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# Collection and review of updated scientific epidemiological data on porcine epidemic diarrhoea

## European Food Safety Authority (EFSA)

### Abstract

Porcine epidemic diarrhoea (PED) is a non-zoonotic viral disease of pigs caused by a coronavirus and characterised by watery diarrhoea and weight loss. PED is not notifiable to the EU or World Organisation for Animal Health listed but it is notifiable at the national level in Finland, France, Ireland and Sweden. PED case reports from seven countries and PED surveillance and monitoring activities in thirteen countries were reported. This information was combined with an extensive literature review to provide an update on global PED occurrence, circulating strains and impact in 2014–2015. PED confirmed cases have been reported in North America, South America, Asia and Europe. PED virus (PEDV) sequences originating from EU pig herds indicate that the strains currently in circulation share nearly 100% sequence identity and have greater than 99% sequence identity with the reference INDEL (insertion/deletion) strain USA/OH851/2014. In 2014–2015, greater genetic variability has been reported in strains circulating in Asia compared with EU Member States and a non-INDEL strain has been detected in the Ukraine in 2014. Data on impact confirms that mortality is higher in suckling piglets and diarrhoea is observed in all age groups. The reported impact is in agreement with that reported in EFSA AHAW Panel (2014) indicating that the impact of recently reported PED outbreaks in Asia and the USA seems to be more severe than that described in EU countries, although the impact of different PEDV strains is difficult to compare between one country and another, as impact is dependent not only on pathogenicity but also on factors such as biosecurity, herd size, farm management, sanitary status or herd immune status.

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**Keywords:** porcine epidemic diarrhoea, PED, pig herds, impact

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**Correspondence:** AMU@efsa.europa.eu

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## 1. Introduction

### 1.1. Background and Terms of Reference as provided by the requestor

In recent years, many porcine epidemic diarrhoea (PED) outbreaks caused by different virus strains have been reported by several countries worldwide with various degrees of impacts on pig production. Only a few Member States of the European Union (EU) have shared information or reported PED clinical cases and/or PEDV seropositive animals, the overall impact of PED in the Union being very limited.

The recent EFSA Scientific Opinion on PED and emerging porcine deltacoronavirus reports that the Czech Republic, Italy, Hungary, Germany and the United Kingdom have reported PED recently with mainly quite mild clinical cases and/or PED virus (PEDV) being isolated or PED seropositive animals being found. In the past weeks information has been made available about sporadic occurrence of PED infected animals in the Netherlands and possibly in other Member States.

PED is not a notifiable disease in the EU and it is not among the World Organisation for Animal Health-listed diseases. There is no evidence that the disease is causing significant health or production problems in the European pig farming system. The current epidemiological situation requires risk managers to obtain up-to-date consolidated information on the distribution and consequences of PED in the EU and worldwide.

Therefore, in the context of Article 31 of Regulation (EC) No 178/2002, the European Commission would like to ask EFSA to provide scientific assistance to the Commission following these terms of reference:

- 1) Guidance on PED data to be collected in Member States in order to optimise the coordination necessary to address the requests below. This may include a basic harmonisation of the case definition, the eligible diagnostic methods, the desired data sets and the frequency of reporting, as well as guidance on epidemiological investigations to facilitate data collection and to carry out the relevant epidemiological analysis.
- 2) An analysis of the epidemiological data and metadata available in the Member States and in recent scientific literature within and outside the EU, focusing on the occurrence of infection with different PEDV strains/types, as well as on the actual morbidity and mortality rates and severity of clinical disease so as to quantify the direct impact on pig production.

In addition, the outcome of the analysis of the above data should allow EFSA to predict possible epidemiological trends of the evolution of the disease within and outside the EU.

### 1.2. Additional information

#### 1.2.1. Pig production in Europe

Eurostat (2014) reports that the pig-producing countries of Europe can be divided into groups based on the type of production and level of commercialisation.

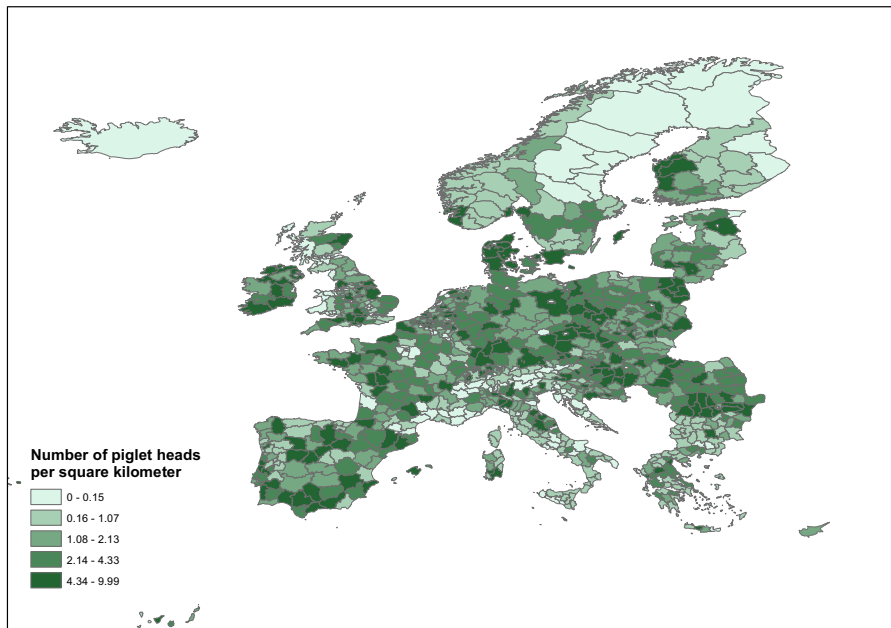
Large-scale fattener herds, characterised by having more than 400 pigs and no sows, are mainly found in Belgium, Denmark, Germany, Spain, Italy, Luxembourg, the Netherlands, Finland, Sweden and the United Kingdom. These 10 countries represent three quarters of EU pork meat production and 69% of the EU pig herd. Fattener herds with more than 400 pigs represent around 1.1% of the pig farms in Europe.

Small-scale/backyard pig farms, characterised by less than 10 pigs, are mainly found in Romania, Hungary, Croatia, Slovenia, Lithuania, Latvia, and Bulgaria. In these countries, pigs are often raised for personal consumption. Small/backyard farms account for 73% of the pig farms in Europe.

Large-scale breeder herds, characterised by more than 400 pigs and 100 sows, are also found in the Czech Republic, Estonia, Ireland, Greece, Cyprus and Portugal. These countries represent half of the EU sow herd and 0.6% of the pig farms in Europe.

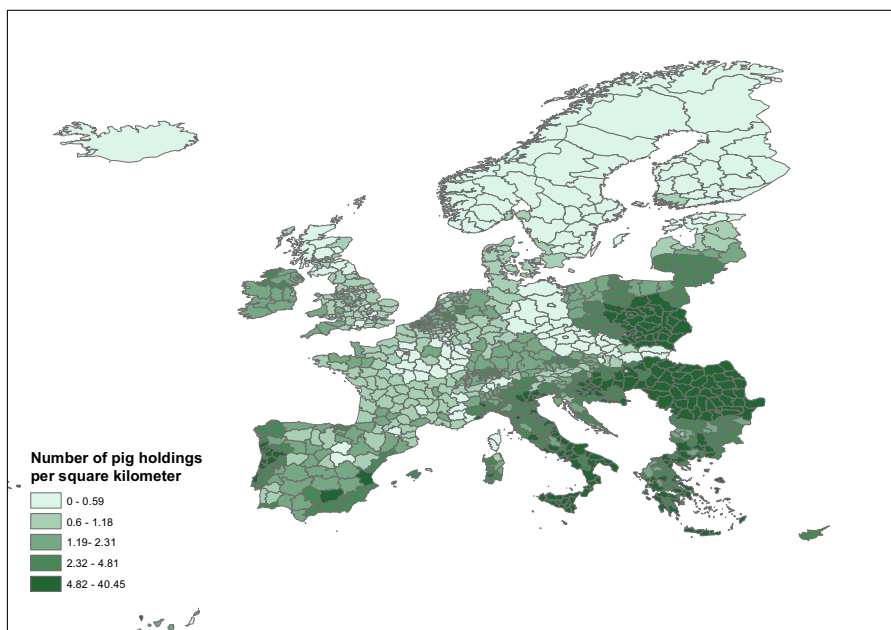
In other countries, for example in Poland, there is a transition from backyard pig farming to larger commercial operations.

In Figures 1 and 2 the difference in farm structures between countries can be clearly seen when the density of pig holdings is compared with the density of piglet heads. When interpreting the results presented in this document, it is important to consider the diversity of pig production and the economic importance of pig production in certain countries.



Source: EUROSTAT farm structures survey 2010 (<http://ec.europa.eu/eurostat/web/agriculture/data/main-tables>)

**Figure 1:** Number of piglet heads per square kilometre in Europe.



Source: EUROSTAT farm structures survey 2010 (<http://ec.europa.eu/eurostat/web/agriculture/data/main-tables>)

**Figure 2:** Number of pig holdings per square kilometre in Europe.

## 2. Data and methodologies

### 2.1. Data

The Chief Veterinary Officers (CVOs) of the EU Member States and the EFSA Scientific Network for Risk Assessment in Animal Health and Welfare were contacted for nominations of experts in the field of pig health and PED. The nominated experts and their affiliation are listed in Appendix B. Over a series of

four web conferences, data-reporting guidelines (Annex A) and procedures were discussed and agreed. The reporting guidelines describe two data models. The first data model (Herd Level) allowed the reporting of pig herds which meet the PED case definition (see Section 2.2.1). This data model was used to collect temporal and spatial information, a description of the production system, reported mortality and morbidity and availability of sequencing data. The second data model (Reporting of serological surveys and other testing) allowed the reporting of monitoring and surveillance activities for PED in European Economic Area (EEA) countries. The data were submitted using Microsoft® Excel templates via the EFSA Data Collection Framework (DCF<sup>1</sup>). Austria, Belgium, Spain, France, Italy and the Netherlands reported Herd Level data, while Austria, Belgium, Denmark, Finland, France, Ireland, the Netherlands, Norway, Sweden and the United Kingdom reported data on PED testing activities. Germany provided information only on the number of herds meeting the case definition not through the DCF, but by e-mail. No data were submitted from Bulgaria, Croatia, Cyprus, Czech Republic, Greece, Hungary, Latvia, Lithuania, Luxembourg, Malta, Poland, Portugal, Romania, Slovakia and Slovenia.

## 2.2. Methodologies

### 2.2.1. Guidance on PED data to be collected

In response to Term of Reference (ToR) 1, guidance on PED data to be collected was developed in consultation with experts of the EFSA Network on PED. The data-reporting guidelines which describe the two data models and the terminology definitions can be found in Annex A. In order for a herd to be reported for the Herd Level data collection, it had to meet the PED case definition. Data were provided for herds affected between 1 January 2013 and 30 September 2015. The second data model could be used to report the results of serological surveys and other PEDV testing not covered by the case definition (for example, negative results or testing of healthy pigs for monitoring or trade purposes). Results could be reported for any time period of testing and for testing of previously stored sera. Outbreaks already included in the Scientific Opinion of the EFSA Panel on Animal Health and Welfare, on PED and emerging porcine deltacoronavirus (EFSA AHAW Panel, 2014) did not need to be reported.

#### **PED case definition, for Herd-level data collection**

**Confirmed cases:** Following suspicion based on clinical signs (described in Annex A), a confirmation of viral infection is necessary, by any of the following tests: RT-PCR, antigen enzyme-linked immunosorbent assay (ELISA), immunohistochemistry, electron microscopy, immunoelectron microscopy or virus isolation.

**Herd case definition:** Any herd with one or more confirmed cases.

#### **Age categories**

Morbidity, mortality and diagnostic testing information was requested separately for each of the following age categories, suckling piglets (newborn to weaning), weaned pigs (from weaning up to 60–80 days of age), fatteners (70–90 days of age, approximately 30–40 kg to slaughter) and adults (breeding pigs, including both sows and boars).

#### **Survey type and sampling strategy, for serological and other PEDV testing**

Using the second data model, data from the following types of surveys could be reported (full definitions can be found in Annex A): **monitoring-active** (based on random sampling), **monitoring-passive**, **surveillance-active** (targeted surveillance involving planned collection of precise field data), **surveillance-passive** (secondary use of data routinely collected for some other purpose), **survey** (a study involving a sample of units selected, randomly, from a larger, well-delineated population) and **clinical investigations** (results obtained as a result of outbreak investigation).

Regarding the sampling strategy, one of the following options could be selected: **objective sampling** (random sample), **selective sampling** (risk-based sample), **suspect sampling** (linked to clinical signs) and **convenient sampling** (units are selected only on the basis of feasibility or ease of data collection). Definitions can be found in Annex A.

The data were analysed using SAS® Enterprise Guide® software Version 5.1 (SAS Institute Inc., Cary, NC, USA) and ArcMap 10.2 (Esri, Redlands, CA, USA).

<sup>1</sup> <http://www.efsa.europa.eu/en/datexsubmitdata/datexdatacollframework.htm>



### 2.2.2. Literature review

An extensive literature review was undertaken in order to collate information on PED for the time period between October 2014 and October 2015. More recent publications identified by the EFSA Network on PED have been included as indicated in footnotes to the respective literature review summary tables. The primary purpose of the extensive literature review was to obtain data in order to update tables 2, 7 and 8 of the 'Scientific Opinion on porcine epidemic diarrhoea and emerging porcine deltacoronavirus' of the EFSA Panel on Animal Health and Welfare (AHAW), published in 2014 (EFSA AHAW Panel, 2014).

The protocol for the extensive literature review is described in Appendix C. The review was designed to address three main questions:

Question 1: Where have cases/outbreaks of pigs with laboratory confirmation of PED been reported in 2014–2015?

Question 2: Sequence identity of full length and partial sequence data of PED isolates from pigs worldwide in 2014–2015 and their similarity to INDEL strain USA/OH851/2014, INDEL strain GER/L00719/2014 and/or CV777 or other strains (e.g. USA/Colorado/2013)

Question 3: What is the impact on pig production of PED reported worldwide for pigs with laboratory confirmation of PED – mortality, morbidity and duration of disease in the four age classes (suckling, weaned, fatteners, adults).

