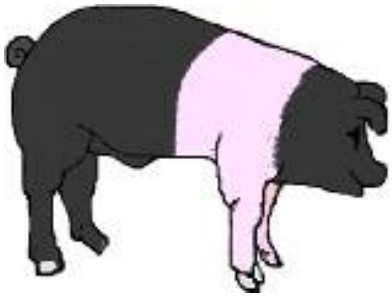
Animal & Plant Health Agency



SRUC

Great Britain pig quarterly report: disease surveillance and emerging threats

Volume 31: Quarter 4 of 2024 (October to December)

Highlights

Contents

Introduction and overview

This quarterly report reviews disease trends and disease threats for the fourth quarter of 2024 (October to December). A full explanation of how data are analysed is provided in the annexe available on GOV.UK.

This report is compiled using data available at the time of writing. It contains analyses carried out on disease data gathered from APHA, Scotland's Rural College (SRUC) Veterinary Services and partner post-mortem providers, as well as intelligence gathered through the Pig Expert Group networks. In addition, links to other sources of information including reports from other parts of the APHA and Defra agencies are included.

Pig disease surveillance dashboard outputs

Diagnoses made most frequently in the fourth quarter of 2024 through the Great Britain (GB; England, Wales and Scotland) scanning surveillance network are listed in Table 1. Note that further diagnoses may be added for submissions made in quarter 4 of 2024 which are finalised after the generation of this report. Diagnoses can be interrogated further using the interactive pig disease surveillance dashboard, which was launched in October 2017. Surveillance data for diagnostic submissions in quarter 4 of 2024 are illustrated in Figures 1a-1c.

These diagnostic submissions are voluntary and subject to several sources of bias. The profile of submissions for the fourth quarter of 2024 was similar to that of the same quarter in 2023, in that the most frequent main clinical sign was diarrhoea and gastro-intestinal and the most frequent syndrome was enteric.

Total GB diagnostic submissions increased in 2024: total submissions were 33% higher than the average for the previous four years and carcase submissions in 2024 increased by 6% compared to the average for the previous four years (2020-2023).

There were fewer submissions in quarter 4 of 2024 compared to the same quarter in 2023, but total submissions were still 15.2% higher in quarter 4 2024 than the average for quarter 4 in the previous four years. The throughput of non-carcase submissions to the GB scanning surveillance network in quarter 4 of 2024 increased by 24% compared to the average for quarter 4 in the previous four years (2020-2023), while the throughput of carcase submissions in quarter 4 of 2024 decreased by 5% compared to the average for quarter 4 in the previous four years. Changes in the number of submissions and the balance of sample types can affect the number and profile of diagnoses achieved. Submission of carcases enables more complete diagnostic investigation.

In terms of numbers of diagnoses, a total of 1577 diagnoses were recorded at the time of writing in 2024, compared to 1352 in 2023. In quarter 4 of 2024, 326 diagnoses were recorded. This compares to 409 diagnoses recorded in quarter 4 of 2023.

There is guidance available for veterinarians on sampling and testing pigs affected with different disease syndromes. Veterinarians are encouraged to contact their regional Veterinary Investigation Centre (VIC) to discuss disease investigations with Veterinary Investigation Officers at APHA and SRUC.

Table 1: GB scanning surveillance 15 most frequent diagnoses in quarter 4 of 2024 and for the same quarter in 2023

15 most frequent diagnoses in quarter 4 of 2024 (total 326)	15 most frequent diagnoses in quarter 4 of 2023 (total 409)
1. *Brachyspira pilosicoli* colitis	1. Colibacillosis - enteric
2. *Lawsonia* sp. associated disease	2. Salmonellosis – *S*. Typhimurium
3. Salmonellosis – *S*. Typhimurium	3. Porcine reproductive and respiratory syndrome (PRRS) - systemic
4. Colibacillosis - enteric	4. *Streptococcus suis* disease
5. Pneumonia associated with PRRSV-1	5. *Brachyspira pilosicoli* colitis
6. Porcine reproductive and respiratory syndrome (PRRS) - systemic	6. *Lawsonia* sp. associated disease
7. Swine influenza	7. Swine influenza
8. *Brachyspira hyodysenteriae* – swine dysentery	8. *Brachyspira hyodysenteriae* – swine dysentery
9. *Streptococcus suis* disease	9. Pneumonia associated with PRRSV-1
10. Pneumonia – *Pasteurella multocida*	10. *Glaesserella parasuis*
11. *Glaesserella parasuis*	11. Pneumonia associated with *Mycoplasma hyopneumoniae*
12. Pneumonia associated with *Mycoplasma hyopneumoniae*	12. Pneumonia – *Pasteurella multocida*
13. Rotavirus	13. Endocarditis
14. Streptococcal infection (excluding *S. suis*)	14. Streptococcal infection (excluding *S. suis*)
15. Fetopathy due to PRRSV-1	15. *Trueperella pyogenes* infection

Figures 1a to 1d: summary surveillance data for 649 submission records in quarter 3 of 2024 (507 in quarter 3 of 2023)

Figure 1a: pig age category

Adult	85
Mixed	7
Neonatal	15
Postwean	241
Prewean	20
Unknown/other	121

Figure 1b: disease syndrome

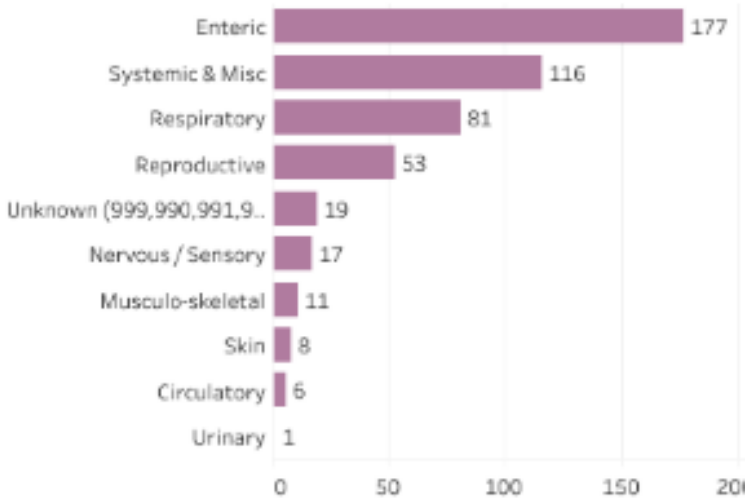
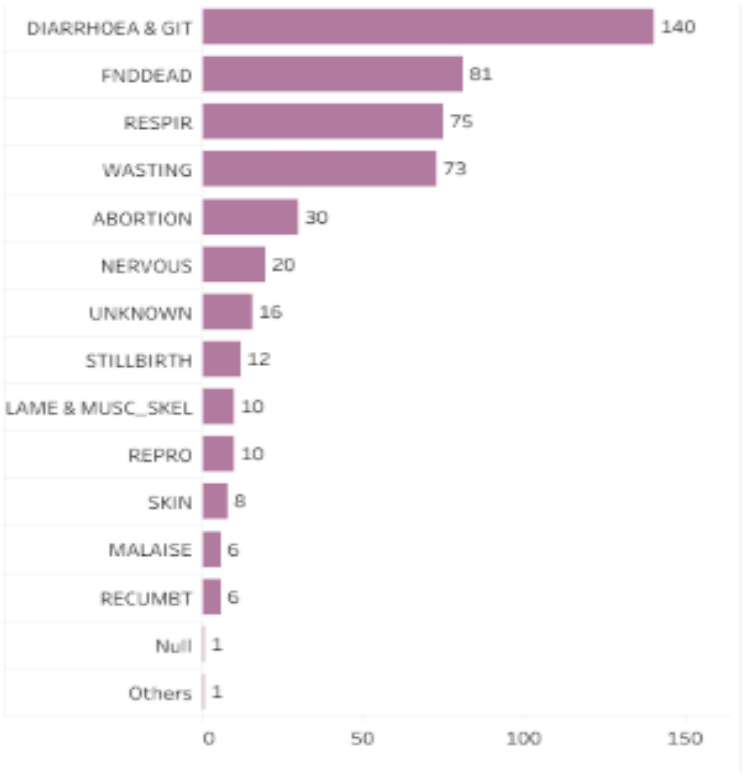


Figure 1c: main clinical sign reported



New and re-emerging diseases and threats

Porcine enteric coronavirus surveillance

Porcine Epidemic Diarrhoea (PED) due to any PED virus strain remains notifiable in England and Scotland and suspicion of disease, or confirmation of infection, must be reported (Defra, 2015; Scottish Government, 2016). No more suspect incidents of PED have been reported since the suspect case in May 2022 on a small pig premises in England, in which PED was ruled out and iron deficiency anaemia was diagnosed.

