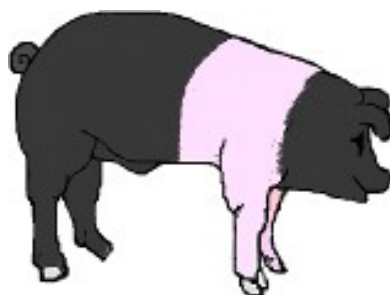




Animal &  
Plant Health  
Agency



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

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Volume 27: Quarter 2 of 2023 (April to June)

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## Introduction and overview

This quarterly report reviews disease trends and disease threats for the second quarter of 2023, April to June. It contains analyses carried out on disease data gathered from APHA, Scotland's Rural College (SRUC) Veterinary Services and partner post-mortem providers and intelligence gathered through the Pig Expert Group networks.

In addition, links to other sources of information including reports from other parts of the APHA and Defra agencies are included. A full explanation of [how data is analysed](#) is provided in the annexe available on GOV.UK.

### Pig disease surveillance dashboard outputs

Diagnoses made most frequently in the second quarter of 2023 compared to the same quarter in 2022 through the Great Britain (England, Wales and Scotland) scanning surveillance network are listed in table 1. These can be interrogated further using the interactive pig [disease surveillance dashboard](#) which was launched in October 2017.

**Table 1: Great Britain scanning surveillance 15 most frequent diagnoses in quarter 2 of 2023**

15 most frequent diagnoses in quarter 2 of 2023 (total 277)	15 most frequent diagnoses in quarter 2 of 2022 (total 221)
1. Salmonellosis – <i>S. Typhimurium</i>	1. <i>Lawsonia</i> sp. associated disease
2. <i>Brachyspira pilosicoli</i> colitis	2. Rotavirus
3. Porcine reproductive and respiratory syndrome (PRRS) - systemic	3. Colibacillosis - enteric
4. PRRS - pneumonia	4. Salmonellosis – <i>S. Typhimurium</i>
5. <i>Lawsonia</i> sp. associated disease	5. <i>Brachyspira pilosicoli</i> colitis
6. <i>Streptococcus suis</i> disease	6. PRRS - pneumonia
7. Colibacillosis - enteric	7. <i>Streptococcus suis</i> disease
8. Streptococcal disease (non- <i>S. suis</i> )	8. PRRS - systemic
9. Swine influenza	9. <i>Pasteurella multocida</i> pneumonia
10. <i>Glaesserella parasuis</i> disease	10. Pneumonia other cause
11. Digestive disease – not listed	11. Swine influenza
12. Streptococcal meningitis	12. Arthritis – non-listed cause
13. Swine dysentery – <i>B. hyodysenteriae</i>	13. Coccidiosis
14. <i>Trueperella pyogenes</i> disease	14. Streptococcal meningitis
15. Systemic disease – not listed	15. Colibacillosis – oedema disease

Note: that further diagnoses may be added for records for submissions made in quarter 2 of 2023 which are finalised at a later date.

Surveillance data for diagnostic submissions in quarter 2 of 2023 are illustrated in Figure 1.

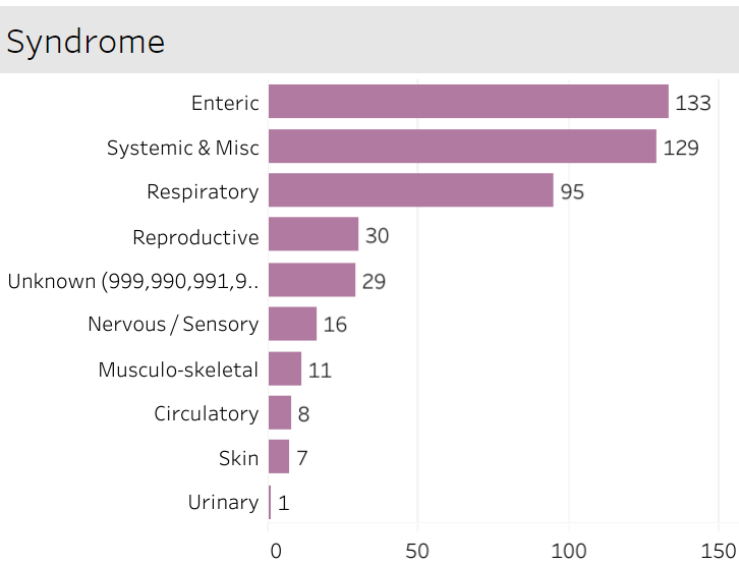
**Figures 1a to 1d: summary surveillance data for 459 submission records in quarter 2 of 2023 (353 in quarter 2 of 2022)**

