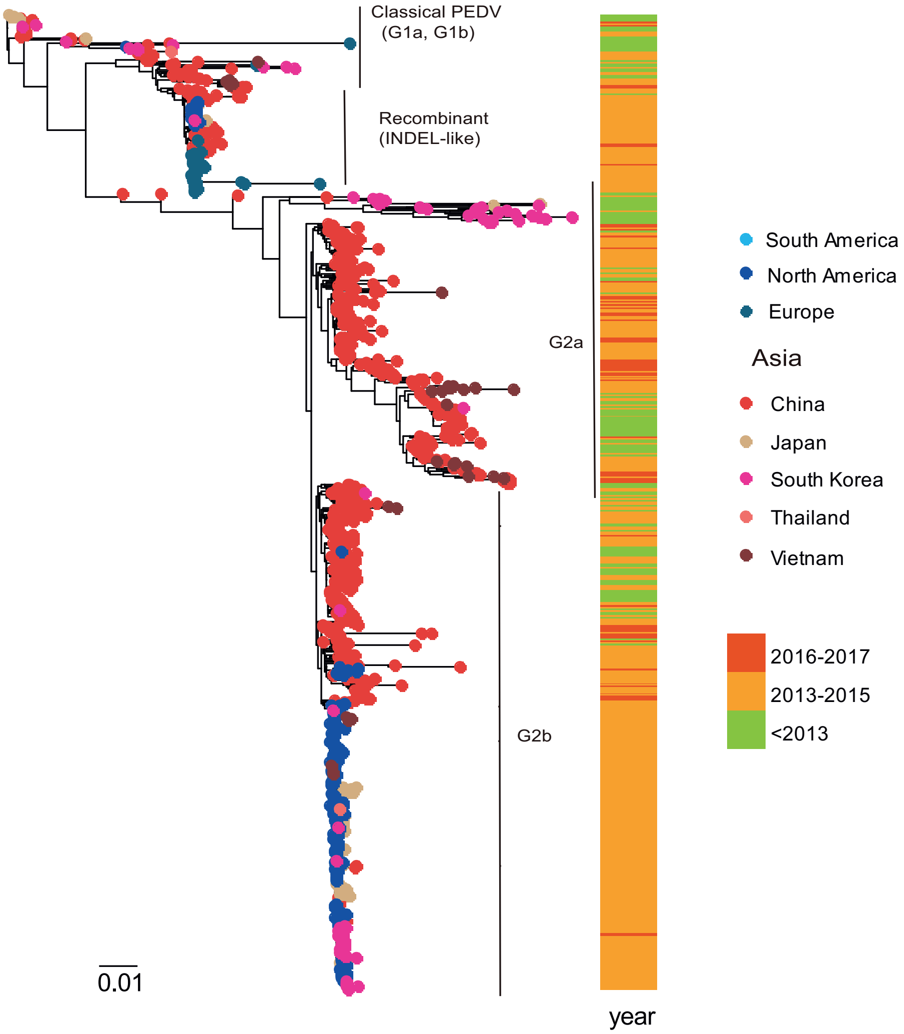

Fig. 1. The phylogenetic tree was constructed for 1075 full-length S sequences of the porcine epidemic diarrhea virus by the maximum likelihood method with GTR + F + I + G4. The regional information of each isolated virus is marked in the branch labels by circles of different colors. The isolated date of strains was corresponded with the tree using a heatmap.

monitor the eradication strategy of PEDV in North America.

The phenomenon of transcontinental spreading of PEDV was illustrated in our analysis. Most of the U.S.–like strains, comprising viruses emerged in North America clustered together as an individual branch, were identified from 2013 to 2015; the PEDV outbreak in the U.S. has been diminishing recently. During an explosive epidemic of PED in North America, the U.S.–like strains were also reported in Asian countries including Japan, South Korea, Vietnam, Thailand and China, and the U.S.–like strains persisted continuously in these regions (Fig. 1).

PEDVs reportedly have a strong ability to survive (Kim et al., 2017). The viruses could suffer long-distance transcontinental transportation accompanied with feed ingredients. Scott et al. identified that the U.S. PEDV outbreak in 2013 had a close relation with China's export of feed ingredients (Dee et al., 2016), and it was evident that spray-dried porcine plasma was associated with PEDV outbreaks in Canada (Aubry et al., 2017). Asia is a vital export source of hog and pork; considering the growing diversities of viral populations and the existence of infection media, the PEDV epidemic in Asia would continuously pose a

Table 1
The number of complete S gene of PEDVs using in this study and the year of the first case in those areas listeded.

Region	Genes (%)	The first case (year)
North America	229 (21.30%)	2013
South America	2 (0.18%)	2014
Europe	47 (4.37%)	1970s
Asia/China	606 (58.43%)	1980s
Asia/Japan	64 (5.95%)	1982
Asia/South Korea	88 (8.18%)	1992
Asia/Thailand	5 (0.46%)	1995
Asia/Vietnam	34 (3.16%)	2009

threat to the global pig industry.

Our findings reveal that the epidemic situation of PEDV in Asia displays an increasingly complex trend and suggest that Asia might become the root cause of the disease outbreak. Efficient preventive strategies, sensitive surveillance systems, and purification measures are urgently required to control the ongoing PEDV outbreaks in Asia.

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Conflict of interests

The authors declare that they have no competing interests.

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