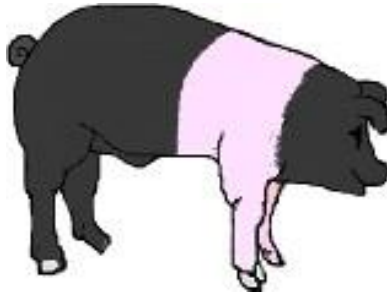




Animal &  
Plant Health  
Agency



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

Volume 36: Quarter 1 of 2026 (January to March)

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# Introduction and overview

This quarterly report reviews potential disease threats for the first quarter of 2026 (January to March). 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; data cannot be extrapolated to determine disease significance or prevalence.

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

### Swine fevers ruled out in feral wild boar found dead

Two feral wild boar were found dead in close proximity to each other in the Forest of Dean in April 2026 by a member of public who informed Forestry England. A Forestry England ranger for the area reported the carcasses to the APHA as suspicious for swine fevers, given that two dead animals had been found close together. An official investigation was initiated and an APHA field veterinarian examined and collected samples from the carcasses, which were severely decomposed. Samples tested negative for African swine fever (ASF) and classical swine fever, which ruled out these notifiable diseases within 30 hours of being reported to APHA.

The degree of carcase decomposition meant that it was not possible to progress testing for differential diagnoses. [Diagnostic investigations into a previous cluster of deaths of wild boar from the Forest of Dean in 2021](#) (which tested negative for ASF as well as anthrax) identified several different diagnoses indicating that the cluster of deaths was not due to a common disease issue (Man and Williamson, 2022). Diagnoses included tuberculosis due to *Mycobacterium bovis*, lungworm, severe metritis and bacterial pneumonia.

The recent negation of swine fevers in wild boar highlights the importance of surveillance for ASF in place for feral wild boar found dead in GB. Rangers working in the Forest of

Dean, the Kent-Sussex border and the Scottish Highlands have been trained by APHA to collect samples from individual wild boar found dead or euthanased due to ill-health, which are tested for ASF at The Pirbright Institute. Activities in England are supported by Forestry England and in Scotland by NatureScot as well as Forestry and Land Scotland. Where more than one wild boar is found dead in the same place, these are reported as suspect swine fevers to APHA for official investigation and sampling, as occurred in the recent case described here.

The case also highlights the need to prevent wild and feral boar encountering material potentially infected with notifiable disease pathogens including the viruses causing swine fevers and foot-and-mouth disease. This is vital to avoid the devastating consequences of a notifiable disease outbreak on livestock health and welfare as well as international trade. People visiting areas inhabited by feral wild boar are reminded of the importance of not feeding these animals and taking away food waste or disposing of it in secure bins. The public should also be aware [of a ban that is currently in place for personal imports](#) of products of ruminant and porcine origin for travellers coming to GB from countries in the European Union. This ban was put in place following two previous outbreaks of foot and mouth disease virus that occurred in Germany, Hungary and Slovakia in 2025.

Suspicion of notifiable disease in animals must be reported immediately to APHA. 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](#).

## Pyometra in a rare-breed sow

A two-year-old rare-breed sow was submitted from a small herd to investigate malaise and inappetence, with infertility also described. The submitted pig first became unwell a week prior to submission and later developed diarrhoea and died. There was no obvious improvement after treatment with penicillin-streptomycin. The group was housed with access to a field. No vaccines had been given to the sow which had been introduced to the herd over a year earlier.

The sow was in good body condition with dark red to purple skin over the ventral body. Lymph nodes were generally slightly enlarged and dark purple. Inguinal lymph nodes and those regional to the reproductive tract were significantly enlarged. The uterus was enlarged, flaccid and fluid-filled (Figure 1) and contained approximately twenty litres of turbid pale yellow to cream liquid with floccular material. The endometrium was dark red with multifocal areas of mild thickening. No foetal material was found. The findings prompted bacterial culture and profuse growths of mixed flora containing heavy growths of a haemolytic Gram-negative rod were obtained from the left and right uterine horns. The Gram-negative rod was identified as *Actinobacillus rossii* from both sites.

