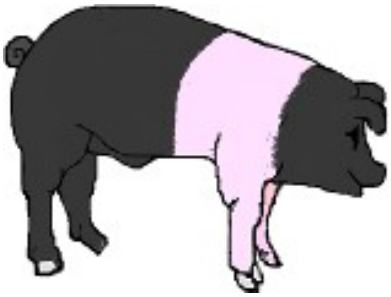
Animal & Plant Health Agency



SRUC

Great Britain pig quarterly report: disease surveillance and emerging threats

Volume 29: Quarter 2 of 2024 (April to June)

Highlights

Contents

Introduction and overview

This quarterly report reviews disease trends and disease threats for the second quarter of 2024, April to June. It contains analyses carried out on disease data gathered from APHA, Scotland's Rural College (SRUC) Veterinary Services and partner post-mortem providers and 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. A full explanation of how data are analysed is provided in the annexe available on GOV.UK.

Pig disease surveillance dashboard outputs

Diagnoses made most frequently in the second 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 records for submissions made in quarter 2 of 2024 which are finalised at a later date. These can be interrogated further using the interactive pig disease surveillance dashboard which was launched in October 2017. Surveillance data for diagnostic submissions in quarter 2 of 2024 are illustrated in Figures 1a-1d.

These diagnostic submissions are voluntary and subject to several sources of bias. The profile of submissions for the second 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. However, enteric disease was more prominent compared to other syndromes in quarter 2 of 2024 compared to the same quarter in 2023.

As noted in the quarterly reports for the last two quarters (APHA, 2023a; APHA, 2024a), total GB diagnostic submissions in this quarter have increased compared to the same quarter in previous years (2020-2023) and total submissions are 37% higher than the average for these previous quarters. This increase is primarily due to a rise in non-carcase submissions with the balance of submission types changing from being 32% carcases in quarter 2 of 2023 to 26% carcases in quarter 2 of 2024, which is the same balance as in quarter 1 of 2024.

The throughput of non-carcase submissions to the GB scanning surveillance network in quarter 2 of 2024 increased by 51% compared to the average for quarter 2 in the previous four years (2020-2023), while the throughput of carcase submissions in quarter 2 of 2024 was the same as the average for quarter 2 in the previous four years.

Changes in the number of submissions and the balance of sample type 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 380

diagnoses were made in quarter 2 of 2024 compared to 280 diagnoses in quarter 2 of 2023 and the most common are shown in Table 1.

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 to discuss investigations with Veterinary Investigation Officers at APHA and SRUC.

Table 1: Great Britain scanning surveillance 15 most frequent diagnoses in quarter 2 of 2024 and for the same quarter in 2023

15 most frequent diagnoses in quarter 2 of 2024 (total 380)	15 most frequent diagnoses in quarter 2 of 2023 (total 280)
1. Colibacillosis - enteric	1. Salmonellosis – *S*. Typhimurium
2. Salmonellosis – *S*. Typhimurium	2. PRRS-1 - systemic
3. *Brachyspira pilosicoli* colitis	3. *Brachyspira pilosicoli* colitis
4. *Lawsonia* sp. associated disease	4. PRRS-1 - pneumonia
5. *Streptococcus suis* disease	5. *Lawsonia* sp. associated disease
6. Swine dysentery – *B. hyodysenteriae*	6. *Streptococcus suis* disease
7. *Glaesserella parasuis* disease	7. Colibacillosis - enteric
8. Porcine reproductive and respiratory syndrome (PRRS) - systemic	8. Streptococcal disease (non-*S. suis*)
9. Swine influenza	9. Swine influenza
10. Rotavirus	10. *Glaesserella parasuis* disease
11. Arthritis other cause	11. Digestive disease – not listed
12. Pneumonia other cause	12. Swine dysentery – *B. hyodysenteriae*
13. Erysipelas	13. Streptococcal meningitis
14. Intestinal volvulus or torsion	14. *Trueperella pyogenes* infection
15. Streptococcal meningitis	15. Systemic disease – not listed

Figures 1a to 1d: summary surveillance data for 581 submission records in quarter 2 of 2024 (462 in quarter 2 of 2023)

Figure 1a: pig age

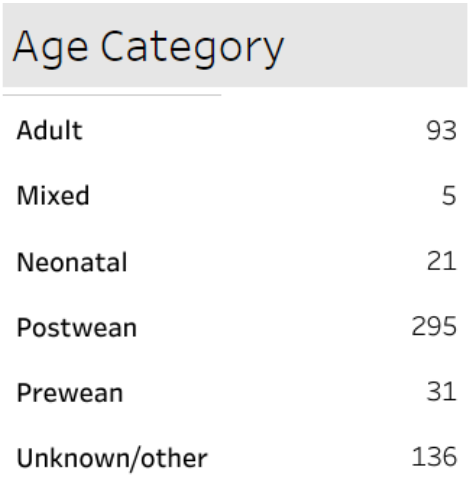


Figure 1b: disease syndrome

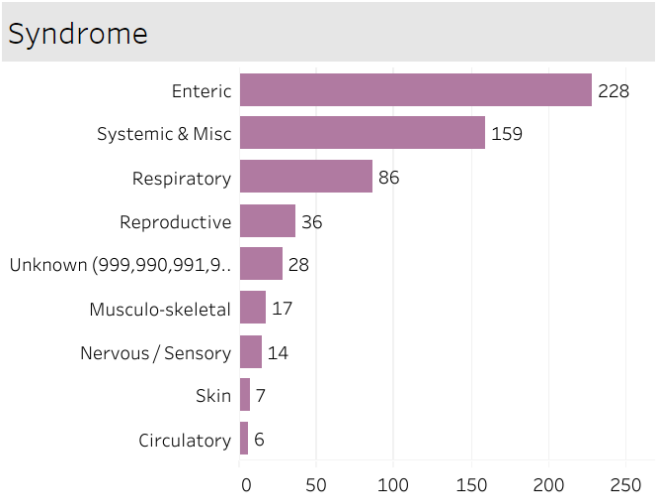


Figure 1c: submission type

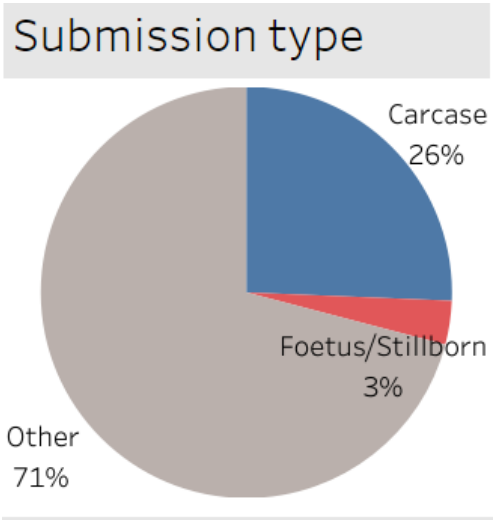
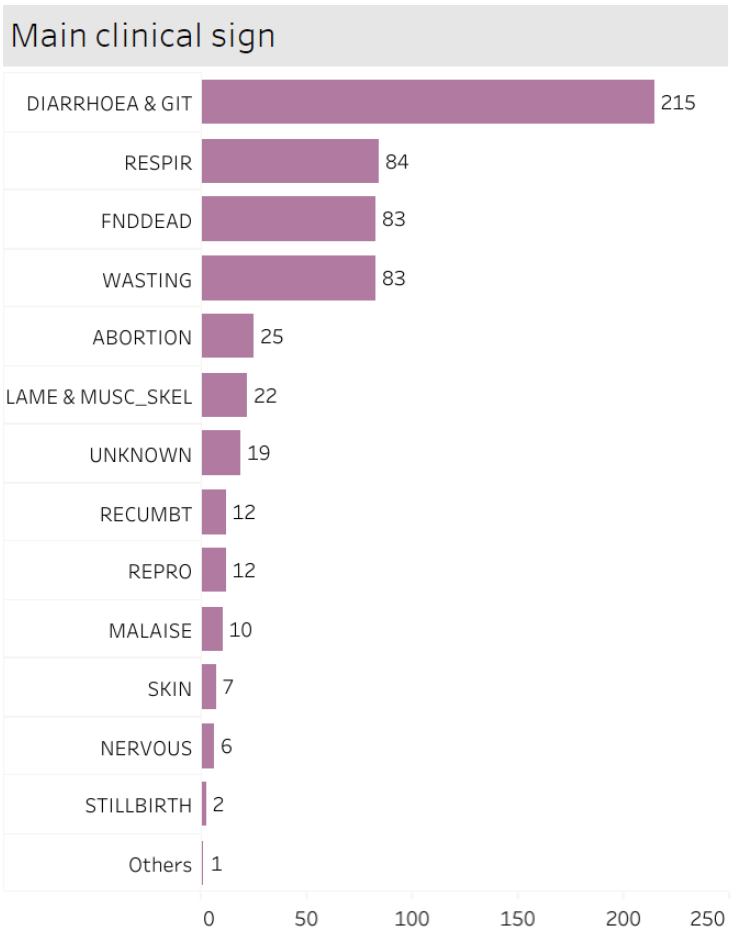


