Porcine epidemic diarrhea (PED) is a highly contagious, intestinal infectious disease caused by porcine epidemic diarrhea virus (PEDV). The disease is characterized by severe diarrhea, vomiting and dehydration. PEDV infections can occur in pigs of all ages, and infections are most serious in piglets, with morbidity and mortality often reaching 100% [9, 40]. Pigs that tolerate PEDV infections usually exhibit growth retardation, reduced food conversion rates, increased feeding costs and the co-occurrence of other diseases. Furthermore, PEDV infections result in reduced pig slaughter rates, insufficient pork supplies and pork price instability, because of a large number of piglet deaths.

PEDV is an enveloped, single-stranded, positive-sense RNA virus that belongs to the order Nidovirales, family Coronaviridae and genus Alphacoronavirus. In 1971, the first reported PED outbreak occurred in pig populations in England, and PEDV was confirmed to cause PED in 1978 [30]. Thus far, PEDV has been reported in swine-farming countries in Asia, Europe, North America [7, 17, 20, 29, 32]. In 1973, an acute diarrheal disease similar to swine transmissible gastroenteritis (TGE) was first reported in Shanghai, China; however, the causative agent of this disease was not confirmed to be PEDV until 1984 [41]. From 1984 to early 2010, PEDV infections occurred in the pig population in China, but there were no large-scale outbreaks [3, 6]. Starting from the end of 2010, PEDV outbreaks occurred in the Chinese pig population and caused enormous economic losses [1, 2, 4, 20, 22, 42]. Because of the severity of PED, extensive, in-depth studies of PEDV have been performed during the past five years in China.

EPIEMIOLOGY

Since 1966, the occurrence of pig diarrheal disease has been recorded in China. The disease showed a local endemic tendency with significant seasonal variations, usually occurring from the end of October to early February, and PEDV was confirmed to be the cause of such outbreaks in 1984 [43]. After PEDV infections in the pig population were confirmed, a series of investigations of PED occurrence were conducted in China. Ji et al. (1987) reported that in farms with PEDV outbreaks, the PEDV incidence was 80% in sows, 100% in suckling pigs and 90% in fattening pigs [18]. Wang et al. (1989) reported that among cases of PED in 1989, the PEDV incidence was 95% in fattening pigs, 60.4% in sows, 78.95% in boars and 100% in sucking pigs (with a mortality rate of 87.9%) [39]. These data suggest that PEDV infections were present in the pig population in China during PED occurred in Europe. However, before 2010, PEDV infections were mostly sporadic or locally endemic, with no large-scale outbreaks in China.