**Figure 1a: pig age**

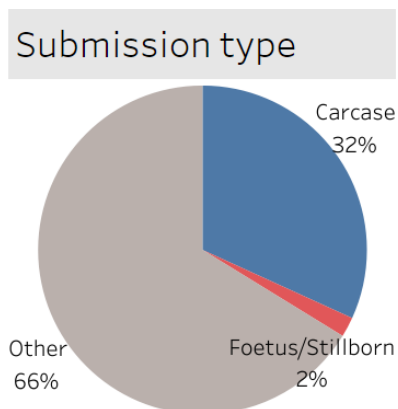
**Age category**

Adult	73
Mixed	2
Neonatal	30
Postwean	222
Prewean	25
Unknown/other	107

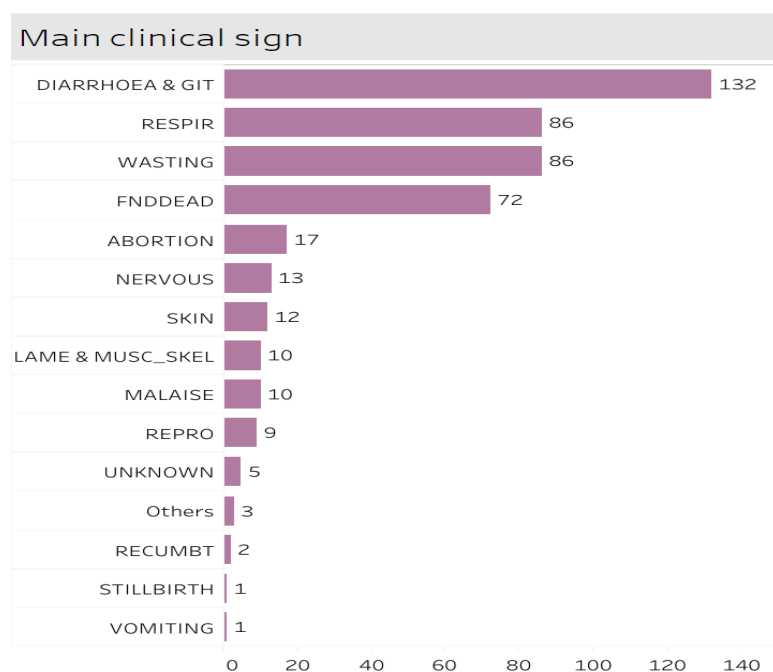
**Figure 1b: disease syndrome**



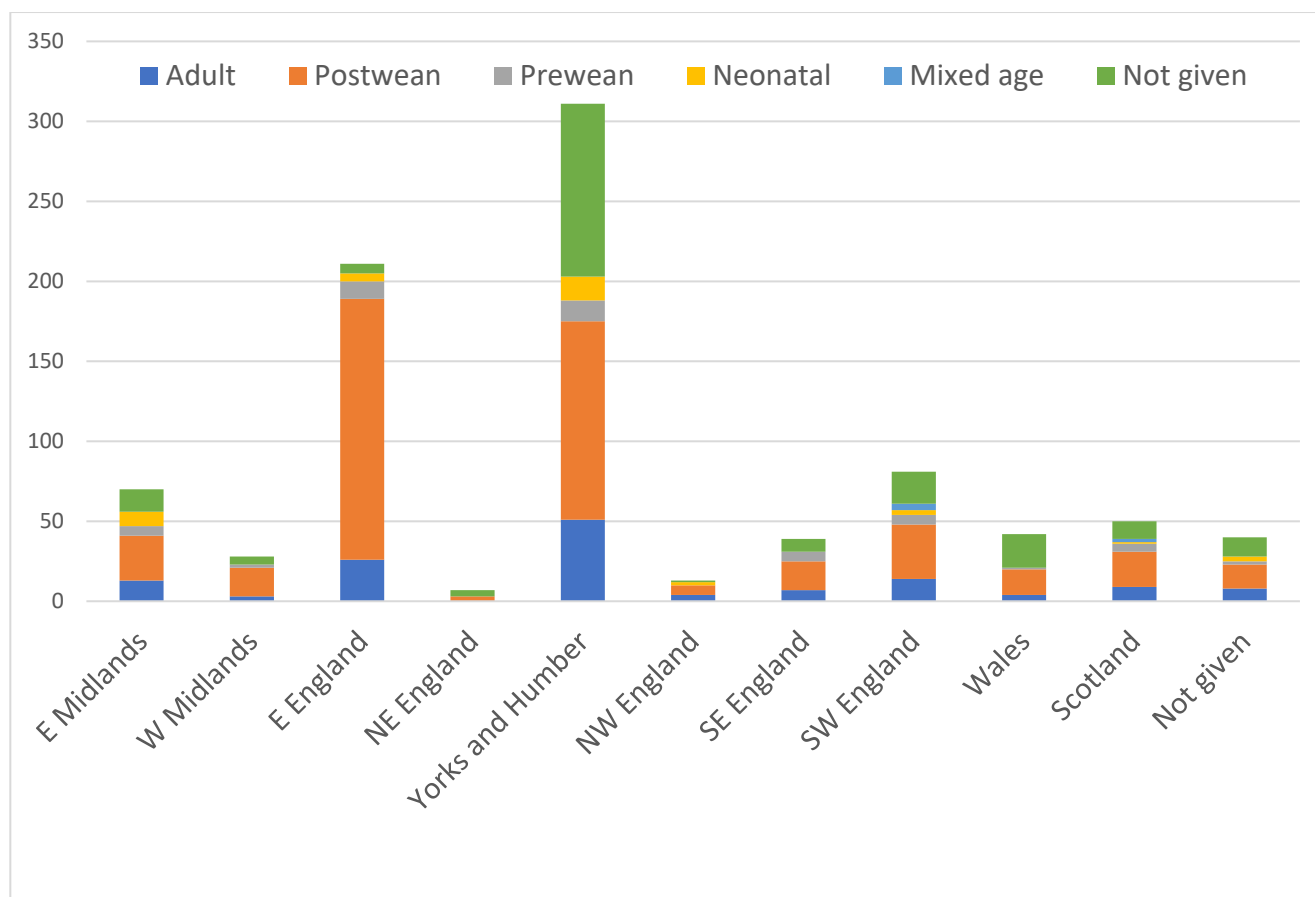
**Figure 1c: submission type**



**Figure 1d: main clinical sign reported**



**Figure 2: Pig diagnostic submission records for January to June 2023 by pig age and region of GB from enhanced dashboard (GB scanning surveillance network)**



These diagnostic submissions are voluntary and subject to several sources of bias. Figure 2 shows the majority of submissions to the GB scanning surveillance network (APHA, partner PME providers, SRUC) are from postweaned pigs and from East England and Yorkshire and Humber, regions with the highest density of pig population, most of which are commercial pigs.

The profile of submissions for the second quarter of 2023 was similar to that of the same quarter in 2022 in that the most frequent main clinical sign was diarrhoea and gastro-intestinal, and the most frequent syndrome was enteric.