Figure 1d: main clinical sign reported



New and re-emerging diseases and threats

African swine fever summary update

African swine fever (ASF) update assessments continue to be published by APHA's International Disease Monitoring (IDM) team on GOV.UK. The most recent update for Europe was published in July 2024 (Defra 2024a), although the situation is quickly developing.

Since mid-June 2024, cases of ASF have been reported in wild boar in the state of Hesse in West Germany, which neighbours the highest pig-producing state (North Rhine-Westphalia) in Germany. In early July 2024, the first domestic pig outbreak was found on a small pig-keeping premises in the same area of Hesse as the infected wild boar were found. Three more domestic pig outbreaks were detected in the same area during July 2024. Spread into the state of Rhineland-Palatinate also occurred in wild boar, with five infected wild boar reported from mid-June to July 2024.

ASF outbreaks in domestic pigs have continued to be reported elsewhere in Europe, with countries including Croatia, Latvia and Lithuania reporting their first outbreaks of ASF in domestic pigs in 2024.

ASF outbreaks have also continued in Northern Italy, despite measures applied in addition to those required by the zonal regulations and movement restrictions. Up until the publication of IDM's previous report in mid-June 2024 (Defra 2024b), ASF in Northern Italy had been confined to wild boar only in 2024. From the end of July 2024 to August 2024, there has been over 23 outbreaks in domestic pigs. The edge of the restriction zone in northern Italy is less than 30km from the border of Switzerland. Some domestic pig outbreaks have been confirmed through surveillance testing either prior to movement to slaughter or through passive surveillance testing of dead pigs, not reported as suspect ASF. Wild boar cases of ASF have also been confirmed in Tuscany for the first time.

ASF has continued to be reported across Asia in domestic pigs and wild boar. The number of reports of ASF has increased in the Philippines, Vietnam, India and South Korea. As described in IDM's recent outbreak assessment for Asia (Defra 2024c) and described in the quarterly report for the last quarter (APHA 2024a), a new variant of ASF has been discovered in domestic pigs across six provinces in northern Vietnam, which is a recombinant virus with features of both genotype I and genotype II. There are two live-attenuated ASF vaccines available in Vietnam, neither of which are effective against the new recombinant strain.

Maps showing information on the European Union (EU) ASF restriction zones are available. Monthly IDM summaries are also included in the disease surveillance items in the Veterinary Record. The Swine Health Information Centre (SHIC) global reports include a round-up of ASF each month.

A report was published on the survival of ASF in feed, bedding materials and mechanical vectors (Blome and others 2024). The report found that infectious virus could only be detected in a few samples (notably beet and potatoes) for several weeks following contamination, at cool temperatures.

The most likely risk of entry of ASF into GB is considered to be through human-mediated pathways and moving porcine products of animal origin. This risk was highlighted for France by the department of agriculture in Paris, who issued warning to those visiting France for the Olympic and Paralympic Games, to take precautions to prevent ASF from entering the country.

EU member states are restricted from exporting pork products from regions impacted by ASF without mitigating measures, such as heat treatment (Defra 2024b). Given the risk that porcine products of animal origin may pose, it is crucial that pig keepers demonstrate strict adherence to legislation around pig feeding. Further, veterinarians and pig keepers must show vigilance to recognise and report clinical suspicions of ASF. Veterinarians are well placed to ensure that keepers are aware of the legislation around pig feeding, including that it is illegal to feed catering waste of any description or domestic food waste to farm animals in the United Kingdom (UK). This includes waste from a vegan domestic kitchen and also covers pigs kept as pets. For the clinical signs of ASF, a helpful guide with images that can be consulted and distributed to pig keepers can be found online.Keep in mind that, at the start of an outbreak, deaths may initially only involve one or two pigs. Significantly increased mortality may only occur once the virus has spread through the herd.

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.

Streptococcus suis disease in negated swine fever case

A small group of eight-week-old pigs were visited for clinical inspection by an APHA vet, after being placed under restriction due to having had access to food scraps from people. On inspection, one of the pigs was pyrexic, depressed, tachypnoeic and recumbent; the pig subsequently died. Given the feeding history, high fever and non-specific clinical signs, the vet reported the pig as suspicious for swine fevers and an official investigation was undertaken. Samples tested negative for African and classical swine fevers and notifiable disease was ruled out within 24 hours.

Once restrictions were lifted, the dead pig was submitted for diagnostic investigation at an APHA Veterinary Investigation Centre. Gross pathology was non-specific but suggested the pig died in lateral recumbency and may have had nervous signs including paddling before death. A smear from the meninges tested positive for *Streptococcus suis* serotype 2 by fluorescent antibody testing and this serotype of *S. suis* was isolated in culture from

the meninges, confirming a diagnosis of streptococcal disease. Histopathological changes in the brain were consistent with a diagnosis of streptococcal meningitis.

Bacterial septicaemia is a differential for the swine fevers in pigs of this age. As in this case, suspicion of swine fevers in pigs must be reported promptly for official investigation. Further description of this case can be found in the April 2024 'disease surveillance in England and Wales' report, which is published in the Vet Record (APHA 2024b).

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 and 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 1600 diagnostic submissions tested under Agriculture and Horticulture Development Board (AHDB) Pork funding from June 2013 to June 2024.

This enhanced surveillance has included testing for porcine deltacoronavirus (PDCoV) since February 2023 under the same funding and no PDCoV has been detected 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 a potential threat to pig health and welfare. The last diagnosis of PED and of TGE recorded in the GB national diagnostic database (VIDA) was in 2002 and 1999, respectively.

PDCoV has not been detected in the UK to date. A paper was published describing PDCoV occurrence in breeding herds in the United States (US), since its emergence in 2014. Kikuti and others 2024 analysed reporting data from a median of 1166 pig herds provided by the Morrison Swine Health Monitoring Project, for which participation is considered to represent over 60% of the US breeding herd. These authors found that the number of cases peaked in winter and incidence ranged from 0.44% in 2017 to 4.28% in 2023.