Enhanced surveillance for PED continues and diagnostic submissions from cases of diarrhoea and/or enteropathy in pigs (non-suspect PED) submitted to APHA have been routinely tested by PCR for PED virus (PEDV) and transmissible gastroenteritis virus (TGEV) on a weekly basis. None have been positive for PEDV or TGEV in 1695 diagnostic submissions tested under Agriculture and Horticulture Development Board (AHDB) Pork funding from June 2013 to December 2024.

This enhanced surveillance has included testing for porcine deltacoronavirus (PDCoV) since February 2023 under the same funding and no PDCoV has been detected in the UK to date. This surveillance aims to detect any of these three porcine enteric coronaviruses, should they occur as a new and (re-)emerging cause of porcine diarrhoea in pigs and thus pose a potential threat to pig health and welfare. The last diagnosis of PED and of TGE recorded in the GB national diagnostic database (Veterinary Investigation Diagnosis Analysis [VIDA]) was in 2002 and 1999, respectively.

Unusual diagnoses or presentations

Congenital tremors in piglets born to parity two sows

Six-day-old piglets were submitted to the Bury St Edmunds VIC from an outdoor breeding herd to investigate congenital tremor. Piglets presented with rhythmic whole-body tremoring and bouncing of the hind legs, which lessened at rest (see video at https://www.youtube.com/watch?v=abu8sSZleFc). Clinical signs were present in just over 10% of the litters born to parity two sows. When this sow batch had farrowed as gilts, 80% of the litters had been affected with congenital tremors. There were no other significant disease issues in the herd; sows of affected litters were healthy and case mortality was low. The clinical signs were typical of congenital tremor type AII and there were no features which raised suspicion of classical swine fever (CSF), which is a notifiable disease and can cause congenital tremor following *in utero* infection (type AI).

There were no gross lesions at postmortem examination other than mildly infected navels. Microscopic changes in the hindbrain and spinal cords revealed hypomyelination and white matter degeneration consistent with congenital tremor type AII. Atypical porcine

pestivirus (APPV) was detected by PCR in the central nervous system tissues of each piglet, confirming the diagnosis.

APPV was first described as the cause of congenital tremor type AII in pigs in 2016, in pigs in the United States (US). Until then a viral cause had been suspected but not identified. All cases of congenital tremors submitted to APHA and its partner PME providers since 2016 have, like the one described here, been found to be type AII and associated with APPV infection. In one case there was concurrent porcine circovirus 3-associated disease. More information on APPV can be found on this factsheet, which represents the US situation.

Other types of congenital tremor are caused by classical swine fever (CSF), recessive genes or teratogens. More information about these is provided in a previous surveillance item (Williamson, 2017). A novel pestivirus (termed porcine abortion-associated pestivirus) was recently detected in samples from an outbreak of reproductive disease and congenital tremors in one herd in China in 2023 (Deng and others, 2025).

APPV is endemic in UK pigs and causes outbreaks of congenital tremor type AII without other clinical signs. APPV is frequently diagnosed presumptively, based on the characteristic clinical history and signs alone, with relatively few confirmed through diagnostic submissions to the GB scanning surveillance network. Diagnostic investigation of congenital tremors is particularly important where the clinical presentation is not typical. Crucially, whenever congenital tremor outbreaks are encountered, it is vital to consider whether clinical or other findings give reason to suspect that it could be due to CSF. In contrast to CSF-associated congenital tremors, type AII (due to APPV) usually results in minimal mortality in affected piglets and tremors are much reduced or absent by the time the piglets are weaned. Type AII usually predominantly affects gilt litters, whereas congenital tremors due to CSF virus would affect litters from all ages of sow in CSF-naïve countries. CSF would also usually be associated with concurrent reproductive disease and systemic disease in older growing pigs and adult pigs. Suspicion of CSF must be reported to Defra Rural Services Helpline on 03000 200 301 in England. In Wales contact 0300 303 8268 and in Scotland contact your local Field Services Office.

The epidemiology of APPV infection is not fully understood but most congenital tremor-affected litters are thought to result from *in-utero* infection in early pregnancy, due to acute infection of the sow. In the incident described here, a high proportion of litters born to gilts had been affected previously. It is likely that the small proportion of parity two sows which produced the congenital tremor-affected piglets at their next farrowing represented some of those without previously affected litters. There were no records available to investigate whether this was the case. An alternative but less likely possibility exists, that the parity two sows producing affected litters were themselves persistently infected with APPV. Empirical advice to control congenital tremor type AII in herds has included avoiding keeping replacement breeding stock derived from affected litters. This case emphasises the value in recording which gilts/sows have litters affected with congenital tremors.

Plant toxicities in woodland dwelling pigs

Plant toxicities are occasionally diagnosed in pigs through the GB scanning surveillance network. These occur more commonly in small-scale herds where pigs may be kept in less controlled conditions with access to a more varied environment than outdoor commercial pigs.

Bracken toxicity

Difficulty breathing, vomiting and a seizure-like episode prior to death was described in an eight-month-old rare traditional breed of pig kept on a small outdoor holding. This was the second pig to have died in ten days from a group of three kept in woodland where bracken was present. The pigs were moved every four weeks, vaccinated for erysipelas and fed pig nuts, apples, bread, and cabbage.

Post-mortem examination revealed excess sanguineous thoracic fluid and dark red, oedematous, firm lungs suggestive of heart failure. Histopathology showed myocardial degeneration and necrosis; lesions of this nature are seen in mulberry heart disease as well as toxicities including bracken, selenium, gossypol and ionophore. Clear exposure to bracken (and not other toxins) and the age of the pigs made bracken toxicity the most likely diagnosis.

Bracken (*Pteridium aquilinum*) toxicity is the most common plant toxicity diagnosed in pigs by APHA. It occurs sporadically in extensively-kept pigs with access to bracken, usually following exposure over a prolonged period (Harwood and others, 2007; Payne and Murphy, 2014). As the rhizomes and young leaves contain the most thiaminase (the toxic component of bracken in pigs), the natural rooting behaviour of pigs, as well as access to growing bracken, can predispose pigs to ingestion and toxicity.

Bracken poisoning is reportable to the Food Standards Agency as a potential food safety incident and pigs must be withdrawn from potential exposure to bracken for at least 15 days prior to slaughter for human consumption. More information can be found in an APHA information note.

In this case, concurrent elevated (but not toxic) liver and kidney lead concentrations were also identified. A visit by APHA's toxicology lead established that the pigs were from area with geographical risk factors for lead. APHA is working with the pig keeper to provide advice on future use of pigs to clear land to ensure that pig health and welfare and food safety are safeguarded.

Bluebell toxicity

Seizure-like episodes and vomiting were described in two native breed pigs prior to death. Three pigs died from a group of four that had access to a forest. Pigs had been moved to a different area nine days before onset of signs. Bluebell bulbs (*Hyacinthoides non-scripta*) were found in the area where the pigs had been rooting.

Post-mortem examination of one pig revealed multiple, firm, white, tuberous fragments of varying size, some with filamentous/root-like projections, which resembled pieces of bluebell bulbs in the stomach (Figure 2). No bacterial pathogens were isolated from a range of systemic sites. Histopathology of a range of tissues was unremarkable.