After the PEDV outbreaks in 2010, detailed studies of the molecular epidemiology and evolution of PEDV were conducted in China, which led to the accumulation of a large amount of data (Table 1). From February 2011 to March 2014, a long-term investigation showed that PEDV was circulating in 29 provinces in China, excluding Tibet and Hainan (Fig. 1A); the positive rates of samples varied from 61.10% to 78.49%, and the positive rates of pig farms varied from 71.43% to 83.47% (Fig. 1B) [10, 45]. The positive rates of PEDV in samples or farms were significantly
<table>
<thead>
<tr>
<th>Investigation time</th>
<th>Geographic location</th>
<th>Number of samples</th>
<th>Target genes</th>
<th>Result description</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>2006.1–2006.6</td>
<td>Harbin, Heilongjiang province; Changsha, Hunan province; Baotou, Inner Mongolia autonomous region; Tongliao, Inner Mongolia autonomous region; Xuzhou, Jiangsu province; Shanghai city.</td>
<td>6 (positive for PEDV by RT-PCR)</td>
<td>M gene of PEDV</td>
<td>There was a new genotype of PEDV prevailing in China.</td>
<td>Chen et al. (2008) [6]</td>
</tr>
<tr>
<td>2006.1–2009.8</td>
<td>Gansu, Heilongjiang, Henan, Hunan, Inner Mongolia, Jiangsu, Jilin provinces and Shanghai city.</td>
<td>12 (positive for PEDV by RT-PCR)</td>
<td>ORF3 gene of PEDV</td>
<td>PEDV field strains in immunized herd have a close phylogenetic relationship to Korean strains and are genetically different from vaccine strain (CV777).</td>
<td>Chen et al. (2010) [3]</td>
</tr>
<tr>
<td>2010.2–2011.11</td>
<td>Yunfu, Zhaoqing, Foshan, Qingyuan, Yangjiang and Sanshui in Guangdong province; Xinfeng, Jiangxi province; Guilin, Guangxi province; Deyang, Sichuan province; Putian, Fujian province; Huaian, Jiangsu province.</td>
<td>127 (feces or intestinal contents)</td>
<td>partial S and M genes of PEDV</td>
<td>43.0% samples were positive for PEDV; 12.0% samples were positive for PEDV and TGEV; all south China PEDV strains have a close relationship with most of the strains in Korea and Thailand, and differ genetically from European strains, early domestic strains and vaccine strain (CV777).</td>
<td>Li et al. (2012) [22]</td>
</tr>
<tr>
<td>2010.10–2011.12</td>
<td>Four provinces located in central China.</td>
<td>15 (positive for PEDV by RT-PCR)</td>
<td>M and ORF3 genes of PEDV</td>
<td>15 PEDV strains showed a close relationship with Korean strains, Thai strains and partial other Chinese strains, but differed genetically from European strains and vaccine strain (CV777). PEDV exhibits rapid variation and genetic evolution, and the currently prevailing PEDV strains in central China are a new genotype.</td>
<td>Yang et al. (2013) [42]</td>
</tr>
<tr>
<td>2010.10–2012.3</td>
<td>Nanning, Guangxi province; Heyuan, Jiangmen, Zhanjiang, Zhongluotan, Zhaoqing, Foshan, Yangjiang, Heshan, and Guangzhou in Guangdong province; Nanyang, Henan province; Zhengzhou, Henan province; Changsha and Cenzhou in Hunan province; Haikou, Hainan province.</td>
<td>70 (rectal swab samples, 16 positive for PEDV by RT-PCR)</td>
<td>partial S, M and ORF3 genes of PEDV</td>
<td>PEDV isolates showed high degree of variation in the genes, particularly S genes, might provide an explanation for the poor immunity and rapid spread of the disease.</td>
<td>Sun et al. (2014) [34]</td>
</tr>
<tr>
<td>2010–2012</td>
<td>Fujian province.</td>
<td>27 (positive for PEDV by PED Ag Test Kit)</td>
<td>ORF3 gene of PEDV</td>
<td>The Fujian strains were very distant from vaccine strain (CV777), which might be the reason why the vaccine was inefficient to control the disease.</td>
<td>Chen et al. (2013) [8]</td>
</tr>
<tr>
<td>2010.2–2012.3</td>
<td>Foshan, Yangjiang, Sanshui, Qingyuanyun and Yunfu in Guangdong Province; Xinfeng, Jiangxi province; Deyang, Sichuan province; Huaian, Jiangsu province; Guilin, Guangxi province.</td>
<td>15 (positive for PEDV by RT-PCR)</td>
<td>N gene of PEDV</td>
<td>These PEDV strains are composed of a separate cluster including three early domestic strains, but differ genetically from the vaccine strain (CV777) and the early Korean strains.</td>
<td>Li et al. (2013) [21]</td>
</tr>
<tr>
<td>2011.1–2011.10</td>
<td>12 provinces in China.</td>
<td>455 (fecal, intestine, S gene of PEDV and milk)</td>
<td>78.95% farms were positive for PEDV; 61.11% samples were positive for PEDV. Three new PEDV variants were identified based on full-length S gene sequences.</td>
<td>Li et al. (2012) [20]</td>
<td></td>
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</table>
higher compared with earlier PEDV outbreaks in China and other countries. In addition to the PEDV, swine transmissible gastroenteritis virus, porcine rotavirus, porcine kobuvirus, porcine bocavirus, porcine enterovirus, porcine teschovirus, *Lawsonia intracellularis* and porcine deltacoronavirus have also been found in diarrhea samples from pigs [10, 12, 44]. These data demonstrated that PED occurred extensively among the pig population in China and that PEDV was the major cause of viral diarrheal diseases in swine during the recent outbreaks. However, co-infections of other intestinal pathogens with PEDV should also be monitored dynamically in future studies in China.