Unusual diagnoses or presentations

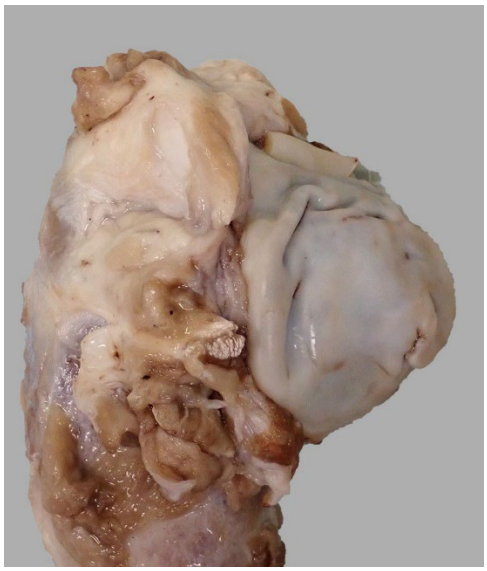
Nutritional osteodystrophy in finishing-age pigs

Severe, chronic lameness affecting a group of eight-month-old male pigs kept outdoors was described on a small-scale pig farm. Pigs were being fed a homemade ration of peas and beans with no extra supplementation.

Two pigs whose clinical signs had progressed to recumbency were euthanised and submitted to Shrewsbury VIC. Postmortem examination revealed soft, flexible, weak bones; severe articular deformities; and healing fractures. In one pig, the right femoral head fractured from the shaft during disarticulation of the hip joint. Histopathology identified severe and chronic dystrophic changes consistent with nutritional osteodystrophy. One pig showed severe pitting and marked deformation of the articular epiphyseal cartilage complex of the humeral head (Figure 2). Biochemistry of bone and liver from both pigs reflected the multifactorial and complex nature of nutritional bone disease with overlapping aetiopathogeneses. Bone ash, calcium and phosphorus levels were low for this age of pig; copper levels in the liver were indicative of hypocuprosis.

Ensuring the welfare of the remaining pigs and the importance of feeding a balanced diet – especially to growing pigs – was highlighted to the submitting vet, who addressed these issues with the owner. This case was described in the August 2024 ‘disease surveillance in England and Wales’ report, which is published in the Vet Record (APHA 2024c). This case resembles a previous one where pigs in a small herd were fed a deficient home-mix diet, which was described in the quarter 1, 2015, pig quarterly report (APHA 2015).

Figure 2: Humeral head of a pig with nutritional osteodystrophy showing marked deformation of the articular cartilage

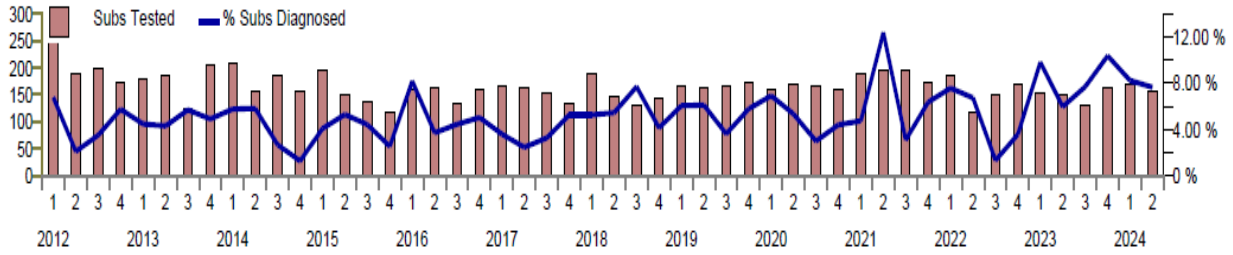


Changes in disease patterns and risk factors

Detections of swine influenza H1N1 clade 1C.2.2

Twenty-seven diagnoses of swine influenza were recorded in VIDA in the first six months of 2024, similar to the same period in 2023 during which 24 diagnoses were made. The rise in diagnostic rate described in quarter 4 of 2023 (APHA, 2023b) did not continue (Figure 3).

Figure 3: Diagnostic rate of swine influenza by year and quarter as a percentage of diagnosable submissions to the Great Britain scanning surveillance network



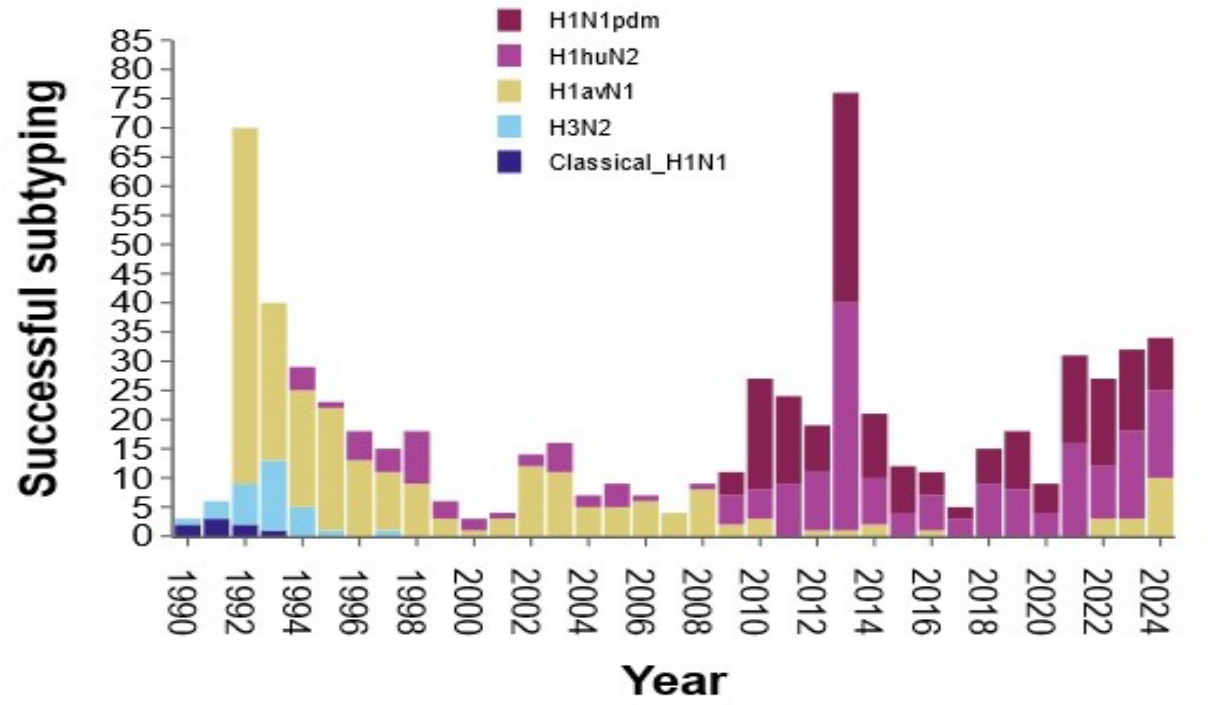
Pigs with respiratory disease in the UK can be tested for swine influenza virus at no charge to the submitting veterinarian through the Government-funded swine influenza surveillance project at APHA. Details on how to access this testing can be found online.

Samples are initially tested for the presence of influenza A Matrix (M) gene RNA. Following a positive detection, molecular assays are applied to determine the hemagglutinin (HA) and neuraminidase (NA) subtype of swine influenza A virus (SwIAV). This is useful for veterinarians considering vaccination of pigs and may help investigation of epidemiological links.