The toxic principles in bluebells are cardiac glycosides; intoxication does not necessarily leave morphological changes in the heart muscle or elsewhere. APHA colleagues have previously described toxicity in pigs following bluebell bulb ingestion, associated with similar gastrointestinal signs, such as vomiting, and cardiac effects (Payne and Murphy, 2014). Given the clinical and post-mortem findings, known exposure and absence of an alternative cause of death, bluebell toxicity was considered the most likely diagnosis in this case.

Figure 2: Tuberous fragments resembling pieces of bluebell bulbs found in the pig's stomach.

Changes in disease patterns and risk factors

Changes in piglet disease due to *Klebsiella pneumoniae* subspecies *pneumoniae*

Three notable findings are described below in relation to disease in piglets caused by *Klebsiella pneumoniae* subspecies *pneumoniae* (*Kpp*).

Sudden death of nine, three-week-old piglets was investigated on a parity one, outdoor breeding herd in December 2024. Piglets submitted to the Bury St Edmunds VIC showed jaundice of the subcutaneous and connective tissues; dark and congested livers; reddened lymph nodes; and red streaking on the cut surfaces of the renal cortices. Milk was present in the stomachs of each piglet, reflecting the sudden deaths described.

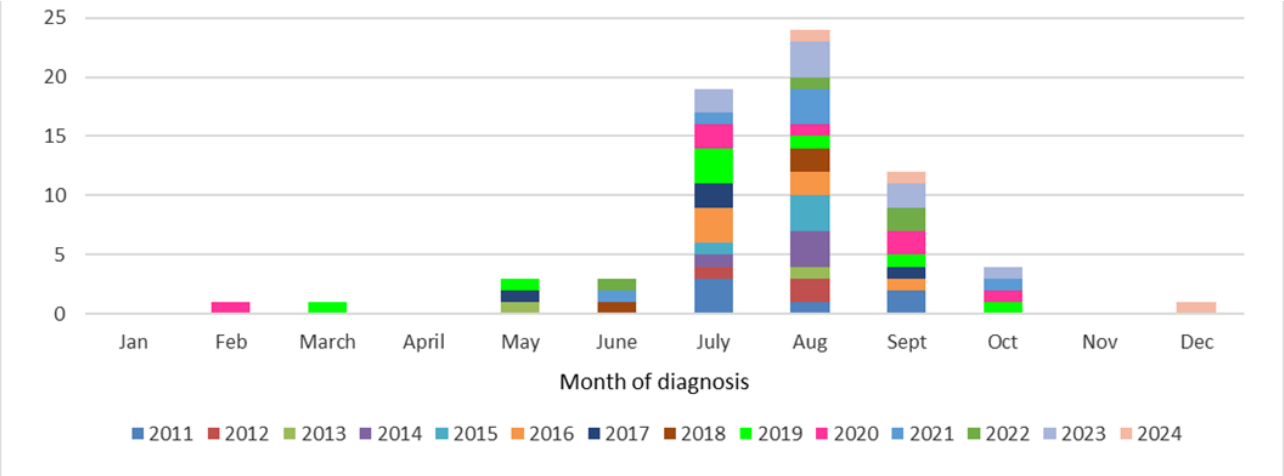
(Kpp) was isolated from the meninges, liver and lung of all piglets, in heavy, pure growth. This fulfils the case definition for a *Kpp* septicaemia outbreak, which is "*pigs found dead with lesions consistent with septicaemia and pure/predominant growths of Kpp isolated from internal sites in multiple pigs*" (APHA, 2016).

Historically, *Kpp* was considered an opportunistic pathogen of pigs, sporadically causing septicaemia or pneumonia in single pigs of any age, or mastitis in sows. In 2011, outbreaks of septicaemia emerged in England in pre-weaned pigs, involving a particular *Kpp* strain: sequence type (ST) 25 (Bidewell and others, 2018; Williamson and others, 2019). These *Kpp* ST25 outbreaks have since occurred annually and show a seasonal pattern, with most cases diagnosed between May and September (Figure 3). This December case represents the first septicaemia outbreak in piglets diagnosed in that month.

The first *Kpp* septicaemia outbreak to have been diagnosed in Scotland was described by SRUC in their recent surveillance report, following submission of three dead two- to three-week-old piglets in September 2024, from a commercial indoor unit (SRUC, 2024). This was also unusual because, historically, most outbreaks have occurred in outdoor breeding herds.

A less common disease manifestation of *Kpp* as meningitis was identified in an individual pig by colleagues at the University of Nottingham partner post-mortem examination provider in November 2024. *Kpp* was isolated from the meninges and liver of a three-week old pre-weaned piglet in heavy, pure growths. Ten of 15 piglets in one litter had died following neurological signs. There was purulent material visible over the meninges grossly and histopathology showed severe inflammation, confirming a diagnosis of severe meningoencephalitis and ventriculitis. As only one piglet was submitted for post-mortem examination, this case did not meet the criteria to fulfil the case definition for a *Kpp* septicaemia outbreak. Sequencing will be undertaken on the *Kpp* isolates associated with the three cases described, to determine whether they involve the emerged *Kpp* ST25 strain.

Figure 3: Outbreaks of Kpp septicaemia in pigs by month of diagnosis within the GB surveillance network, from 2011 to 2024.



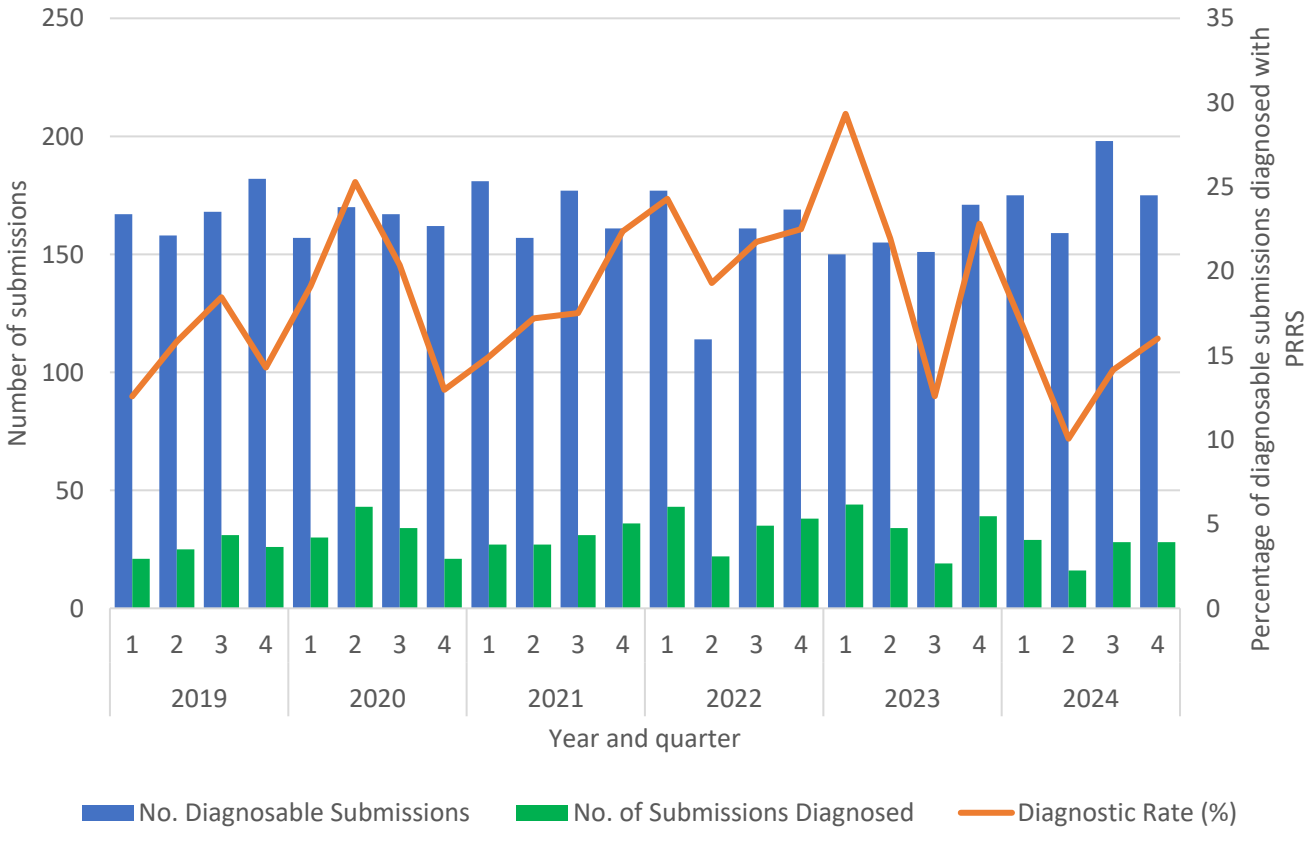
Porcine reproductive and respiratory syndrome virus (PRRS) update