Total Great Britain (GB) diagnostic submission records for quarter 2 of 2023 were higher than the total for the same quarter in 2022, 2020 and 2019 and very similar to quarter 2 of 2021. The balance of submission types changed slightly from being 25% carcasses in quarter 2 of 2022 to 32% carcasses in quarter 2 of 2023. This can affect the number of diagnoses achieved as carcasses enable full diagnostic investigation and this may have contributed to the greater number of diagnoses made in quarter 2 of 2023 (277) compared to the same quarter in 2022 (221).

## New and re-emerging diseases and threats

### African swine fever

[Updated assessments continue to be published on African swine fever \(ASF\)](#) on GOV.UK.

Updates on the [ASF situation in Europe](#) were issued in this quarter in April, May and June 2023. Maps showing information on the [European Union \(EU\) ASF restriction zones](#) are available.

Monthly IDM summaries are also included in the [disease surveillance items in the Veterinary Record](#). The [Swine Health Information Centre \(SHIC\) global reports](#) include a round-up of ASF each month.

Global ASF Research Alliance (GARA) is to establish and sustain global research partnerships that will generate scientific knowledge and tools to contribute to the successful prevention, control and, where feasible, eradication of ASF. Their news and activities are accessible on the [GARA website](#).

The use of two ASF vaccines on a commercial basis is being progressed in Vietnam according to [SHIC's August global report](#) and a [Pig Progress report](#). These vaccines differ from one another in several respects such as recommended pig age at vaccination and duration of immunity and the importance of farmers adhering to each of the vaccine's use guidelines is emphasised to ensure optimum vaccinal immunity to ASF and minimise the risk of adverse effects. Neither vaccine has DIVA (Differentiating Infected from Vaccinated Animals) features making it difficult to distinguish vaccinated animals from infected ones.

Zhao and others (2023) published a paper about the field detection of a new virulent ASFV strain which is the result of a recombination of genotype I and genotype II. This was detected during routine surveillance in Henan, Inner Mongolia and Jiangsu provinces with lower virulence genotype I virus initially detected and deeper analysis revealing characteristics of genotype II leading to the finding of the recombinant virus. The recombinant strains were isolated from the field but it is not known how they originated, natural recombination during dual field infection with both genotype I and II is one possibility. It is not known how prevalent this recombinant strain is although it has spread to different provinces in China. The highly virulent recombinant strain would out-compete more attenuated ASFV in pigs.

This finding is concerning, particularly as the recombinant virus is still highly transmissible and highly pathogenic. Also, the live attenuated vaccine derived from genotype II ASFV appears not to be protective against challenge with this recombinant virus.

It should also be noted that Italy has genotype I and II in Sardinia and genotype II in several regions of mainland Italy, thus it is not impossible that a similar recombinant event could happen in Europe independently. ASF is a relatively complex DNA virus and does not evolve as rapidly as some viruses, particularly not RNA viruses like swine influenza or porcine reproductive and respiratory syndrome virus (PRRSV). Molecular epidemiology has been used to determine possible virus origins at a regional level, rather than being able to elucidate spread between individual premises as used for FMDV.

Information on ASF is disseminated to veterinary practices and Pig Veterinary Society members. The assistance of veterinary practitioners in raising awareness about ASF amongst their pig-keeping clients in the UK is vital, together with advising them on resolving biosecurity weaknesses to reduce the risk of introduction.

The biggest risk for ASF virus entering the UK's pig population continues to be pigs or wild boar eating pork or pork products derived from infected animals. ASFV can survive for months in smoked, dried and cured meats, and for years in frozen meat.

Meat and meat products brought into the UK from affected countries as personal imports and illegal imports represent the most significant risk of introduction of exotic notifiable diseases including ASF, Classical swine fever and foot and mouth disease (FMD), the commercial trade of such products is not permitted from ASF-affected areas. The Government announced new restrictions on the movement of pork and pork products into Great Britain to help safeguard pigs from the threat of ASF. These came into force from 1 September 2022 and mean it is no longer legal to bring non-commercial pork or pork products weighing over two kilograms in from EU member states and European Free Trade Association states unless they are produced to the EU's commercial standards. This does not apply to commercial imports. It remains illegal to trade in pork or wild boar meat from ASF-affected areas or to bring in meat products from Asia or Africa.

Pig keepers are reminded that it is illegal to feed pigs catering, kitchen or domestic waste, or meat or meat products. Providing dedicated clothing and boots for staff and visitors, limiting visitors to a minimum, and preventing outside vehicles or equipment which may be contaminated from coming on to the farm, are also all valuable procedures to reinforce. [Images of the clinical signs and pathology of ASF](#) are available. Suspect cases must be [reported promptly to APHA](#) and this is followed by an official veterinary investigation.

### **Differential diagnosis negated notifiable disease report case**

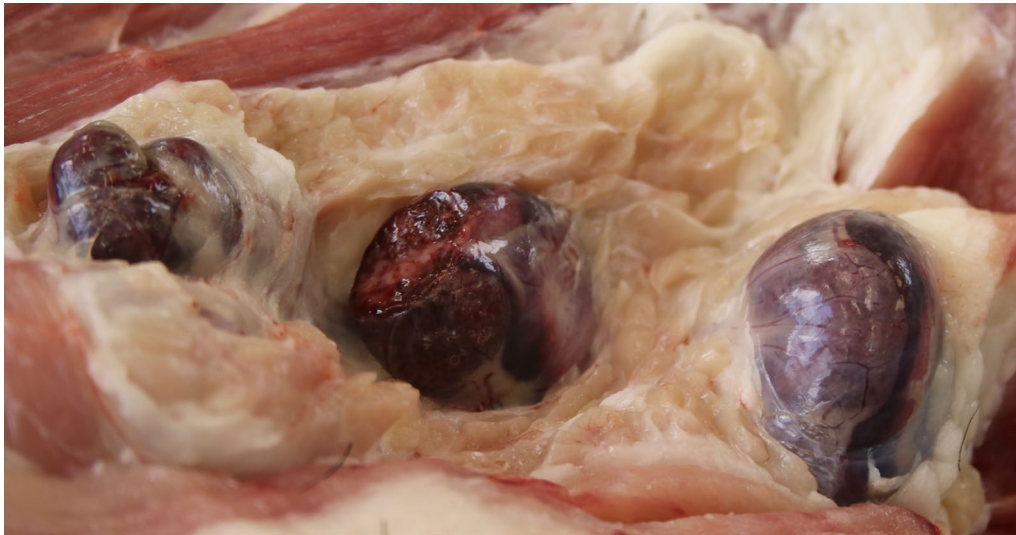
An investigation took place into a report of suspect swine fever during quarter 2 of 2023 and ruled out notifiable disease involvement. This case is described below.