The SwIAV subtypes identified as endemic in GB pigs remain pandemic 2009 H1N1 (clade 1A.3.3.2) and H1huN2 (clade 1B.1.1) and, less frequently, H1N1 (clade 1C.2.2 or Eurasian avian-like) viruses that have been enzootic in pigs in Europe for over 40 years. The clade 1C H1N1 viruses had been detected at a lower frequency in GB since 2009 and were reassortants incorporating gene segments from pandemic 2009 H1N1 viruses.

However, in GB submissions since 2022, 1C H1N1 detections have been more frequent (Figure 4) and these viruses have been detected in most of the recent quarters, mainly from pigs in northern England. In this quarter, SwIAV reassortants have been detected that incorporate an HA from the Eurasian-avian 1C.2.2 clade and N1 commonly paired with this HA. Interestingly, the remaining gene segments in these reassortant viruses originate from H1N1 clade 1A.3.3.2 (pandemic 2009) viruses, except for the M gene segment, which is phylogenetically related to M gene segments from the original Eurasian-avian-like (1C) viruses circulating in Europe.

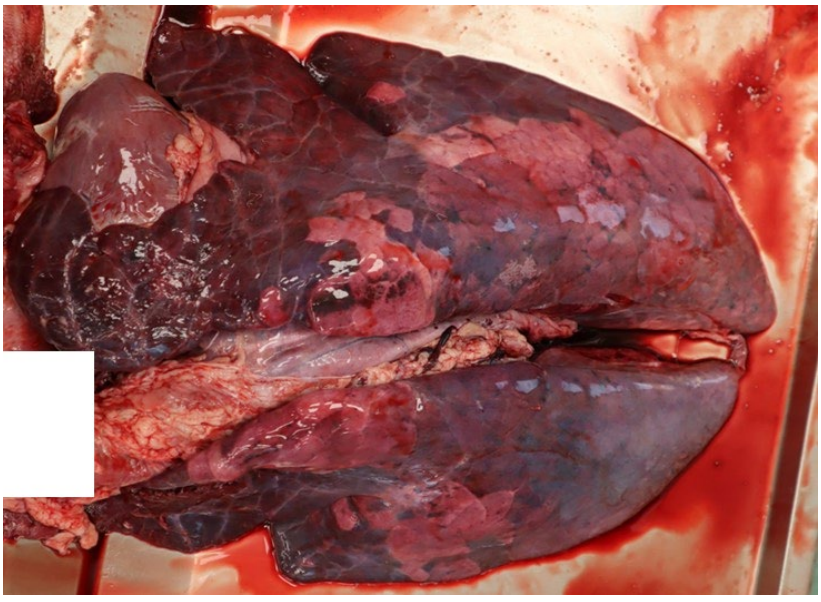
Figure 4: Swine influenza subtypes identified in Great Britain by year through scanning surveillance



It is worth noting that Figure 4 shows only those SwIAV detections in which the full subtype was successfully identified, thus these numbers do not represent the numbers of diagnoses or detections each year.

A severe outbreak of influenza in breeding gilts was described in the June 2024 surveillance report in the Veterinary Record (APHA 2024d). Secondary bacterial infection with *Streptococcus dysgalactiae* subspecies *equisimilis* was also identified and was likely to have influenced the severity of clinical disease (Figure 5).

Figure 5: Lungs of a sow in which active swine influenza virus and Streptococcus dysgalactiae subspecies equisimilis were detected



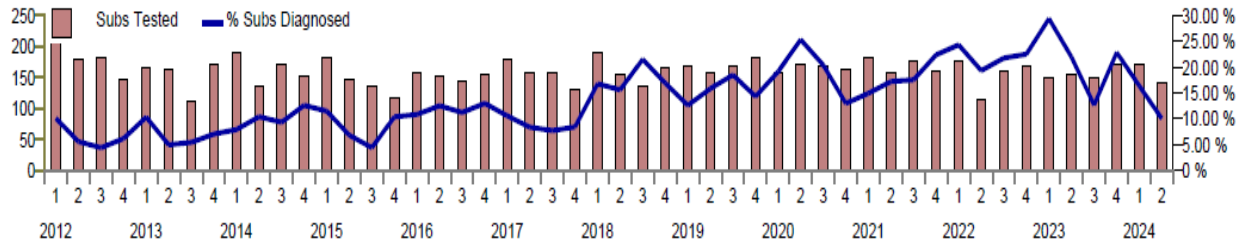
Subtyping identified human-like H1N2 swine influenza virus. As this subtype was included in one of the swine influenza vaccines used in the group of gilts, it was recommended that the incident be reported as a vaccine failure to the Veterinary Medicines Directorate.

A recent detailed publication from the US reviews the progress and challenges to swine influenza vaccine research, including novel vaccine approaches (Petro-Turnquist and others 2024). It also details current licensed vaccines and their potential limitations.

Porcine reproductive and respiratory syndrome virus 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.

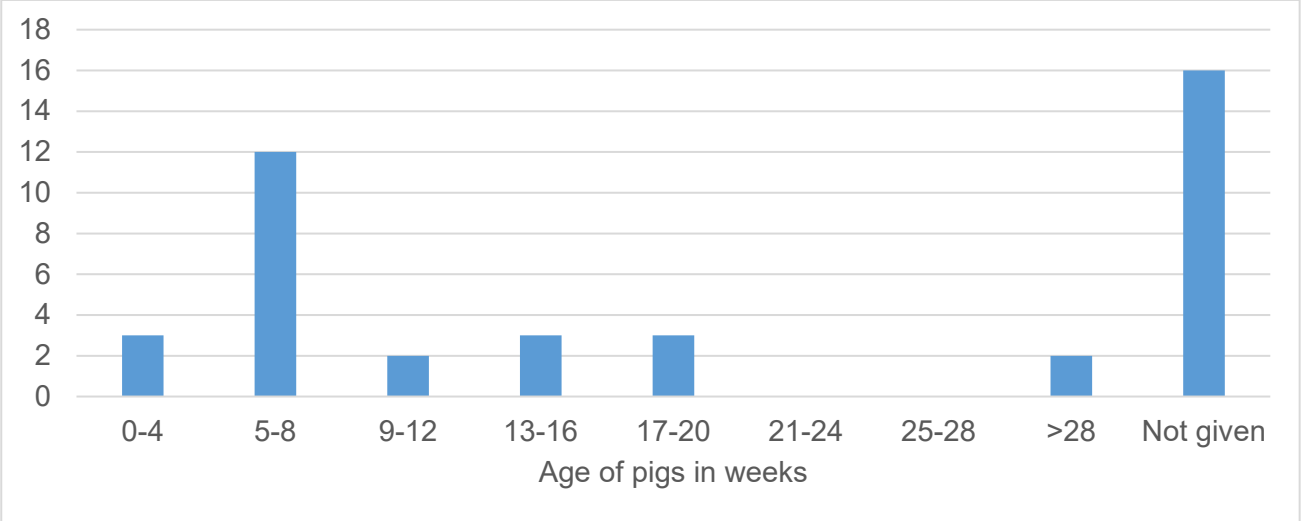
Figure 6: Diagnostic rate of PRRS by year and quarter as a percentage of diagnosable submissions to the Great Britain scanning surveillance network



The diagnostic rate for PRRS in GB fell in the first six months of 2024 but remains at a rate of around 10% of diagnosable submissions (Figure 6). 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.

In the first two quarters of 2024 there have been 45 diagnoses of PRRS, four of these related to reproductive disease in breeding pigs and 41 to systemic or respiratory disease. Excluding reproductive disease cases, the ages of pigs in which PRRS was diagnosed are illustrated in Figure 7, with the most diagnoses made in pigs in the weeks immediately after weaning. This is likely to reflect the opportunity for PRRSV spread following mixing of pigs at weaning, when their maternal immunity is waning and vaccinal immunity, where vaccines are used at or near weaning, is still establishing.

