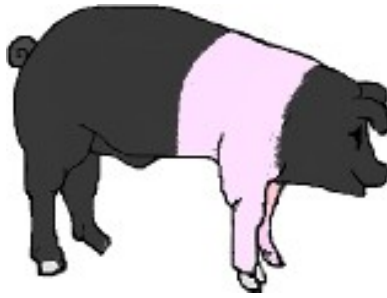




Animal &  
Plant Health  
Agency



## Great Britain pig quarterly report: disease surveillance and emerging threats

Volume 35: Quarter 4 of 2025 (October to December)

### Highlights

- H3N2 influenza A virus detected in a pig herd in England – page 1
- Two separate cases of cerebrospinal angiopathy – page 4
- Arthritis associated with *Actinobacillus pleuropneumoniae* in piglets – page 5
- New guidance for investigation of infectious causes of porcine fetopathy – page 9

# Contents

Introduction and overview.....	1
Unusual diagnoses or presentations.....	1
H3N2 influenza A virus detected in a pig herd in England.....	1
Detection of deltacoronavirus of likely wild bird origin in a pig sample.....	3
Two separate cases of cerebrospinal angiopathy.....	4
Arthritis associated with <i>Actinobacillus pleuropneumoniae</i> in piglets.....	5
Horizon scanning.....	7
Virus with similarity to fur seal faeces-associated circular DNA virus identified in pigs in southern China.....	7
Information sources on global notifiable disease.....	8
Ongoing scanning surveillance initiatives.....	9
New guidance for investigation of infectious causes of porcine fetopathy.....	9
<i>Brachyspira hyodysenteriae</i> – swine dysentery.....	9
Porcine enteric coronavirus surveillance.....	10
Porcine circovirus 3-associated disease.....	10
Porcine reproductive and respiratory syndrome.....	11
Seneca Valley virus.....	12
Contact.....	12
References.....	12

## Introduction and overview

This quarterly report reviews potential disease threats for the third quarter of 2025 (October to December). A full explanation of [how data are analysed](#) is provided in the annexe available on GOV.UK. Submissions to and diagnoses made through the Great Britain (GB; England, Wales and Scotland) scanning surveillance network can be interrogated further using the interactive pig [disease surveillance dashboard](#). Diagnostic submissions are voluntary and subject to several sources of bias.

This report is compiled using data available at the time of writing. It contains disease findings gathered from APHA, Scotland's Rural College (SRUC) Veterinary Services and surveillance pathology partners, 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.

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

## Unusual diagnoses or presentations

### H3N2 influenza A virus detected in a pig herd in England

Very mild respiratory signs among piglets on a breeding herd in Yorkshire prompted molecular testing for swine influenza A virus through a private laboratory in December 2025. In January 2026, the herd veterinary practitioner informed APHA's Pig Expert Group that this testing had resulted in detection of influenza A virus subtype H3N2 in one pooled sample. Whilst swine influenza infection of pigs is non-notifiable and non-reportable, it is monitored because of the impact on pork production as well as the zoonotic and pandemic potential of mammalian influenza A viruses.

H3N2 influenza A virus had not been detected in pigs in GB since 1997. Previous monitoring of this herd had detected H1N2 and H1N1 (1C 'Eurasian avian-like' clade) swine influenza A viruses but not H3N2. Following the H3N2 detection in December, respiratory signs spread to other stages of production in the herd and became less mild, suggesting that the H3N2 virus may have recently been introduced to this herd.