### **Haemorrhagic disease in a young Kune-kune with megakaryocyte hypoplasia**

A four-month-old castrated Kune-kune pig in good to fat body condition was submitted to the Shrewbury Veterinary Investigation Centre. The pig had died after a two-day history of illness including epistaxis then bleeding from rectum and was euthanased. No information was available about whether the pig was pyrexemic. Anthrax was ruled out by examination of polychrome methylene blue-stained blood smears from the carcass. Post-mortem examination revealed widespread haemorrhagic lesions throughout the carcass, dark-red enlarged marbled lymph nodes (Figure 3) and haemorrhagic large intestinal contents. In view of the resemblance of these lesions to swine fevers, the case was reported as suspect notifiable disease and an official veterinary investigation visit was undertaken. The remaining pig on the premises was found to be healthy and samples from the dead pig tested negative for African and Classical swine fever. Once restrictions were lifted, diagnostic investigation continued and found no evidence of infectious disease. The main histopathological finding was marked megakaryocyte hypoplasia in bone marrow with a notable complete absence of megakaryoblasts/megakaryocytes. An acquired immune-mediated thrombocytopaenia considered most likely. This has been encountered previously in sporadic individual cases of haemorrhagic disease investigated in pigs (Bidewell and others, 2013) and a similar case which also prompted a suspect swine fever investigation was described in the March 2023 APHA surveillance report in the Veterinary Record (APHA, 2023a).

### **Figure 3: enlarged haemorrhagic submandibular lymph nodes in pig with megakaryocyte hypoplasia**





Cases of multifocal haemorrhages in pigs affecting the skin, mucosal and serosal surfaces and viscera with lymphoid lesions may raise concern when the lesions resemble those described for the porcine notifiable diseases, African and classical swine fevers. This concern is significantly increased where several pigs are unwell and pyrexia with mortality.

### **Porcine epidemic diarrhoea and other porcine enteric coronavirus surveillance**

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

Enhanced surveillance for PED continues and diagnostic submissions from cases of diarrhoea and/or enteropathy in pigs (non-suspect PED) submitted to APHA have been routinely tested by PCR for PED virus (PEDV) and transmissible gastroenteritis virus (TGEV) on a weekly basis. None has been positive for PEDV or TGEV in over 1,470 diagnostic submissions tested under Agriculture and Horticulture Development Board (AHDB) Pork funding from June 2013 to June 2023.

This enhanced surveillance has included testing for porcine deltacoronavirus (PDCoV) since February 2023 under the same funding. This surveillance aims to detect any of these three porcine enteric coronaviruses, should they occur as a new and (re-)emerging cause of porcine diarrhoea in pigs and thus a potential threat to pig health and welfare. The last diagnosis of PED and of TGE recorded in the Great Britain national diagnostic database (VIDA) was in 2002 and 1999, respectively. PDCoV has not been detected to date.

## **Unusual diagnoses or presentations**

### **Sudden deaths in outdoor pigs due to water dropwort toxicity**

An unusual diagnosis was made when sudden deaths were investigated in a group of nine eight-month-old pigs kept outdoors. The group were part of a small rare-breed breeding herd with six sows, several boars and fatteners, that were moved into a paddock with an ark and



electric fencing. A week later, the owner came in the morning to find two of them dead with bloody froth around their noses and mouths. One other non-pyrexia pig in the group showed non-specific severe malaise although it was able to stand and the other six pigs appeared perfectly well. The group had been fed their usual commercial pig food the previous evening and mains water was provided from a large dispenser via nipple drinkers to which pigs had free access. The owner was certain that the water had not run out. The pigs were sometimes fed vegetables but none had been given for the previous week.

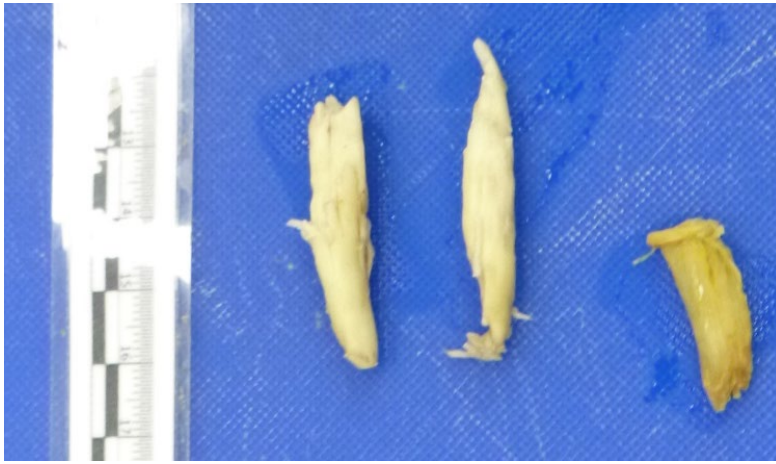
One dead pig in good body condition was submitted to APHA's partner postmortem provider at Bristol University. There was blood-stained fluid around the mouth, the sclera were markedly congested and there was diffuse skin congestion around the head and the thorax. The stomach was relatively full of concentrate-like food with some straw and several sections (up to 5 cm long and one cm wide) of white, tuberous plant material (Figure 4) and segments of fibrous plant matter that did not resemble straw. Amongst other non-specific findings there was haemorrhage/blood pooling over the cerebral and cerebellar surfaces of the brain.