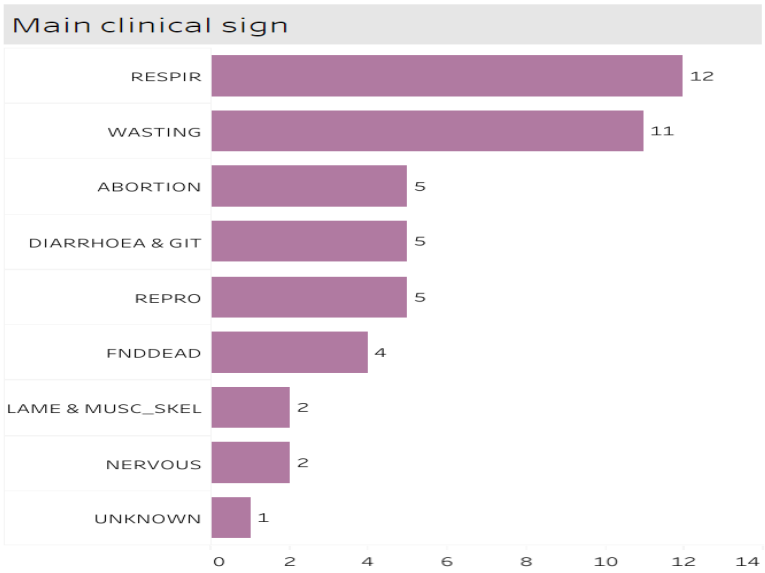
Figure 7: Age of pigs in which systemic or respiratory porcine reproductive and respiratory syndrome was diagnosed during first six months of 2024



Fifty one percent of PRRS diagnoses were made in carcase submissions, in which full diagnostic investigation can be undertaken. Concurrent diseases were found in all but two of the 41 diagnoses of systemic and respiratory PRRS made in carcases. This compared to only four of the 18 non-carcase submissions which had diagnoses in addition to PRRS. Swine influenza was diagnosed in six submissions and was the most common concurrent diagnosis made in the first six months of 2024. The other most frequent concurrent diagnoses were disease due to *Pasteurella multocida*, *Glaesserella parasuis*, *Mycoplasma hyorhinis* and *Brachyspira pilosicoli*. 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 are shown in Figure 8. Clinical signs may reflect the concurrent diagnoses made rather than being directly due to PRRS.

Figure 8: Main clinical signs in submissions in which PRRS was diagnosed.



As part of PRRS surveillance at APHA, ORF-5 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 the first six months of 2024 has not detected any which suggest a novel introduction. The genetic diversity of those sequenced continues to evolve and at least 13 different lineages/clades are seen.

The presence of diverse and, sometimes, more pathogenic PRRSV-1 in parts of Europe, as well as PRRSV-2 in Europe, the Americas and Asia, emphasises the importance of preventing strains exotic to the UK from being introduced. It is vital that veterinarians involved in importation of live pigs or semen into the UK remember of the importance of taking measures to ensure that they are sourced from PRRSV-negative herds, with testing before and after importation to prevent the introduction of exotic PRRSV strains into the UK. Raising awareness amongst vets less familiar with pigs, smaller pig producers and owners of non-assured pig herds is especially important.

The National Pig Association live pig import protocol was established by the NPA in consultation with pig breeding companies and includes recommendations about import conditions and testing for PRRSV. This has become a Red Tractor standard for assured pig premises to follow this protocol when importing live pigs. As around 95% of commercial pigs in the UK are Red Tractor assured, this is now mandatory for the majority of commercial pig herds.

Viruses in which the ORF-5 gene sequence has 98.5% or greater similarity to one of the live PRRSV vaccines are termed “vaccine-like”. As the ORF-5 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. Since a recombinant PRRSV-1 vaccine (or vaccine-like) and field virus was described in pigs in England (Frossard and others, 2013), no further recombinants have been found. 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 which may have reflected, in part, issues with the supply of certain live vaccines. In 2024, vaccine-like viruses represent 19% of those sequenced so far in the first six months of 2024.

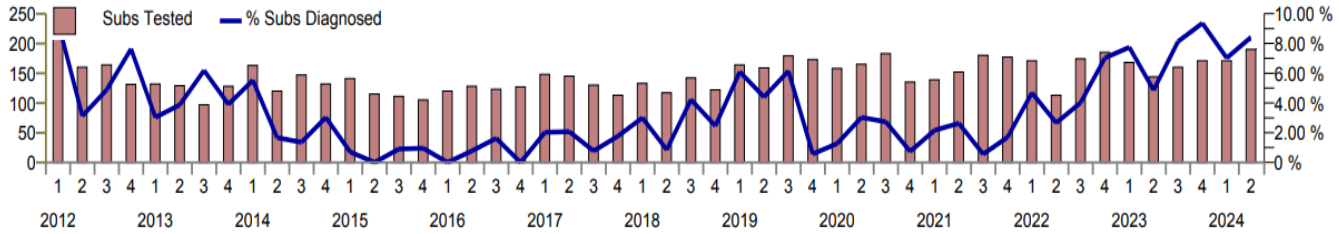
Swine dysentery diagnoses continue in 2024

An upward trend in the number of diagnoses of swine dysentery made through the GB scanning surveillance network (at APHA and SRUC laboratories) has been noted since the end of 2021 (Figure 9) and cases have continued to be diagnosed in 2024. In more recent years, veterinarians have noticed that some confirmed cases of swine dysentery have

been in pigs showing mild to moderate diarrhoea rather than the typical muco-haemorrhagic diarrhoea that is associated with swine dysentery.

Sixteen diagnoses have been recorded in VIDA during quarter 2 of 2024 to date. Submissions were from 14 premises in nine counties in GB (East Riding and North Lincolnshire, Essex, Lincolnshire, Norfolk, North Yorkshire, Northumberland, Powys, Suffolk and Wiltshire). This compares to quarter 1 of 2024 when 12 diagnoses were made on nine premises in five counties in GB and to quarter 2 of 2023 when seven diagnoses were made on six premises in six counties. These diagnoses can be seen on the interactive GB pig disease surveillance dashboard. 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 9: Diagnostic rate of swine dysentery by year and quarter as a percentage of diagnosable submissions to the Great Britain 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 multilocus sequence types 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 2 shows the STs identified so far for isolates from submissions to APHA or SRUC in the first six months of 2024. Five different STs were identified in 2021, seven in 2022, ten in 2023 and nine so far in 2024.

Each year several novel allelic profiles are identified; these are submitted to the pubMLST database and allocated a new ST. There are already three novel STs identified in 2024 (ST339, 340 and 341). Since an isolate was first identified as ST341 in March 2024, there have been a total of eight isolates identified as ST341, these originate from six premises in five counties. ST341 is the most frequently identified ST this year. None of the isolates tested to date from this emerging ST341 have shown clinical resistance to antimicrobials licensed for use in pigs.

In recent years (2016 onwards), one ST (ST251) has been associated with multi-drug resistance including clinical resistance to tiamulin. One ST251 isolate has been identified so far in 2024, for which MIC testing is ongoing. Apart from ST251-associated cases, clinical antimicrobial resistance does not appear to be a main factor behind the upward trend in swine dysentery diagnoses since 2021.