Fourteen bibliographic databases were queried in order to identify information on PED that has been published within the specified time period, appropriate to address these three questions. Additionally, the CVOs of the EU Member States were asked to provide any relevant information on country reports on PED that may have been published within the last few months. In addition a search was performed on websites of Veterinary Authorities, other governmental organisations and International Organisations and disease reporting databases as well as a search using Google, in order to identify web sites which contained .pdf files reporting on PED. Information to be retrieved was limited to publications in English, German, French, Italian and Spanish.

The information extracted from the reviewed literature can be found in Appendix A.

## 3. Assessment

In response to ToR 2, countries reported data via the DCF. These data and the results of the literature review are summarised in the sections below.

### 3.1. Occurrence of PED in 2014–2015

The literature review identified 19 reports of PEDV detection published between October 2014 and October 2015, while two additional reports published after October 2015 have been also included in the respective table, in order to include information that was made available after the literature review. PEDV-confirmed cases/outbreaks have been reported in North America (USA, Canada), South America (Colombia), Asia (Japan, China, South Korea, Thailand, Taiwan, Vietnam) and Europe (Portugal, Spain, Slovenia, Germany, France, Belgium, Italy, Ukraine) (Appendix A).

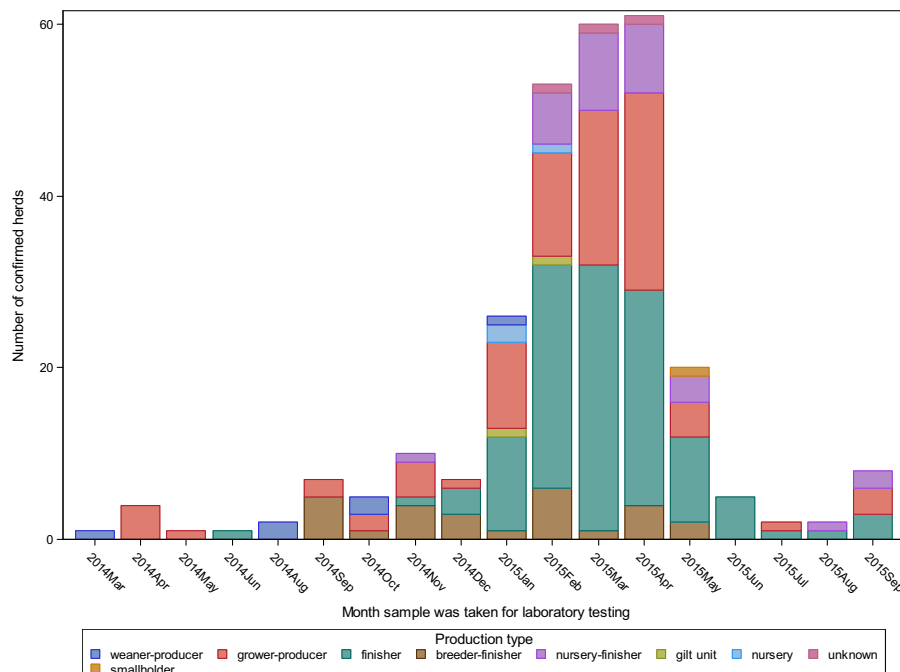
PED is only notifiable in the following Member States: Finland, France, Ireland and Sweden (and is likely to become notifiable in the United Kingdom from late 2015/early 2016). The EFSA Network on PED representing EEA countries voluntarily reported 245 case reports of pig herds meeting the PED case definition and 71 pig herds with PCR confirmation of PEDV-genome were reported via e-mail by a private laboratory. The PEDV-confirmed cases were reported by Austria, Belgium, Spain, France, Italy, the Netherlands and Germany. Laboratory testing for PED is often not centralised within each MS and there exists a diverse range of laboratories testing for PED both in the private and public sector; there is also no official EU reference laboratory for this disease.

Belgium, Spain, Italy, Germany and the Netherlands are among the largest producers of pork in Europe, while globally, China, USA, Brazil, Germany and Vietnam are among the highest producers of pork (number of heads in average 2012–2013).<sup>2</sup> Farms in these countries are generally large commercial operations under continuous veterinary supervision.

<sup>2</sup> FAOSTAT: <http://faostat3.fao.org/browse/Q/QA/E>

Based on the data reported by the EFSA Network on PED via the DCF, Figure 3 shows the PED case reports by date of sampling and type of production system, prior to 30 September 2015. For the reported herds, the first confirmed sample was taken in March 2014. A greater number of case reports were reported in the beginning of 2015 and this could be due to an increasing number of clinical cases, increased vigilance for signs or changes in laboratory protocols and the range of tests applied to samples. In May 2015, the number of PED case reports decreased until August 2015, while a slight increase was again observed in September 2015. As the disease is not notifiable to the EU (only at national level in a few countries), any temporal distribution should only be considered to be indicative as there are likely to be infected herds which have not been reported or tested. Forty-three percent of case reports were finisher herds and 31% were grower-producer herds; all pig herds were raised indoors with only 3% having outdoor access. As clinical signs are more noticeable in piglets, it is surprising that the majority of herds for which confirmed cases were reported are finishers; however, this production system is the dominant type of pig production in the reporting countries; moreover, frequent movements of animals both on and off farm in rearing herds may increase the risk of PEDV introduction.

Based on the low number of case reports that have been submitted for the 2014–2015 period, the number of PED-affected herds in the EU is very low.



**Figure 3:** Reported porcine epidemic diarrhoea-confirmed herds by month of sampling and production type

### 3.2. Virus strains circulating in 2014–2015

The literature review retrieved information on full length PEDV genome sequences from virus strains from pigs in Belgium, France, Germany, Ukraine, USA, Mexico, China, Japan, South Korea, Taiwan, Thailand and partial sequences (predominantly the S gene), from strains sampled in China, Korea, Portugal, Vietnam and the USA (Appendix A). In addition, the EFSA Network on PED provided information on full-length sequences of strains from France and Spain and partial sequences of strains obtained in Austria, Belgium, Spain, Italy and the Netherlands.

Vlasova et al. (2014) reported that sequencing and analysis of 74 strains from North America resulted in two distinct clades. Within Clade II there is a cluster of PEDV variants with insertions and deletions (INDEL) in the S gene (USA/Indiana12.83/2013 and USA/OH851/2014 fall within this cluster) which share 99.8–100% identity with each other and 96.2–96.7% identity to the strains initially detected in North America. The reference INDEL strain USA/OH851/2014 was isolated from a farm in Ohio (USA) in January 2014 where sows were known to be infected but piglets showed minimal to no



clinical signs and no piglets had died (Wang et al., 2014). This PEDV variant is characterised by three deletions and one insertion in the S gene.

Phylogenetic analysis of full-length genome sequences from EU MS indicated that INDEL strain USA/OH851/2014 shared greater than 99% sequence identity with the German, French, Belgian and Spanish strains (Hanke et al., 2015; Grasland et al., 2015; Stadler et al., 2015; Theuns et al., 2015) (Table 1).

The German INDEL strain GER/L00719/2014 isolated from a fattening pig farm in May 2014 (Hanke et al., 2015) had 99.9% identity with strain no. KR011756 from France (Grasland et al., 2015). The Belgian strain (BEL/15V010/2015) had 99.9% identity with L00721 also isolated in Germany in 2014 and 97% identity with the older European strain CV777 (Theuns et al., 2015).

In Italy, comparative analysis of partial sequences of the RdRp and M genes and the total spike (S1) gene of the circulating strains responsible for the outbreaks in 2014 showed a high nt identity with the S-INDEL strain USA/OH851/2014 from the USA (98.7, 99.8, 99.3–99.5%, respectively) and with the strains detected in Germany (100, 100, 99.7%) (Boniotto et al., 2016). This differs from the PEDV strains previously circulating from 2007 to 2012 in Italy, which showed a high genetic variability.

In the Netherlands, partial sequence analysis (orf1b + S segment, 1,400 bp) of 11 PCR products from 11 farms showed that all viruses were > 99.5% similar to the German isolate and the US INDEL USA/OH851/2014 strain.

In Austria, sequencing of the complete or nearly complete S gene (> 4 kb) obtained from affected farms showed over 99.5% sequence identity to other recent PEDV strains from Western and Central Europe (Steinrigl et al., 2015).

In Portugal, analysis of amplified sequences of the S gene shared a very high (99.0%) identity with the INDEL strain USA/OH851/2014 and were identical (100%) to the strains recently reported in Germany (Mesquita et al., 2015).

Greater genetic diversity is seen in Asian strains compared to European MS strains (Table 1). Analysis of 38 full genome sequences from Japan found 4 strains, which clustered with North American INDEL strain in Clade II and that 34 clustered with Korean and North American strains in Clade I (Suzuki et al., 2015). The authors concluded that recent PED outbreaks in Japan were caused by PEDV that has a common origin with those circulating in other swine-producing countries. Also in Japan, a strain isolated from the Tottori Prefecture had highest sequence identity to Iowa 103 and clustered with the North American isolates in Clade I (Masuda et al., 2015; Murakami et al., 2015). The authors speculated that the large deletion in the S gene may affect virulence. A full-length genomic sequence from an isolate obtained from pigs with diarrhoea in South Korea in March 2014 has 99.7% sequence

**Table 1:** Summary of whole genome phylogenetic sequence analysis of porcine epidemic diarrhoea virus isolates from USA, Asia and Europe isolated in 2014–2015, reported in Table A.2 of Appendix A

Origin	Comparison to USA strains	Similarity (%)	Comparison to European strains	Similarity (%)	Similarity (%) to strain CV777
Belgium 2015	USA/OH851/2014	99.4	GER/L00721/2014	99.9	97
France 2014	USA/OH851/2014	99.4	GER/L00719/2014	99.9	
Germany 2014	USA/OH851/2014	99.4–99.5			
Spain 2014	USA/OH851/2014	> 99			
Ukraine 2014	USA/Kansas29/2013, USA/Colorado30/2013	99.8	GER/L00719/2014	98.5	96.5
USA 2014	USA/Colorado/2013	> 99			
South Korea 2014	USA/OH851/2014	99.7			
Japan 2013–2014	USA and Korean (Clade I) INDEL Clade II	99.77–99.99 98.65–99.96			
Japan 2014	Iowa103 North America Clade I North America Clade II US INDEL strains	99.87 99.73–99.87 99.64–99.69 98.90–99.45			

**Table 2:** Descriptive epidemiology information submitted through the DCF by the members of the EFSA Network on PED for the herds where full length genome sequences or published partial sequences are available

GenBank accession number	Production	Herd size	Date of appearance of clinical signs	Suckling symptomatic (%)	Suckling mortality (%)	Weaned symptomatic (%)	Weaned mortality (%)	Adult symptomatic (%)	Adult mortality (%)	Fatteners symptomatic (%)	Fatteners mortality (%)
Unpublished	Grower-producer	3,160	April 2014	80	18	80	5	90	0	0	0
Unpublished	Grower-producer	7,197	April 2014	70	29	20	2.99	100	0	0	0
Unpublished	Grower-producer	19,376	April 2014	90	13.7	30	1.5	100	0	0	0
Unpublished	Breeder-finisher	1,243	September 2014	95	0	95	0	95	0	95	0
Unpublished	Breeder-finisher	1,361	September 2014	95	0	95	5	95	0	70	1
Unpublished	Weaner-producer	4,053	October 2014	90	70	0	0	25	0	0	0
KR011756	Breeder-finisher	4,610	November 2014	100	12.1	0	0	13	0	50	2
KR003452	Finisher	1,000	January 2015							20	0
KT206204	Finisher	1,400	December 2014							80	0
KT206206	Finisher	200	March 2015							70	0
KT895907	Finisher	450	April 2015							10	0
KT895908	Finisher	500	June 2015							100	0
KR011121	Finisher	1,832	October 2014							72	0
KR011122	Finisher	2,107	December 2014							100	0

identity with INDEL strain USA/OH851/2014. In Taiwan, phylogenetic analysis of nine S gene sequences indicated that strains from three farms in early 2014 have highest sequence identity within Clade I strains (Sung et al., 2015).

Strains isolated from 5 regions in China between 2011 and 2014 were sequenced and the 11 whole genomes exhibited nucleotide sequence identities ranging from 97.5% to 99.7%, with no insertions or deletions (Sun et al., 2015). These strains clustered with strains from China and North America which had been isolated after 2008. These genomes of PEDV field isolates from China showed a wide range of genetic variation and highlight the risk of further PEDV outbreaks caused by novel variants.

In the USA, a strain isolated in Minnesota in January 2014 had nucleotide identities of 99.9% to USA/Colorado/2013 strain and clustered within Clade II (Marthaler et al., 2014). The clinical presentation was reported as equal to or more severe than the presentation of cases caused by the prototype PEDV Colorado/2013.

Closer to the EU, a strain (Ukraine/Poltava01/2014) isolated from an outbreak in a farm in Poltrava in the Ukraine in 2014 had 99.8% sequence identity to strains USA/Kansas29/2013 and USA/Colorado30/2013 and only 98.5% sequence identity with the German strains all of which cluster within Clade II. This Ukraine strain is, therefore, distinct from the strains currently circulating in the MS.

Descriptive epidemiology for the herds where a full length genome sequence or published partial sequences are available indicated that the impact is variable between farms (Table 2) even though the sequence identity is high between these PEDV strains. From the literature review there is limited information available about the production systems, breeds and ages of the animals, clinical signs and impact and conclusions of the outbreak investigation. The linking of epidemiology and outbreak data with sequence data is required to understand the contribution of insertion/deletion events to PEDV virulence and impact and predict epidemiological trends.

### 3.3. Impact of PED infections within farms

The data model allowed the reporting of the proportion of animals with clinical signs and the number of dead animals for the four age classes (suckling piglets, weaned pigs, fatteners and adult animals) as well as the duration of clinical signs on the affected holding (in days). Box-and-whisker plots of the percentage of symptomatic animals and of PED-associated mortality by age category are shown in Figures 4 and 5. The descriptive statistics for these values are presented in Table 3. It is important to note the number of missing values; for all variables this is high and very high for the mortality figures. For various reasons, follow-up visits to, or contact with, confirmed holdings to collect information on the severity or otherwise of the disease may not occur. It is for this reason that impact analysis is difficult for diseases which are not notifiable and this is particularly problematic if the impact is low. Additionally, impact analysis would need to consider baseline values, in the absence of the disease, accounting for production types and age classes, and this information is often missing. High proportions of missing data (in particular for mortality) may be an indicator for disease with low production impact. Due to missing data, the results should be viewed with caution; however, based on the reported data, there is some indication that mortality was higher in the suckling piglet age group with a mean of 18%, and the range of mortality in this age group from 0% to 84% was greater than in other age groups. The mean proportion of pigs with clinical signs was between 48% and 60% across the four age groups. The impact indicators reported (morbidity, mortality, duration of clinical signs) varied between farms. The duration of clinical signs on the farm for affected herds was between 6 and 90 days with a mean of 23 days.