A farm visit and follow-up sampling was conducted by an APHA Veterinary Investigation Officer at no charge to the veterinary practitioner and farmer under Defra-funded projects for swine influenza surveillance and scanning surveillance for diseases of pigs in England and Wales. Nasal swabs were collected from piglets and weaners with and without clinical

signs. Diagnostic testing of samples was completed by the National Reference Laboratory for swine influenza. More than half of the 58 pigs sampled tested positive in the influenza A virus M-gene molecular test. Molecular HA and NA subtyping tests detected both H3N2 and H1N2 influenza A viruses. No pig samples were positive for both H3N2 and H1N2. Where present, clinical signs in pigs which tested positive for H3N2 were mild and included sneezing, coughing and ocular and nasal discharges. Whole-genome sequencing was completed in samples with sufficient viral RNA which confirmed the two influenza A virus HA sub-clades:

- H1N2 (H1B.1.1.1)
- H3N2 (G.2, human influenza A virus HA gene nomenclature)

The H1N2 viruses detected are similar to those already circulating in GB pig herds. They incorporate HA (1B.1.1.1) and N2 genes, with the remaining genes (the internal gene cassette) belonging to the pandemic 2009 lineage.

The HA (H3 gene) in the H3N2 viruses from this case clusters genetically with the human seasonal G.2 clade. This clade was frequently detected in humans globally in 2023 but has rarely been detected since then. The N2 sequences are genetically related to human seasonal N2 sequences associated with the G.2 HA clade. In contrast, the remaining genes belong to the pandemic 2009 lineage, which is a genetic constellation commonly detected in GB pigs. Human seasonal H3N2 influenza A viruses typically have a genetically distinct internal gene constellation.

Although pig-origin H3N2 viruses continue to be detected in pigs at low levels in the EU, the H3 HA gene in the H3N2 viruses from this case clusters separately from the H3 genes detected in swine influenza strains in European herds, including that of the H3N2 strain in the European-licensed swine influenza vaccine. Instead, the H3 HA gene clusters more closely with 2023 human seasonal strains. Further characterisation is ongoing.

Public health experts have indicated that there are no signals of increased risk to human health from this H3N2 strain, compared to the human seasonal influenza viruses circulating this year. That said, it is important to note the zoonotic potential of influenza viruses. People in contact with pigs, particularly pigs with influenza-like clinical signs or diagnosed with influenza, should note and follow the guidance in the [swine influenza in pigs code of practice](#) which also details biosecurity recommendations.

Given that H3N2 virus has not been detected in pigs in GB since 1997, immunity of the national pig herd to H3N2 viruses may be low. [There is free surveillance for influenza virus in pigs at APHA](#). If veterinarians use other laboratories to test for swine influenza virus and detect H3N2 or other unusual swine influenza subtypes in pigs in England or Wales, please contact the [Pig Expert Group](#). APHA's swine influenza national reference laboratory can assist in further investigation and analysis of detected viruses. SRUC also offers advice and supports vets to undertake diagnostic investigations in pigs in England, Wales and Scotland.

## Detection of deltacoronavirus of likely wild bird origin in a pig sample

APHA has carried out enhanced surveillance for porcine deltacoronavirus (PDCoV) since February 2023 on diagnostic submissions from cases of diarrhoea and/or enteropathy in pigs. An inconclusive PCR result for PDCoV was obtained from one sample of pig faeces from four-week-old pigs with diarrhoea on an outdoor premises in England in July 2025. The sample was pooled from several faeces and was collected from the floor. A farm visit and follow-up sampling was conducted by an APHA Veterinary Investigation Officer at no charge to the veterinary practitioner or farmer under the Defra-funded projects for scanning surveillance for diseases of pigs in England and Wales. No positive PDCoV PCR results were obtained from testing pig faeces and pooled bird faeces collected on this visit.

The original inconclusive PCR result was investigated further by APHA virology using PCR primers from the literature. One set of primers, designed to target the M gene of the virus, produced the expected amplicon in PCR. Sequencing of this amplicon yielded a 440-nucleotide sequence. A BLAST search against sequences published in the public domain (GenBank) showed the highest nucleotide identity to deltacoronavirus sequences reported from magpies in China. Thus, a deltacoronavirus was detected which is considered likely to have a wild bird origin. The sequencing information provided an explanation for the inconclusive porcine deltacoronavirus PCR result and confirmed that it did not represent a detection of PDCoV, which has never been detected in GB pigs to date.