Table 2: Sequence types of Brachyspira hyodysenteriae isolates from submissions received in the first six months of 2024

Note that further STs of isolates from the first six months 2024 may be identified if 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
88	4	East Riding and North Lincolnshire and North Yorkshire	Yes
242	1	East Riding and North Lincolnshire	Yes
243	1	Derbyshire	No (previously identified in Europe)
251	1	East Riding and North Lincolnshire	Yes
319	1	Northumberland	Yes (first detection 2023)
339	1	Fife	No
340	1	Norfolk	No
341	8	Norfolk, Suffolk, Northumberland, Tyne and Wear	No

Increased diagnostic rate of disease due to *Escherichia coli*

The diagnostic rate of disease due to *Escherichia coli* increased in quarter 2 of 2024, having fallen in quarter 1 of 2024 from the peak in the last quarter of 2023 (Figure 10). The majority of the diagnoses due to E. coli recorded in VIDA to date for the second quarter of

2024 (91%, n=54) were enteric colibacillosis, with four diagnoses of oedema disease (one diagnosis of enteric colibacillosis was concurrent with oedema disease) and two diagnoses of colisepticaemia. Fifty-one of the 54 diagnoses were in England, two were in Scotland and one was in Wales. The primary presenting clinical sign described most frequently for enteric colibacillosis diagnoses was diarrhoea, with wasting or pigs found dead the next most frequent clinical signs (see Figure 11). The ages of pigs in which enteric colibacillosis was diagnosed (where age information was provided) is shown in Figure 12. The majority of diagnoses were made in pigs aged between four and seven weeks old, which are likely to be in the first four weeks after weaning.

This recent increase in diagnostic rate is similar to the trend described in quarter 4 of 2023 (APHA 2023c) and may, in part, reflect the effect of the removal of zinc oxide from pig feed as a means of controlling post-weaning diarrhoea since product authorisation expired in June 2022. The UK Veterinary Medicines Directorate (VMD) granted an extension in the UK, allowing the industry to use up any product purchased before the authorisation expired in June 2022. The diagnostic trend for disease due to *Escherichia coli* will be kept under review.

Figure 10: Diagnostic rate of disease due to Escherichia coli by year and quarter as a percentage of diagnosable submissions to the Great Britain scanning surveillance network.

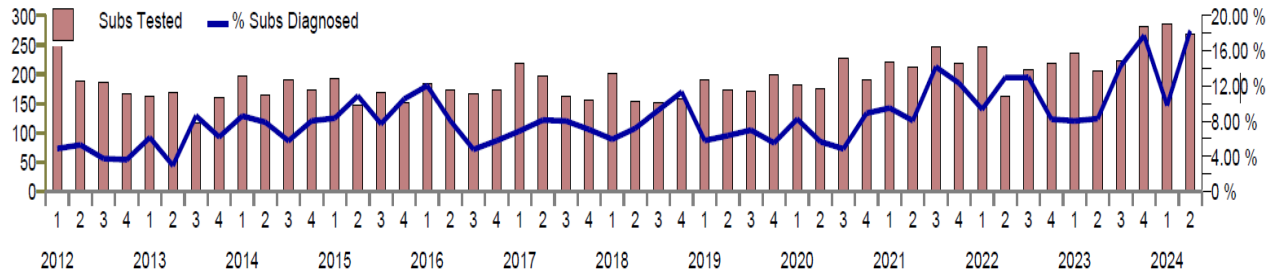


Figure 11: Main presenting signs of pigs diagnosed with enteric colibacillosis through the GB scanning surveillance network (where presenting sign information provided) during quarter 2, 2024.

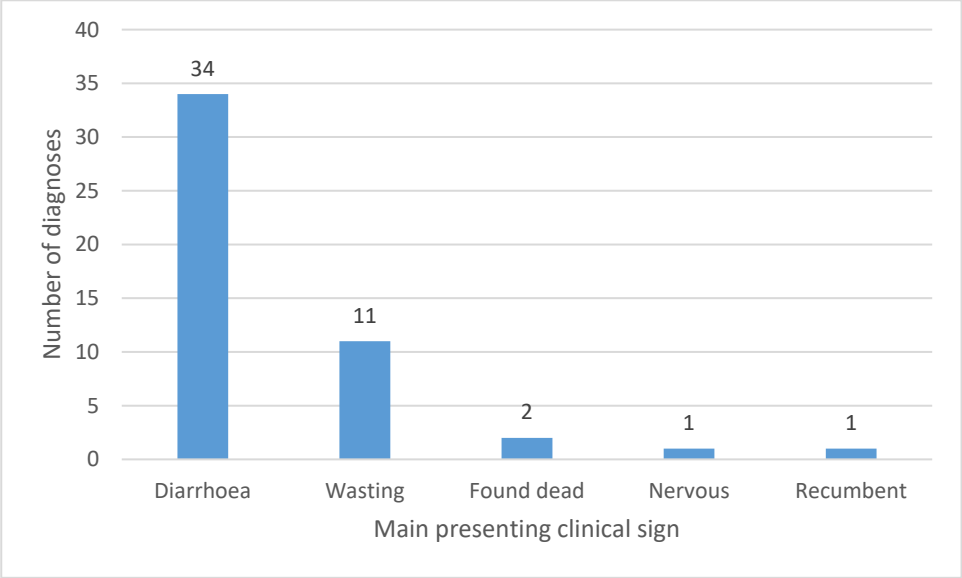
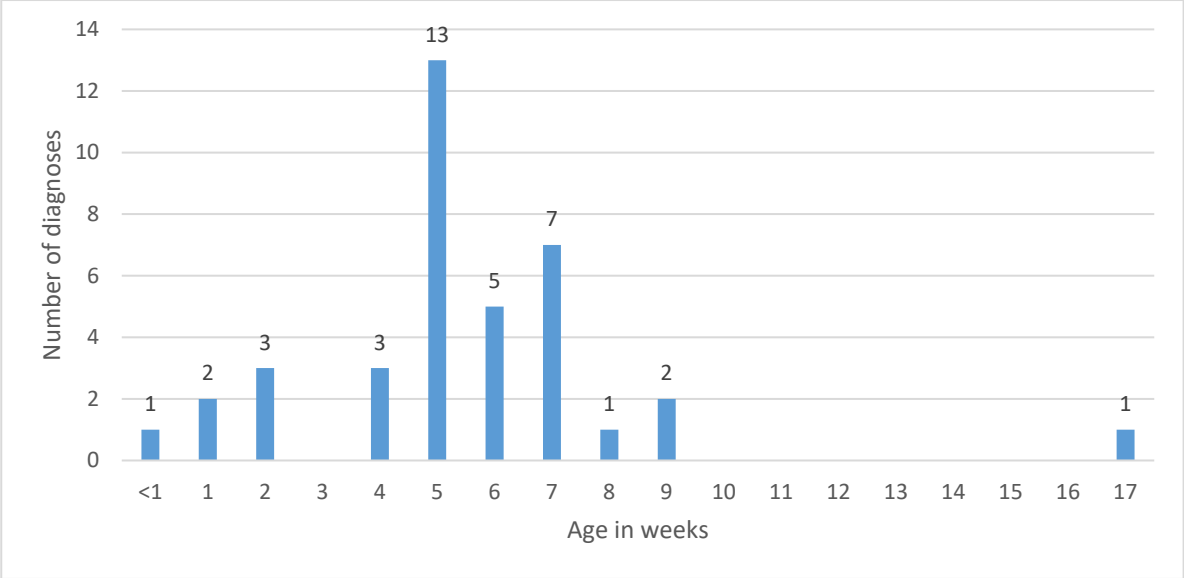


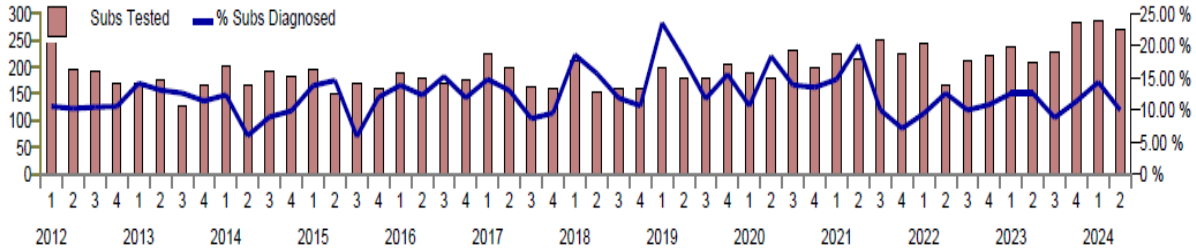
Figure 12: Ages of pigs diagnosed with enteric colibacillosis through the GB scanning surveillance network (where age information provided) during quarter 2, 2024.



