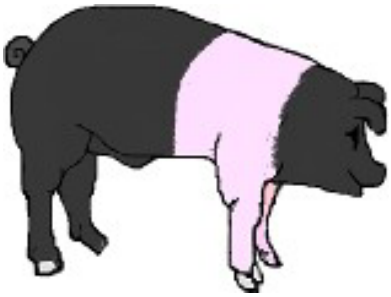
Animal & Plant Health Agency



SRUC

Great Britain pig quarterly report: disease surveillance and emerging threats

Volume 33: Quarter 2 of 2025 (April to June)

Highlights

- Diagnostic investigation of negated vesicular disease report case – 1
- Unusual bacterial abortions – 3
- Two different causes of hindlimb paresis in sows – 3
- Experimental infection with porcine astrovirus 4 in the US – 9

Contents

Introduction and overview

This quarterly report reviews potential disease threats for the second quarter of 2025 (April to June). 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

Diagnostic investigation of negated vesicular disease report case

An official APHA investigation took place into a report of suspect vesicular disease in sows which resulted in notifiable diseases (foot-and-mouth disease, vesicular stomatitis and swine vesicular disease) being ruled out by laboratory testing. The herd was an outdoor single-parity (parity 3) breeding herd in England. Sudden onset of clinical signs were reported to have begun after some particularly hot weather in a batch of very recently served sows. Fifty percent of the affected group were found to be reluctant to leave their arcs but still ate and drank. Twenty-five percent of the group were lame, five of which were described as having ulcers at the coronary bands. One sow had a lesion on her snout that was later assessed to be a traumatic lesion, rather than a vesicular lesion. Affected sows were not pyrexic and no other clinical signs were described on the farm which appeared relevant to the disease being reported.

Samples collected from affected sows were tested for Seneca Valley virus (SVV) by The National Reference Laboratory for Vesicular diseases at The Pirbright Institute and were negative for viral nucleic acid by RT-PCR and for SVV-specific antibodies by the virus neutralisation test (VNT).

A visit to investigate the cause for this negated report case was undertaken by an APHA Pig Expert Group veterinarian three days after the initial description of clinical signs. No fresh lesions were found in dry sows and lesions in the affected sows had begun to heal (Figure 1). A few sows were cautious in placing their hindfeet, but sows otherwise appeared clinically well. More vertical hoof fissures were noted amongst the affected group of sows than the unaffected groups (Figure 2). No obvious causes of trauma were identified for the affected group; the farm was very well-managed and biosecurity protocols were stringent. Although the ground was hard and stoney, given the dry weather, there was not a noticeable difference between the environments of the affected and unaffected groups. Epithelial tissue was collected three days after the initial description of clinical signs and have been tested by next generation sequencing at APHA Weybridge, with results awaited.

Similar but less severe clinical signs were noted after the following batch of sows were served and a second visit was made to the farm. Five sows with very mild lameness were identified, three of which had vertical hoof fissures, some with wounds or bruising at the coronary band, but no vesicular lesions were found. Further blood samples were collected. Five from the currently affected group tested negative for SVV by RT-PCR. Four out of five from the previously affected group were seronegative to SVV by VNT and one tested SVV antibody positive. Serology by VNT was repeated on this sow, as well as 17 more sows, six weeks after the initial clinical signs. All 18 tested negative for antibodies to SVV. These results provide evidence that the clinical signs demonstrated were not associated with

infection with SVV. Goolia and others (2017) indicate that pigs seroconvert to SVV within around seven days and that positive antibody titres are maintained in most pigs for at least six months.

Hoof lesions (including hoof fissures) in sows are described as being multifactorial in cause. To name just two of the nutritional factors associated with foot health in pigs, biotin and zinc are crucial to horn integrity (van Riet and others, 2013). Supplementation of biotin has been shown to reduce claw lesions and lameness in sows (De Jong and Sytsema, 1983). The same has been shown for zinc in dairy cattle (Moore and others, 1989). For these reasons, the 10 sera from the second visit were tested for zinc and biotin. The concentrations detected did not suggest zinc or biotin deficiency in the sows tested (De Jong and Sytsema, 1983; Elbers and others, 1994), although serum reference ranges for zinc and biotin are not well established for the modern sow. As serum biotin levels are considered to fluctuate significantly – measurements on two different days are recommended in people (Trüeb, 2016) – and to ensure that dietary biotin was adequate, dietary biotin levels for sows were increased following this incident. No further clinical signs were noted in subsequent sow batches.