Plant toxicity was suspected, with other differentials being a different toxicity, acute septicaemia/meningitis, electrocution, inhalation toxicity (slurry gas, carbon dioxide), and oedema disease. However, the clinical and epidemiological findings pointed away from some of these.

No bacterial pathogens were isolated and kidney lead concentration was not elevated. A farm visit was promptly undertaken by the private vet. No further pigs were affected in this group or elsewhere in the herd. The pigs were moved out of the paddock which was found to border a hedge and ditch draining into a rhyne, a local term for draining ditches on the Somerset levels and in which water dropwort often grows in profusion. Plants with tuberous roots and leaves matching those of *Oenanthe crocata* were found. Overall the findings were strongly supportive of toxicity due to eating the roots of *Oenanthe crocata*, known as hemlock water-dropwort and also called "dead man's fingers" due to the appearance of the roots. All parts of the plant are highly toxic and the oenanthotoxin causes seizures and sudden death (also vomiting in pigs). This is thought to be the first GB diagnosis of water dropwort toxicity in pigs recorded in the VIDA database and was described in the June 2023 APHA surveillance report in the Veterinary Record (APHA, 2023b). It is not an uncommon diagnosis in cattle and occasionally sheep. Payne and Murphy (2014) published a review of plant poisoning in farm animals and included several that have been identified in pigs, the most common being bracken which causes acute heart failure with lung oedema and body cavity effusions.

Pigs in small herds may be kept outdoors in less controlled situations than on commercial pig herds, with access to a range of wild plants in woodland or rough grazing, there is a higher risk of toxicity incidents. Certain plant toxicities have food safety implications if the pigs are destined for the food chain and APHA reports these to the Food Standards Agency as potential food safety incidents which sometimes require a period of voluntary restriction of pigs to protect the food chain.

**Figure 4: Tuber-like material found in stomach contents in case of water dropwort toxicity**



### **Abnormal hindlimb gait associated with possible pantothenic acid deficiency**

A private veterinarian contacted the Shrewsbury Veterinary Investigation Centre after encountering an unusual clinical presentation in well-grown 18-week-old commercial finisher pigs on an all-in, all-out single age indoor finisher unit. Around six pigs were affected in different pens in a batch of 1000 with hindlimb ataxia and paresis, and some showed hindlimb hypermetria (“goose-stepping”) as shown in Figures 5 and 6. Signs were gradual in onset and progressive and, when seen by the vet, pigs had been affected for around seven days and had not responded to antibiotic treatment. The pigs appeared otherwise well and alert and were eating and drinking. They were housed on straw and fed commercial pig pellets. There had been possible feed quality issues and some diarrhoea earlier in rear. Two typical cases were euthanased on farm with barbiturate and submitted.

Differentials initially considered included spinal trauma/abscess or other trauma from fighting/riding, neurotropic viral infection, an immune-mediated radiculopathy, pantothenic acid deficiency, and selenium or other toxicity. Other causes of nervous disease such as bacterial meningitis, water deprivation and subacute to chronic oedema disease were considered unlikely given the apparently normal mental state of the pigs. It can be hard to differentiate clinically, especially in larger pigs, whether hindlimb gait issues are due to musculoskeletal or nervous disease except by postmortem examination (PME).

**Figure 5: Pig with hindlimb hypermetria (courtesy of Tom Hill, George Veterinary Group)**



**Figure 6: Pig with ataxia and hindlimb paresis (courtesy of Tom Hill, George Veterinary Group)**



PME was grossly unremarkable with no evidence of disc protrusion, vertebral instability, abscesses, trauma or osteomyelitis, or of musculoskeletal disease involving the hindlimbs. However, histopathology revealed axonal degeneration affecting the proprioceptive pathways of the spinal cord and dorsal spinal nerve roots which are changes consistent with the neurological signs observed. No lesions were found in the brains, peripheral nerves and skeletal muscle and toxic, metabolic or genetic causes were considered as possible differentials. These included chronic arsenic toxicity, organophosphate toxicity, copper deficiency, pantothenic acid (B5)

deficiency and pyridoxine (B6) deficiency. Heritable forms of myelopathy with similar pathology have been described in Brown Swiss and Murray Grey cattle, but no such conditions have been observed in pigs.

Immediate concerns about toxicities were investigated with APHA's toxicologist and through liaison with the vet who indicated that there was no credible source of organophosphates, but confirmed there was a spring water source and groundwater contamination with arsenic was thus a theoretical possibility. A paper from Italy described an incident of chronic arsenic poisoning in pigs associated with groundwater contamination in pigs on a finishing unit on which the contaminated water was used for liquid feeding and as source of water with enteric and nervous disease manifestations (Scollo, 2022). In the case seen by APHA, both arsenic and selenium toxicities were ruled out by estimation of liver concentrations allaying potential food safety concerns. Liver copper concentrations were found to be low, however hypocuprosis was not considered likely to be the primary diagnosis as copper was only marginally low and the nature and distribution of degenerative changes in the spinal cord were different from those described in copper deficiency.

Feed analysis to investigate possible deficiencies was recommended, to include trace elements and vitamins, but was not possible as insufficient sample had been retained. No tissue testing is available for pantothenic acid or pyridoxine. No definitive diagnosis was possible in this case and no further cases occurred to investigate, however, histopathological lesions were most suggestive of pantothenic acid (B5) and/or pyridoxine (B6) deficiency. One might have expected more pigs to show signs and the other pig batches on the same diet to be affected, unless the deficiency was quite marginal, however past reports of pantothenic acid (MacLean, 1965 and Oakley 1965) mention that nervous signs develop later and do not always manifest, that earlier diarrhoea is seen and that pigs are most susceptible from six to 14 weeks of age. These descriptions also mention predisposing circumstances for pantothenic acid deficiency to include pigs growing particularly rapidly and modification of a diet to take advantage of a low market price of an ingredient, such as a cereal.