Systemic cultures were sterile; it is likely that the pyometra found led to a terminal toxæmia. It is uncertain whether the *A. rossii* was the original cause of the pyometra or was an opportunist pathogen. *A. rossii* is a normal inhabitant of the porcine vagina but can cause ascending infection and has been associated with abortions. A recent case of abortions due to *A. rossii* is described in the [quarterly GB pig disease surveillance and emerging threats report for quarter 2 of 2025](#). *A. rossii* is more usually thought to cause sporadic abortions rather than the infertility described in this herd.

There was a history of past importation into the herd from a country in Europe where *Brucella suis* has been described in wild boar. This information, together with the history of infertility, prompted *Brucella* selective cultures and Modified Ziehl-Neelsen-stained smears to be undertaken on the reproductive tract. These did not detect any *Brucella* species. *B. suis* is a reportable pathogen in the UK and has never been detected in the country. APHA undertakes routine surveillance testing for *B. suis* including bacterial cultures on selective media for *B. suis* on porcine foetopathy and musculoskeletal cases as well as spinal lesions.

**Figure 1: Enlarged uterus containing purulent liquid.**



## Coal tar toxicity in growing pigs

Coal tar poisoning was diagnosed in eight-week-old pigs on an outdoor unit. The farm had been experiencing disease issues for approximately two weeks. There were around 30 deaths and live pigs showed clinical signs including purple discolouration of the ears and loss of body condition. No pigs in the other pens on the farm were affected. Post-mortem examinations carried out on farm by the herd veterinarian identified anaemia and markedly enlarged, friable and mottled livers (as illustrated in Figure 2). The stomach of one pig contained a small amount of dark material. The discoloured ears and presence of petechial haemorrhages over the renal cortices and across the serosa of the intestine

prompted the vet to call the Thirsk VIC for advice, in particular about whether the pathology could be due to swine fevers. The striking hepatic pathology and absence of pyrexia in affected pigs, together with other pathological and epidemiological findings, meant that swine fevers were not suspected and coal tar toxicity was considered a possibility.

**Figure 2: A previous case of coal tar toxicity which had a mottled enlarged liver and mesenteric oedema.**



Fixed liver was submitted to APHA Weybridge for histological examination. This confirmed moderate to severe hepatic necrosis and haemorrhage consistent with a diagnosis of coal tar poisoning. A search on the farm found evidence of previous shooting activity (unspent old shotgun cartridges), with clay pigeon shooting suspected to have taken place previously on the site. Bitumen was a constituent of old clay pigeons and is a source of coal tar if fragments are ingested by pigs. It was also revealed that the site was historically used as an airfield and was ploughed prior to use as pig paddocks without being cleared first, thus it was possible that asphalt fragments containing coal tar remained. Given that just one pen of pigs were affected, this latter theory may be less likely. As the liver pathology in coal tar cases is indistinguishable from that resulting from *hepatosis dietetica*, the clinical history and identification of exposure to sources of coal tar were vital to establish a diagnosis in this case.

Cartridge cases were amongst items found and, as a precaution and due to potential access by pigs to material which may contain lead, blood lead concentrations are being monitored in the group of exposed pigs to protect food safety.

The affected group of pigs were moved and the veterinary lead for toxicology at APHA was notified. The incident was raised to the Food Standards Agency as a potential food safety issue. This resulted in an agreed restriction of the pigs from the food chain for over 28 days following their removal from the source of coal tar, although the affected pigs were not destined for the food chain for a few months. There is an APHA [note on coal tar poisoning](#) for more information.

# Disease patterns and risk factors

## 2025 *Brachyspira hyodysenteriae* whole genome sequencing and antimicrobial sensitivity findings

*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 for 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 1 shows the STs identified by WGS completed for isolates from submissions to APHA or SRUC in 2025. WGS was successfully undertaken on 22 isolates. Eleven different STs were identified in 2025. Each year several novel allelic profiles are identified; these are submitted to the pubMLST database and allocated a new ST. Four new STs were identified in 2025. There was just one ST341 isolate in 2025, which is notably fewer than the 13 ST341 isolates in 2024. ST341 was detected for the first time in early 2024.