In addition to the data submitted by the EFSA Network on PED; information on the impact of PED on pig production was retrieved from the literature review and is summarised in Table A.3 in Appendix A. This table includes information from France, Germany, Spain, Canada, the USA and Colombia. Usually, morbidity and mortality were higher in piglets than in adult animals, in some cases reaching 100%. The duration of clinical signs of the disease was very variable, ranging from 2 days in individual adult animals to up to 15 weeks in some piglet groups.

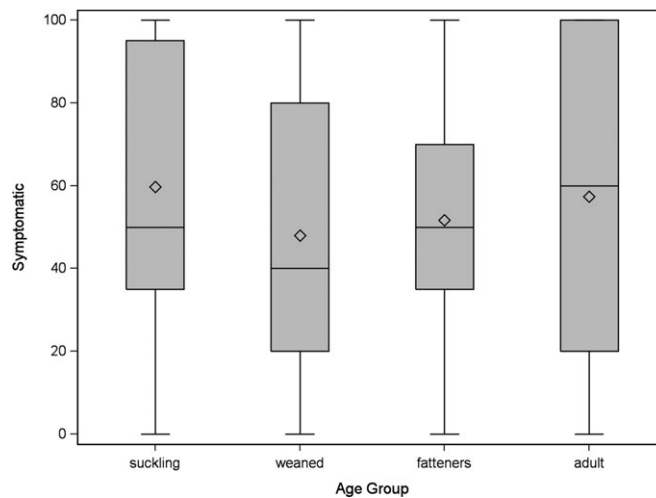
Documenting production losses usually requires the analysis of high quality data that have been collected in combination with suitable baseline production values. A few studies have attempted to quantify PED impact in production terms. This information can be found in Table A.3 in Appendix A. Effects reported include reduced feed consumption (and, respectively, milk output in affected post-partum sows), reduced average daily weight gain and increased feed conversion ratio, a longer fattening period, reduced number of piglets per litter and reproductive losses (abortions, returns to

heat, etc.). Two studies reported that the period for performance indicators to return to the values observed before the outbreaks were 6 and 20 weeks, respectively (Dastjerdi et al., 2015; Stadler et al., 2015).

The reported impact is in agreement with EFSA AHAW Panel (2014) which indicates that the impact of recently reported PED outbreaks in Asia and the USA seems to be more severe than that described in EU countries, but the impact of different PEDV strains is difficult to compare between one country and another, as it is dependent not only on pathogenicity but also on factors such as biosecurity, herd size, farm management, sanitary status or herd immune status.

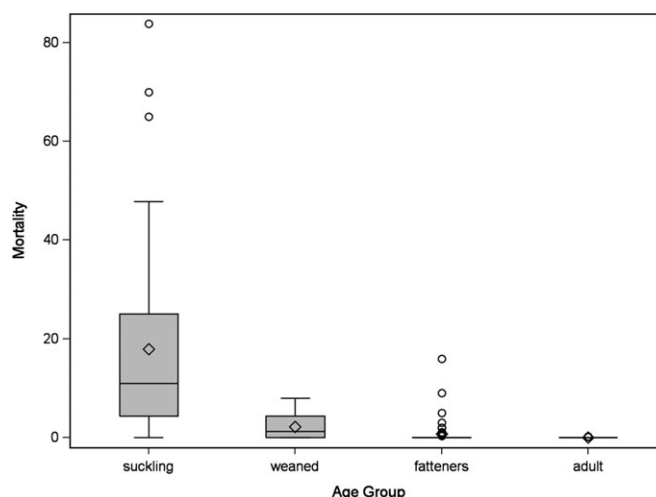
**Table 3:** Descriptive statistics for impact indicators for reported herds with confirmed porcine epidemic diarrhoea

Age group	Outcome	No. of herds	Herds with missing information (%)	Minimum of the outcome (%)	Mean outcome (%)	Median outcome (%)	Maximum of the outcome (%)
Suckling	Symptomatic	64	55	0	59.7	50	100
	Mortality	45	69	0	18	11	83.9
Weaned	Symptomatic	55	67	0	48	40	100
	Mortality	34	80	0	2.2	1.25	8
Fatteners	Symptomatic	82	67	0	51.7	50	100
	Mortality	53	79	0	0.8	0	16
Adult	Symptomatic	67	53	0	57.4	60	100
	Mortality	50	65	0	0.01	0	0.2



The bottom and top edges of the box indicate the intra-quartile range, the marker inside the box indicates the mean value and the line inside the box indicates the median value, the whiskers that extend from each box indicate the range of values that are outside of the intra-quartile range.

**Figure 4:** Box-and-whisker plot of the percentage of pigs with clinical signs by age category



The bottom and top edges of the box indicate the intraquartile range, the marker inside the box indicates the mean value and the line inside the box indicates the median value, the whiskers that extend from each box indicate the range of values that are outside of the intraquartile range, points that are a distance of more than 1.5 × intraquartile range from the box are considered to be outliers.

**Figure 5:** Box-and-whisker plot of porcine epidemic diarrhoea-associated mortality by age category

### 3.4. Suspected sources of PEDV infection and disease control methods

Concerning possible suspected sources of PEDV infection for affected farms and specific disease control methods applied in relation to PED, the information reported for confirmed herds is categorised in Table 4. Among the six countries that reported relevant information in Table 4, five indicated transportation as a suspected source of PEDV infection. Concerning disease control measures, management, biosecurity and/or cleaning and disinfection measures were reported in all countries that reported herds with confirmed PED (through the DCF – for Germany this information is not available, as it reported only the number of confirmed cases by e-mail). From the literature review it seems that biosecurity plays an important role in prevention and that particular attention should be paid also to the cleaning of transportation trucks.

**Table 4:** Suspected sources of PEDV infection and disease control methods in herds with confirmed PED. Compilation of some of the reported responses

Country	Suspected source of PEDV infection				Disease control methods	
	Transportation of animals or of manure or collection of carcasses	Proximity and/or connections to other farms or businesses	Introduction of infected animals	Personnel of the farm or of other companies	Management and/or biosecurity measures and/or cleaning and disinfection	Exposure of sows to contaminated faeces from piglets or sows
Austria					+	
Belgium	+				+	
France	+				+	
Italy	+				+	
Netherlands	+		+	+	+	+
Spain	+	+	+	+	+	+

PEDV: porcine epidemic diarrhoea virus; PED: porcine epidemic diarrhoea.

### 3.5. Surveillance and monitoring activities for PED in Europe

Austria, Belgium, Denmark, Estonia, Finland, France, Germany, Ireland, Italy, the Netherlands, Norway, Sweden and the United Kingdom reported surveillance and monitoring activities. Among these countries, Denmark, Finland, Ireland, Norway and the United Kingdom did not confirm any PED cases in their country's pigs through these activities between June 2013 and 30 September 2015.

Activities based around serological testing for PED are listed in Tables 5 and 6. Table 6 describes surveys reporting the results as prevalence estimates. Sweden has had an active surveillance programme for PED between 1993 and 2005, but is not now performing surveillance for PED. Denmark had active surveillance using an in-house ELISA to detect PEDV-specific antibodies which tested approximately 2,500 swine sera each year between 2000 and 2006 with no positive results reported during this period of time. In the Netherlands, in 2014, a retrospective serological survey of 838 serum samples from sows obtained from herds and slaughterhouses resulted in two positive samples as determined by an indirect ELISA and subsequent confirmation using a virus neutralisation test. In Belgium, in 2014, sow serum samples from 12 herds randomly selected from each province were tested using an immunoperoxidase monolayer assay (IPMA) method and no samples tested positive.

The United Kingdom reported the results of a seroprevalence survey conducted in 2013 using serum samples obtained at the slaughterhouse (Table 6). The results showed that a small proportion (9%) of the pigs sampled at the slaughterhouse were seropositive to PEDV using a blocking ELISA (Cheney et al., 2014). The blocking ELISA test used for this survey (van Nieuwstadt and Zetstra, 1991) is known to be capable of detecting antibody to virulent US and historic Great Britain PEDV strains; however, the authors identified some uncertainties with respect to the antibody results and false-positive results are recognised to occur. As indicated in Table 7, there have been no PED PCR-positive samples from diarrhoeic UK pigs tested in passive surveillance activities from 2013 to 2015.

AFBI Stormont Veterinary laboratory tested 200 randomly selected sera obtained from pigs in Northern Ireland mainly at slaughter during late 2014 and 2015, for the purpose of evaluating a commercial antibody ELISA kit. No samples tested positive.

France conducted a prevalence survey in 2014 of serum samples from 300 breeding sows in 30 herds using an indirect ELISA test (Table 6). The test performance parameters were estimated from pig farms samples from Canada. After correcting for herd clustering and test sensitivity and specificity the frequency of seropositive sows was 3.6% with a 95% confidence interval of 1.55–6.47%.

Austria, Belgium, Denmark, Estonia, Finland, France, Ireland, Italy and the United Kingdom reported activities related to laboratory testing (of potentially infected materials, e.g. intestine, faeces, rectal swabs) where PED was suspected on farms with clinical signs (Table 7). In Belgium, in 2015, faecal samples and intestinal content from suspect carcasses were tested by RT-PCR and one positive result was obtained; ELISA analysis of serum from some of the herds also tested positive (Table 7 and Table 5, respectively). France is performing a passive surveillance on herds presenting clinical signs (surveillance programme implemented as the disease is notifiable as an emergent disease since July 2014). In Germany, there are no official surveillance or monitoring activities for PED but private laboratories are providing testing upon request.

There is uncertainty about the sensitivity and specificity of existing antibody tests when used for the assessment of exposure to emerging PEDV strains. Many tests were developed using strains circulating in Europe in the 1970s and 1980s (for example, CV777 isolated from a swine breeding farm in Belgium in 1977 (Pensaert and de Bouck, 1978)) and the ability to detect the new strains from outside Europe requires further investigation.

As a consequence, there has been a ring-test performed between five EU national veterinary public health institutes, organised by DTU National Veterinary Institute, Denmark (partners within CoVetLab; CVI, Central Veterinary Institute, the Netherlands; Animal & Plant Health Agency (APHA), UK; ANSES, Agence nationale de sécurité sanitaire, de l'alimentation, de l'environnement et du travail, France; SVA, National Veterinary Institute, Sweden). An interlaboratory comparison of assays for detection of antibodies against PEDV has been conducted using a single panel of sera (> 50 samples) collected from the field both in Europe and in the USA and also from animal experiments including infections by PEDVs from both Europe and the USA. A variety of assays, based on either IPMA or ELISA technologies, including a commercial test kit, were included in the ring-test.

Differences were found in the ability of the various assays to detect anti-PEDV antibodies and also the specificity of the assays seemed to be variable. An 'in-house' blocking ELISA used at DTUVet, Denmark was used as reference and seemed to have the overall highest sensitivity and specificity. In



**Table 5:** Reported serology-based porcine epidemic diarrhoea testing activities in Europe

Country	Year	Activity	Location	Unit	Units sampled	Sample	Matrix	Method	Method details	No. of positive units
Belgium	2015	Monitoring – active	Farm	Animal	61	Mixed pig herds	Serum	Indirect ELISA (I-ELISA)		17
	2014	Survey – national survey	Farm	Animal	488	Breeding pigs	Serum	Immunoperoxidase monolayer assay (IPMA)		0
Denmark	2014	Surveillance active	Slaughterhouse	Animal	2,383	Breeding pigs	Serum	ELISA, Blocking ELISA (B-ELISA)	In-house blocking ELISA using a cell culture grown isolate of PEDV (BR1/87) as antigen in combination with a pig polyclonal anti-PEDV antiserum; sensitivity 100% 10 days after infection (EU and US strains) and specificity > 99.9%	0
	2015	Surveillance active	Slaughterhouse	Animal	2,970	Breeding pigs	Serum	ELISA, Blocking ELISA (B-ELISA)	In-house blocking ELISA using a cell culture grown isolate of PEDV (BR1/87) as antigen in combination with a pig polyclonal anti-PEDV antiserum; sensitivity 100% 10 days after infection (EU and US strains) and specificity > 99.9%	0
Italy	2014	Surveillance active	Farm	Herd	21	Mixed pig herds	Serum	MAb-based competitive ELISA	In-house (Sozzi et al., 2007)	11
Netherlands	2014	Survey – national survey	Slaughterhouse	Animal	838	Breeding pigs	Serum	IgG ELISA and virus neutralisation test	ELISA based on a recombinant S1-antigen of PEDV, specificity = 99.17, sensitivity = 100	2
	2015	Surveillance active	Farm	Herd	41	Breeding pigs	Serum	Indirect ELISA (I-ELISA)	Swinecheck® PED indirect	0
Norway	2015	Surveillance active	Slaughterhouse	Herd	27	Fattening pigs	Serum	Indirect ELISA (I-ELISA)	Swinecheck® PED indirect	0
	2015	Surveillance active	Slaughterhouse	Herd	395	Mixed pig herds	Serum	Indirect ELISA (I-ELISA)	Swinecheck® PED indirect	0
Sweden	2005	Surveillance active	Farm	Animal	3,000	Breeding pigs	Serum	Enzyme-linked immunosorbent assay (ELISA)	Knuchel et al. (1992)	0

**Table 6:** Results of reported seroprevalence studies in Europe

Country	Year	Programme	Location	Unit	Units sampled	Sample	Matrix	Method	Method details	Seroprevalence	Uncertainty	Remarks
United Kingdom	2013	Survey – national survey Objective sampling	Slaughterhouse	Animal	554	Mixed pig herds	Serum	ELISA, Blocking ELISA (B-ELISA)	van Nieuwstadt and Zetstra (1991)	9%	95% CI 6.3–11.7	Serological survey on pigs at abattoir using plasma samples originally collected for food-borne zoonoses survey
France	2014	Surveillance – passive Convenient sampling	Farm	Animal	300	Breeding pigs	Serum	Indirect ELISA (I-ELISA)	Swinecheck® PED indirect	4%	95% CI 1.55–6.47	Serological survey