Porcine reproductive and respiratory syndrome (PRRS) remains one of the most significant endemic viral infections in UK pigs. The APHA's interactive PRRS dashboard provides surveillance and diagnostic data from the GB scanning surveillance network for submissions diagnosed with PRRS from 2012 to 2023. All diagnoses made through the GB surveillance network were due to PRRSV-1, with no PRRSV-2 detected in British pigs to date.

The Pig Expert Group recently published an information note on preventing the introduction of exotic PRRSV strains into GB in imported live pigs or semen. A recent publication describes a new scheme for classifying PRRSV-1 strains (Yim-Im and others, 2025) based on the open reading frame (ORF) 5 gene. The lineage of PRRSV sequenced at APHA is now provided in ORF5 gene sequence reports.

The diagnostic rate for PRRS in GB for 2024 was around 14% of diagnosable submissions, which was less than in 2023 (Figure 4). The data underline the importance of PRRS as an endemic pathogen in GB pigs. PRRS is the priority for disease control in the pig component of the Animal Health and Welfare pathway, alongside a focus on biosecurity improvements to control endemic pig diseases and prevent the introduction of exotic disease threats.

Figure 4: Diagnostic rate of PRRS by year and quarter as a percentage of diagnosable submissions to the GB scanning surveillance network.

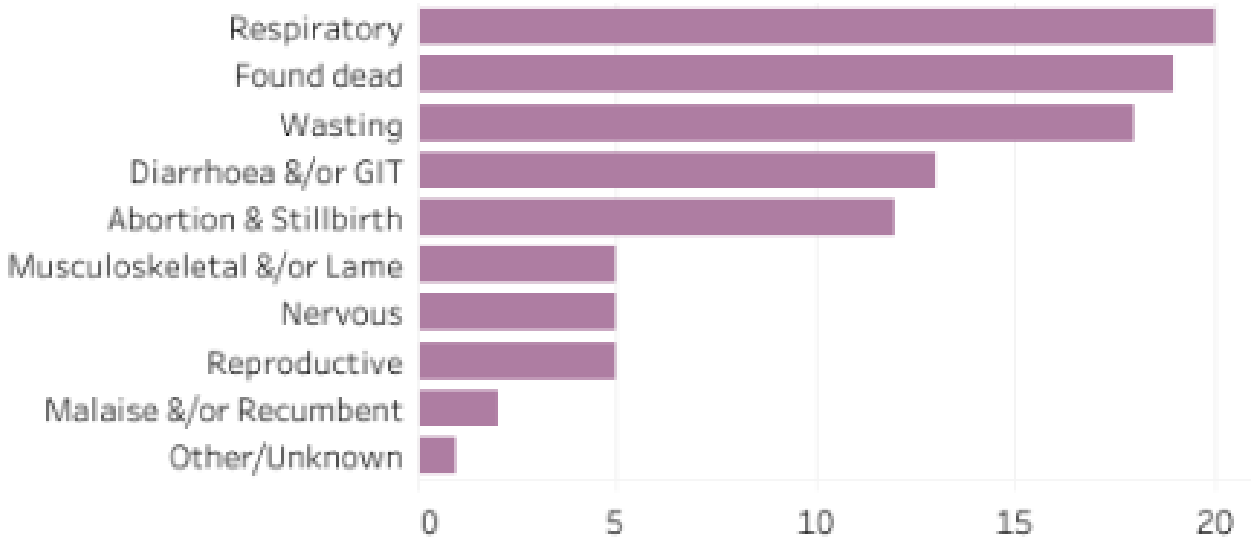


For 2024 submissions, 107 diagnoses of PRRS have been recorded in VIDA to date. Twelve of these related to reproductive disease in breeding pigs and 95 to systemic or respiratory disease. Just under half of diagnoses were made in pigs of four to eight weeks of age (where the age of pigs was provided), which are likely to be post-weaned pigs. This likely reflects the opportunity for PRRSV spread following mixing of pigs at weaning, when pig's maternal immunity is waning and vaccinal immunity, where vaccines are used at or near weaning, is still establishing.

Fifty-five percent of PRRS diagnoses were made in carcase submissions, in which full diagnostic investigation can be undertaken. Concurrent diseases were found in all but six of the 59 diagnoses of systemic and respiratory PRRS made in carcase submissions in the first four quarters of 2024. In contrast, concurrent diagnoses were made in 14 of the 48 non-carcase submissions in which systemic or respiratory PRRS was diagnosed. Swine influenza was diagnosed with PRRS in 15 submissions and was the most common concurrent diagnosis made in 2024. The other most frequent concurrent diagnoses were disease due to *Pasteurella multocida*, *Glaesserella parasuis*, *Mycoplasma hyorhinis* and *Streptococcus suis*. The presence of these additional diseases reflects the immunosuppressive effect of PRRS. This adds to the adverse impact that PRRS has on pig health and welfare and drives antimicrobial use to treat the bacterial infections which result from, or are exacerbated by, PRRS.

The main clinical signs described in submissions in which PRRS was diagnosed in 2024 are shown in Figure 5. Clinical signs may reflect the concurrent diagnoses made, rather than being directly due to PRRS.

Figure 5: Main clinical signs in submissions in which PRRS was diagnosed in 2024.



As part of PRRS surveillance at APHA, ORF5 gene sequencing is undertaken under pig disease surveillance funding on the sample with the lowest Ct value (likely highest viral load) in each PCR-positive submission to APHA. This monitors diversity in the PRRSV detected and checks there have not been introductions of novel genetically diverse

PRRSV-1 strains into the UK. Sequencing completed so far in 2024 has not detected any which suggest a novel introduction. The genetic diversity of the PRRS sequenced continues to evolve and at least 17 different lineages/clades are seen.

Viruses in which the ORF5 gene sequence has 98.5% or greater similarity to one of the live PRRSV vaccines are termed “vaccine-like”. As the ORF5 sequence analysis is based on just 4% of genome, vaccine-like viruses are analysed further by sequencing part of the nonstructural protein 2 (nsp2) to help identify any potential recombinants. No further recombinants have been found since a recombinant PRRSV-1 vaccine (or vaccine-like) and field virus was described in pigs in England (Frossard and others, 2013). All of the other vaccine-like PRRSV examined to date have had nsp2 and ORF5 sequences that are consistent and do not raise concern that they represent potential recombinants.

The proportion of sequenced PRRSV found to be vaccine-like ranged from 22 to 31% in the years 2019 to 2022. In 2023, only 13% of the PRRSV sequenced at APHA were found to be vaccine-like. This may have reflected, in part, issues with the supply of certain live vaccines. Vaccine-like viruses represent 18% of those sequenced so far in 2024.

Pig holding size and pig movements on premises on which PRRS was diagnosed

To improve understanding of the nature of pig holdings on which PRRS was diagnosed in submissions to the GB scanning surveillance network, ten years of data (2014 to 2024) were analysed, alongside pig movement data for each of the premises diagnosed with PRRS.