The S1 regions of the spike (S) protein-encoding gene of 99 selected PEDV strains were divided into two groups (GI and GII) in a phylogenetic tree. The GI group consists of two subgroups (GIa and GIb), while the GII group also consists of two subgroups (GIIa and GIIb) (Fig. 2). Ten Chinese PEDV strains isolated from 2004 to 2015, which exhibited
a close relationship with PEDV strains from Vietnam and the U.S.A., were placed into the GIIa group; four Chinese PEDV strains, LZC, CH/JL/2011, SC-L and CH/BJSY/2011, which had a close relationship with the classic PEDV strain CV777, were placed into the GILb group, as well as early PEDV strains from Japan and South Korea. Fifty-one Chinese PEDV strains isolated from 2011 to 2015, as well as 22 selected reference strains that were recently circulating in the U.S.A., Canada, Taiwan, Mexico, South Korea, Vietnam and Thailand, were placed into the Gla group, which exhibited twelve clusters (C1–C12). The clusters from C1–C3 and C7–C10 were composed of the Chinese PEDV strains; the Chinese PEDV strains from C1–C4 clusters differed genetically from these from C7–C11 clusters. In the Gla group, the genetic diversity of the 51 Chinese PEDV strains from 2011 to 2015 may be associated with the introduction of PEDV strains from other countries, self variation of the PEDV as one of the RNA viruses and the prolonged immune pressure from vaccine or infection. Of the G1 group, three PEDV strains (Chinju99, Spk1 and KNU-0901) from South Korea and two Japanese strains (KH and NK) formed one specific GIIb group. In summary, the phylogenetic analysis of the S1 region of the S gene of PEDV strains from 2004 to 2015 in China revealed that the PEDV field strains circulating in China showed varying degrees of variability and that Chinese PEDV strains from 2011 to 2015 exhibited specific evolutionary lineages compared with PEDV strains from early China, Europe, North America, South America and other Asian countries. In addition, the variations in Chinese PEDV isolates attracted the attention of researchers seeking to determine whether the PEDV vaccine strain (CV777) can effectively prevent PEDV variant strain infections in China. Several reports indicated that for PEDV field strains, the neutralizing epitopes of the major antigenic protein, the S protein, showed high conservation and were highly similar to that of the vaccine strain CV777 [2, 15, 33]. These data suggest that in China, the traditional PEDV vaccine strain (CV777) still could prevent infections by PEDV field strains and provide effective cross-protection. However, the protective effect of the PEDV vaccine needs to be dynamically monitored in future due to the increasing trend of PEDV variants in China.

Recombination of the S gene of coronaviruses has been frequently reported [24, 31]. The PEDV S protein binds to a host cell receptor and triggers fusion of the viral and cellular membranes. It is likely that PEDV variants will continue to emerge, because of naturally occurring recombination events and mutations in the S gene. To identify possible recombination events within the S gene of PEDV, the S1 regions of 65 selected S genes from Chinese PEDV strains isolated from 2004 to 2015 (see Fig. 2) were screened using the Recombination Detection Program (RDP), GENECONV, Bootscan, MaxChi, Chimaera, 3Seq, PhyloPro, LARD and SISscan methods embedded in RDP4. The recombination analysis revealed that four potential recombination events occurred between the 65 PEDV strains from China (Table 2), and confirmation of the four potential recombination events was carried out by bootscan analysis and fast neighbor-joining trees, respectively (Fig. 3). Of the four potential recombination events, one potential recombinant event occurred between a GI group strain and a GII group strain, and three potential recombinant events occurred within GI group strains. Most of the GI group Chinese strains consisted of PEDV strains that emerged from 2011 to 2015. The limited data demonstrated that recently emerging PEDV strains in China exhibited high variability and potential recombination of the S gene. In summary, although the evidence of naturally occurring recombination events is limited, possible recombination events between the S genes of Chinese PEDV strains should be monitored by extensive molecular epidemiology investigations in the future.

**Vaccine**

Conventional vaccine: Wang et al. reported that a tissue-inactivated PEDV vaccine was prepared using PEDV strain
Fig. 2. Phylogenetic analysis of selected PEDV strains among Europe, North America, South America and Asia from 1988 to 2015 based on the S1 gene. The phylogenetic trees were generated from the ClustalX-generated alignments by MEGA6.06 software using the neighbor-joining method, respectively. The reliability of the generated phylogenetic tree was assessed by bootstrapping, using 1,000 bootstrap replications. ● China.
The inactivated, bivalent TGEV and PEDV vaccine (1999-2006) are extensively used in the Chinese pig population, and they play important roles in the control of TGEV and PEDV infections. After the outbreak of PED at the end of 2010, there was a renewed demand for live vaccines that could effectively prevent viral diarrhea diseases of swine. Based on the attenuated, bivalent TGEV and PEDV vaccine, Feng et al. prepared a trivalent TGEV, PEDV and PRoV (G5 type) live vaccine (consisting of an attenuated H strain, an attenuated CV777 strain and the attenuated NX strain), which was licensed on December 31, 2014, by the Chinese Ministry of Agriculture. The results of vaccine clinical trials showed that the immunization protection rate was over 95%, and the incidence of viral diarrheal diseases of swine in experimental farms was reduced from 8–12% to 3–5% [5]. In the future, the TGEV, PEDV and PRoV trivalent live vaccine will serve as an effective tool for the control of viral diarrheal diseases of swine in China, especially PEDV infections.