Streptococcus suis serotypes associated with disease

Disease due to *Streptococcus suis* is consistently one of the most common diagnoses made in pigs through the GB scanning surveillance network (Table 1) with the diagnostic rate shown in Figure 13 indicating its importance as an endemic disease.

Figure 13: Diagnostic rate of streptococcal disease by year and quarter as a percentage of diagnosable submissions to the Great Britain scanning surveillance network.



Primary disease due to *S. suis* mainly manifests as septicaemia, meningitis, polyserositis, polyarthritis and/or endocarditis. The disease is a significant reason for antimicrobial treatment in growing pigs.

Amongst the measures taken to control disease, autogenous vaccines for the *S. suis* strain causing disease on farm are sometimes used. Farms have different serotypes and different strains of *S. suis* causing disease in their pigs, although spread from sows to their progeny may result in similarity in the *S. suis* in different pig flows from the same breeding sources and within the same breeding pyramids.

The *S. suis* isolates from diseased pigs at APHA and SRUC laboratories are serotyped at APHA Starcross. The serotypes identified in submissions to the GB scanning surveillance in the first six months of 2024 are summarised in Table 3. *S. suis* serotype 2 is predominant with serotype 7 the second most frequently identified. These findings are in line with expectations.

Table 3: Streptococcus suis serotypes identified in GB pig diagnostic submissions

Year and Quarter	Total	1	2	3	4	5	7	8	9	10	12	13	14	16	21	23	25	1/2	NT
Q1 2024	27	1	7	1	0	2	6	1	1	0	0	1	1	0	0	1	0	1	4
Q2 2024	19	1	7	0	0	0	2	1	0	0	1	0	1	0	0	0	1	0	5
Q1-2 2024 totals	46	2	14	1	0	2	8	2	1	0	1	1	2	0	0	1	1	1	9

NT = non-typeable

The four serotypes most commonly associated with primary disease, due to *S. suis* in GB diagnostic submissions are serotypes 1, 2, 7 and 14. *S. suis* serotype 2 is predominant in most quarters. Other serotypes can occasionally cause primary disease in individual pigs but are less or uncommonly associated with ongoing outbreaks. A wide range of serotypes can be involved in secondary infections, following viral disease, in particular PRRS or

swine influenza. The interactive PRRS dashboard shows that disease due to *S. suis* is one of the most common diagnoses found concurrent with PRRS.

Horizon scanning

Increased mycotoxin risk in cereals and forage crops

The Agriculture and Horticulture Development Board (AHDB) released an alert in late July 2024 regarding the potential risk to livestock posed by fusarium and ergot in grain (AHDB 2024). Risk assessments based on rainfall and temperatures during the 2024 growing season suggested that the presence of both of these fungi was likely to be more frequent in 2024. Since then, agronomists and grain merchants have reported that this is the case. This could lead to an increased risk of contamination of grain and forage crops with these fungi and therefore also with their associated mycotoxins. The growing period for crops has been wetter than average in the UK in 2024. AHDB's alert encouraged farmers to familiarise themselves with the clinical signs of ergotism and fusarium toxicity.

Ergot causes vasoconstriction of the peripheral blood vessels resulting in tail-end and ear-tip loss, and lower limb and hoof tissue damage and sloughing. Lameness, weight loss, and neurological signs may also be exhibited. Fusariotoxins can cause gastrointestinal tract lesions, oedema, respiratory distress and general malaise. WOAH has information on mycotoxicoses (WOAH 2021).

This issue was discussed with APHA's toxicology lead and an alert was sent out through APHA's Endemic and Emerging Disease Alert System (EEDAS) to raise awareness.

Porcine circovirus 3 knowledge review

A review article was published on porcine circovirus 3 (PCV3) which highlights questions currently remaining unanswered for this relatively recently detected virus (Silva and others 2024). The significance of PVC3 detection in pigs not showing clinical signs of disease (asymptomatic carriers), or where presence of the virus cannot be demonstrated in lesions for pigs showing clinical signs, remains unclear. There is also a poor understanding of the impact of PCV3 when found in co-infections with other pathogens, including atypical porcine pestivirus, PRRS and ASF.

PCV3 was first detected in 2016 and was associated with porcine dermatitis and nephropathy syndrome (PDNS) -like skin lesions in sows, increased sow mortality, abortions, increased mummies and stillborn rates, as well as decreased conception rates (Kroeger and others 2022). The presence of multisystemic inflammation has also frequently been associated with the virus (Kroeger and others 2022). Experimental studies infecting pigs with PCV3 have improved the understanding of the role of PCV3 in causing disease (Silva and others 2024). Following inoculation with PCV3, four-week-old pigs have

exhibited clinical signs including pyrexia, coughing and anorexia (Jiang and others 2019). In the same study, eight-week-old pigs exhibited PDNS-like skin lesions.

Case definitions for diagnoses of PCV3-associated disease have been developed. APHA/SRUC's Veterinary Investigation Diagnosis Analysis (VIDA) coding reflects case definitions proposed by Saporiti and others (2021; Table 8) for PCV3-reproductive disease and PCV3-systemic disease. For a submission to be coded as systemic PCV3-associated disease by APHA/SRUC, histopathology must demonstrate myocarditis or multi-systemic inflammation associated with PCV3. Presence of PCV3 is confirmed using *in situ* hybridisation and/or qPCR demonstrating high viral loads of PCV3 in lesioned tissue(s).

Diagnoses of PCV3 associated disease have been made in GB; an update on PCV3 associated disease for GB can be found in the 2023 quarter 4 pig report (APHA 2023d). Two diagnoses of PCV3-associated disease were made in quarters 1 and 2 of 2024, one was an incident of fetopathy associated with PCV3 and the other was an individual pig with PCV3-systemic disease.

First detection of porcine circovirus 4 in the US

Kroeger and others (2024) have published the first report of detection of porcine circovirus 4 (PCV4) in pigs in the US. The initial report of PCV4 as a novel virus followed its first detection in 2019 in diseased pigs in Hunan province, China (Zhang and others, 2020). This was described in the quarterly surveillance report (APHA, 2019). Since then, PCV4 has been detected in pigs in other parts of China and in South Korea and studies demonstrated it had been present earlier than 2019. Detection has not yet been associated with any specific disease or syndrome. In a study from China, an infectious clone of PCV4 replicated in cell culture and piglets but did not result in clinical signs, although pathological changes were found in several organs.

The first detection in Europe was reported in Spain (Holgado-Martín and others 2023) in retrospective samples from 1998 to 2022 from wild boar and domestic pigs from mid-south-western Spain. Interestingly, PCV4 DNA was not detected in other commercial pig samples tested from north-eastern Spain or in domestic swine (backyard and intensively raised) or wild boar from Italy. The relatively high virus prevalence in wild boar and low prevalence in Iberian pigs from the same areas raised the possibility of intra- and interspecific transmission, and wild boar being a potential virus reservoir.