A recent case report describes pantothenic acid-responsive degenerative myelopathy in two Brazilian pig herds (Lorenzetti and others, 2023). The neurological signs and white matter changes in the spinal cord are consistent with this case, although neuronal degeneration is a key feature absent here and described as a primary change and consistent feature in pantothenic acid-responsive myelopathy in pigs.

The case was described in the Veterinary Record surveillance report (APHA 2023c) and illustrates the value of submitting pigs with unusual clinical signs for full diagnostic investigation. APHA are interested to learn if others see similar presentations or pathology.

## Changes in disease patterns and risk factors

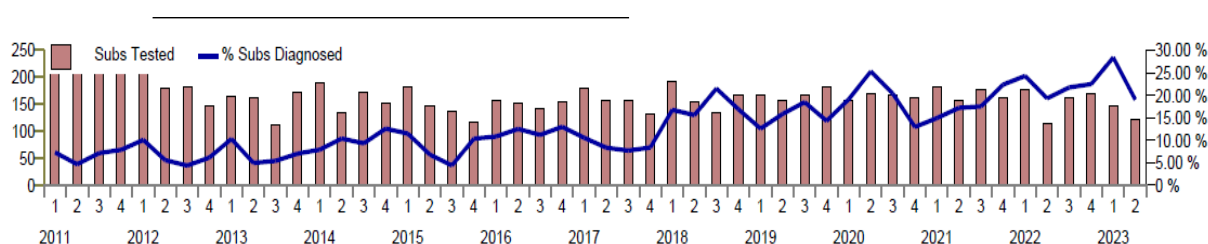
### Monitoring of genetic diversity of PRRSV in pigs in Great Britain

The diagnostic rate for porcine reproductive and respiratory syndrome (PRRS) in Great Britain showed a reduction in quarter 2 following the peak in the first quarter of 2023 when the diagnostic rate exceeded the highest most recent peak in quarter 2 of 2020 (Figure 7). The data underline the importance of PRRS as an endemic pathogen in GB pigs. PRRS is the

priority for disease control in the [pig component of the Animal Health and Welfare pathway](#) alongside a focus on biosecurity improvement to control endemic pig diseases and help prevent the introduction of exotic disease threats. No PRRSV-2 has been detected in UK pigs to date.

Pig keepers in England with over 50 pigs can join the Animal Health and Welfare (AHW) Pathway which funds a veterinary annual review visit and testing to determine their herd's PRRSV status. Further details are available [here](#) and comprehensive [guidance to vets](#) undertaking AHW pathway visits is provided on AHDB webpages.

**Figure 7: Diagnostic rate of PRRS by year and quarter as a percentage of diagnosable submissions to the Great Britain scanning surveillance network**



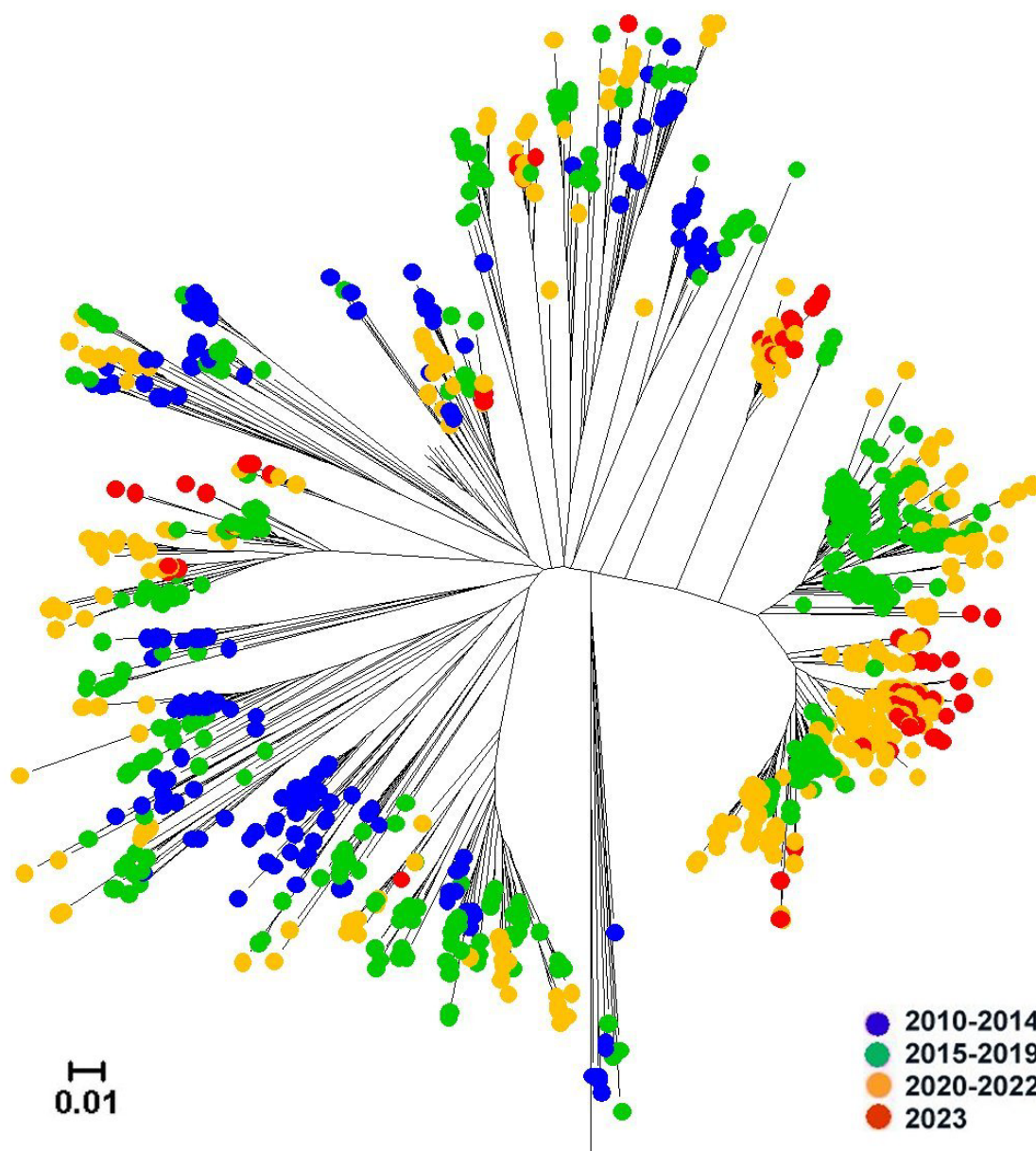
As part of PRRS surveillance at APHA, ORF-5 gene sequencing is undertaken under pig disease surveillance funding on the sample with the lowest Ct value (likely highest viral load) in each PCR-positive submission. Over recent years, phylogenetic analysis of these ORF-5 sequences has shown a continued increase in the genetic diversity of the PRRSV-1 strains detected as illustrated in Figure 8. The sequencing has not shown evidence of introductions of exotic PRRSV-1 strains from outside clades present in the UK. Increasing genetic diversity over time is a feature of PRRSV which, as an RNA virus, has a relatively high mutation rate and could allow new variants to evolve from resident PRRSV strains which escape, partially or totally, field or vaccinal immunity as well as posing a challenge to diagnostic tests for virus detection. This increasing genetic diversity occurs in all countries in which PRRSV occurs.