**Genetically engineered vaccines:** mucosal immunity plays an important role in the immune mechanism of viral diarrheal diseases. Immunoglobulin A (IgA) antibodies secreted by the intestinal mucosa can defend against invading pathogens. Oral vaccines can stimulate mucosal immunity and produce protective mucosal and serum IgA antibodies, and they are an effective method for prevention of intestinal infectious diseases. For PEDV oral vaccines, Hou et al. reported that lactic acid bacteria expressing the PEDV N protein could activate the production of mucosal IgA and circulating IgG antibodies against the PEDV N protein [16]. Ge et al. reported that recombinant lactobacilli expressing

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**Table 2. Potential recombination analysis of the S1 genes from Chinese PEDV strains**

<table>
<thead>
<tr>
<th>Potential recombinant events</th>
<th>Recombinant strains (accession no./year/group*)</th>
<th>Major parent strains (accession no./year/group*)</th>
<th>Minor parent strains (accession no./year/group*)</th>
<th>Breakpoint Positions in recombinant sequences</th>
<th>Program or method of recombination detection</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>CH-ZWBZa-01-2015 strain (KR296680/2015/GII)</td>
<td>CHJL/2011 strain (JQ638924/2011/GII)</td>
<td>CH-ZWBZb-01-2015 strain (KR296681/2015/GII)</td>
<td>11–762</td>
<td>RDP (P=7.15E-22); GENECONV (P=6.89E-20); Maxchi (P=3.39E-16); Chimaera (P=3.04E-16); SiSscan (P=3.04E-17); 3Seq (P=8.95E-18).</td>
</tr>
<tr>
<td>2</td>
<td>JS-2004-2 strain (AY653204/2004/GII)</td>
<td>PJ1407 strain (KM406184/2014/GI)</td>
<td>ZJ-2011-1 strain (JN825710/2011/GI)</td>
<td>50–767</td>
<td>RDP (P=5.91E-03); Maxchi (P=4.73E-10); Chimaera (P=3.12E-06); SiSscan (P=2.71E-21); 3Seq (P=2.31E-12).</td>
</tr>
<tr>
<td>3</td>
<td>GDS01 strain (AB857233/2012/GI)</td>
<td>JY7C strain (KF177256/2013/GI)</td>
<td>MX1405 strain (KM406182/2014/GI)</td>
<td>1455–2093</td>
<td>RDP (P=6.38E-03); GENECONV (P=2.58E-02); Chimaera (P=2.79E-02); SiSscan (P=1.47E-05); 3Seq (P=7.89E-05).</td>
</tr>
<tr>
<td>4</td>
<td>FJ-YX 2013 strain (KJ646590/2013/GI)</td>
<td>JY7C strain (KF177256/2013/GI)</td>
<td>MX1405 strain (KM406182/2014/GI)</td>
<td>1359–1974</td>
<td>GENECONV (P=3.71E-02); Maxchi (P=1.87E-02); SiSscan (P=1.27E-06); 3Seq (P=2.23E-03).</td>
</tr>
</tbody>
</table>

*Group was defined based on the phylogenetic tree of S1 gene of the selected PEDV strains in our study (see Fig. 2).
the N protein and the core neutralizing epitope (COE) could stimulate the intestines to produce local immune responses, as well as systemic immune responses, after oral immunization [13, 14]. Liu et al. constructed recombinant lactobacilli expressing the PEDV N gene or the S1 region of the S gene, and an oral inoculation showed that lactobacilli expressing the N protein could enhance the mucosal and systemic immune responses mediated by recombinant lactobacilli expressing the S1 fragment of the S protein [25].

The S protein of PEDV is a peplomer glycoprotein that is located on the surface of viral particles, and it can mediate the production of neutralizing antibodies; therefore, it is a target for vaccine research. However, the S protein is a highly glycosylated protein, and in vitro expression of recombinant S protein usually results in the loss of immunogenicity. To produce a highly effective PEDV vaccine, Meng et al. used a eukaryotic expression vector to construct a DNA vaccine expressing the PEDV S gene. This vaccine was able to effectively activate cell-mediated immunity and mediate the production of high levels of antibodies in immunized animals [28]. Liang et al. used a eukaryotic expression vector to construct a recombinant plasmid expressing the S1 region of the PEDV S gene, and they further constructed an attenuated Salmonella enterica serovar Typhimurium strain that carried a recombinant plasmid expressing the S1 region of the S gene [23]. Currently, although PEDV oral vaccines and DNA vaccines are still at the research stage and have not been applied in Chinese pig populations, these studies have broadened our understanding of PEDV vaccines, and they have provided a foundation for the future development of highly effective PEDV vaccines.

CONCLUDING REMARKS

Recently, a large number of studies of PEDV have provided an in-depth understanding of PEDV infections in the pig population in China. In particular, a trivalent live vaccine for viral diarrheal diseases of swine has been authorized for
use, and it is a powerful tool for the control of PED. However, virus variability and co-infections of PEDV with other enteric viruses are unpredictable. These factors make it difficult to understand and control PEDV infections. Therefore, future work should continue to trace the variability of PEDV strains and co-infections of other enteric viruses, improve PEDV vaccines using variant strains as candidates and elucidate the pathogenicity of PEDV variant strains.

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