**Table 7:** Reported surveillance and monitoring activities based around suspect sampling in Europe

Country	From	To	Activity	Location	Unit	Units sampled	Sample	Matrix	Method	Method details	No of positive units
Austria	2014	2015	Clinical investigations	Farm	Herd	102 <sup>(a)</sup>	Mixed pig herds	Faeces, intestine	Reverse-transcription PCR	Commercial kit	4
Belgium	2015	2015	Monitoring – active	Farm	Animal	78	Mixed pig herds	Intestine	Reverse-transcription PCR		1
Denmark	2014	2015	Surveillance passive	Farm	Animal	69	Breeding piglets	Faeces, intestine	Reverse-transcription PCR	In-house; Adapted from Kim et al. (2007)	0
Estonia	2010	2015	Monitoring – passive	Farm	Animal	98	Mixed pig herds	Faeces, intestine	Anigen Rapid PED Ag Test Kit (Chromatographic immunoassay)	No PCR confirmation	21
Finland	2010	2010	Monitoring – passive	Farm	Herd	1	Breeding piglets	Intestine	Anigen Rapid PED Ag Test Kit (Chromatographic immunoassay)	Confirmation by reverse-transcription PCR	0
	2011	2013	Monitoring – passive	Farm	Herd	19	Mixed pig herds	Faeces, intestine	Anigen Rapid PED Ag Test Kit (Chromatographic immunoassay)	Confirmation by reverse-transcription PCR	0
	2014	2015	Monitoring – passive	Farm	Herd	17	Mixed pig herds	Intestine	Anigen Rapid PED Ag Test Kit (Chromatographic immunoassay)	Confirmation by reverse-transcription PCR	0
France	2014	2014	Surveillance passive	Farm	Animal	5	Fattening piglets	Faeces, intestine	Reverse-transcription PCR	Based on N gene. Tested on CV777, INDEL strain and virulent US strain	5
	2014	2014	Surveillance passive	Farm	Animal	1	Breeding pigs	Faeces	Reverse-transcription PCR	Based on N gene. Tested on CV777, INDEL strain and virulent US strain	0

Country	From	To	Activity	Location	Unit	Units sampled	Sample	Matrix	Method	Method details	No of positive units
	2014	2014	Surveillance passive	Farm	Animal	4	Mixed pig herds	Intestine	Reverse-transcription PCR	Based on N gene. Tested on CV777, INDEL strain and virulent US strain	0
Ireland	2015	2015	Monitoring – passive	Farm	Animal	2	Breeding pigs	Faeces, rectal swabs	Reverse-transcription PCR		0
	2015	2015	Monitoring – passive	Farm	Animal	56	Fattening piglets	Faeces, rectal swabs	Reverse-transcription PCR		0
	2015	2015	Monitoring – passive	Farm	Animal	33	Fattening pigs	Faeces, rectal swabs	Reverse-transcription PCR		0
Italy	2008	2014	Surveillance active	Farm	Animal	1,756	Mixed pig herds	Faeces, intestine	IEM and MAb-based ELISA. Reverse-transcription PCR	IEM (Lavazza et al., 2015) MAb-based ELISA (Sozzi et al., 2010)	73
	2015	2015 (30 Sept)	Surveillance active	Farm	Herd	396	Mixed pig herds	Faeces, intestine	MAb-based ELISA Reverse-transcription PCR	Commercial kit PEDV-TGEV-Deltacoronavirus	172
Netherlands	2014	2015	Clinical investigations	Farm	Animal	222	Mixed pig herds	Faeces, intestine	Reverse-transcription PCR		62
United Kingdom	2013	2015 (March)	Clinical investigations	Farm	Animal	352	Mixed pig herds	Faeces, intestine	Reverse-transcription PCR	Based on S gene. Tested on CV777, INDEL (OH851) and virulent US PED strains	0
	2013	2014	Surveillance active	Farm	Animal	79	Mixed pig herds	Faeces	Reverse-transcription PCR	Based on S gene. Tested on CV777, INDEL (OH851) and virulent US PED strains	0

Country	From	To	Activity	Location	Unit	Units sampled	Sample	Matrix	Method	Method details	No of positive units
	2014	2015 (March)	Surveillance active	Farm	Animal	2,265	Breeding pigs	Faeces	Reverse-transcription PCR	Based on N gene. Tested on CV777 and virulent US PED strains	0
	2015 (April)	2015 (September)	Surveillance active	Farm	Animal	515	Mixed pig herds	Faeces	Reverse-transcription PCR	Based on N gene. Tested on CV777 and virulent US PED strains	0
	2015 (April)	2015 (September)	Clinical investigations	Farm	Animal	123 <sup>(b)</sup>	Mixed pig herds	Faeces, intestine	Reverse-transcription PCR	Virotype PED/TGE real time RT-PCR from Qiagen used from May 2015 at APHA and assay described in Ojkic et al. (2015) used at AFBI Stormont Veterinary Laboratory	0

(a): This number includes repeated submissions from some farms

(b): From 80 diagnostic investigations.

this 'in-house' blocking ELISA, a cell culture-grown isolate of PEDV (BR1/87) was used as antigen in combination with a pig polyclonal anti-PEDV antiserum. More than 2,000 pig sera from Denmark (which has not experienced cases of PED) tested negative in this assay, but pigs experimentally infected with PEDV (both EU and US strains) were shown to seroconvert within 10 days post-infection. Other tests, including a commercial test kit commonly used in many European laboratories were found to have lower specificity and/or sensitivity, giving rise to false positive or negative results.

There is uncertainty about serological test performance; therefore, negative or positive results without confirmation of the presence of the virus and/or possibly existing relevant clinical or epidemiological information should be interpreted with caution.

## 4. Conclusions

In collaboration with experts nominated by the CVOs of the EU Member States and the EFSA Scientific Network for Risk Assessment in Animal Health and Welfare, data collection and reporting guidelines for two data models were developed, one at herd level, used to report data for an epidemiological analysis and the second used to collect data to describe surveillance and monitoring activities. During this process, a harmonised case definition was agreed for PED-confirmed herds based on clinical signs and laboratory confirmation of the PEDV.

The data collected by the EFSA Network on PED were combined with data retrieved from an extensive literature review covering the period of October 2014–October 2015 and collated information on PEDV occurrence, circulating strains and impact.

PED-confirmed cases/outbreaks have been reported in North America, South America, Asia and Europe in 2014–2015. Herds meeting the case definition for PED were reported voluntarily by Austria, Belgium, Spain, France, Italy, the Netherlands and Germany. Thirteen countries reported PED surveillance and monitoring activities and among these, Denmark, Finland, Ireland, Norway and the United Kingdom did not confirm any PED cases in their country's pigs through these activities between June 2013 and 30 September 2015. No data were submitted from Bulgaria, Croatia, Cyprus, Czech Republic, Greece, Hungary, Latvia, Lithuania, Luxembourg, Malta, Poland, Portugal, Romania, Slovakia and Slovenia.

Sequencing of virus isolates from EU pig herds indicated that the strains currently in circulation shared nearly 100% sequence identity and had greater than 99% sequence identity with the reference INDEL strain USA/OH851/2014. Italy has reported that the observed high sequence identity contrasts with PEDV strains previously circulating from 2007 to 2012 in Italy, which showed a high genetic variability. However greater genetic variability is observed in Asia compared with EU MS and a non INDEL strain has been detected in an outbreak in Ukraine in 2014. This highlights the possibility of further outbreaks in pig populations naive to a novel PEDV variant.

Data provided by the EFSA Network on PED and information from the literature review confirmed that mortality is higher in suckling piglets and diarrhoea is observed in all age groups for strains circulating globally in 2014–2015. Two published studies reported the time period required for the return of production to pre-outbreak levels, and this was variable for the described outbreaks (6 and 20 weeks, respectively) (Stadler et al., 2015, Dastjerdi et al., 2015).

These findings are in agreement with those reported in EFSA AHAW Panel, (2014) that the impact of recently reported PED outbreaks in Asia and the USA seems to be more severe than that described in EU countries, but the impact of different PEDV strains is difficult to compare between one country and another, as impact is dependent not only on pathogenicity but also on factors such as biosecurity, herd size, farm management, sanitary status or herd immune status.

## 5. Recommendations

- Increase awareness of clinical signs; high morbidity diarrhoea in pigs of any age is a good indicator of the need for PEDV testing.
- Biosecurity, in particular for vehicles, is important to prevent introduction of the virus on farm.
- Maintain vigilance as the EU pig herd is likely to be susceptible to novel PEDV variants.
- Link PEDV genome sequence data to epidemiological and outbreak investigation information in order to predict the contribution of insertion/deletion events to PEDV virulence and impact.
- Transparency and open communication concerning the occurrence of outbreaks of PED between farms and between countries is key for prevention of the spread of the virus and for effective response.



- Impact analysis requires a comparison with baseline values, where no disease is present and therefore more specialised studies might need to be conducted in order to clarify the disease impact in a farm.

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## Abbreviations

CVO	Chief Veterinary Officer
DCF	Data Collection Framework
EEA	European Economic Area
ELISA	enzyme-linked immunosorbent assay
INDEL	insertion/deletion
IPMA	immunoperoxidase monolayer assay
MS	Member States
PED	porcine epidemic diarrhoea
PEDV	porcine epidemic diarrhoea virus
RT-PCR	reverse transcription polymerase chain reaction
ToR	Term of Reference

## Appendix A – Tables summarising information from the extensive literature review

**Table A.1:** Information on PEDV occurrence in the period 2014–2015 obtained by an extensive search of the scientific literature and relevant websites

Country	Region	Time period of outbreaks	Number of reported cases	Diagnostic methods	Number of positive/ tested samples	Reference	RefID <sup>(a)</sup>
Europe							
Belgium		January 2015	Farm: 1	RT-qPCR		Theuns et al. (2015)	276
France	Northern France	December 2014	Herd: 1	Sequencing		Grasland et al. (2015)	2300
Germany	Federal State of Baden-Wuerttemberg	May 2014		RT-PCR		Hanke et al. (2015)	79
Portugal	Southern and Central regions	January, 2015 – April, 2015	Farms: 44	RT-PCR	55/84	Mesquita et al. (2015)	175
Spain		8 August 2014 – 29 May 2015	Farms: 10	RT-qPCR	278/962	Laranjo et al. (2015)	2425
Slovenia		December 2014 – February 2015	Farms: 2	RT-PCR		Toplak et al. (2015)	2621
Ukraine	Poltava	Summer 2014	Farm: 1	RT-PCR		Dastjerdi et al. (2015)	2620
Asia							
Japan	Hokkaido (1) Tohoku (2) Kanto (3) Chubu (4) Kinki (5) Chugoku/Shikoku (6) Kyusyu/Okinawa (7)	1 October 2013 – 31 August 2014	(1) Farms:23/Pigs:1427 (2) Farms:81/Pigs:56397 (3) Farms:225/Pigs:127934 (4) Farms: 140/Pigs: 45578 (5) Farms: 0/Pigs:0 (6) Farms:19/Pigs: 5863 (7) Farms:329/Pigs: 372942 Total Farms: 817/5570 Total Pigs: approximately 1,227,000/9,685,000	RT-PCR		Yamakawa (2014)	2536
Japan	Kagoshima and Miyazak	3 December 2013 – 24 July 2014	3 Clusters determined by Bernoulli model: Kanoya cluster, reproduction farms:24/35 Miyakonojo cluster, integrated farms: 32/81 Miyazaki north cluster, integrated farms: 10/45			Makita et al. (2015)	1353

Country	Region	Time period of outbreaks	Number of reported cases	Diagnostic methods	Number of positive/ tested samples	Reference	RefID <sup>(a)</sup>
Thailand	Eastern Thailand	2013–2014	Two PEDV variants from 3-day-old pigs with PED	Virus isolation		Cheun-Arom et al. (2015)	36
Taiwan	Central and Southern Taiwan	Early 2014		RT-PCR	Piglets: nine 1- to 7-day-old dead piglets from 3 farms	Chiou et al. (2015)	38
China	Jiangxi	2014 – March 2015		RT-PCR	In 2014, 129/194 In 2015, 28/56	Song et al. (2015a)	248
South Korea	Kyungpook Province	March 2014	Farm: 1	RT-PCR-PEDV/TEGV		Lee et al. (2014)	2268
Vietnam	6 provinces in the north and 1 in the central region of Vietnam	November 2013 – April 2014		RT-PCR	30/160	Kim et al. (2015a)	111
<b>The Americas</b>							
United States of America		5 June 2014 – 21 November 2015		PCR	1827 Confirmed Positive Premises <sup>(b)</sup> (cumulative since June 5, 2014), 524 Presumptive Positive <sup>(c)</sup> Premises (cumulative since June 5, 2014). From 5 June 2014 to Nov, 2015: 73155 Biological accessions tested, 12984 PEDV Positive, 17.7% Positive	USDA, Animal and Plant Health Inspection Service (2015)	3000
United States of America	Ohio, Michigan, Illinois and Iowa	May 2013 – February 2014		RT-q-PCR, IFA, EM, Sequence analysis	9/88	Oka et al. (2014)	2273

Country	Region	Time period of outbreaks	Number of reported cases	Diagnostic methods	Number of positive/ tested samples	Reference	RefID <sup>(a)</sup>
United States of America	Ohio	January 2014	Confirmed disease was present on multiple sites within and across breeding and post weaning production flows	RT-PCR		Bowman et al. (2015)	22
United States of America	Northeast Nebraska	January 2014	Boars in one board stud	PCR		McCarty et al. (2015)	1049
Canada	Quebec: (1) Région de Granby, Montérégie, (2) St-Denis-sur-Richelieu, Montérégie, (3) St-Aimé, Montérégie, (4) St-Liboire, Montérégie, (5) St-Hugues, Montérégie, (6) Montérégie Ouest (7) Montérégie	22 February 2014 – 5 February 2015	(1) 2 sites (2) 4 sites (3) 2 sites (4) 1 sites (5) 1 sites (6) 1 sites (7) 1 sites			Misener (2015)	2570
	Ontario	22 January 2014 – 20 February 2015	76 cases				
	PEI (Prince Edward Island)	February 2014	Farm: 1				
	Manitoba		Farms: 5 Assembly yards:3				
Colombia	Huila	7 March 2014 – 9 June 2014	750 cases in 12 outbreaks	RRT-PCR		Piñeros and Mogollón Galvis (2015)	1395