In this study from the US, PCV4 was detected by PCR in 8.6% of the 512 samples tested with lung, faeces, spleen, serum and lymphoid tissue all represented in the PCR-positive samples. Lymphoid tissue had the highest frequency of detection. Two ORF2 sequences were obtained from lymphoid tissue samples. PCV4 was most commonly detected in nursery to finisher pigs with respiratory and enteric disease and the authors noted frequent co-infection with PCV2, PCV3 and other endemic pathogens.

The epidemiology, clinical significance and pathogenesis of PCV4 all remain poorly understood and further research is likely to follow this finding in pigs in the US.

It has been agreed that the 2023-24 abattoir serum archive established by AHDB and APHA from pigs in England will be tested for the presence of PCV4.

Contact

Editors: Susanna Williamson, Claire Scott

Address: APHA, Bury St Edmunds

Telephone: + 44 (0) 2080 264990

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

References

AHDB (2024) Farmers warned of potential risk to livestock posed by fusarium and ergot in grain. https://ahdb.org.uk/news/farmers-warned-of-potential-risk-to-livestock-posed-by-fusarium-and-ergot-in-grain

APHA (2015). Illthrift and lameness in growers associated with deficient home-mix diet. Quarter 1 of 2015 (January to March). https://webarchive.nationalarchives.gov.uk/ukgwa/20200806095813mp_/https:/assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/430707/pub-survrep-p0115.pdf

APHA (2019). Novel circovirus species (PCV4) identified in pigs in China. Volume 23: Quarter 4 of 2019 (October to December) page 19 https://webarchive.nationalarchives.gov.uk/ukgwa/20200806210308mp_/https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/873051/pub-survrep-p-Q4-19.pdf

APHA (2023a). Pig disease surveillance dashboard outputs. Great Britain pig quarterly report: disease surveillance and emerging threats. Volume 27: Quarter 4 of 2023 (October to December) page 2 https://assets.publishing.service.gov.uk/media/663b5a0774933dccbbb6c3bd/Quarterly-GB-pig-disease-surveillance-emerging-threats-report-October-December-2023.pdf.pdf

APHA (2023b). Rise in swine influenza diagnoses and diagnostic rate. Great Britain pig quarterly report: disease surveillance and emerging threats. Volume 27: Quarter 4 of 2023 (October to December). https://assets.publishing.service.gov.uk/media/663b5a0774933dccbbb6c3bd/Quarterly-GB-pig-disease-surveillance-emerging-threats-report-October-December-2023.pdf.pdf

APHA (2023c). Rise in diagnostic rate for enteric colibacillosis. Great Britain pig quarterly report: disease surveillance and emerging threats. Volume 27: Quarter 4 of 2023 (October to December). https://assets.publishing.service.gov.uk/media/663b5a0774933dccbbb6c3bd/Quarterly-GB-pig-disease-surveillance-emerging-threats-report-October-December-2023.pdf.pdf

APHA (2023d). Porcine circovirus-3 associated disease update. Great Britain pig quarterly report: disease surveillance and emerging threats. Volume 27: Quarter 4 of 2023 (October to December). https://assets.publishing.service.gov.uk/media/663b5a0774933dccbbb6c3bd/Quarterly-GB-pig-disease-surveillance-emerging-threats-report-October-December-2023.pdf.pdf

APHA (2024a). Great Britain pig quarterly report: disease surveillance and emerging threats. Volume 28: Quarter 1 of 2024 (January to March). https://assets.publishing.service.gov.uk/media/66e2f5393f1299ce5d5c3da4/2024_Q1_Pigs_final_revised.pdf

APHA (2024b). Streptococcus suis infection in negative swine fever case, April 2024. *Veterinary Record*, 194: 339-342. https://doi.org/10.1002/vetr.4228

APHA (2024c). Non-infectious causes of lameness in finishing age pigs. Disease surveillance in England and Wales, August 2024. https://bvajournals.onlinelibrary.wiley.com/doi/epdf/10.1002/vetr.4670

APHA (2024d). Severe respiratory disease in sows with swine influenza. Disease surveillance in England and Wales, June 2024. Veterinary Record, 195: 20-24. https://doi.org/10.1002/vetr.4454

Blome, S., Schäfer, M., Ishchenko, L. and others (2024). Survival of African swine fever virus in feed, bedding materials and mechanical vectors and their potential role in virus transmission. *EFSA Supporting Publications*, *21*(4), 8776E.

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 (2024a). Updated Outbreak Assessment #36, African swine fever in Europe, 24 July 2024. https://assets.publishing.service.gov.uk/media/66a3c644ab418ab055592e3a/african-swine-fever-in-europe-update-36.pdf

Defra (2024b). Updated Outbreak Assessment #35, African swine fever in Europe, 17 June 2024. https://assets.publishing.service.gov.uk/media/667444bb64e554df3bd0dbed/Update_ASF_in_Europe_35.pdf

Defra (2024c). Updated Outbreak Assessment #26, African swine fever (ASF) in Asia, 19 August 2024. https://assets.publishing.service.gov.uk/media/66c85e381f215d9f0a913535/asf_asia_update_26.pdf

Holgado-Martín, R., Arnal, J.L., Sibila, M. and others (2023). First detection of porcine circovirus 4 (PCV-4) in Europe. Virol J 20, 230. DOI: 10.1186/s12985-023-02181-1

Jiang, H., Wang, D., Wang, J. and others (2019). Induction of porcine dermatitis and nephropathy syndrome in piglets by infection with porcine circovirus type 3. *Journal of Virology*, *93*(4), pp.10-1128. DOI: 10.1128/jvi.02045-18

Kikuti, M., Picasso-Risso, C. and Corzo, C.A. (2024). Porcine Deltacoronavirus Occurrence in the United States Breeding Herds since Its Emergence in 2014. *Viruses*, *16*(3), p.445. DOI: 10.3390/v16030445

Kroeger, M., Temeeyasen, G. and Piñeyro, P.E. (2022). Five years of porcine circovirus 3: What have we learned about the clinical disease, immune pathogenesis, and diagnosis. *Virus Research*, *314*, p.198764.

Kroeger, M., Vargas-Bermudez, D.S., Jaime, J. and others (2024). First detection of PCV4 in swine in the United States: codetection with PCV2 and PCV3 and direct detection within tissues. Sci Rep 14, 15535. DOI: 10.1038/s41598-024-66328-y

Petro-Turnquist E., Pekarek Matthew J., Weaver Eric A. (2024). Swine influenza A virus: challenges and novel vaccine strategies. Frontiers in Cellular and Infection Microbiology 14:1336013. DOI: 10.3389/fcimb.2024.1336013

Saporiti, V., Franzo, G., Sibila, M. and Segalés, J. (2021). Porcine circovirus 3 (PCV-3) as a causal agent of disease in swine and a proposal of PCV-3 associated disease case definition. *Transboundary and Emerging Diseases*, *68*(6), pp.2936-2948.

Silva, R.R.D., Silva, D.F.D., Silva, V.H.D. and Castro, A.M.D. (2024). Porcine circovirus 3: a new challenge to explore. *Frontiers in Veterinary Science*, *10*, p.1266499.

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

WOAH (2021). Mycotoxicosis. https://www.woah.org/app/uploads/2021/05/mycotoxicosis.pdf

Zhang H.H., Hu W.Q., Li J.Y. and others (2020). Novel circovirus species identified in farmed pigs designated as Porcine circovirus 4, Hunan province, China. Transboundary and Emerging Diseases 67(3):1057-1061. DOI: 10.1111/tbed.13446

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:

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