A definitive diagnosis was not reached and it remains possible that the hard ground and weather conditions affected the recently weaned and served sows more than other groups. Importantly, the farmer and submitting veterinarian showed diligence in promptly reporting suspect notifiable disease to APHA. This enabled rapid investigation, negation of notifiable disease and lifting of restrictions.

Figure 1: Coronary band lesion in a sow in which notifiable diseases had been ruled out.

Figure 2: Vertical fissure in the hoof of a sow.

Unusual bacterial abortions

Abortions affecting two successive batches of breeding pigs were investigated on a recently established single parity (parity 1) herd. The abortion rate was 4% for one batch and 3% for the other. Affected gilts had been due to farrow in three to seven weeks. Gilts were vaccinated against common endemic pathogens which cause fetopathy including erysipelas, leptospirosis and parvovirus.

Four separate submissions of foetal material (making up five litters) were provided for diagnostic investigation to the Bury St Edmunds VIC. Aborted piglets weighed between 235 and 870g. There were piglets with reddened skin lesions in three of the four submissions (Figure 3) and placentae were semi-opaque in two of the four submissions. Bacterial culture of foetal stomach contents of five piglets from three of the submissions grew mixed flora containing light to very heavy or pure growths of an *Actinobacillus* species identified as *A. rossii*, for which the species was additionally confirmed by MALDI ToF sequencing. Bacterial culture of foetal stomach contents of two different piglets from two submissions grew mixed flora containing heavy growths of *Streptococcus suis*; one was identified as serotype 2 and the other as serotype 28. No other abortifacient agents were detected by diagnostic testing including pathogenic *Leptospira* and porcine reproductive and respiratory syndrome virus.

A mild necrosuppurative placentitis was confirmed in two placentae (Figure 4) from one submission and a Gram stain highlighted colonies of bacteria characteristic of *Actinobacillus* (a mix of Gram-negative pleomorphic rods and coccoid bacteria) as well as a smaller number of Gram-positive ovoid cocci in short chains and pairs (resembling *Streptococcus* or *Staphylococcus* species).

A. rossii has been associated with sporadic abortions in past submissions to APHA (APHA, 2015; 2020; 2023), but has not previously been confirmed in multiple submissions over a short time frame from a breeding herd. Holyoake and Thompson (2017) described isolation of *A. rossii* from an abortion outbreak in sows in Australia but isolated *A. rossi* from only one piglet. The case here, therefore, represents the first time, to our knowledge, that *A. rossii* has been isolated from more than one piglet in several aborted litters from one herd. Interestingly, Holyoake and Thompson (2017) also described reddening of the skin of an aborted foetus as well as (moderate to severe) necrosuppurative placentitis, although the skin reddening likely represents a non-specific finding possibly related to the placentitis.

Both *A. rossii* and *S. suis* are normal inhabitants of the porcine vagina but may cause abortion through ascending infection, and for *S. suis* also through haematogenous infection. Potential factors underlining an increase in bacterial abortions were explored for the farm but were not identified. Abortions ceased after the two batches were affected without specific intervention.

Figure 3: A piglet from which *Actinobacillus rossii* was isolated from the stomach contents with areas of reddened skin (ears and distal limbs).