Country	Region	Time period of outbreaks	Number of reported cases	Diagnostic methods	Number of positive/ tested samples	Reference	RefID <sup>(a)</sup>
Colombia	Cundinamarca	8 March 2014 – 9 June 2014	2475 cases in 30 outbreaks	RRT-PCR		Piñeros and Mogollón Galvis (2015)	1395
	Tolima	4 April 2014 – 9 June 2014	3 cases in 1 outbreak				
	Boyacá	24 April 2014 – 9 June 2014	27 cases in 1 outbreak				
	Santander	12 May 2014 – 9 June 2014	72 cases in 1 outbreak				

(a): RefID is an internal reference identification number which is used for easy identification of the references included in each of the tables

(b): Published in November 2015

(c): A confirmed positive premises is a premises where pigs tested positive and have clinical signs. A presumptive positive premises is a premises where pigs tested positive but have non-specific, unknown, or no clinical signs consistent with SECD. Please see the official SECD Case Definition for more information ([www.aphis.usda.gov/animal-health/secd](http://www.aphis.usda.gov/animal-health/secd))

**Table A.2:** Information on sequence differences between porcine epidemic diarrhoea virus (PEDV) strains reported in 2014-2015 and obtained by an extensive search of the scientific literature

Country (region)	Date of isolation	Sample description and sequence information	Strain sequenced	Reference	RefID <sup>(a)</sup>
Europe					
Belgium	January 2015	An outbreak of diarrhoea occurred in a fattening pigfarm Full-length genome analysis – BEL/15V010/2015 was most closely related to strain GER/L00721/2014 (99.9% nucleotide similarity), and the prototype US INDEL strain OH851 (99.4%). In contrast, BEL/15V010/2015 was less closely related to strain CV777 (97.0%)	BEL/15V010/2015 (GenBank accession number: <a href="#">KR003452</a> )	Theuns et al. (2015)	276
France (Northern France)	December 2014	Full-length genome analysis – The strain was found to be genetically related to the recent German strain GER/L00719/2014 (99.9% identity) and with USA/Indiana12.83/2013 (99.8% identity), a US strain detected in June 2013. The USA/OH851/2014 strain shared 99.4% identity with the German and French isolates. The French and German PEDV isolates are more related to the USA/Indiana 12.83/2013 strain than to the USA/OH851/2014 isolate	PEDV FR/001/2014 to FR/003/2014 (GenBank accession number: <a href="#">KR011756</a> )	Grasland et al. (2015)	2300
Germany (Federal State of Baden-Wuerttemberg)	May 2014	Full-length genome analysis – The strains share a very high identity (99.5%) with the new variant OH851 recently reported from the United States. However, differences exist that distinguish the strains from Germany from the highly virulent PEDV strains that caused the major losses in the United States	GER/L00719/2014 and GER/L00721/2014 (GenBank accession number: <a href="#">LM645057-8</a> )	Hanke et al. (2015)	79
Germany (South-Western Germany)	May and November 2014	Full-length genome analysis – Comparative analyses of the full-length genomes revealed up to 98.7% identity with currently circulating highly virulent US strains and strains from China. Strains were most closely related to S INDEL PEDV strains described in the US (99.4% identity with OH851). Much lower overall similarity was found between the current German S INDEL strains and the European isolate CV777 from the late 1970s	GER/L00719/2014, (GenBank accession number: <a href="#">LM645058</a> ) L00721/GER/2014, (GenBank accession number: <a href="#">LM645057</a> ) K14/14 (GenBank accession number <a href="#">L00855</a> ) K16/14 (GenBank accession numbers: <a href="#">L00906</a> , <a href="#">L00907</a> , <a href="#">L00908</a> )	Stadler et al. (2015)	256

Country (region)	Date of isolation	Sample description and sequence information	Strain sequenced	Reference	RefID <sup>(a)</sup>
Italy (Northern Italy)	July 2014	Comparative analysis of partial sequences of the RdRp and M genes and the total spike (S1) gene showed a high nt identity with the S-INDEL strain OH851 from US (98.7%, 99.8%, 99.3–99.5%, respectively) and with the strains detected in Germany (100%, 100%, 99.7%)	PEDV/Italy/178509/2014; PEDV/Italy/200885/2014 GenBank accession numbers: KT027397-8; KT027413-4; KT027429-30	Boniotti et al. (2016) <sup>(b)</sup>	2622
Portugal (Southern and Central regions)	January 2015	Comparative analyses of a 440 bp region of the spike protein gene of PEDV revealed a very high (99.0%) identity with the new PEDV variant OH851 of the US. Interestingly, the amplified sequences showed to be identical (100%) to the strains recently reported in Germany PEDV/GER/L00719/2014 and PEDV/GER/L00721/2014	PEDV Portugal 2015	Mesquita et al. (2015)	175
Ukraine (Poltava)	Summer 2014	Full-length genome analysis of the isolate showed the highest similarity to USA/Kansas29/2013 and USA/Colorado30/2013 (99.8% nucleotide identity). The nucleotide identity was substantially lower (98.5%) when compared to strains isolated in Germany in 2014 and CV777 strain (only 96.5% homology).	Ukraine/Poltava01/2014 (GenBank accession number: KP403954)	Dasfjerdi et al. (2015)	2620 <sup>(c)</sup>
<b>The Americas</b>					
United States of America (Ohio, Michigan, Illinois and Iowa)	From May 2013 to February 2014	Phylogenetic analysis on both, the nearly full genomic sequences and partial S proteins, demonstrated that the 8 PEDV isolates [with the exception of Iowa106 (PV39) strain] were clustered with the original US PEDV strains, and Iowa106 (PV39) was clustered together with the S INDEL strain OH851. Further analysis indicated that the major differences among strains were mainly in the N-terminal region of the S protein (aa 1-388 according to USA/Colorado/2013 strain [GenBank KF272920]). Based on the analysis of this region, the nine strains were distributed between two major distinct clusters: (1) a major clusters similar to the original highly virulent US PEDV strains; and (2) similar to S INDEL US PEDV strain, OH851.	Cluster (1): PC22A-P10, PE103(PC21A)-P4, PC168-P2, PC170-P2, PC173-P2, PC177-P2, PC180-P2, PC182-P2, (GenBank accession numbers: KM392224-231); Cluster (2): Iowa106 (PV39)-P1 (GenBank accession number: KM392232)	Oka et al. (2014)	2273

Country (region)	Date of isolation	Sample description and sequence information	Strain sequenced	Reference	RefID <sup>(a)</sup>
United States of America (Minnesota)	January 2014	Phylogenetic analysis on both, the full genomic sequences and S gene, of a PEDV isolated from intestines of a deceased neonatal piglet. The Minnesota188 strain was aligned with the other complete genome of PEDV available in GenBank (n = 113); it had a 99.9% nucleotide percentage identity to Colorado/2013 and clustered in the North America clade II (Figure, panel A, <a href="http://wwwnc.cdc.gov/EID/article/20/12/14-0908-F1.htm">http://wwwnc.cdc.gov/EID/article/20/12/14-0908-F1.htm</a> ). The spike gene segment had a 99.7% nucleotide percentage identity (99.4% amino acid identity) with Colorado/2013 and clustered with the non-North America INDEL strains (Figure, panel B)	USA/Minnesota188/2014 (GenBank accession number: <a href="#">KM077139</a> )	Marthaler et al. (2014)	166
United States of America (Iowa)	May 2013	NPL-PEDV/2013 strain was isolated from a pig with diarrhoea and complete genome sequencing found > 99% nucleotide identity to others US PEDV [(Minnesota isolate MN (GenBank accession number: <a href="#">KF468752</a> ) and an isolate from Ohio (GenBank accession number: <a href="#">KJ408801</a> )]	NPL-PEDV/2013 (GenBank accession number: <a href="#">KJ778615</a> )	Collin et al. (2015)	41
USA and Mexico	From May 2013 to February 2014	Out of 25,762 diagnostic samples, a total of 74 PEDV-positive samples (72 from the United States, 2 from Mexico) were randomly selected for genome sequencing. Full-length genome sequences – Most of the PEDV strains from the U.S. shared complete genome nucleotide identities of 98.6–100% and were distributed between 2 clades (I and II). Compared with the initially reported prototype strains from the U.S., 7 of the 72 newly identified US strains had an S INDEL. These 7 PEDV strains were from 4 US States, shared 99.8–100% nt identity with each other and 96.2% nt identity with the prototype North American strains, and formed a separate cluster in Clade II. Two isolates from Mexico, Mexico124/2014 and Mexico104/2013, belonged to Clades I and II, respectively. In addition, phylogenetic analysis confirmed a recent common ancestor with PEDV strains from China ( <a href="#">AH2012</a> ) and all PEDV strains from North America, as was suggested previously. S gene – In contrast to findings from complete-genome analysis, findings from S gene analysis indicated that S INDEL and non-S INDEL PEDV strains from the U.S. were most closely related to strain CH7ZMZDY/11, but not to strain AH2012, from China. Additional information about E, M, and N genes are present in the paper.	US PEDV strains: GenBank accession numbers: <a href="#">KJ645635-699</a> Mexico PEDV strains: Mexico124/2014 (GenBank accession number: <a href="#">KJ645700</a> ) Mexico 104/2013 (GenBank accession number: <a href="#">KJ645708</a> )	Vlasova et al. (2014)	294

Country (region)	Date of isolation	Sample description and sequence information	Strain sequenced	Reference	RefID <sup>(a)</sup>
Asia China (Jiangxi Province)	2013	<p>Faecal and intestinal samples were collected from suckling piglets with severe watery diarrhoea, vomiting and dehydration from different premises</p> <p>Full-length genome analysis – The nucleotide identity between the Jiangxi PEDV strains and strains identified post-2010 ranged from 97.3% to 99.7%, while the nucleotide identity with those determined ante-2010 (CV777, attenuated vaccine_KC189944, SM98, JS2008, JS2008new and LZC) ranged from 96.3% to 97.0%</p> <p>The two strains showed the highest nucleotide identity (&gt; 99%) with six newly confirmed US strains (IA1, Co/13, USA/Indiana, ISU13-22038-IA-homogenate, ISU13-22038- IA-P9, and 13-019349) and five Chinese strains (GD-B, AH2012, BJ-2011-1, CH/ZMD/ZY, and CH-HZ/2012) identified post-2010, suggesting these PEDV strains might have evolved from the same origin. Interestingly, a comparison analysis revealed that CH/JX-1/2013 and CH/JX-1/2013 had 99.7% nucleotide identity to the strain of GD-B (GenBank accession number: <a href="#">JX088695</a>) isolated from Guangdong, an adjacent province of Jiangxi, in October 2010</p> <p>In conclusion, the two Jiangxi strains defined in this study had a close relationship with the recent prevailing field PEDV strains in China and the United States</p> <p>S gene sequences – The two Jiangxi strains had a 99.8% nucleotide identity with each other, and 96.7% nucleotide identity with CV777</p>	CH/JX-1/2013 and CH/JX-2/2013 (GenBank accession numbers: <a href="#">KF760557</a> and <a href="#">KJ526096</a> )	Song et al. (2015b)	249
China (Zhejiang, Jiangxi, Shandong and Hubei provinces of Eastern China)	From January 2012 to July 2013	<p>A total of 169 faecal and intestinal samples were collected from pigs with typical PED symptoms on 26 farms</p> <p>Comparative genomic, phylogenetic and recombination analyses was determined for 24 PEDV-positive representative samples (twenty-one S-ORF3-E-M-N genes, two S genes, and one full-length genomic cDNA)</p> <p>The S genes of the 24 samples have a 4,161-nt sequence that, compared with the prototype CV777 strain, shows 97.9–100% sequence identities</p> <p>Analyses using new and known sequence data demonstrated that the AH2012 strain is likely not the direct progenitor of emergent US PEDV strains during 2013</p>	CH/ZIQZ-2w/2012 CH/ZJHY-2/2012 CH/ZJJS-1Z/2012 CH/JXZS-3H/2012 CH/JXZS-2H/2012 CH/ZJXS212/2012 CH/ZJHZHY-6/2013 CH/JXJZ-F/2012 CH/ZJJS-2Z/2012 CH/JXZS-3L/2012	Tian et al. (2014)	2269

Country (region)	Date of isolation	Sample description and sequence information	Strain sequenced	Reference	RefID <sup>(a)</sup>
China (Guangdong in Southern China)	2014	The full-length genome analysis of a variant porcine epidemic diarrhoea virus (PEDV) strain, CH/GDZQ/2014, was determined. The isolate was a variant strain with a relatively far relationship with the PEDV strains previously identified in the same area between 2011 and 2012 and was genetically distinct from the CV777-based vaccine strain currently being used in China. Full-length genome analysis – Phylogenetic analysis demonstrated that the CH/GDZQ/2014 strain had a relatively far relationship with four variant PEDV strains (CH/GD-01, CH/GDGZ/2012, GD-A, and GD-1) identified in Guangdong between 2011 and 2012, indicating that CH/GDZQ/2014 was genetically distinct from these strains. Sequence homology analysis showed that CH/GDZQ/2014 had 96.7% nt identity with the prototype CV777 strain but shared 97.8–99.0% nt identity with the variant PEDV strains that have emerged since 2010 in China and 98.8% nt identity with two newly identified US strains. S gene sequences – The S protein of CH/GDZQ/2014 had 93.1–98.6% nt identity with the reference strains, showing the lowest identity with the CV777-based vaccine strain (NC_003436) and the highest identity with two Chinese strains (BJ-2011-1 and JS-HZ/2012).	CH/JXZS-1223L/2012 CH/SDZD-1/2012 CH/SDZD-2/2012 CH/HuBWHYQ/2012 CH/ZJQZ-2/2012 CH/ZJHZ-1C/2012 CH/ZJHZ-2C/2012 CH/JXJZ-1/2012 CH/ZJJS-4X/2012 CH/ZJXC-1/2012 CH/ZJDX-1/2012 CH/JSZL-2/2013 CH/JSZL-3/2013 CH/ZJJS-Z/2012 (GenBank accession numbers: KF840537-KF840858, KF840861, KF840862)	Song et al. (2014)	250