Two datasets were extracted from the GB scanning surveillance network database – Veterinary Investigation Diagnosis Analysis (VIDA). Data for submissions with a diagnosis of PRRS were extracted from 2014 to October 2024 (inclusive), including herd size data provided by private veterinary surgeons. The same data were extracted for all diagnosable submissions for PRRS, to provide a denominator. The diagnosable submissions for PRRS are those from which PRRS could have been diagnosed.

The pig holdings represented in each of these GB scanning surveillance network datasets were matched to holdings in the Livestock Data Demographics Group (LDDG) pig population dataset, using the CPH and postcode provided for each submission. The LDDG pig population dataset includes the incoming or outgoing pig movements for a holding within a two-year time period and this is used to provide an estimate of holding size. Further information on methodology for how movement data are collected for each holding and how this is used to predict holding size is provided in LDDG reports (APHA, 2024). Descriptions of the five estimated herd size categories based on the numbers of pigs moved are given in Table 2.

Table 2: Estimated herd size categories based on the numbers of pigs moved (APHA, 2024).

Size category of holding	Numbers of pigs moved in 24-month period	Comments
1	1 to 25	Size suggests pet pig owners or small holdings
2	26 to 300	Size suggests small holdings
3	301 to 2,000	Size suggests small commercial farms
4	2,001 to 8,000	Size suggests medium commercial farms
5	8000+	Size suggests large commercial farms

Where exact matches existed, the LDDG estimated holding size category and total number of pigs moved on and off the holding during the two-year period most closely related to the submission were attributed to each scanning surveillance submission. For example, samples submitted in 2014 were matched with the LDDG 2014 to 2015 dataset. LDDG data are available until the period 2022-2023, therefore, 2024 submissions were matched to this most recent time period.

Diagnostic rates for PRRS were calculated for each LDDG pig holding size category by dividing the number of submissions diagnosed with PRRS for each size category, by the number of diagnosable submissions received from each size category. Average size category and total numbers of pigs moved were calculated for the submissions diagnosed with PRRS and compared to the same data for the diagnosable submissions for PRRS. Statistical analysis was completed using t-tests for continuous data and chi-squared tests for categorical data.

A total of 1088 submissions were diagnosed with PRRS from 2014 to October 2024. CPH and postcodes for 51% of submissions diagnosed with PRRS (556) could be matched to an exact holding in the LDDG dataset. This compared to 53% matching (3852) for the diagnosable submissions for PRRS over the same time period. The most common reason for an exact match not being made was that the CPH or postcode was not provided (or was provided in part) by the submitting private veterinary surgeon.

Table 3 and Figure 6 show the number of submissions diagnosed with PRRS, the diagnosable submissions for PRRS and the diagnostic rate, stratified for each LDDG size category (where submissions could be assigned a category). The correlation between LDDG category (excluding unknown LDDG category submissions) and the diagnostic rate for PRRS (shown in Figure 6) was 0.96. Proportionally more submissions from an LDDG 4 or 5 category holding were diagnosed with PRRS than those from an LDDG 1, 2 or 3 holding ($p_{chi\text{-}sq}<0.01$). The diagnostic rate of PRRS was higher for LDDG category 5 farms than each of the other categories ($p_{chi\text{-}sq}<0.01$).

Table 3: Submissions diagnosed with PRRS, diagnosable submissions for PRRS and diagnostic rates, stratified by size category (where a category could be assigned).

LDDG Size Category	Number of submissions diagnosed with PRRS	Number of diagnosable submissions for PRRS	PRRS diagnostic rate (%) with 95% confidence interval
1 (suggests pet pig owner or small holding)	0	123	0% ± 0
2 (suggests small holding)	4	275	1.45% ± 0.09
3 (suggests small commercial farm)	11	207	5.31% ± 0.21
4 (suggests medium commercial farm)	84	532	15.79% ± 0.13
5 (suggests large commercial farm)	457	2715	16.83% ± 0.02
Total 1, 2, 3	15	605	2.48% ± 0.05
Total 4 and 5	541	3247	16.66% ± 0.02
Total all categories	556	3852	14.43% ± 0.02
No category assigned due to no exact CPH/postcode match	532	3365	15.81% ± 0.02
Total all categories and no category assigned due to no exact match	1088	7217	15.08% ± 0.01

Figure 6: Diagnostic rates of PRRS, stratified by size category.

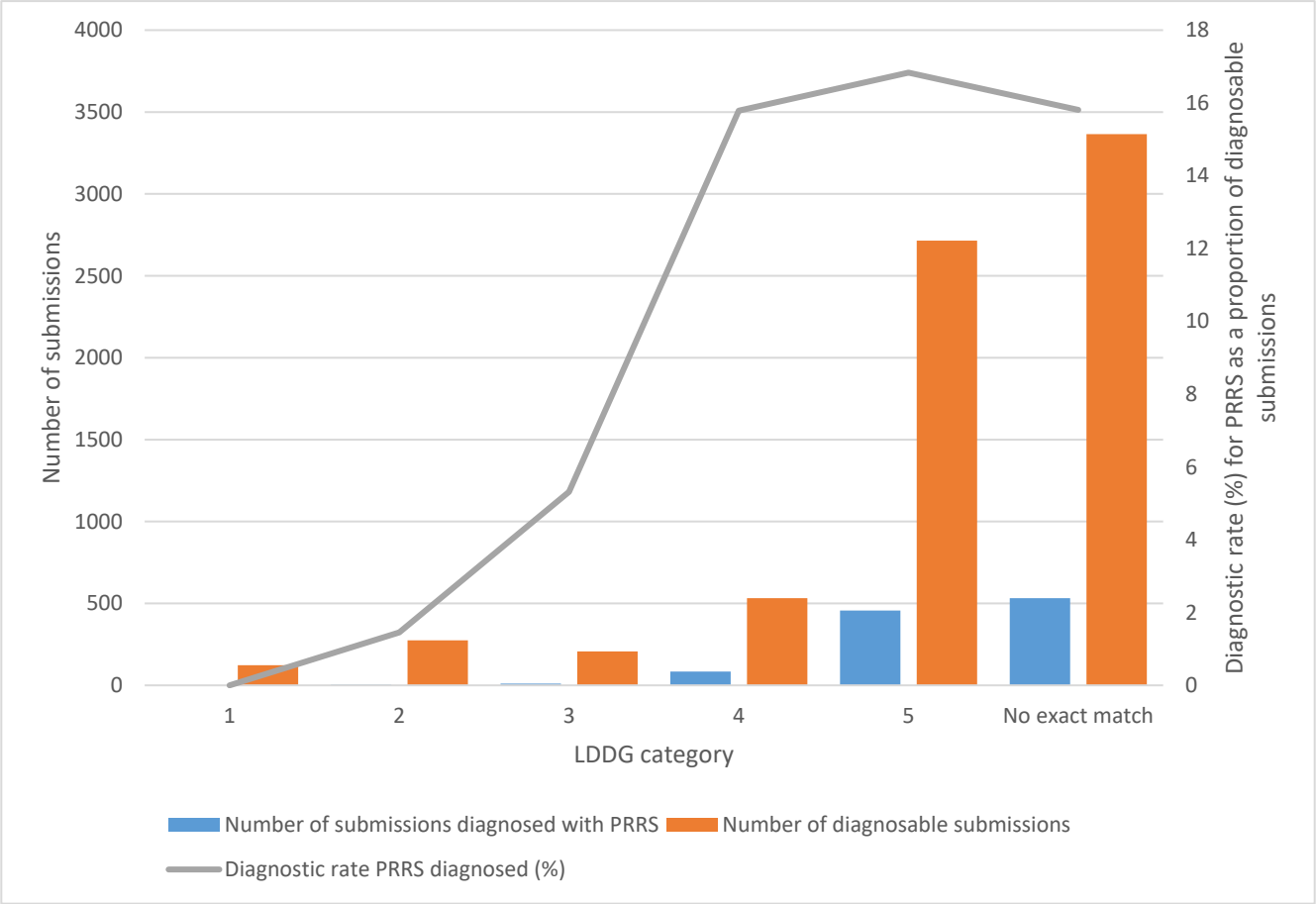


Table 4 shows the means and medians of total pigs moved for submissions diagnosed with PRRS versus the same for diagnosable submissions for PRRS, where the LDDG size category could be matched. The mean total pigs moved for submissions diagnosed with PRRS was significantly greater than the mean for diagnosable submissions ($p_{t\text{-test}}<0.01$).