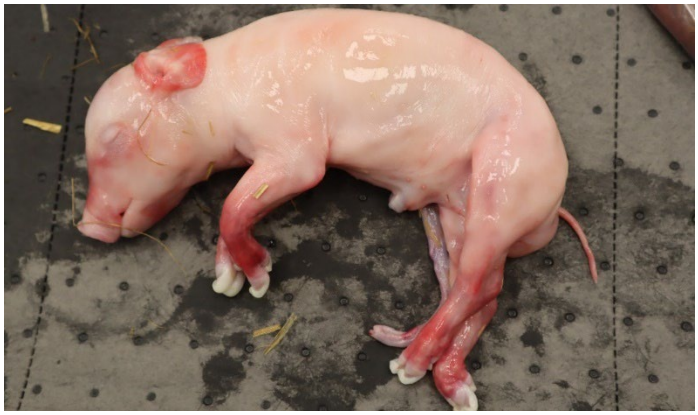
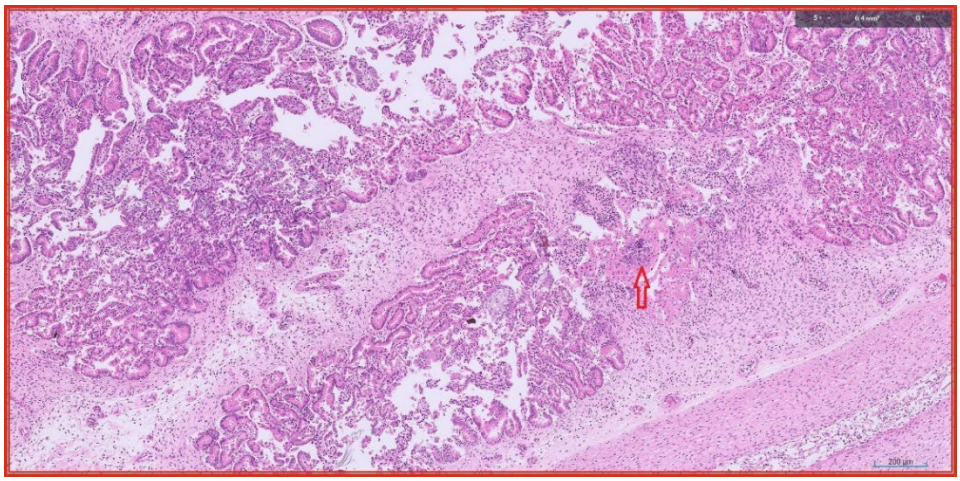


Figure 4: Mild necrosuppurative placentitis (red arrow) in a placenta from which *Actinobacillus rossii* was isolated. Pig placenta, HE stain. Image courtesy of Sionagh Smith, Finn Pathologists.



Two different causes of hindlimb paresis in sows

Two sows were euthanased on-farm and submitted to the Thirsk VIC from a single-parity herd (at parity 2) to investigate the cause of acute onset hindlimb weakness and paralysis. Both sows were affected around six weeks prior to their farrowing date and were in fair body condition. Videos showed the sows struggling to lift their bodyweight using their hindlimbs as well as knuckling of the hindlimb feet (Figure 5). There had been no response to antimicrobial and non-steroidal anti-inflammatory treatment.

In video footage received from the practitioner, the first sow demonstrated marked hindlimb weakness and knuckling, suggesting a lesion in the lumbosacral intumescence. There were no grossly visible lesions in the spinal column or hindlimbs at postmortem examination, but microscopic survey of the spinal cord revealed a focal area of necrosis at the level of L6 resulting from fibrocartilaginous embolism (FCE).

FCE is well recognised as a sporadic cause of spinal disease in pigs and other species and has been described in pigs of various ages (Pass, 1978; Piva and others, 2022;

Tessaro and others, 1983). The aetiopathogenesis remains poorly understood, but the end result is embolization of intervertebral disc material into the vasculature of the spinal cord and ischaemic necrosis. Heavy muscling, carcase weight, vigorous activity/exercise, metabolic bone disease, and degenerative spine disease are putative risk factors for the condition in pigs (Benson and Schwartz, 1998; Done and others, 2012), but these are unproven.