The presence of a deltacoronavirus of likely wild bird origin in a pig faecal sample could have been the result of bird faeces contaminating the pig sample which was collected from multiple faeces from the lairage floor; as a spill-over of infection from birds into a pig; or due to mechanical transmission of wild bird-derived virus through a pig's gastrointestinal tract. Both the veterinary practitioner and the APHA vet noted a high wild bird population on the premises (ravens, rooks and gulls) with areas of high faecal contamination from birds including water troughs. Advice was provided to the veterinary practitioner on wild bird control. Diagnostic testing on the submitted pigs, and similar ones from linked premises established diagnoses for the diarrhoea and wasting (coccidiosis and rotaviral enteritis).

Deltacoronaviruses have been frequently detected in a wide variety of bird species (waterfowl, seabirds, passerines, birds of prey, columbids) without signs of disease globally, including in Asia, South America, Russia, Europe, Antarctica and Australia (Rahman and others, 2021; Wille and Holmes, 2020). There is wide viral diversity in the deltacoronaviruses detected; some are, to date, only described from a single bird species, or within a single order. Although this case represents the first known detection of deltacoronavirus of likely wild bird origin by APHA, no surveillance has been undertaken in GB birds for this group of viruses. Given their global distribution in birds, this incidental finding is, perhaps, not surprising.

This situation is a reminder to pig keepers to minimise contact between wild birds and pigs. This can be difficult in outdoor production systems, however there are other good reasons to promote effective separation, for example, for *Salmonella* and erysipelas control. It is also important that any dead birds seen are [removed promptly for disposal](#).

It is uncertain whether the potential for zoonotic transmission of deltacoronaviruses from wild birds to humans exists. This case was discussed at the Human Animal Infections and Risk Surveillance group who agreed that [advice is already available which recommends minimising contact between people and wild birds in relation to avian influenza](#).

## Two separate cases of cerebrospinal angiopathy

Cerebrospinal angiopathy is an uncommon, chronic manifestation of vascular injury due to Shigatoxin-producing *Escherichia coli* strains – the cause of oedema disease. Two unrelated cases of cerebrospinal angiopathy in pigs were diagnosed by APHA in late 2025.

The first was from a submission of three pigs which were humanely euthanased for post-mortem examination at the Thirsk VIC. The pigs were from a group of 9-week-old Duroc-cross pigs with neurological signs including circling, head tilts, head pressing and paddling. Pigs were also anorexic and some had joint swellings. The pigs were from an indoor farrow-to-finish herd.

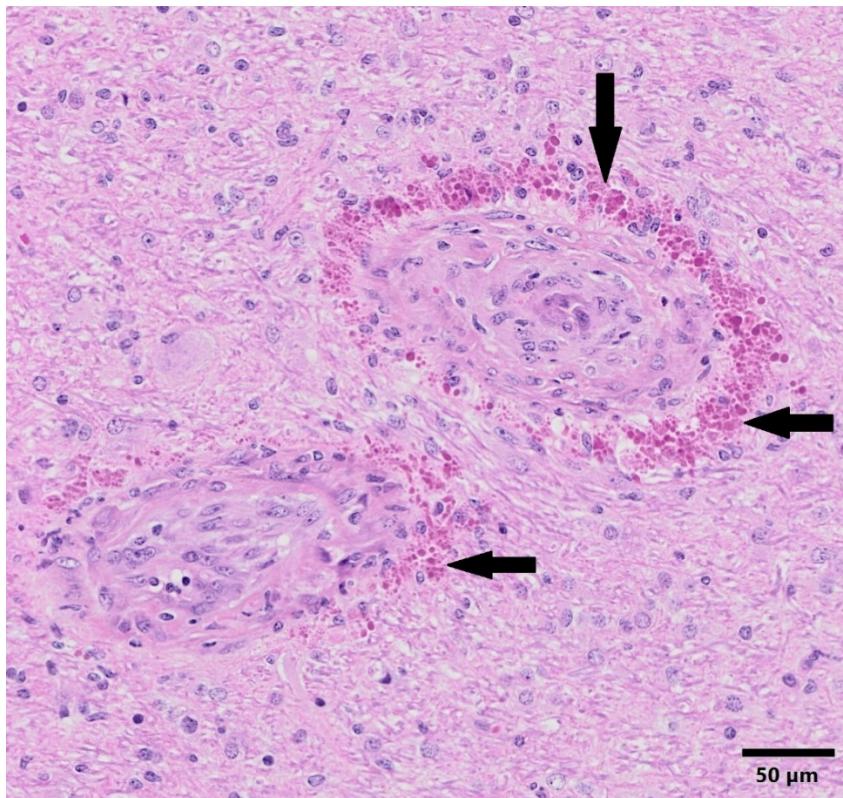
The second case involved a second parity sow which was found recumbent with knuckling on all four limbs when prompted to stand and had 'exaggerated head movements'. She was humanely euthanised following poor response to antimicrobial and non-steroidal anti-inflammatory treatment and submitted to the Bury St Edmunds VIC. She had farrowed 10 days earlier and her litter of 14 piglets was healthy. She was from an outdoor, single parity herd.