In recent years (2020 onwards), one particular ST (ST251) has been associated with multi-drug resistance, including clinical resistance to tiamulin. Two ST251 isolates were identified in 2025 from two counties. MIC testing of one of these isolates showed clinical resistance to tiamulin, tyvalosin, lincomycin and tylosin and both contained genes associated with reduced susceptibility to pleuromutilins, tiamulin, valnemulin, lincomycin, tylosin, tyvalosin and doxycycline. Apart from the ST251 isolate, no other isolates showed clinical resistance to tiamulin.

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 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).

**Table 1: Sequence types of *Brachyspira hyodysenteriae* isolates detected in submissions received in 2025.**

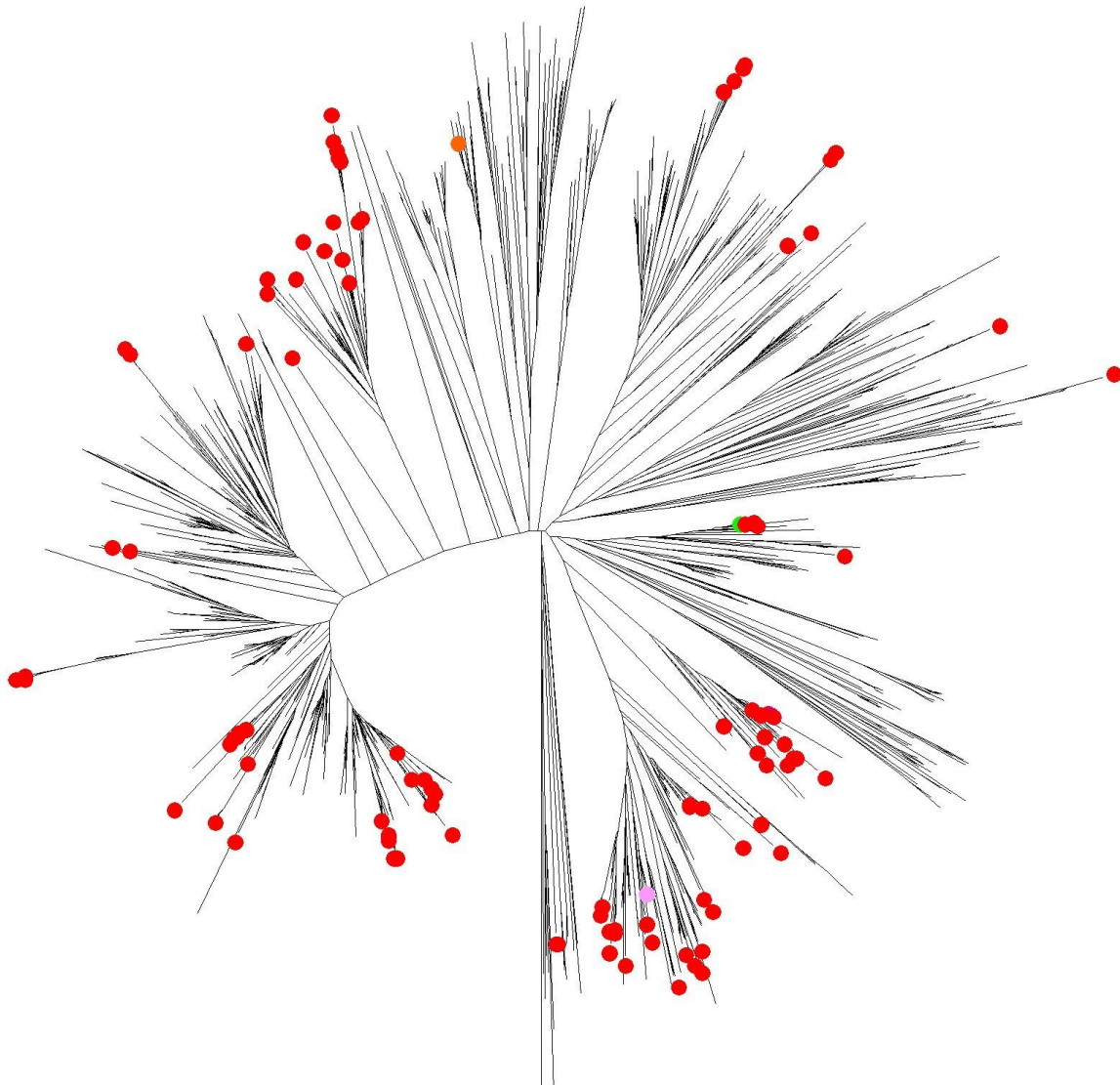
| ST identified | Number of isolates | Counties of origin in 2025                                           | ST identified in UK isolates prior to 2025 |
|---------------|--------------------|----------------------------------------------------------------------|--------------------------------------------|
| 52            | 4                  | Dorset, East Riding and North Lincolnshire, Worcestershire, Somerset | Yes                                        |
| 88            | 2                  | East Riding and North Lincolnshire and Norfolk                       | Yes                                        |
| 242           | 4                  | North Yorkshire                                                      | Yes                                        |
| 251           | 2                  | Lincolnshire and East Riding and North Lincolnshire                  | Yes                                        |
| 270           | 2                  | South Yorkshire                                                      | Yes                                        |
| 341           | 1                  | Norfolk                                                              | Yes                                        |
| 344           | 1                  | Scottish Borders                                                     | Yes                                        |
| 348           | 2                  | Norfolk                                                              | No                                         |
| 352           | 1                  | Norfolk                                                              | No                                         |
| 356           | 2                  | Norfolk and Lincolnshire                                             | No                                         |
| 358           | 1                  | Norfolk                                                              | No                                         |