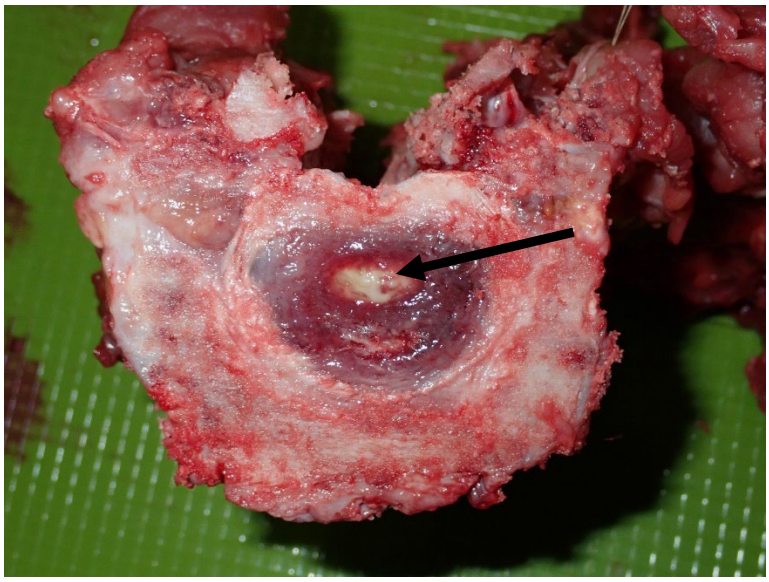
In the second sow, there was a fibrous and bony protuberance over the ventral aspect of the spinal column approximately at the level of lumbar vertebra L1, with multiple purulent tracts through surrounding soft tissue. On sectioning of this portion of the spinal column, a focal abscess occupying the intervertebral disc (Figure 6) and part of the vertebral body was found. This finding was consistent with the clinical signs described. There are various reasons for spinal abscesses occurring in pigs, including haematogenous infection following tail biting or other trauma, haematogenous spread from sites of bacterial infection elsewhere in the body (e.g. arthritis) and suboptimal injection hygiene. *Brucella suis* is a notifiable disease and is a recognised cause of spinal abscessation; the UK is free of *B. suis* and lesions of the nature found in this sow are routinely selectively cultured for *B. suis* as part of surveillance to provide evidence of freedom. Aerobic bacterial cultures did not yield *B. suis*, or any other bacterial pathogen.

It was interesting that a similar clinical presentation in sows at the same stage of production and in a close time frame was found to be due to differing mechanisms and the wider significance of these cases to the herd is uncertain. Inflammation of the intervertebral disc (diskospondylitis) and FCE have been described to occur together in pigs (Haynes and Benson, 1999); it is suggested that diskospondylitis predisposes an animal to intervertebral disc collapse, with subsequent embolization of nucleus pulposus to the spinal cord. The primary disease process resulting in FCE in the first sow from this case was not identified at postmortem examination, and it is possible that this sow had intervertebral disc disease or osteomyelitis that was overlooked.

Some causes of acute hindlimb lameness in sows can be diagnosed through on-farm post-mortem examination (e.g. pathological fractures due to lactational osteoporosis, infectious arthritis or osteochondrosis dissecans). However, cases such as those described here, where examination of the spinal column and canal and collection of nervous tissues are essential, demonstrate the value of full post-mortem examination and laboratory-based diagnostic investigations. Full clinical histories together with videos are vital for such investigations. Careful removal of the brain and spinal cord and sectioning of the spine for examination are time-consuming exercises that benefit from the use of appropriate equipment in the hands of experienced technicians.

Figure 5: Image captured from video of the sow with FCE showing hindlimb weakness and knuckling.

Figure 6: Diskospondylitis: infected intervertebral disc (abscess) in a sow, with purulent material replacing the nucleus pulposus. Arrow showing purulent material.



Another detection of *Brachyspira hampsonii* in finishing pigs

Brachyspira hampsonii was detected in a faecal sample from 15-week-old pigs with diarrhoea and some mild loss of condition. The diarrhoea was cow pat to watery in consistency and coloured dark to light-grey and sometimes brownish. Seven faecal samples were submitted to SRUC in December 2024; all tested positive for *B. pilosicoli* by PCR and culture. Culture and presumptive identification through biochemical testing also identified an isolate of *B. hampsonii* from one sample and the species identity was confirmed by whole genome sequencing (WGS) at APHA. The contribution of the *B. hampsonii* to the clinical disease is uncertain in this case given the presence of *B. pilosicoli*, a cause of spirochaetal colitis, in all the samples. This detection of *B. hampsonii*

was on an all-in-all-out rearing unit in South-East England, which has since depopulated. The isolate contained no AMR genes or SNPs associated with reduced susceptibility to pleuromutilins (tiamulin and valnemulin), lincomycin, tylosin and tylvalosin or doxycycline. Minimum inhibitory concentration (MIC) testing indicated sensitivity to the antimicrobials tested and showed no clinical resistance to antimicrobials licensed and commonly used to treat diarrhoea due to *Brachyspira* species in pigs.