Table 4: Mean and median total pigs moved for submissions diagnosed with PRRS versus diagnosable submissions for PRRS.

Scanning surveillance submissions	Mean total pigs moved in two-year period with 95% confidence interval	Median total pigs moved in two-year period
Submissions diagnosed with PRRS	43813.36 ± 4166.31	27271
Diagnosable submissions for PRRS	38139.75 ± 1547.62	22628

There is acknowledged bias in scanning surveillance data from which the datasets used for this analysis were extracted. Further, diagnoses of PRRS may be made outside the GB scanning surveillance network. This means that GB scanning surveillance data cannot be used to estimate the prevalence of diseases. The high proportion of submissions which could not be exactly matched to a holding in the LDDG dataset by CPH and postcode reflects missing data that exist for submissions to the GB scanning surveillance network. These missing data may affect the certainty with which conclusions can be drawn in studies such as this and highlights the importance of submitting veterinarians providing complete information during submissions in order to fulfil surveillance goals.

Notwithstanding these limitations, the results of this study show potential value in combining datasets from the GB scanning surveillance network and the LDDG to provide inferences about holdings diagnosed with certain conditions, where prevalence data do not exist. Such analyses could help inform the suitability of proposed interventions and provide an evidence base for policy decisions relating to disease control.

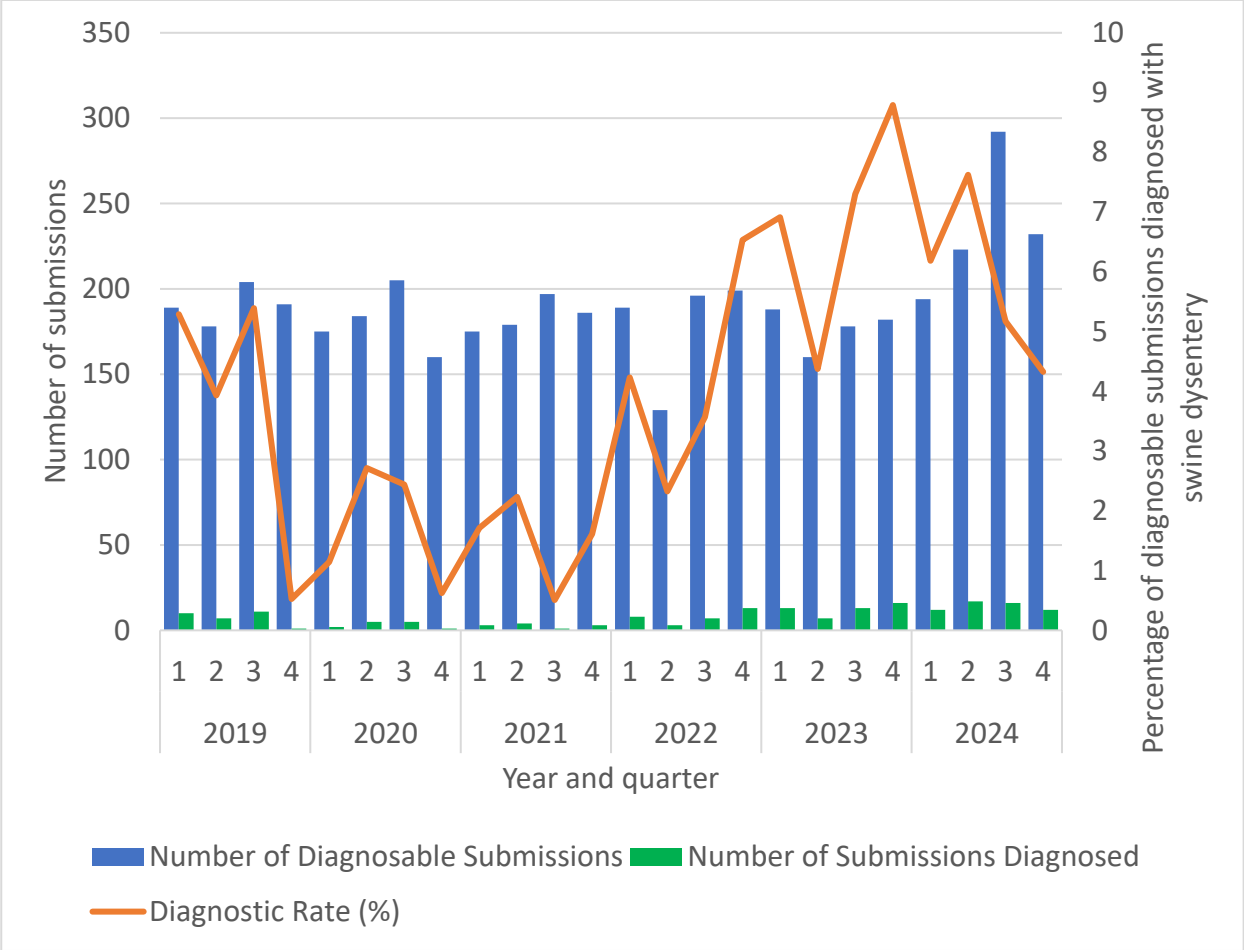
Swine dysentery diagnoses continue in 2024

An upward trend in the number of diagnoses of swine dysentery made through the GB scanning surveillance network (at APHA and SRUC laboratories) was noted from the end of 2021 to the first quarter of 2024. Cases have continued to be diagnosed but at a lower rate during the last three quarters of 2024 (Figure 7). In more recent years, veterinarians have noticed that some confirmed cases have been in pigs showing mild to moderate diarrhoea rather than the muco-haemorrhagic diarrhoea that is typically associated with swine dysentery.

Twelve diagnoses have been recorded to date in VIDA during quarter 4 of 2024. These were made on 10 premises in six counties in GB (East Riding and North Lincolnshire, Essex, Lincolnshire, Norfolk, Northeast Wales, North Yorkshire, Powys, and Surrey). This compares to quarter 3 of 2024 when 14 diagnoses were made on 13 premises in eight counties in GB. These diagnoses can be seen on the interactive GB pig disease surveillance dashboard.

AHDB's webpages on biosecurity and swine dysentery, including the #MuckFreeTruck campaign, contain comprehensive information on appropriate biosecurity before, during and after a visit to a pig holding. Farms which are signed up to the pig industry's Significant Diseases Charter (which is now a requirement for Red Tractor assured farms) must report a diagnosis of swine dysentery to the Charter. Alerts are then issued to participants of the Charter to raise awareness about swine dysentery outbreaks.

Figure 7: Diagnostic rate of swine dysentery by year and quarter as a percentage of diagnosable submissions to the GB scanning surveillance network.



Whole genome sequencing (WGS) and minimum inhibitory concentration (MIC) testing by broth microdilution is undertaken on a representative *B. hyodysenteriae* isolate from a submission from each premises (where successfully isolated and provided to APHA) under funding from APHA's pig disease scanning surveillance project. WGS enables multilocus sequence typing (MLST). MLST is a tool for characterisation of isolates of a bacterial species by analysing sequence data of seven conserved genes in each *B. hyodysenteriae* isolate. This results in a combination of alleles known as a sequence type (ST) for each isolate. The MLSTs of *B. hyodysenteriae* isolates from pigs in GB, as well as the genes or SNPs associated with reduced antimicrobial susceptibility that they possess, are represented on the *B. hyodysenteriae* MLST dashboard.

Table 5 shows the STs identified by WGS completed so far for isolates from submissions to APHA or SRUC in 2024. Fifteen different STs have been identified so far in 2024. One ST (ST 243) was identified for the first time in GB in a March 2024 isolate from pigs.