Gross pathological changes in both cases were limited and non-specific. Microscopic examination of the fixed brain and spinal cord revealed widespread chronic injury to small vessels in the neural tissue and meninges consistent with cerebrospinal angiopathy (Figure 1). The non-haemolytic *E. coli* isolates cultured from terminal small intestine contents in both cases did not possess genes coding for Shiga toxin type 2 (Stx2e) or other common *E. coli* virulence factors.

Pigs with cerebrospinal angiopathy typically present with nervous signs like ataxia and circling, as well as loss of condition. As in these cases, pigs rarely have significant oedema in, for example, the stomach wall, mesocolon or eyelid. Due to the chronicity of the condition, Shiga-toxin producing *E. coli* strains are often not isolated. As in the first case, [oedema disease and cerebrospinal angiopathy typically affect pigs in the post-weaning period but cases are seen sporadically in other ages of pig](#) (Joint Pathology Centre, 2023).

Both cases highlight the importance of a thorough pathological examination of the brain, spinal cord and spinal column in cases of unexplained recumbency and nervous disease.

**Figure 1:** Two arterioles in the brainstem of a pig showing endothelial, medial and adventitial proliferation and perivascular droplets of hyaline material (black arrows).



## Arthritis associated with *Actinobacillus pleuropneumoniae* in piglets

Three, three-week-old piglets from an indoor breeding unit were humanely euthanased and submitted to the Shrewsbury VIC to investigate an increase in lameness and swollen joints among piglets from approximately two weeks of age, with clinical signs worsening after weaning.

At post-mortem examination, there was marked joint swelling affecting one or more limbs of all three piglets. Stifle, carpal, hock and fetlock joints were affected and were distended with markedly thickened joint capsules, pink and reactive synoviae and thick fibrin deposits. Subcutaneous oedema was associated with some joint lesions. One pig also had swellings on and communicating with the phalangeal joints which were filled with thick yellow purulent material (Figure 2).

*Actinobacillus pleuropneumoniae* was isolated in pure growths under standard aerobic conditions from two joints each from two of the piglets. No bacteria were cultured from the joints of the third pig. No *Brucella suis* was isolated from the joints by selective culture.

Histopathology on the joint tissues was consistent with the gross findings of chronic bacterial polyarthritis. No bacteria were visualised for the two pigs from which *A. pleuropneumoniae* was isolated, however filamentous bacilli resembling *Fusobacterium* species were visualised in the third pigs in which lesions appeared more chronic. There was no evidence of porcine reproductive and respiratory syndrome virus (PRRSV) involvement, with spleens from all three pigs testing negative by PCR.