WGS and MIC testing was completed at no charge to the submitting vet, under funding from APHA's pig disease scanning surveillance project. The isolate was confirmed as ST 23 from the *B. hampsonii* MLST scheme. This sequence type has been identified in eight previous submissions in 2020 to 2021 from South-East England, East of England, East and West Midlands (APHA, 2021). WGS of the 2025 isolate also determined it to be closely genetically related to the 2020 to 2021 pig isolates. The first detection of *B. hampsonii* by APHA was in April 2019 in finishers with loose faeces (APHA, 2019). This first isolate detected in 2019 was of a different ST and is not genetically related to the other isolates that have been detected from pigs in GB from 2020 to the current isolate.

B. hampsonii was described as a new potentially pathogenic species in pigs in North America in 2012 (Chander and others, 2012). *B. hampsonii* has strong haemolysis in culture and is regarded as a causative agent of diarrhoea in pigs, which is sometimes muco-haemorrhagic in nature (Wilberts and others, 2014). *B. hampsonii* was identified by APHA in a captive rhea (Rhea sp.) with severe typhlocolitis in 2019 (McFadzean and others, 2021).

B. hampsonii has been reported in European pigs imported to Germany from Belgium (Rohde and others, 2014) and pigs imported to Belgium from the Czech Republic (Mahu and others, 2014). *B. hampsonii* has also been detected in wild waterfowl (greylag geese and mallards) in Europe, which may be implicated in transmission of infection (Martínez-Lobo and others, 2013). Transmission of *Brachyspira* species is oro-faecal*; B. hampsonii* is not a notifiable or reportable disease. It is not zoonotic and pork/pork products are not a recognised route of transmission.

This finding highlights the importance of carrying out cultures for *Brachyspira* species in tandem with PCR testing in order to identify emerging *Brachyspira* species and obtain isolates for WGS and antimicrobial sensitivity testing. Recently, SRUC have introduced a new *Brachyspira* RT-PCR test which specifically detects four pathogenic species of *Brachyspira* (*B. hyodysenteriae, B. pilosicoli, B. hampsonii and B. suanatina*). The test is expected to enhance the ability of the GB scanning surveillance network to detect emerging *Brachyspira* species.

Changes in disease patterns and risk factors

Porcine circovirus detection in abattoir serum archives

An archive of just over 800 sera from pigs sent to abattoirs in England was established in 2023-24 through collaboration between Agriculture and Horticulture Development Board (AHDB) Pork and APHA. The sera derived from pigs from approximately 600 premises in England and Wales. The serum archive was tested by APHA Virology for three porcine circoviruses by PCR; PCV2, PCV3 and PCV4. Table 1 shows the results with a comparison to those from testing the 2019 archive for PCV2 and PCV3.

Table 1: Porcine circovirus prevalences in pigs sampled at abattoirs in England and Wales.

Year	% PCV2 PCR +ve	% PCV3 PCR +ve	% PCV4 PCR +ve
2019	16.0 *(95% CI 13.3-18.8)*	38.3 *(95% CI 34.7-42.0)*	Not tested
2023-24	19.2 *(95% CI 16.5-21.9%)*	26.3 *(95% CI 23.3-29.3%)*	0.7% *(95% CI 0.1-1.3%)*
Prevalence change 2019 to 2023-24	Not significant	Significant reduction (p<0.001)	Not applicable

PCV2 and PCV3 are both considered endemic in pigs in GB with subclinical infection being a common feature. The findings of the archive testing confirm this to be the case.

PCV2 – abattoir study

PCV2 prevalences described in healthy pigs in other countries vary widely and depend on the number and types of samples and the sampling strategy, making them not directly comparable with the results found here. However Saporiti and others (2020b) detected a similar prevalence of PCV2 by PCR in 21% of 624 sera from fattening pigs in nine European countries.

In the current study, the majority of PCV2 PCR-positive sera had high Ct values, equating with low viral loads in the blood. Consequently, it was not possible to sequence all the PCR-positive samples. All 20 sera which yielded an ORF2 sequence were genotype PCV2d. This reflects the genotype shift from PCV2b to PCV2d that has been described globally over time. APHA PCV2 disease-associated cases that have been genotyped in

recent years have also shown this shift to being predominantly due to PCV2d, with a few due to PCV2b (APHA, 2020).