Country (region)	Date of isolation	Sample description and sequence information	Strain sequenced	Reference	RefID <sup>(a)</sup>
China (Jiangsu province)	July 2013	A PEDV-positive sample from a sow with very mild clinical sign was used to inoculate in Vero cells to isolate the virus The phylogenetic trees based upon either the complete genome or S gene showed that the FL2013 strain belongs to the genogroup G2bstrains prevalent in the U.S. and China currently, but had a short deletion at the 3'-end of the spike gene	FL2013 (GenBank: KP765609)	Zhang et al. (2015)	342
China (regions, when specified: ChongQing, JiangXi, JiangSu, ZheJiang, ShanDong)	From April 2011 to March 2014	Nine intestinal homogenates and two faeces samples were collected from pigs that had severe diarrhoea and a high mortality rate at 11 farms Full-length genome analysis – The 11 whole genomes exhibited nucleotide sequence identities ranging from 97.5% to 99.7%, with no insertions or deletions. The phylogenetic tree of 49 PEDV genomes indicated that the PEDV isolates could be divided into two clusters, designated the pandemic group and the classical group. Thirty-nine Chinese and American strains isolated after 2008 comprised the pandemic group. The classical group comprised 10 strains, including 3 Korean strains (SM98, DR13, and attenuated DR13), 6 Chinese strains (CH/S, LZC, SD-M, attenuated vaccine, JS2008, and JS2008 new), and 1 European strain (CV777)	PEDV-15F PEDV-7C PEDV-8C PEDV-10F PEDV-14 PEDV-LY PEDV-CHZ PEDV-LS PEDV-1C PEDV-LYG and PEDV-WS (GenBank accession numbers: KM609203-13)	Sun et al. (2015)	261
China (Shanghai)	2013	Intestinal tracts were collected from dead piglets during an outbreak of diarrhoea on a breeding farm in Shanghai in 2013 Full-length genome sequencing – Identities ranging from 96.6% to 99.8% to other strains; the highest level of similarity, with JS-HZZ2012, was 99.8%. Based on analysis of the nucleotide sequences of the PEDV ORF1a and ORF1b, all of the PEDV strains could be divided into three groups. Group 1 comprised one Chinese strain (LZC), one Korean strain (SM98) and one European strain (CV777). Group 2 consisted of vaccine strains (attenuated DR13) and two Chinese PEDV field strains (SD-M and JS2008). Group 3 was made up of virulent DR13, 10 USA strains isolated in 2013 and 16 Chinese strains (except CH/S), which were isolated from China during PED outbreaks in 2011–2013. The S gene shared 93.8–99.4% nucleotide sequence identity with those of other PEDV strains (Table 2). SHQP/YM/2013 belonged to Group 3, which also including four Korean field strains (KNU-0802, KNU-0902, CNU-091222-01 and CNU-091222-02) from 2008 to 2009, 10 USA field isolates from 2013, and 15 Chinese strains, which were isolated during severe PED outbreaks in China during 2011–2013	SHQP/YM/2013 (GenBank accession number: KJ196348)	Yang et al. (2014)	324

Country (region)	Date of isolation	Sample description and sequence information	Strain sequenced	Reference	RefID <sup>(a)</sup>
China (Henan province)	January 2013	<p>Four intestinal samples were obtained from 3-day old piglets with diarrhoea from one farm</p> <p>S gene nucleotide sequence – The isolate exhibited highest nucleotide sequence similarity (99.6%) to strains JS-HZ2012 and HB-2012-1 from China, but most closely related to strain CH/XCYL/11. The complete S gene of PEDV HN1303 was sequenced and analysed, and the results showed that HN1303 shares 94.0% and 92.8% nucleotide and amino acid identities with CV777 vaccine strain, respectively. Phylogenetic tree based on S gene indicates that the HN1303 strain belongs to genotype IIa, a recently prevalent genotype in China and USA</p>	HN1303 (GenBank accession number: <a href="#">KR080551</a> )	Wang et al. (2015)	306
Japan (Tottori prefecture)	October 2014	<p>Suckling pigs from several sows showed mild diarrhoea and vomiting in a breed-to-wean farm</p> <p>Full-length genome sequence – Comparative sequence analysis showed that the complete genome of Tottori2/JPN/2014 strain had 99.73–99.87%, 99.64–99.69% and 98.90–99.45% nucleotide sequence identity with those of North American clades I and II and US S INDEL PEDV strains used in this analysis, respectively. A phylogenetic dendrogram constructed using the sequence data without considering gaps indicated that the Tottori2 PEDV strain was included in a cluster in North American clade I and was most closely related to US PEDV strain Iowa103</p> <p>S gene sequences – Phylogenetic analysis of S genes demonstrated that the Tottori2 PEDV strain belonged to a cluster including the reference PEDV strains and showed the closest genetic relationship to the US PEDV strain TC-PC177 (97.89% identity at the nucleotide sequence level)</p>	Tottori2/JPN/2014 (GenBank accession number: <a href="#">LC022792</a> )	Masuda et al. (2015)	170
Japan (Tottori Prefecture)	October 2014	<p>A unique case of PED, associated with no mortality rates among piglets, was observed in Tottori Prefecture</p> <p>Full-length genome analysis – The strain had 99.73–99.87%, 99.64–99.69% and 98.90–99.45% nt identities with those of North American Clades I and II and US S INDEL PEDV strains used in the phylogenetic analysis, respectively. The strain was classified into a cluster of North American Clade I and was most closely related to the US PEDV strain Iowa103</p> <p>S gene sequences – The strain had the closest genetic relationship with the US PEDV strain TC-PC177 (97.89% nt identity)</p>	Tottori2/JPN/2014 (GenBank accession number: <a href="#">LC022792</a> )	Murakami et al. (2015)	2249

Country (region)	Date of isolation	Sample description and sequence information	Strain sequenced	Reference	RefID <sup>(a)</sup>
Japan (18 prefectures)	From October 2013 to May 2015	<p>Full-length genome analysis – The 38 PEDV strains clustered into two major clades, North America (NA) Clade I (n = 26) and NA Clade II (n = 12), each including recent PEDV strains from the US and other countries. The complete genomes of the Japanese PEDV strains were almost identical to those of the US and Korean PEDV strains within each clade (Clade I: 99.77–99.99%; Clade II: 98.65–99.96%)</p> <p>S gene – The 38 PEDV strains clustered into two major clades, the North American (NA) type (n = 34), and the INDEL type (n = 4), each of which included the recent US and/or Korean PEDV strains. The 4 INDEL PEDV strains from Japan shared 99.76–99.95% nt sequence identity with each other, and shared 96.55–98.24% nt sequence identity with the 34 NA PEDV strains from Japan, respectively. These findings indicated that the 38 PEDV strains from Japan were more closely related to the global PEDV strains from the US and Korea than to the classical PEDV strains from Japan</p>	<p>AOM-1 to 3/JPN/2014, EHM-1/JPN/2014, FKO-1/JPN/2014, GNM1 to 2/JPN/2014, HRS-1/JPN/2014, IBR-1 to 2/JPN/2013, IBR-3 to 8/JPN/2014, IWT-1 to 4/JPN/2014, KCH-1 to 2/JPN/2014, KGS 1 to 2/JPN/2013, KGS-4/JPN/2014, KGW-1/JPN/2014, KMM-1 to 2/JPN/2014, MIE-1/JPN/2014, MYG-1/JPN/2014, MYZ-1/JPN/2013, NIG-1 to 2/JPN/2014, OKN-1 to 2/JPN/2013, OKY-1/JPN/2014, TTR-1 to 2/JPN/2014 (GenBank accession numbers: LC063810-47)</p>	Suzuki et al. (2015)	265
South Korea (9 provinces)	From January to December 2008	<p>A total of 2,634 faecal and intestinal samples were collected from pigs exhibiting diarrhoea from 569 swine farms</p> <p>S gene complete sequence – The complete S gene sequence MF3809 showed a high (93.3–98.5% nt; 92.0–98.0% aa) sequence identity to all known PEDV strains for which full-length S gene sequences were available in GenBank, except that MF3809 has the large deletion in its S gene. Phylogenetic analysis confirmed that MF3809 belonged to a cluster containing a PEDV reference strain, not a cluster that included any other coronaviruses, and showed the closest genetic relationship with PEDV strains from South Korea in 2009</p> <p>M gene – The entire M gene of MF3809 had 96.6–100% nt (96.0–100% aa) sequence identity to all known PEDV strains available in GenBank, and phylogenetic analysis showed that MF3809 belonged to a cluster containing PEDV reference strain and showed the closest genetic relationship with 2007 Korean PEDV strains</p>	<p>MF3809/2008/South Korea (GenBank accession numbers: KF779469 and KF779470)</p>	Park et al. (2014)	211

Country (region)	Date of isolation	Sample description and sequence information	Strain sequenced	Reference	RefID <sup>(a)</sup>
Korea (8 provinces)	From 1998 to 2013	A total of 27 samples of diarrhoea and intestinal tissue from piglets were collected from farms in Korea The full S gene sequences of a total of 27 PEDV strains and 48 reference strains were compared. Based on the phylogenetic trees the Korean strains could be divided into two groups (G1 and G2) at the nt and aa levels. Vaccine strains, reference strains, and several of the Korean and Chinese strains were found to belong to G1, whereas all Korean field strains clustered together within G2. Interestingly, three strains (KGG13_2DJ, KGG14_6IC, and KDG13_295BG) in G2-2 were highly similar to the US strains that spread in 2013, with 99.2–99.8% and 98.8–99.7% identity at the nt and aa level, respectively	GenBank accession numbers: <a href="#">KJ857352</a> – <a href="#">KJ857481</a>	Kim et al. (2015b)	108
South Korea (Kyungpook Province)	March 2014	Faecal samples were collected from pigs exhibiting PED-like symptoms Full-length genome analysis – Nucleotide identity of 96.6–99.7% with other complete PEDV genomes available in GenBank, with the highest nucleotide identity (99.7%) with a new variant US strain, OH851 ( <a href="#">KJ399978</a> ) S gene sequences – Nucleotide sequencing analysis showed 99.8–99.9% nt identity to a new variant strain OH851 from the United States	KOR/KNU-1406/2014 (GenBank accession number: <a href="#">KM403155</a> )	Lee et al. (2014)	2268
Taiwan (Central and Southern Taiwan)	Early 2014	A total of nine intestinal samples were collected from nine 1- to 7-day-old dead piglets, which showed signs of watery diarrhoea and dehydration from three farms S gene sequences – Phylogenetic analysis revealed two major clusters. All new PEDVs isolated from Taiwan in this study belonged to the Group 1 (G1). They were very closely related to the US non-S INDEL(USA-Iowa 28-2013, USA-Kansas 29-2013, USA-Texas 39-2013) strains and the Canada PEI-023 strain (ranging from 99.7% to 99.8%); but relatively less related to other Asia strains in the same group, including the China PEDV strains isolated from the PED outbreaks during 2011–2012, and the Vietnam strains isolated from the PED outbreaks in 2013 (VN/JFP1013_1/2013, VN/VAPI113_1/2013 and VN/KCHY-310113/2013, ranging from 96.9% to 97.1%) The S gene sequences of the Taiwan PEDV variants were separated from the Group 2 (G2) viruses, which comprised the European CV777-based vaccina strain (lower identity to the CV777 and DR13 vaccine strains, ranging from 93.9% to 94.2%), Korean DR13 strain, the Taiwan and global historic strains, and the US S INDELs strains, such as USAIndiana128, USA-Ohio126 and USA-Iowa107 strains Phylogenetic analysis also revealed that the Taiwan strains and the US non-S INDEL PEDV strains were the most closely related to China CH/ZMZDY/11 and CH/ZY/11 strains (99.2–99.3% nucleotide sequence identity)	TW-Chiayi-12, 24 and 32, TW-Yunlin-71, 82 and 91, TW-Pingtung-41, 52 and 63 (GenBank accession numbers: <a href="#">KP276244</a> – <a href="#">KP276252</a> )	Chiou et al. (2015)	38

Country (region)	Date of isolation	Sample description and sequence information	Strain sequenced	Reference	RefID <sup>(a)</sup>
Taiwan		<p>NSP3 gene complete sequence – the NSP3 genes from three clinical samples of swine with PEDV infection were obtained and aligned with 34 NSP3 genes available in GenBank as of February 2014. The results suggested that the viruses from the 2014 PEDV epidemic in Taiwan were highly clustered with the viruses from the US within Genogroup 2</p> <p>Comprehensive PEDV full-genome sequences collected from the US were obtained and the phylogenetic tree was further constructed based on the nsp3 gene including 74 and 3 PEDV sequences from the US and Taiwan, respectively. The results suggested that the virus responsible for the 2014 PEDV outbreak in Taiwan clustered closely together with Clade I from the US</p>	TW369-NTNSP3 and TW298-TY NSP3 (GenBank accession numbers: KR632490-2)	Sung et al. (2015)	263
Thailand (Eastern region)		<p>Two PEDV variants, designated CBR1 and EAS1, were isolated from 3-day-old pigs</p> <p>Full-length genome analysis - CBR1 shares a high similarity (98.3–98.7% and 96.3–97.0% at the nucleotide and amino acid levels, respectively) with more recent isolates from China. In contrast, EAS1 shares a high similarity with LZC, SM98, and CV777 (99.1% to 99.5% and 98.3% to 98.8% at the nucleotide and amino acid levels, respectively)</p> <p>S gene sequences – CBR1 shared 94.2–98.5% and 92.2%–98.0% nucleotide sequence and amino acid similarity with the prevalent PEDV variant in China and Thailand</p> <p>EAS1 has a close relationship with CV777, LZC, and SM98 vaccine strains, sharing 98.4–98.9% and 96.6–97.5% nucleotide sequence and amino acid similarity and is genetically distinct from the prevalent PEDV variant in Thailand</p>	CBR1 (GenBank accession no. KR610993) EAS1 (GenBank accession no. KR610991)	Cheun-Arom et al. (2015)	36