The presence of diverse and, sometimes, more pathogenic PRRSV-1 in parts of Europe, as well as PRRSV-2 in Europe, the Americas and Asia, emphasises the importance of preventing strains exotic to the UK from being introduced. The Pig Veterinary Society, liaising with APHA, the National Pig Association (NPA), British Pig Association and AHDB Pork, have been active in reminding veterinarians involved in importation of live pigs or semen into the UK of the importance of taking measures to ensure that they are sourced from PRRSV-negative herds, with testing before and after importation to prevent the introduction of exotic PRRSV strains into the UK.

**Figure 8: Phylogenetic analysis of ORF5 nucleotide sequences of PRRSV detected in GB**

The evolutionary history was inferred using the Neighbor-Joining method. The evolutionary distances were computed using the Kimura 2-parameter method. The rate variation among sites was modelled with a gamma distribution (shape parameter = 0.66). The scale bar corresponds to 0.01 substitution per nucleotide.





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

However, there are no statutory requirements for PRRSV testing pre or post-import of live pigs or semen and the risk of introducing exotic PRRSV strains remains if importers to non-assured herds do not follow the NPA import protocol.

Communications to vets and pig farmers were disseminated to raise awareness of the risks of importing PRRSV as well as other non-statutory diseases either not present in the UK, or where there are different strains that represent a threat to the national herd. These included a [Pig World article](#). Raising awareness amongst vets less familiar with pigs, smaller pig producers and owners of non-assured pig herds is especially important.

## Multi-drug resistant *Brachyspira pilosicoli* isolates identified

*Brachyspira pilosicoli* is one of the causative agents of porcine intestinal spirochetosis. It has a worldwide distribution in pigs, causing a non-haemorrhagic colitis usually in the grower or finisher stages and milder less persistent disease than swine dysentery due to *B. hyodysenteriae*.

Thirty-one diagnoses of colitis due to *B. pilosicoli* were made in the first six months of 2023 through the GB scanning surveillance network. Treatment of clinical disease relies on the same antimicrobials as used for treatment of swine dysentery.

Whole genome sequencing (WGS) and minimum inhibitory concentration (MIC) testing by broth microdilution was undertaken retrospectively on 22 archived *Brachyspira pilosicoli* isolates from clinical cases during 2021 (19) and the first quarter of 2022 (3) funded from APHA's pig disease scanning surveillance project. The 22 isolates were from 14 different APHA pig submissions (one submission had two isolates) provided by APHA Starcross and seven different SRUC submissions provided by SRUC Edinburgh. A one control *B. pilosicoli* strain were included. The isolates derived from pigs in England (n= 20) and Wales (n= 2).

In interpreting the MIC results, in the absence of cut-off values for *Brachyspira pilosicoli*, epidemiological cut-off (ECOFF) values and clinical breakpoints (Pringle and others, 2012; Duinhof and others, 2008) proposed for *B. hyodysenteriae* were used as others have (Hampson et al. 2019). Clinical breakpoints are available for agar dilution; for broth microdilution breakpoints are usually considered to be one dilution lower than for agar dilution; for example, for tiamulin the suggested clinical breakpoint for broth microdilution is >2 µg/ml.

WGS showed that six isolates (27%) had no antimicrobial resistance (AMR) genes or single nucleotide polymorphisms (SNPs) associated with the six antibiotics in the MIC panel tested (tiamulin, valnemulin, tylosin, tylvalosin, lincomycin and doxycycline). Thirteen isolates (59%) contained one AMR genetic determinant; 12 isolates containing just *tva*(B) associated with pleuromutilin (tiamulin and valnemulin) reduced susceptibility and one isolate had just the 16S rRNA SNP associated with reduced susceptibility to doxycycline.

Two isolates (9%) contained two AMR genetic determinants: one had *tva*(B) and *lnuC* genes associated with pleuromutilin (tiamulin and valnemulin) and lincomycin. The remaining isolate had *tva*(B) and 23S rRNA A2059G SNP, the presence of both being associated with reduced susceptibility to multiple antibiotics (tiamulin, valnemulin, lincomycin, tylosin and tylvalosin) used in the treatment of *Brachyspira*-associated enteric disease. One isolate had genetic determinants associated with reduced susceptibility to all six antibiotics tested by MIC, with *tva*(B) gene and 16S rRNA G1058C SNP and 23S rRNA A2059G SNP present.