PCV2 emerged causing widespread severe multisytemic disease in pigs in GB from 1999. PCV2 disease diagnoses in British pigs have been at a low level since commercial PCV2 vaccines became widely used in commercial pigs from the mid-2000s. The persistent detection of PCV2 in the serum archives from healthy pigs sampled in abattoirs at two time points indicates that this virus remains prevalent as a subclinical infection in pigs and presents a continued threat to unvaccinated pigs.

PCV3 - abattoir study

PCV3 is distinct from PCV2. PCV3 has been described in pigs since 2016 in many countries globally, including the UK, since the first report from the US (Palinski and others, 2017). It has been detected in healthy and diseased pigs. For diseased pigs, it has been associated with a variety of disease manifestations for which case definitions have been established (Saporiti and others, 2021). Most notably, this is foetopathy with myocarditis (presenting as outbreaks of stillbirths and weak neonatal piglets) and, more sporadically, postnatal multisystemic inflammation. Research indicates that this virus, although newly discovered in pigs, has been present in pig populations for a number of years.

The APHA Pig Expert Group has surveillance in place for PCV3-associated disease through use of myocardial histopathology on all submitted pigs, foetuses and stillborn piglets. Those found to have non-suppurative myocarditis are investigated further for involvement of PCV2 or PCV3. To date, APHA has detected PCV3-associated disease at relatively low frequency (APHA, 2023; 2025).

The PCV3 prevalence in the 2023-24 serum archive shows that this virus, like PCV2, is a common virus in the national pig population. PCV3 prevalence has not increased and, in fact, is significantly lower than in the 2019 archive.

Direct comparison of the 2023-24 PCV3 prevalence with those reported in studies in other countries is not possible as the sera tested are sourced in diverse manners, not usually at the national level, and some are tested in pools not individually. A study in Spain compared PCV3 prevalence in the sera of pigs with respiratory or enteric disease with the prevalence in sera from healthy age-matched pigs and found no difference (Saporiti and others, 2020a). The percentage of PCV3 positive sera was generally lower in their study than detected here with 6.7% of the healthy pigs testing PCR positive, although only 60 healthy pigs were tested. Klaumann and others (2019) describe longitudinally sampling pigs and testing for PCV3 on four pig farms in Spain; the frequency of infection was not consistently higher at any particular age and the prevalence at 25 weeks old ranged from around 10 to 32%.

In the current study, there was no significant association between the detection of PCV2 DNA and PCV3 DNA. ORF2 sequences were successfully obtained for 31 of the PCV3

PCR-positive sera and showed high sequence homology with previous PCV3 strains sequenced by APHA.

First detection of PCV4 in pigs in England

PCV4 was first identified as a new circovirus in 2019 in diseased pigs in Hunan Province, China (Zhang and others, 2020). Until 2023, PCV4 was only described in Asia and the USA and a few studies in South America and Europe failed to detect it. Spain confirmed the first detection of PCV4 in Europe in 2023 (Holgado-Martín and others, 2023). To our knowledge, this PCV4 detection in the 2023-24 abattoir serum archive is the first detection of PCV4 in GB pigs. There was no specific surveillance for PCV4 in pigs in England and Wales prior to testing the 2023-24 archive.

PCV4 shows highest genomic identity to mink circovirus (66.9%) and has genetic homology of only 43.2%-51.5% to the other pig porcine cirvovirus genomes. The clinical significance of PCV4 remains unclear and, to date, it has not been associated with any specific disease syndrome.

The prevalence was low (PCV4 prevalence 0.7%; 95% CI 0.1-1.3%); just six sera tested positive for PCV4 by PCR. These derived from pigs from premises in three different geographic regions of England. As with PCV2 and PCV3, high PCR Ct values indicated low PCV4 loads and likely subclinical infection.

The specificity of the PCV4 PCR was confirmed by sequencing a small fragment of the PCV4 genome (165-nucleotides) in three samples. Further work will try to obtain longer sequences to enable comparison with PCV4 detected elsewhere.

This testing provides a baseline prevalence for the porcine circoviruses which can be monitored for changes over time. The archive data assists interpretation and investigations in the event of any change in, for example, the frequency of disease incidents associated with porcine circoviruses, or a change in their manifestation.