Each year several novel allelic profiles are identified; these are submitted to the pubMLST database and allocated a new ST. Five novel STs isolated from pigs in 2024 have been identified so far (ST339, 340 and 341, 343 and 347). An isolate was first identified as ST341 in March 2024. Since then, a total of 13 ST341 isolates have been identified,

making ST341 the most frequently identified ST this year. These ST341 isolates originate from eight premises in five counties. None of the isolates tested by MIC to date from this emerging ST341 have shown clinical resistance to antimicrobials licensed for use for treatment of swine dysentery in pigs.

Figure 9 shows that the number of different STs identified by the GB scanning surveillance network is higher in 2024 than in each of the previous three years. The number of STs newly detected (either novel or first detection of a known ST) in GB was also higher in 2024. The reason for this is not known and trends will be kept under review.

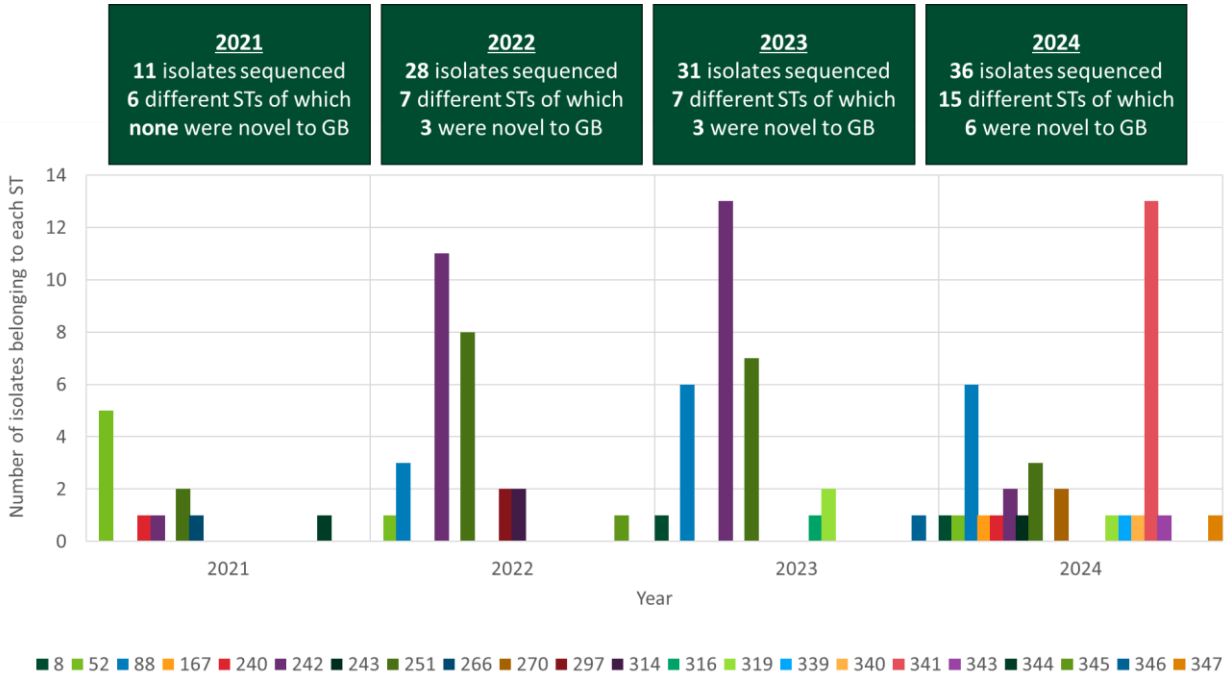
In recent years (2020 onwards), one particular ST (ST251) has been associated with multi-drug resistance, including clinical resistance to tiamulin. Three ST251 isolates have been identified so far in 2024, all of which originated from the same holding. MIC testing of one of these isolates showed clinical resistance to tiamulin, doxycycline and tylosin. The second isolate showed clinical resistance to tiamulin, lincomycin and tylosin and the third isolate showed clinical resistance to tiamulin and tylosin.

Apart from these ST251 isolates, only one other isolate (ST167) has shown clinical resistance to tiamulin and clinical resistance to licensed antimicrobials does not appear to be a main factor behind the upward trend in swine dysentery diagnoses since 2021. The ST167 isolate was identified associated with a weakly haemolytic variant of *B. hyodysenteriae*. The haemolytic activity of *B. hyodysenteriae* is considered contributory to virulence *in vivo* (Card and others, 2019). Weakly haemolytic *B. hyodysenteriae* isolates have been detected sporadically in GB between 2008 and 2024. STs associated with weakly haemolytic isolates have mostly been ST167. They have also been reported in Europe (Card and others, 2019); European weakly haemolytic isolates were different STs from ST167 and their core genomes were very different from those in GB pigs (>7000 single nucleotide polymorphisms, SNPs).

Table 5: Sequence types of *Brachyspira hyodysenteriae* isolates detected so far in submissions received in 2024. *Note that further STs from 2024 may be identified as more isolates are sequenced from this time period.*

ST identified	Number of isolates	Counties of origin in 2024	ST identified in UK isolates prior to 2024
8	1	East Riding and North Lincolnshire	Yes
52	1	Devon	Yes
88	6	East Riding and North Lincolnshire and North Yorkshire	Yes
167	1	East Riding and North Lincolnshire	Yes
240	1	North Yorkshire	Yes
242	2	East Riding and North Lincolnshire and North Yorkshire	Yes
243	1	Derbyshire	No (previously identified in Europe)
251	3	East Riding and North Lincolnshire	Yes
270	2	Essex	Yes
319	1	Northumberland	Yes (first detection 2023)
339	1	Fife	No
340	1	Norfolk	No
341	13	Norfolk, Suffolk, Northumberland, Tyne and Wear, Worcestershire	No
343	1	Essex	No
347	1	Norfolk	No

Figure 9: Details of *Brachyspira hyodysenteriae* isolate STs detected so far in submissions made from 2021 to 2024. 'Partial' ST matches have been allocated to the most closely matched ST.



Horizon scanning

Publications evidence vertical transmission of Seneca Valley virus

Two recent papers describe some evidence which supports vertical transmission of Seneca Valley virus (SVV). In the first, Kim and others (2024) inoculated five sows in late gestation with a strain of SVV which had produced vesicular lesions in eight-month-old gilts in a separate study. All sows showed evidence of virus replication and seroconverted, only one developed a vesicular lesion. Viraemia and antibody were detected in piglets prior to ingesting colostrum, from one sow infected with SVV ten days pre-farrowing, suggesting transplacental SVV infection in this litter. No vesicular lesions were noted in any of these piglets, or others in the study.

In the second paper, Schaefer and others (2024) provide evidence of vertical transmission of SVV in naturally infected sows in a pig herd which had experienced an SVV outbreak five years earlier. In this later outbreak, sows were viraemic with vesicular disease at the point of farrowing. Piglets were viraemic (with high viral loads) within 24 hours of birth, at which time approximately 25% of piglets also had vesicular lesions. Possible sources of SVV infection for piglets included *in-utero* infection, the birth canal, colostrum, the sow or the environment. The early viraemia and vesicular lesions in new-born piglets supports congenital/vertical transmission as most likely. Whilst the researchers were not able to

sample piglets before colostral intake, the fact that viral loads were highest in the samples taken within 24 hours of birth also supports congenital/vertical transmission.

It should be noted that there have been no SVV vesicular disease cases in GB during 2023 or 2024 and none to date in 2025. Also, vesicular disease in piglets was not a feature of the clinical SVV outbreaks in England in 2022 which affected breeding pigs (APHA, 2022).