Country (region)	Date of isolation	Sample description and sequence information	Strain sequenced	Reference	RefID <sup>(a)</sup>
Vietnam (6 provinces in the north and 1 in the central region)	From November 2013 to April 2014	Complete sequence analysis of two (spike and ORF3) genes in 30 positive samples (diarrhoea and intestinal samples from piglets) identified 8 strains. Complete S gene sequences demonstrated that HUA-PED45 has high similarity (99.7% and 99.4% at the nt and aa level, respectively) to HUA-PED47 and 97.6–97.8% nt sequence similarity to Vietnamese strains (VN/KCHY-310113, VAP1113-1, and JFP1013-1) responsible for the 2013 outbreaks Phylogenetic analysis based on a complete spike gene fragment of Vietnamese field strains, together with other PEDV reference strains from GenBank, divided the sequences into four groups (Fig. 1)	HUA-PED55, -PED58, -PED60, -PED63, -PED67, -PED68, -PED45 and -PED47 (GenBank accession numbers: KP455313-KP455320 and KP455967-KP455974)	Kim et al. (2015a)	111
Vietnam (Northern and Southern provinces)	From January to November 2013	Whole-genome sequences are reported for three PEDV strains isolated from pigs displaying severe diarrhoea from three different farms Full-length genome analysis - the three isolates were grouped together in Group G2 (along with PEDV isolates from China after 2010, Korea and the United States), and in sub-cluster 2-1 (along with, in addition to Vietnam isolates, isolates from China that were reported to be a new variant). These isolates were separated from Chinese (AH2012), US and US-like Korean isolates, which were included in sub-cluster 2-2. These findings suggest that the PEDV strains isolated in Vietnam are new variants. In addition, the results of genetic analysis suggest a close relationship between Vietnamese isolates and new variants of Chinese PEDV isolates from 2011 to 2012	VN/KCHY-310113 (GenBank accession number: KJ960180), VAP1113-1 (GenBank accession number: KJ960179) and JFP1013-1 (GenBank accession number: KJ960178)	Vui et al. (2015)	297

(a): RefID is an internal reference identification number which is used for easy identification of the references included in each of the tables

(b): Publication in January 2016

(c): Publication in December 2015



**Table A.3:** Reported information on clinical signs and pathological lesions and production losses for different age groups of PEDV in 2014–2015 obtained by an extensive search of the scientific literature and relevant websites

Country and time period	Age of the animals	Morbidity and description of clinical signs and/or pathological lesions	Mortality and production losses	Virus strain	Reference	refID <sup>(a)</sup>
Europe						
France (Northern France); December 2014	Piglets, fatteners		The mortality rate ranged between 3.3% and 5.5% in the fattening building and reached 12% in piglets after 1 week and 25% at weaning in the farrowing building	PEDV FR/001/2014 (KR011756)	Grasland et al. (2015)	2300
Germany (Federal State of Baden-Wuerttemberg); May 2014	Pig fattening farm: all age groups (feeders to slaughter animals)	Watery diarrhoea	Clinical signs were present for at least 1 week; ≈20 pigs died	GER/L00719/2014 (GenBank accession number: <a href="#">LM645058</a> ) GER/L00721/2014 (GenBank accession number: <a href="#">LM645057</a> )	Hanke et al. (2015)	79
Germany (South-Western Germany); October/ November 2014	Sows  Piglets	The group of sows weaned on the first day of the outbreak had > 95% morbidity: severely reduced feed intake for the first 7–8 days after weaning and yellowish, watery diarrhoea  From one farrowing group diarrheic (yellowish, pasty to watery diarrhoea), gaunt and dehydrated piglets, covered with feces were found in 30 out of 35 (86%) litters  Gross lesions were limited to the intestines and characterized by distended, thin and transparent intestinal walls, mainly observed in the small intestines but partially also in the colon region  Histology was characterized by atrophic enteritis, which included shortening, blunting and fusion of the villi, occasionally with vacuolation and exfoliation of enterocytes		K16/14-01 (L00906) K16/14-02 (L00907) K16/14-03 (K00908)	Stadler et al. (2015); FARM C	256
			67.6% of piglets from this farrowing group died or had to be euthanized before weaning. Mortality in the nursery reached up to 7.1% during the outbreak Clinical signs subsided within 4 weeks after the onset of diarrhoea			



Country and time period	Age of the animals	Morbidity and description of clinical signs and/or pathological lesions	Mortality and production losses	Virus strain	Reference	refID <sup>(a)</sup>
Germany (South-Western Germany); September 2014	Sows and boars	First clinical signs were characterised by anorexia in lactating sows. Up to 100% of the sows in the farrowing unit were affected by watery diarrhoea. Within 1 week after the onset of first clinical signs, diarrhoea had spread to all age groups of pigs present at the farm including boars and nursery pigs	Clinical signs were present for approximately 4 weeks and performance data returned to normal within 6 weeks after the outbreak of PED	K14/14-02 (L00855)	Stadler et al. (2015); FARM B	256
	Piglets	Pasty diarrhoea, which progressed to watery greyish feces with variable degrees of dehydration, affecting about 70% of piglets from one farrowing batch Gross and histologic lesions were commonly described for animals from all three farms (A, B,C, see above)	During the outbreak, mortality ranged from 5.5% in suckling piglets to 8.8% in nursery pigs			
Germany (Southern Germany); May 2014	Fattening farm – all age groups affected	95% of all growing and finishing pigs developed diarrhoea accompanied by anorexia and lethargy. Vomitus was apparent in individual pigs. The affected pigs showed varying degrees of weight loss and dehydration. At the peak of clinical signs, 5 days after the onset of first clinical signs, feed consumption severely declined	Within the first 10 days after the onset of clinical signs 20 pigs had died; 80% of them originated from the youngest age group. During the outbreak of PED an overall mortality rate of 4.5%, an average daily gain (ADG) of 600 g and a prolonged fattening period of 30 days were documented. Prior to the outbreak, performance data accounted for 750 g ADG and 2% mortality Feed consumption returned to normal within 6 days in the older age groups but was compromised in the youngest age groups for several weeks Clinical signs subsided within 3 weeks in the older age groups, but recurrent diarrhoea persisted in the youngest age group for up to 15 weeks	GER/L00719/2014 <sup>(b)</sup> (GenBank accession number: LM645058) L00721/GER/2014 (GenBank accession number: LM645057)	Stadler et al. (2015); FARM A	256

Country and time period	Age of the animals	Morbidity and description of clinical signs and/or pathological lesions	Mortality and production losses	Virus strain	Reference	refID <sup>(a)</sup>
Spain; from August 2014 to May 2015	Suckling piglets, fatteners	Disease was most severe among piglets < 10 days of age. Diarrhoea was the predominant clinical sign	The mortality rate was up to 90% in new born piglets Decreased weight in suckling piglets (< 0.5–0.3 Kg per piglet) and increased time for fattening		Laranjo et al. (2015)	2425
	Sows	Decrease of appetite (10–80% of sows) and, in less proportion of animals, diarrhoea (4–30%) and, eventually vomiting (2–5%). The clinical course among adult pigs lasted 2–5 days. Necropsy of affected piglets reveal a severe catarrhal enteritis and histologically villus atrophy was observed that affected mainly jejunum and ileum	In a period of 8 weeks the decrease of number of piglets per litter ranged from a negligible value up to 2.9 piglets. Clinical signs were observed between 2 and 11 weeks depending on different factors such as using of controls measures (eg. feedback of sows with infected faeces)			
Spain (3 provinces); March 2014		In all cases high morbidity was observed in affected holdings, the predominant symptom was higher in piglets under 1 week of age (up to 44%), over 1 week of age, mortality of 2 weeks old piglets decreased considerably (16.9%), being non-existent in older animals.	The average duration of an outbreak has been 16.9 days with complete recovery in all cases. Spanish strains have produced losses of 0.66 piglets per sow per year on average while in the USA it has been of 1.67 piglets		ANPROGAPOR-Dirección General de Sanidad de la Producción Agraria, 2014.	2623

Country and time period	Age of the animals	Morbidity and description of clinical signs and/or pathological lesions	Mortality and production losses	Virus strain	Reference	refID <sup>(a)</sup>
Ukraine (Poltava region); summer 2014	Sows	Vomiting and profuse diarrhoea. Disease was less severe in adults, whose appetite returned and diarrhoea ceased within 3 days	Abortions occurred immediately following the outbreak in 38% of 1 batch of sows that were at 28–35 days'gestation; no diagnostic investigation was made to determine the cause. Abortions did not occur in other groups of sows and have not been reported as a feature of PED outbreaks in North America. The reproductive status of sows at other stages of gestation was not substantially affected by the initial PED outbreak, and no higher return rate was observed. Postpartum sows did not fail to produce milk, but those affected by PEDV had a reduced feed intake and associated reduced milk output.		Dastjerdi et al. (2015) <sup>(c)</sup>	2620
	Piglets	Disease was most severe among piglets <10 days of age. Vomiting and profuse watery diarrhoea. Piglets >10 days old became sick, but most (95%) survived.	The case-fatality rate reached nearly 100%. The decision was made to euthanize piglets <10 days of age during a 3-week period from the start of the outbreak. The performance of the pig unit took 20 weeks to return to pre-outbreak levels. During that time, a total of 30,000 piglets died, which equates to a loss of 6 weaned piglets per sow per year.	Ukraine/Poltava01/2014 (GenBank accession number: KP403954)		

Country and time period	Age of the animals	Morbidity and description of clinical signs and/or pathological lesions	Mortality and production losses	Virus strain	Reference	refID <sup>(a)</sup>
The Americas						
Canada (Southwestern Ontario); January 2014	Piglets	Occurred in January of 2014 in a 500 sow farrow-to-finish herd. Diarrhoea and vomiting in piglets. Piglet morbidity was 100%. Small and large intestine were distended with watery yellow translucent content; intestinal serosae were congested; moderate to marked atrophy and fusion of intestinal villi; villus tip epithelium was columnar but vacuolated	Piglet mortality was 100%	N and S gene conventional PCR assays produced amplicons of the predicted size for all 4 colon samples. Sequencing of these PCR products showed that this Ontario PEDV was 99% identical to recent PEDV isolates from the USA and China.	Ojkic et al. (2015)	197
United States of America (one large swine system with several farms located in the Midwest); between March 1, 2013 and June 1, 2014.	Weaned pigs	Retrospective cohort study based on 18 eligible pairs of batches: control (before Porcine Epidemic Diarrhoea—PED - detection) and infected (first batch after PED detection).	Mortality was significantly ( $p < 0.001$ ) higher in PED-positive batches compared with the control pigs, with an overall mean difference of 12.5% (95% confidence interval = 6.4–18.4). Average daily gain (ADG) and feed conversion ratio (FCR) were significantly worse in case batches, with a 0.16 lb mean decrease of the former (95% CI = 0.07–0.26) and a 0.55 increase in the latter (95% CI = 0.30–0.79). Average daily feed intake (ADFI) remained largely unaffected ( $p = 0.9$ ).		Alvarez et al. (2015)	8

Country and time period	Age of the animals	Morbidity and description of clinical signs and/or pathological lesions	Mortality and production losses	Virus strain	Reference	refID <sup>(a)</sup>
United States of America (Ohio); January 2015	Sows	Multi-site swine operation. 80% of sows on one site experienced diarrhoea, vomiting, and dehydration.			Bowman et al. (2015)	22
	Piglets, weaned pigs	Diarrhoea, vomiting, and dehydration. Several units in the same or other production flows reported signs and/or confirmation of the virus by RT-PCR.	Forty-two percent mortality was observed in piglets in one of the farrowing units. In one of the production flows, Overall, mortality among neonatal piglets was close to 100% one of the production flows.			
Colombia (Huila, Cundinamarca, Tolima, Boyacá, and Santander); from March to May 2014	Piglets	Morbidity was 18%. Diarrhoea and death in piglets	Case fatality rate was 31.67% Proportion susceptible animals lost = Removed from the susceptible population through death, destruction and/or slaughter (5.68%)		Piñeros and Mongollón Galvis (2015)	1395 <sup>(d)</sup>

(a): RefID is an internal reference identification number which is used for easy identification of the references included in each of the tables

(b): Personal communication with Dr. Sandra Blome

(c): Publication in December 2015

(d): Final report submitted by the World Organisation for Animal Health (OIE) - "Information received on 09/06/2014 from Dr Luis Humberto Martínez Lacouture, Gerente General, Instituto Colombiano Agropecuario (ICA), Ministerio de Agricultura y Desarrollo Rural, Bogotá, Colombia"; [http://www.oie.int/wahis\\_2/public/wahid.php/Reviewreport/Review?reportid=15389](http://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?reportid=15389) [Accessed 7 December 2015]

## Appendix B – Members of the EFSA Network on PED

**Table B.1:** Members of the Network on PED

Country	Name	Affiliation
Austria	Steinrigl, Adolf	Austrian Agency for Health and Food Safety (AGES)
Belgium	Cay, Brigitte	Veterinary and Agrochemical Research Centre (CODA-CERVA)
	Christiaens, Isaura	Ghent University
	Desmarets, Lowiese	Ghent University
	Nauwynck, Hans	Ghent University
	Theuns, Sebastiaan	Ghent University
	Van der Stede, Yves	Veterinary and Agrochemical Research Centre (CODA-CERVA)
Croatia	Brnić, Dragan	Croatian Veterinary Institute Virology Department
Denmark	Bøtner, Anette	Technical University of Denmark, National Veterinary Institute
	Strandbygaard, Bertel	Technical University of Denmark, National Veterinary Institute
Estonia	Nurmoja, Imbi	Estonian Veterinary and Food Laboratory
	Tedersoo, Triin	Estonian Veterinary and Food Laboratory
Finland	Laine, Taina	Finnish Food Safety Authority (EVIRA)
	London, Laura	Finnish Food Safety Authority (EVIRA)
France	Evain, Loic	Bureau de la Santé animale, Direction générale de l'alimentation, Ministère de l'Agriculture, de l'Agroalimentaire et de la Forêt
	Grasland, Beatrice	French Agency for Food, Environmental and Occupational Health and Safety (ANSES)
	Marcé, Clara	Bureau de la santé animale Sous-direction de la santé et de la protection animales Service de la prévention des risques sanitaires de la production primaire Direction Générale de l'Alimentation
	Rose, Nicolas	French Agency for Food, Environmental and Occupational Health and Safety (ANSES)
Germany	Blome, Sandra	Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health
	Schwarz, Bernd-Andreas	VAXXINOVA GMBH diagnostics
Greece	Fortomaris, Paschalis	Aristotle University of Thessaloniki
	Kritas, Spyridon	Aristotle University of Thessaloniki
Hungary	Bálint, Ádám	National Food-chain Safety Office, Veterinary Diagnostic Directorate
	Dán, Ádám	National Food-chain Safety Office, Veterinary Diagnostic Directorate
Ireland	Moriarty, John	Virology Division, Central Veterinary Research Laboratory, Backweston Campus, Celbridge, Co. Kildare
	Ryan, Eoin	Virology Division, Central Veterinary Research Laboratory, Backweston Campus, Celbridge, Co. Kildare
Italy	Alborali, Giovanni	Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna
	Boniotti, Beatrice	Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna

Country	Name	Affiliation
	Ceroli, Monica	Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna
	Lavazza, Antonio	Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna
Lithuania	Masiulis, Marius	Emergency Response Department, State Food and Veterinary Service of Lithuania
Netherlands	Franssen, Paul	GD, Animal Health Service
	Van der Poel, Wim	Wageningen University & Research Centre
	Van der Wolf, Peter	GD, Animal Health Service
Norway	Grøntvedt, Carl Andreas	Norwegian Veterinary Institute
	Heier, Berit Tafjord	Norwegian Veterinary Institute
Portugal	Vilhena Clemente, Patrícia Isabel	Direcção de Serviços de Protecção Animal DGAV
	Vaz, Yolanda	Direcção-Geral de Alimentação e Veterinária
	Correia, Maria Jorge	Direcção de Serviços de Protecção Animal Divisão de Bem Estar Animal DGAV-DSPA
Slovak Republic	Mojzis, Miroslav	State Veterinary Institute – Zvolen
	Ondrejková, Anna	Univerzita veterinárskeho lekárstva a farmácie v Košiciach
	Polak, Dalibor	Animal Health and Welfare Department of State Veterinary and Food Administration of the Slovak Republic
Spain	Cáceres Garrido, Germán	Ministry of Agriculture, Food and Environment (MAGRAMA)
	Gonzalo Martínez, Beatriz	Ministry of Agriculture, Food and Environment (MAGRAMA)
	Romero, Luis	Ministry of Agriculture, Food and Environment (MAGRAMA)
Sweden	Hultén, Cecilia	National Veterinary Institute
United Kingdom	Roberts, Helen	Animal and Plant Health Agency (APHA)
	Steinbach, Falko	Animal and Plant Health Agency (APHA)
	Williamson, Susanna	Animal and Plant Health Agency (APHA)



## Appendix C – Details on extensive literature review on PED

The primary purpose of the extensive literature review is to obtain data in order to update tables 2, 7 and 8 of the 'Scientific Opinion on porcine epidemic diarrhoea and emerging porcine deltacoronavirus' of the EFSA Panel on Animal Health and Welfare (AHAW), published in 2014.

The main review questions are:

- Question 1: Where have cases/outbreaks of pigs with laboratory confirmation of PED been reported in 2014–2015?
- Question 2: Sequence identity of full length and partial sequence data of PED isolates from pigs worldwide in 2014–2015 and their similarity to INDEL strain USA/OH851/2014, INDEL strain GER/L00719/2014 and/or CV777 or other strains (e.g. USA/Colorado/2013)
- Question 3: What is the impact on pig production of PED reported worldwide for pigs with laboratory confirmation of PED – mortality, morbidity and duration of disease in the four age classes (suckling, weaned, fatteners, adults).

In order to address these questions an extensive literature search will be performed in bibliographic databases, sources of grey literature and the web.

The literature search will be conducted using a range of relevant information sources, including searches in several relevant data bases.

Network members will also be asked to provide relevant country reports, grey literature, research studies or any other relevant information, provided that the information is allowed to be published in the EFSA Scientific Report.

Specific search strings, encompassing terminology related to Porcine Epidemic Diarrhoea (PED), will be used to search published literature (see Tables 1–5). The following bibliographic databases will be searched:

Web of Science, encompassing the following databases:

- Web of Science™ Core Collection
- BIOSIS Citation Index<sup>SM</sup>
- CABI: CAB Abstracts<sup>®</sup>
- Chinese Science Citation Database
- Current Contents Connect<sup>®</sup>
- Data Citation Index<sup>SM</sup>
- BMC Genomics
- FSTA<sup>®</sup>—the food science resource
- KCI – Korean Journal Database
- SciELO Citation Index
- Zoological Record<sup>®</sup>
- MEDLINE<sup>®</sup>

Scopus

PubMed

Information will be also searched in ProMED-mail, Google Scholar and the OIE website, including the World Animal Health Information Database Interface (WAHID).

The final search string that was used for the database searches was: ((((((porcine epidemic OR PEDV OR PED))) OR diarrh\*)) AND (swine OR pig OR porcine)). Concerning the Google Advanced Search the search string was porcine epidemic (diarrhoea OR diarrhea) filetype:pdf. The time period of publication was specified at the most detailed level available in each database. Therefore, when this was allowed, a detailed time period was specified as 1 October 2014 to 31 October 2015, while sometimes the period could only be specified as 2014–2015 and the actual publication date of the retrieved publications was accessed later during the process in order to assess their eligibility for inclusion in the review.

The output from the searched databases, including all indexed fields per hit (e.g. title, authors, abstract), will be exported into separate Endnote 7 files, allowing a count of the individual hits per database. Files will then be combined and duplicate records will be removed.

The files obtained will be transferred into DistillerSR Web-Based Systematic Review Software (Evidence Partners, Ottawa, Canada). Using the Distiller duplicate detection function, duplicates will be identified and removed (quarantined).

**Table C.1:** Details of search strings used for literature searches in support of review questions — search strings for Web of Science

Set number	Search	Number of hits	Commentary
14	TITLE: ((((((porcine epidemic OR PEDV OR PED))) OR diarrh*)) AND (swine OR pig OR porcine)) OR TOPIC: ((((((porcine epidemic OR PEDV OR PED))) OR diarrh*)) AND (swine OR pig OR porcine)) Timespan = 2014–2015 Search language = Auto	1,262	
13	TITLE: ((((((porcine epidemic OR PEDV OR PED))) OR diarrh*)) AND (swine OR pig OR porcine)) Timespan=2014-2015 Search language=Auto	313	
12	TOPIC: ((((((porcine epidemic OR PEDV OR PED))) OR diarrh*)) AND (swine OR pig OR porcine)) Timespan = 2014–2015 Search language = Auto	1,262	
11	TOPIC: ((((((porcine epidemic OR PEDV OR PED))) OR diarrh*)) AND (swine OR pig OR porcine)) Timespan = 2014–2015 Search language = Auto	1,262	
10	#9 AND #1 Timespan = 2014–2015 Search language = Auto	1,262	
9	#4 OR #3 Timespan = 2014–2015 Search language = Auto	Approximately 35,476	
8	#7 AND #1 Timespan=2014-2015 Search language=Auto	Approximately 83,818	
7	#3 OR #1 Timespan = 2014–2015 Search language = Auto	Approximately 114,147	
6	#4 AND #2 AND #1 Timespan = 2014–2015 Search language = Auto	270	
5	#4 OR #3 OR #1 Timespan = 2014–2015 Search language = Auto	Approximately 116,245	
4	TOPIC: (porcine epidemic OR PED OR PEDV) Timespan = 2014–2015 Search language = Auto	1,255	
3	TOPIC: (diarrh*) Timespan = 2014–2015 Search language = Auto	Approximately 33,237	
2	TOPIC: (porcine Swine pig) Timespan = 2014–2015 Search language = Auto	Approximately 5,233	
1	TOPIC: (porcine OR swine OR pig) Timespan = 2014–2015 Search language = Auto	Approximately 83,809	

**Table C.2:** Details of search strings used for literature searches in support of review questions — search strings for Scopus

Set number	Search	Number of hits	Commentary
5	History Search Terms((TITLE-ABS-KEY (porcine epidemic OR pedv OR ped) OR TITLE-ABS-KEY (diarrh*)) AND (TITLE-ABS-KEY (swine OR pig OR porcine)) AND (LIMIT-TO (PUBYEAR, 2015) OR LIMIT-TO (PUBYEAR, 2014)))	633	Search strings have been searched in Article Title, Abstract, Keywords; Date Range (inclusive) have been applied (from 2014 to 2015)
4	(TITLE-ABS-KEY(porcine epidemic OR PEDV OR PED) OR TITLE-ABS-KEY(DIARRH*))	212,307	Search strings have been searched in Article Title, Abstract, Keywords
3	TITLE-ABS-KEY(swine OR pig OR porcine) AND PUBYEAR > 2013 AND PUBYEAR < 2016	20,621	Search strings have been searched in Article Title, Abstract, Keywords; Date Range (inclusive) have been applied (from 2014 to 2015)
2	TITLE-ABS-KEY(diarrh*) AND PUBYEAR > 2013 AND PUBYEAR < 2016	18,926	Search strings have been searched in Article Title, Abstract, Keywords; Date Range (inclusive) have been applied (from 2014 to 2015)
1	TITLE-ABS-KEY(porcine epidemic OR PEDV OR PED) AND PUBYEAR > 2013 AND PUBYEAR < 2016	196	Search strings have been searched in Article Title, Abstract, Keywords; Date Range (inclusive) have been applied (from 2014 to 2015)

**Table C.3:** Details of search strings used for literature searches in support of review questions — search strings for PubMed

Set number	Search	Number of hits	Commentary
9	Search (((((diarrh*[Title/Abstract] AND ("2014/10/01"[PDat]: "2015/10/31"[PDat]))) AND (((porcine epidemic[Title/Abstract] OR PED[Title/Abstract] OR PEDV[Title/Abstract]))) AND ("2014/10/01"[PDat]: "2015/10/31"[PDat]))) AND ("2014/10/01"[PDat]: "2015/10/31"[PDat]))) AND (((swine[Title/Abstract] OR pig[Title/Abstract] OR porcine[Title/Abstract]))) AND ("2014/10/01"[PDat]: "2015/10/31"[PDat])) Filters: Publication date from 2014/10/01 to 2015/10/31	118	Filters activated: Publication date from 1/10/2014 to 31/10/2015
8	Search (swine[Title/Abstract] OR pig[Title/Abstract] OR porcine[Title/Abstract]) Filters: Publication date from 2014/10/01 to 2015/10/31	7,715	Filters activated: Publication date from 1/10/2014 to 31/10/2015
7	Search ((diarrh*[Title/Abstract] AND ("2014/10/01"[PDat]: "2015/10/31"[PDat]))) AND (((porcine epidemic[Title/Abstract] OR PED[Title/Abstract] OR PEDV[Title/Abstract]))) AND ("2014/10/01"[PDat]: "2015/10/31"[PDat])) Filters: Publication date from 2014/10/01 to 2015/10/31	118	Filters activated: Publication date from 1/10/2014 to 31/10/2015
6	Search diarrh*[Title/Abstract] Filters: Publication date from 2014/10/01 to 2015/10/31	5,060	Filters activated: Publication date from 1/10/2014 to 31/10/2015

Set number	Search	Number of hits	Commentary
5	Search (porcine epidemic[Title/Abstract] OR PED[Title/Abstract] OR PEDV[Title/Abstract]) Filters: Publication date from 2014/10/01 to 2015/10/31	436	Filters activated: Publication date from 1/10/2014 to 31/10/2015
4	Search (((((porcine epidemic OR PEDV OR PED))) OR diarrh*)) AND (swine OR pig OR porcine) Filters: Publication date from 2014/10/01 to 2015/10/31	351	Filters activated: Publication date from 1/10/2014 to 31/10/2015
1	Search (((((porcine epidemic OR PEDV OR PED))) OR diarrh*)) AND (swine OR pig OR porcine)	5,310	
3	Search ((((((porcine epidemic[Title/Abstract] OR PEDV[Title/Abstract] OR PED))) [Title/Abstract] OR diarrh*)) [Title/Abstract] AND (swine[Title/Abstract] OR pig[Title/Abstract] OR porcine)[Title/Abstract]) Schema: all	0	
2	Search ((((((porcine epidemic[Title/Abstract] OR PEDV[Title/Abstract] OR PED))) [Title/Abstract] OR diarrh*)) [Title/Abstract] AND (swine[Title/Abstract] OR pig[Title/Abstract] OR porcine)[Title/Abstract])	0	

**Table C.4:** Details of search strings used for literature searches in support of review questions — search strings for ProMED-mail

Set number	Search	Number of hits	Commentary
1	Porcine epidemic (diarrhoea OR diarrhea)	13	Filters activated: Publication date from 1/10/2014 to 23/10/2015

**Table C.5:** Details of search strings used for literature searches in support of review questions — search strings for Google Advanced Search

Set number	Search	Number of hits	Commentary
1	Porcine epidemic (diarrhoea OR diarrhea) filetype:pdf	242 .pdf filetype results out of 510 results	Search strings have been searched in file type Adobe Acrobat PDF (.pdf); Date Range (inclusive) have been applied (from 1/10/2014 to 31/10/2015); last update: past year;

Eligible data include both individual and aggregated data that address the objectives of the review questions illustrated above. Information sources are: peer-reviewed journals; country reports that can become publicly available; dedicated web pages; publicly available laboratory reports, conference abstracts and presentations (that include enough information to allow the appraisal of the data reported), grey literature, unpublished research studies for which the researchers agree to make their data available to be included in the report and any other source of relevant information that can be identified.

Studies need to have been published or the information to have become available between October 2014 and October 2015, however, the information in the studies may concern previous time periods as well.

The studies may describe PED occurrence in any type of pig farming setting and for any pig ages.  
Selection criteria

- 1) Report relates to farmed domestic pigs (Yes = Include) and/or
- 2) Report indicates that laboratory testing was used to confirm PED infection (to include also serological information as optional) (Yes = Include) and/or

- 3) Report is primary research or data collection (Yes = Include) and/or
- 4) Report describes (Yes = include)
  - (a) prevalence, incidence, occurrence of the virus
  - (b) full length or partial sequencing results
  - (c) impact of the virus (morbidity, mortality, production losses, duration of disease)
  - (d) vaccination and intervention strategies (e.g. biosecurity and bio-containment)
  - (e) risk assessments for transmission between farms or between countries (e.g. feed and spray-dried porcine plasma (SDPP) used as a feed supplement)

Reports including information on points d. and e. above will not be included in the current literature review but will be identified and kept in the database for future reference.

All studies will be initially screened for their relevance to the review questions and allocated for inclusion in the literature review. Initial screening will be based on titles and abstracts and subsequent screening (for studies passing the first screening) will be based on the full article. Studies will be grouped by review questions.

## **Annex A – Porcine epidemic diarrhoea (PED) data reporting guidelines**

An annex to this document is published in the EFSA Journal as a separate file (<http://www.efsa.europa.eu/en/efsajournal/pub/4375>).