Horizon scanning

Experimental infection with porcine astrovirus 4

A preliminary Swine Health Information Centre (SHIC) report describes a study in the US in which 17 piglets were experimentally infected with porcine astrovirus genotype 4 (PoAstV4). This was prompted by detection of PoAstV4 in respiratory disease samples where no diagnosis had been reached, described in a joint SHIC/American Association of Swine Veterinarians webinar. The current study found that PoAstV4 was shed in nasal secretions as early as two days post infection (all pigs tested negative by 14 days post challenge). Necropsy at five- and eight-days post infection demonstrated that infected pigs developed tracheitis and bronchitis and virus was detected in these lesioned tissues. Anti-

PoAstV4 antibodies were detected in serum. The findings of the study described suggest that PoAstV4 should be considered a differential diagnosis for respiratory signs, particularly coughing, in suckling and early nursery pigs, and where common viral pathogens like swine influenza virus are not detected.

Porcine astroviruses (PoAstVs) have been detected in porcine faeces by APHA in a metagenomics study which tested samples from a small number of pigs. PoAstVs (genotypes 1, 2, 4 and 5) were detected in both diarrhoeic and age-matched non-diarrhoeic pigs in the postweaning period, with a higher viral load in diarrhoeic pigs. No investigation into the role of PoAstV4 in respiratory disease has been undertaken at APHA however further findings from the US and elsewhere will be kept under review by the Pig Expert Group.

Prion detection in wild pigs in the US

A recently published study identified prions in tissues from wild pigs (using an ultrasensitive prion detection method) trapped in areas of the US with chronic wasting disease (CWD) in cervids (Soto and others, 2025). Prions were primarily detected in the lymph nodes of pigs, with fewer detections in brains. In some CWD-endemic areas in the US, wild pigs coexist with cervids and reportedly prey on fawns and scavenge deer carcasses. Although the current study did not provide evidence of disease in pigs, the study provides evidence that wild pigs are exposed to cervid prions in some environments and may act as carriers. Authors describe how scavenging pigs could contribute to the spread of CWD (which has uncertain zoonotic potential [Otero and others, 2021]) in such areas, through environmental contamination.

There are no documented reports of natural interspecies transmission of CWD and experimental infections of pigs have identified some resistance to infection amongst pigs (Otero and others, 2021). Given that the UK is free of CWD, the environmental CWD prion burden in the endemic areas studied in the US results in a significantly higher exposure risk to wild pigs. Further, it is likely that the interface between wild pigs and cervids also differs in GB in comparison to the US. Therefore, the results of this study have limited relevance to the GB pig population currently.

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. Outbreak assessments which detail such outbreaks are published here. Monthly IDM summaries are also included in the disease surveillance items in the Veterinary Record.

For foot-and-mouth disease, visit the .GOV.UK website for information on the latest situation. For African swine fever (ASF), visit here. European Commission information on ASF is accessed here 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 the swine fevers. ASF is a notifiable disease, meaning that suspicions must be reported immediately. In England, this is by calling the Defra Rural Services Helpline on 03000 200 301. In Wales, contact 0300 303 8268 and in Scotland, contact your local APHA Field Services Office. For information on notifiable diseases in animals, including disease controls, visit .GOV.UK.

Ongoing scanning surveillance initiatives

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 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.

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 1947 diagnostic submissions tested under AHDB Pork funding from June 2013 to June 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 PCV-3 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 which provides key features of PCV3 as well as APHA surveillance findings up to June 2021 is available here. Useful literature reviews on PCV3 include Klaumann and others (2018) and Kroeger and others (2022).

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 were due to PRRSV-1, with no PRRSV-2 detected in British pigs to date. The Pig Expert Group recently published an information note on preventing the introduction of exotic PRRSV strains into GB in imported live pigs or semen.

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 2025 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. No further recombinants have been found since a recombinant PRRSV-1 vaccine (or vaccine-like) and field virus was described in pigs in England (Frossard and others, 2013). All of the other vaccine-like PRRSV examined to date have had nsp2 and ORF5 sequences that are consistent with the expected result and do not raise concern that they represent 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. Details on how to access this testing is given here.

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. 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.

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