## PRRSV-1 recombinant viruses identified from 2021 and 2025

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. Viruses in which the ORF5 gene sequence has 98.5% or greater similarity to one of the live commercial 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.

The phylogenetic tree below is based on ORF5 gene sequences from GB, with the 153 sequences identified in 2025 in red. The sequences originated from 135 submissions. The percentage of vaccine-like sequences found was 13% Porcilis® PRRS, 13% Unistrain® PRRS, 1% Suvaxyn® PRRS, and 3% Ingelvac PRRSFLEX® EU/ReproCyc® PRRS.

**Figure 3: Phylogenetic tree based on ORF5 gene sequences of PRRS viruses from GB, with the 153 sequences identified in 2025 in red.**



Two recombinant PRRSV-1 viruses involving vaccine strains have been identified during recent sequencing at APHA. One was identified through sequencing a retrospective PCR-positive sample from 2021 and the other was identified in a 2025 submission. Clinical signs were not described in either case and the 2025 case was from a monitoring submission.

The first virus, from the 2021 submission, exhibited close (99.5%) similarity to a vaccine strain at the ORF-5 gene. The nsp2 gene was only 84.6% similar to that same vaccine strain. Whole genome sequencing (WGS) found the genome contained portions of another vaccine strain. The two vaccine strains involved were also identified in a previous recombinant PRRSV-1 which was associated with disease in pigs in Denmark (Genís and others, 2020; Kvisgaard and others, 2020). However, the WGS in this case was genetically different and distinct from the disease-associated recombinant identified in Denmark. Further, no closely related viruses to the 2021 GB recombinant virus have been identified from sequencing almost 800 PRRSV-1 since 2021.

The second virus, from a 2025 submission, exhibited 98% similarity to a different vaccine strain at the ORF-5 region, while the nsp2 region was only 62% similar to that same vaccine strain. WGS found the genome contained portions of a field strain of PRRSV-1 which had been detected in a historic sample submitted from the same farm. Whole genome sequencing of a PRRS virus detected from further samples collected from the farm six months after the submission is ongoing. The farm in question was a breed-to-finish herd. APHA have not found evidence of this same recombinant virus on other farms.