Foot and Mouth Disease in Germany and Hungary

APHA's International Disease Monitoring (IDM) team have published a preliminary outbreak assessment after Germany reported Foot and Mouth Disease (FMD) in one herd of buffalo in Märkisch-Oderland on 10 January 2025. The risk level for incursion of FMD to the UK was increased to medium. The commercial import of cattle, pigs, sheep, deer, buffaloes and their products such as meat, and dairy from Germany was banned. Travellers were also prevented from bringing unpackaged meat, meat products, milk and dairy products, certain composite products and animal by products of pigs and ruminants into GB from the European Union, European Free Trade Association states, the Faroe Islands and Greenland.

On 07 March 2025, the UK government announced a ban on commercial imports of susceptible species of live animals and their untreated products from Hungary and Slovakia, following a confirmed case of FMD in the northwest of Hungary, near the border with Slovakia. In addition, as of 08 March, travellers were prevented from bringing meat, meat products, milk and dairy products, certain composite products and animal by products of pigs and ruminants, or hay or straw, from Hungary and Slovakia to GB. Livestock keepers were reminded of the need to practice stringent biosecurity, remain vigilant to the clinical signs of notifiable diseases and report suspicion immediately by calling the Defra Rural Services Helpline on 03000 200 301. In Wales, contact 0300 303 8268 and in Scotland, contact your local APHA Field Services Office. For up to date information on notifiable diseases in animals, including disease controls, visit .GOV.UK.

African swine fever

Comprehensive information on African swine fever (ASF) in Europe and Asia is available from several sources. African swine fever (ASF) update assessments are published by APHA's International Disease Monitoring (IDM) team on GOV.UK. The most recent update for Europe was published in July 2024 (Defra and APHA, 2024), although the situation has developed since this update. Monthly IDM summaries are also included in the disease surveillance items in the Veterinary Record.

European Commission information is accessed here and maps are available showing the current European Union (EU) ASF restriction zones. The Food and Agriculture Organisation (FAO) Emergency Prevention System for Animal Health (EMPRES-AH) produces regular ASF disease situation updates for ASF in Asia and the Pacific. The

Swine Health Information Centre (SHIC) global reports includes a detailed round-up of ASF in their global disease monitoring report each month.

Several pig media articles on aspects of ASF in have been published. Articles include those describing ASF outbreaks in Sri Lanka, vaccination use for ASF in the Philippines and successful eradication in Sweden. The Agriculture and Horticulture Development Board (AHDB) issued a reminder to pig producers in England of the threat of ASF to the national pig herd. AHDB offers resources for ASF contingency planning, including webinars, workshops, podcasts and advice on contingency planning.

EU member states are restricted from exporting pork products from regions impacted by ASF without mitigating measures, such as heat treatment (Defra and APHA, 2024). A significant recent development was the introduction of new measures on 27 September 2024 to restrict personal imports of pork and pork products from the EU single market area to GB, unless produced and labelled to EU commercial standards. No personal imports of unpackaged pork and pork products are permitted and the personal allowance of commercially produced and labelled goods is limited to 2kg (Defra, 2024). Additional restrictions on products of animal origin are currently in place in response to the foot and mouth disease outbreak detected in Germany as described above.

Given the risk that illegally imported porcine meat and products pose, it is crucial that pig keepers strictly adhere to legislation around pig feeding under which it is illegal to feed catering waste of any description or domestic food waste to farm animals in the UK. This includes waste from a vegan domestic kitchen and covers pigs kept as pets.

A helpful on-line guide, with images of the clinical signs and pathology of ASF, can be distributed to veterinarians and pig keepers. This notes that, at the start of an outbreak, deaths may initially just involve one or two pigs. Significantly increased mortality may only develop later once the virus has spread further in the herd.

Veterinarians and pig keepers must show vigilance and be familiar with the clinical signs of the swine fevers. ASF is a notifiable disease, meaning that suspicions must be reported immediately. In England, this is by calling the Defra Rural Services Helpline on 03000 200 301. In Wales, contact 0300 303 8268 and in Scotland, contact your local APHA Field Services Office.

Contact

Editors: Claire Scott, Susanna Williamson

Address: APHA, Bury St Edmunds

Telephone: + 44 (0) 2080 264990

Email: Claire.scott@apha.gov.uk, susanna.williamson@apha.gov.uk

References

APHA (2022). Great Britain pig quarterly report: disease surveillance and emerging threats. Volume 26: Quarter 2 of 2022 (April to June). https://assets.publishing.service.gov.uk/media/63331d2d8fa8f51d1f8339a1/2022_Q2_Pigs_final.pdf.

APHA (2024). Livestock Demographic Data Group: Pig population report. Livestock population density maps for Great Britain, using 2022 to 2023 data. https://assets.publishing.service.gov.uk/media/674f2908d7e2693e0e47d02f/LDDG_Pig_Population_data_2022-23_published_2024-25_v3_Final.pdf.

Card, R. M., et al. (2019). Weakly haemolytic variants of Brachyspira hyodysenteriae newly emerged in Europe belong to a distinct subclade with unique genetic properties. *Veterinary research* **50**: 1-13. https://doi.org/10.1186/s13567-019-0639-x.

Defra (2015). Porcine epidemic diarrhoea: how to spot and report the disease. http://www.gov.uk/guidance/porcine-epidemic-diarrhoea-how-to-spot-and-report-the-disease.

Defra (2024). OVS NOTE 2024/43 - Increased restrictions on personal imports of pork and pork products from the EU. https://assets.publishing.service.gov.uk/media/67b4b754b56d8b0856c2fe85/ovs-note-2024-43.pdf.

Defra and APHA (2024). African swine fever in pigs and wild boars in Europe. Retrieved 2nd December 2024, https://www.gov.uk/government/publications/african-swine-fever-in-pigs-and-boars-in-europe.

Deng, L., et al. (2025). Emergence of a novel porcine pestivirus with potential for cross-species transmission in China, 2023. *Veterinary research* **56**(1): 32 DOI: https://doi.org/10.1186/s13567-025-01472-5.

Frossard, J.-P., et al. (2013). Porcine reproductive and respiratory syndrome virus: genetic diversity of recent British isolates. *Veterinary Microbiology* **162**(2-4): 507-518. https://doi.org/10.1016/j.vetmic.2012.11.011.

Harwood, D., et al. (2007). Suspected bracken poisoning in pigs. *The Veterinary Record* **160**(26): 914 DOI: https://doi.org/10.1136/vr.160.26.914-c.

Kim, H., et al. (2024). Experimental Seneca Valley virus infection in sows and their offspring. *Veterinary Microbiology* **289**: 109958 DOI: https://doi.org/10.1016/j.vetmic.2023.109958.

Payne, J. and A. Murphy (2014). Plant poisoning in farm animals. *In Practice* **36**(9): 455-465 DOI: https://doi.org/10.1136/inp.g6148.

Schaefer, R., et al. (2024). Evidence of vertical transmission of Senecavirus A in naturally infected sows. *Virology* **600**: 110248 DOI: https://doi.org/10.1016/j.virol.2024.110248.

Scottish Government (2016). The Specified Diseases (Notification) Amendment (Scotland) Order 2016. http://www.legislation.gov.uk/ssi/2016/41/contents/made.

Williamson, S. (2017). Congenital tremor associated with atypical porcine pestivirus. *VetRecord* **180**(2): 42-43 DOI: https://doi.org/10.1136/vr.j121.

Yim-Im, W., et al. (2025). Refining genetic classification of global porcine reproductive and respiratory syndrome virus type 1 (PRRSV-1) and investigating their geographic and temporal distributions. *Veterinary Microbiology*: 110413 DOI: https://doi.org/10.1016/j.vetmic.2025.110413.

Data Protection:
For information on how we handle personal data visit www.gov.uk and search Animal and Plant Health Agency Personal Information Charter.

This publication is available at www.gov.uk/government/publications

Any enquiries regarding this publication should be sent to us at:

Claire.scott@apha.gov.uk, Susanna.williamson@apha.gov.uk

APHA is an Executive Agency of the Department for Environment, Food and Rural Affairs and also works on behalf of the Scottish Government, Welsh Government and Food Standards Agency to safeguard animal and plant health for the benefit of people, the environment and the economy.