Virulence in *A. pleuropneumoniae* is multifactorial and is influenced by exotoxin production and other factors. One *A. pleuropneumoniae* isolate from this case was tested by PCR for the presence of exotoxins. The isolate tested positive for Apx4, which confirmed the species assigned by bacteriological methods. In addition, the isolate tested positive for Apx toxin 2 and negative for Apx 1 and 3, so is considered to be of lower virulence than isolates producing Apx1 or isolates with both Apx2 and Apx3.

Isolation of *A. pleuropneumoniae* from sites other than the respiratory tract and from pigs without respiratory disease is infrequently described in the literature (Hoeltig and others, 2018; Jensen and others, 1999). Interestingly, there was no lung pathology in these piglets or respiratory disease described on the farm. The chronic appearance of these abscesses prompted measures to improve early piglet hygiene for this farm, particularly the addition of navel dipping. The clinical issue has now improved, without the use of metaphylactic antimicrobials in litters.

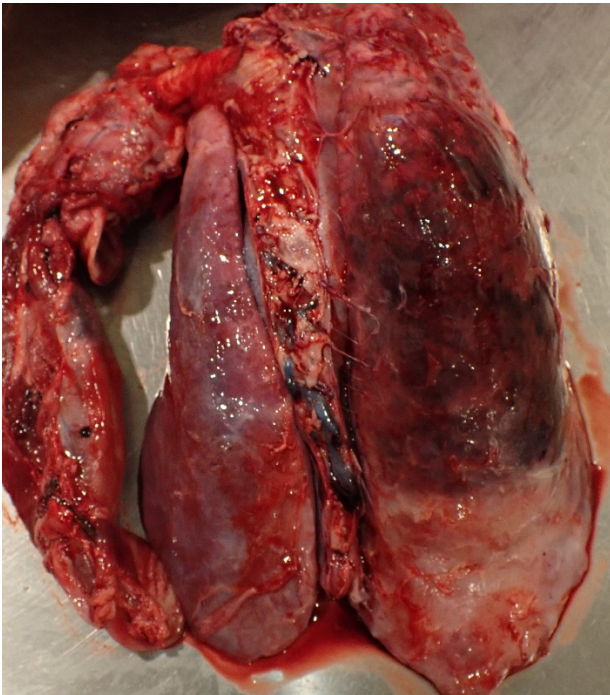
Figure 2: Abscesses over and communicating with the phalangeal joints in a piglet from which *Actinobacillus pleuropneumoniae* was isolated from joints.



A case of sudden death in finishers with porcine respiratory disease complex (PRDC) and severe respiratory pathology which also involved *A. pleuropneumoniae* infection was investigated by the Thirsk VIC. Focally extensive lung purpling and swelling with consolidation and overlying fibrinous pleurisy (Figure 3), typical of *A. pleuropneumoniae*, was present. *A. pleuropneumoniae*, *Streptococcus suis*, *Streptococcus dysgalactiae* and *Pasteurella multocida* were all isolated from the lesioned lungs and *S. dysgalactiae* was

also isolated from the meninges of one pig. Viral involvement in the PRDC was confirmed by all three submitted pigs testing positive for PRRSV by PCR. ORF-5 gene sequencing showed that the virus was a field strain and not vaccine-like. The *A. pleuropneumoniae* isolate was shown to possess Apx toxins 2 and 3 by PCR, so is considered to be of lower virulence than isolates producing Apx1. The veterinarian is now focusing on achieving better PRRS stability in the herd using vaccination as well as other measures.

Figure 3: Focally extensive consolidation of the right lung with pleurisy in a pig with pneumonia due to *Actinobacillus pleuropneumoniae*.



## Horizon scanning

### Virus with similarity to fur seal faeces-associated circular DNA virus identified in pigs in southern China

Liu and others (2025) [have published information](#) about a virus with similarity to fur seal faeces-associated circular DNA virus (FSfaCV) that they have described as a new circovirus (tentatively designated as porcine circovirus [PCV] 5). The virus was identified by PCR in samples collected from pigs on several farms in southern China between October 2021 and June 2023 with respiratory, enteric and reproductive disease issues.