These viruses represent the second and third detections of recombination involving vaccine or vaccine-like viruses in GB; the first previously detected recombinant virus likely resulted from a recombination event between a field strain of PRRSV and a vaccine or vaccine-like strain (Frossard and others, 2013). Such detections underline the potential for recombinant events between different PRRSV strains; the [importance of following guidelines for the use of modified live PRRSV vaccines](#) (such as that simultaneous or consecutive use of different vaccine strains should be avoided as much as possible); and the value of sequencing of PRRS viruses to detect such events. The relevant vaccine companies and the Veterinary Medicines Directorate have been made aware of these cases.

## Horizon scanning

### First outbreak in Poland of *Klebsiella pneumoniae* septicaemia in piglets

*Klebsiella pneumoniae* subsp. *pneumoniae* (Kpp) is a component of the intestinal flora of mammals and has long been considered an opportunistic pathogen causing sporadic disease in pigs, usually manifesting in individual pigs as mastitis, septicaemia or pneumonia. In recent years, several countries including Australia (Bowring and others, 2017), GB (Bidewell and others, 2018) and [the Netherlands](#) (Van Hout, 2019) have described emergence of outbreaks of septicaemia in preweaned piglets caused by the emergent Kpp ST25.

[The first report of septicaemia in sucking piglets due to Kpp in Poland has recently been published](#) (Cybulski and others, 2026). Molecular characterisation of the isolates from this outbreak showed similarity to those associated with disease outbreaks in pigs in the literature in other countries and the Polish outbreak involved Kpp ST25. There was also broad similarity between the outbreak described in Poland and those occurring in GB with respect to the young age of pigs affected, septicaemic disease manifestation and summer occurrence. However, there are also differences as outbreaks in GB have been predominantly in outdoor herds, whereas the outbreak in Polish piglets was on an indoor farm. Further, very few outbreak-associated Kpp ST25 isolates from GB have shown acquired antimicrobial resistance, whereas there was some acquired antimicrobial resistance detected in the Kpp isolates from the outbreak in Poland.

The paper from Poland serves as a reminder of the upcoming season for Kpp septicaemia outbreaks; outbreaks in GB typically have a summer occurrence and most diagnoses by APHA since the emergence of this disease in 2011 are recorded between May and October. More information including the Kpp outbreak case definition is in a surveillance focus article on [Kpp septicaemia outbreaks in pigs in England](#). Diagnosis is confirmed by bacterial culture from pigs with septicaemia.

## 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 digital learning resource on diagnostic investigation of nervous signs

The Pig Expert Group have recently published a [digital learning resource](#) exploring diagnostic investigation for a common presentation of nervous disease in pigs, including differential diagnoses. It includes fact sheets, videos and a quiz with signposting to extra information. It will take approximately one hour to complete. It can be [accessed directly](#) or from the [APHA vets page](#) where further resources will be published in the future. APHA hopes it will be of use to vet students, pig vets early in their career and general practice farm vets.

### New 'Dissecting Animal Diseases' APHA podcast

APHA's new '[Dissecting Animal Diseases](#)' podcast involves discussions around diagnostic investigations completed at APHA. Listen to the first two episodes, '[investigating a case of lameness and recumbency in breeding sows](#)' and '[investigating diarrhoea in a small-scale pig herd](#)'. Follow the podcast on [Spotify](#) or [Apple podcasts](#) to never miss an episode.

### 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 1979 diagnostic submissions tested under AHDB Pork funding from June 2013 to March 2026. 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, diagnoses of systemic disease due to PCV3 in postnatal pigs have been sporadic and have affected a single pig from the batch of pigs submitted in all but three occasions.

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](#).

## 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 [one H3N2 detection](#), 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 between 1997 and late 2025 when H3N2 was detected in one herd.

## Seneca Valley virus

In 2022, [APHA confirmed vesicular disease due to Seneca Valley virus \(SVV\) 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, 2024 and 2025 and none to date in 2026. Key facts about SVV are provided [here](#) and more information about the SVV outbreaks in pigs in England was [recently published](#) (Armson and others, 2026).

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