Samples from pigs from 17 out of 70 farms across a range of ages tested positive for the new circovirus by PCR. The authors propose a tentative association between disease and PCV5 infection as they saw correlation between the viral load in tissues and more severe

pathology, however no evidence of causation was presented nor was any other diagnostic testing described or viruses investigated. Healthy pigs were also stated to be infected with the new circovirus at lower viral loads and lower prevalence.

Four porcine circovirus species are already recognised in pigs within the genus Circovirus: non-pathogenic PCV1; pathogenic PCV2 and PCV3; and a relatively recently discovered PCV4, for which pathogenicity remains uncertain. The tentative designation of a fifth – PCV5 – reflects its host and genomic organization; however, phylogenetic analysis indicates that the virus clusters outside the family Circoviridae and is most closely related to FSfaCV. The authors speculate that a cross-species transmission event could account for its origin, however the species origin of FSfaCV is not certain.

FSfaCV was first identified in faeces of New Zealand fur seals in 2013 and then in 2017 in pig faeces in Japan. FSfaCV was also detected in nasal swabs from pigs sampled in 2017 in Anhui Province, China, and showed 91.3% and 90.9% genome-wide nucleotide sequence similarities with the New Zealand fur seal strain FSfaCV-as50 and Japanese pig strain FSfaCV-JPN1, respectively (Shi and others, 2021).

Information in this publication and other findings related to viruses found in pigs with similarity to FSfaCV will be kept under review by APHA's Pig Expert Group.

## Information sources on global notifiable disease

APHA's International Disease Monitoring (IDM) team monitor any major, notifiable or new and emerging animal disease outbreaks worldwide. [See IDM's outbreak assessments which detail such outbreaks](#). Monthly IDM summaries are also included in the [disease surveillance items in the Veterinary Record](#).

Visit the .GOV.UK website for information on the latest situation on [foot-and-mouth disease](#) and [African swine fever \(ASF\)](#). The [European Commission also publishes information on ASF](#) and maps are available showing the current [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.

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. Information on what food items or products of animal origin may be brought into the UK is found via [.GOV.UK](#) and [Food Standards Agency](#).

An [on-line guide with images](#) of the clinical signs and pathology of ASF is available 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 a group.

Veterinarians and pig keepers must show vigilance and be familiar with the clinical signs of all notifiable diseases, so that suspicions are 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](#). For information on notifiable diseases in animals, including disease controls, visit [.GOV.UK](#).

## Ongoing scanning surveillance initiatives

### New guidance for investigation of infectious causes of porcine fetopathy

[A new information note](#) has been published by the APHA's Pig Expert Group: "Investigating porcine abortions, stillbirths and mummified piglets: Guidance for veterinarians submitting samples to APHA". This provides veterinary practitioners with guidance on suitable samples to submit to APHA to investigate infectious causes of porcine abortions, stillbirths and mummified piglets. Ideally, whole litters, with individual placentas, [should be submitted to an APHA Veterinary Investigation Centre or surveillance pathology partner](#) where possible. However, where this is not possible, the guidance in the information note assists veterinary practitioners to examine affected litters, collect a specified range of samples and submit these to APHA. The guidance details the steps involved in collecting and submitting these samples and has two tables which act as aide memoires to be completed and sent with submissions.

### *Brachyspira hyodysenteriae* – swine dysentery

*Brachyspira hyodysenteriae* is the cause of swine dysentery. 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). This is completed at no charge to the submitting veterinarian, under APHA's pig disease scanning surveillance and 'Monitoring of Antimicrobial Resistance in Bacteria from Animals and their Environment' projects. 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](#).

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. The Pig Expert Group recently collaborated with key representatives from the pig sector to publish an article describing [prevention, diagnosis and management of swine dysentery for the general farm animal vet](#) (Scott and others, 2025).

## Porcine enteric coronavirus surveillance

APHA carries out enhanced surveillance for porcine epidemic diarrhoea (PED) virus, transmissible gastroenteritis virus (TGEV) and porcine deltacoronavirus (PDCoV). 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 and transmissible gastroenteritis virus (TGEV) on a weekly basis. None have been positive for PEDV or TGEV in 1936 diagnostic submissions tested under AHDB Pork funding from June 2013 to December 2025. 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. 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. 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).

## Porcine circovirus 3-associated disease

Porcine circovirus 3 (PCV3) is a relatively recently discovered pig virus. Since 2016, PCV3 has been described in pigs in an increasing number of countries globally, including the US, China, Poland, Italy and Spain (Palinski and others, 2017). It was first detected in archived samples from UK pigs in 2017 (Collins and others, 2017).

PCV3 detection has been reported in samples from both healthy pigs and from pigs with a variety of disease presentations; Saporiti and others (2021) proposed case definitions for PCV3-associated disease. No zoonotic concern is reported. Experimental PCV3 infection of weaned pigs (Jiang and others, 2019) induced disease which resembled PDNS in some respects.

Enhanced surveillance at APHA for disease associated with porcine circovirus 3 (PCV3) began in 2021, using histopathology on pig hearts as an initial screen to detect non-suppurative myocarditis and/or periarteritis in foetuses, pigs or plucks received by APHA VICs for postmortem examination. Where such lesions are detected, further investigation

is progressed for detection of involvement of PCV2 by immuno-histochemistry (IHC) or PCV3 by *in situ* hybridisation (ISH).

Two main disease manifestations have been recognised in submissions to APHA; PCV3-associated foetopathy and PCV3-associated systemic disease in postnatal pigs. This enhanced surveillance since 2021 has to date detected a relatively low number of PCV3 diagnoses in APHA submissions each year. Whilst PCV3 foetopathy outbreaks have been diagnosed, systemic disease diagnoses in postnatal pigs have been sporadic and have only once involved more than one pig in the batch of pigs submitted.

A narrated [APHA presentation provides key features of PCV3 as well as APHA surveillance findings up to June 2021](#). Useful literature reviews on PCV3 include Klaumann and others (2018) and Kroeger and others (2022). The results of testing an archive of just over 800 sera from pigs sent to abattoirs in England in 2023-24 by PCR for PCV2, PCV3 and PCV4 at APHA (funded by AHDB) were described in the [April to June 2025 pig disease surveillance quarterly report](#).

## Porcine reproductive and respiratory syndrome

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 and has been updated to include data for 2024. All diagnoses made through the GB surveillance network have been 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.

As part of PRRSV 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 assesses for introduction or development of novel or genetically diverse PRRSV-1 strains into GB. Sequencing completed so far in 2026 has not detected any suspected new introductions. 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 the genome, vaccine-like viruses are analysed further by sequencing part of the nonstructural protein 2 (nsp2) to help identify any potential recombinants.

## Swine influenza

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](#).

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. This is useful for veterinarians considering vaccination of pigs and may help investigation of epidemiological links. Apart from the H3N2 detection described earlier in this report, the subtypes detected in the last year were all H1 viruses, belonging to three main genetic clades: H1N1 that emerged in the 2009 pandemic (Clade 1A.3.3.2), H1N2 viruses of the 1B.1.1.X clade that is unique to GB and was linked to the human case in Nov 2023 and H1 viruses of the 1C.2.2 or 'Eurasian avian-like' clade that were prevalent in Europe before 2009 and have re-emerged in recent years. No H3N2 viruses were detected in GB pigs from 1997 to late 2025.

## Seneca Valley virus

In 2022, [APHA confirmed vesicular disease due to Seneca Valley virus on five commercial breeding pig premises in one geographical area of England between June and September](#). No cases of vesicular disease in pigs due to Seneca Valley virus were identified in GB in 2023 and 2024, 2025 and none to date in 2026.

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