MIC testing was performed on 20 of the 22 isolates and showed 13 (65%) were susceptible to all six antibiotics tested. Five isolates (25%) showed reduced susceptibility to one antibiotic class, namely doxycycline, lincomycin or the pleuromutilins (tiamulin and valnemulin).

Two 2021 isolates from the same premises obtained ten months apart had MICs exceeding the clinical breakpoint for all five antimicrobials tested that are licensed for treatment. This is significant and emphasises the need for disease control using alternative interventions (all-in, all-out management systems; cleaning and disinfection) to prevent persistence and the development of wider antimicrobial resistance.



Although a relatively small number of isolates were assessed in this study, overall there was less evidence of a reduction in antibiotic susceptibility to licensed antimicrobials in these GB *B. pilosicoli* compared to isolates in studies in some other countries (Hampson and others, 2019; Arnold and others, 2022).

### **Genetic diversity shown in *Brachyspira pilosicoli* isolates**

The WGS data obtained in the study described allowed multi-locus sequence typing (MLST) to be undertaken using the *B. pilosicoli* MLST database and the isolates were found to be new sequence types (ST), with potentially 18 new allelic profiles identified. Further work is needed to assign new alleles and STs on the *B. pilosicoli* pubMLST database.

The detection of new *B. pilosicoli* STs is not unexpected; the *B. pilosicoli* MLST database had only 181 STs described at the time of analysis. Within this there were only three UK *B. pilosicoli* isolates, all obtained from pigs in the 1970s. The database contains some European isolates, predominantly from Switzerland, with a few from Italy, France and Sweden. A Swiss study also showed high genetic diversity with 44 *B. pilosicoli* STs detected in the 80 isolates tested (Arnold and others, 2022).

The WGS data and analysis of core genome SNPs for these isolates, with a further 56 publicly available *B. pilosicoli* genomes, showed little similarity between GB pig and chicken *B. pilosicoli* isolates, with SNP distances of 860 or more SNPs. There was also no close association between the GB pig isolates and non-UK *B. pilosicoli* published genomes, with at least 1980 SNPs between them. Within the pig isolates in this study, there were two pairs of isolates from different submissions which showed close genetic similarity to each other (0 or 1 SNP difference) suggesting an epidemiological link, the remaining isolates were not similar to each other (>450 SNP difference). The diversity in *B. pilosicoli* is an area to be explored further, however early indications from this small study is that WGS would also be useful for *B. pilosicoli* in a similar manner to its use in swine dysentery surveillance to assist epidemiological investigations and antimicrobial treatment choices. If funding allows, this may be undertaken periodically on a batch basis.

### **Porcine circovirus-2 genotyping**

Porcine circovirus 2 (PCV2) is a DNA virus with a relatively high evolutionary rate compared to some DNA viruses and has been classified into several genotypes, nine of which have been proposed to date (a-i). Some (PCV-2a, PCV-2b, and PCV-2d) have a worldwide distribution while others (e.g. 2c and 2e) appear to be more restricted to certain geographical regions and/or limited time periods. Since 2011, APHA has periodically genotyped PCV2 involved in confirmed cases of PCV2-associated disease (PCV2-AD) diagnosed at APHA, based on analysis of the ORF-2 gene to monitor genotype. From 2011 to 2016, PCV2b was the only, or the predominant, genotype detected in APHA's disease-associated cases, with genotype 2d first detected in APHA cases in 2013 (Sylvia Grierson and others, 2018). Since then PCV2d has become predominant with PCV2b less often detected. In the latest batch of genotyping at APHA, the PCV2 detected in disease-associated cases from lymphoid tissues of eight confirmed cases were all PCV2d except for one case which was PCV2b. This shift from PCV2b to 2d follows a similar global shift that has occurred in other pig-producing countries. No other genotypes have been detected in GB pigs to date, apart from PCV2a in the past. Global shifts may have been influenced by vaccination pressure or it is possible that new variants have better fitness.

The overall opinion is that current PCV2 vaccines based on genotype 2a (or 2a and 2b) are controlling clinical disease due to PCV2a, 2b and 2d, however the efficacy for protecting against the other genotypes not widely detected, should they be found associated with disease, is not clear. Also, the possibility exists that differences in virological/immunological responses could become more important in relation to differences between vaccine and field genotype if vaccination is not optimal (Franzo and others, 2020).

PCV2 virus prevalence in the APHA-AHDB Pork 2019 abattoir pig serum archive was also assessed by the colleagues in the Virology department at APHA Weybridge. In 681 English and Welsh serum samples tested for PCV2 by qPCR, 109 tested positive equating to 16.0% PCV2 prevalence (95% confidence intervals 13.3-18.8). Ct values ranged from 28.24 to 43.75 (mean 38.91) indicating that the viral loads in PCR-positive sera were mainly low, consistent with subclinical infection. Interestingly, there was no significant association in PCV2-positive pigs with positive PRRSV or PCV3 results. This underlines the continuing presence of PCV2 within the national pig population and the need for vaccination which has been very successful in protecting pigs against PCV2-AD since becoming available in 2007.

APHA and AHDB Pork are collaborating to enable a new 2023-24 serum-tonsil archive to be established. The sampling strategy will, like the 2019 archive, be similar to that used in the 2013 study described by Powell and others (2015).

## Horizon scanning

### **Detection of porcine circovirus genotype 2e in rural pig farms in Northern Italy**

Porcine circovirus genotype 2e is present in Asia and North America and was recently detected on one farm in Italy (Franzo and others, 2022) which is the only detection of PCV2e described to date in Europe. The report of incidental detection of PCV2e in a breeding farm in northeastern Italy was included in a previous quarterly report (APHA, 2021). Another recent publication from Italy describes further investigation of this finding (Faustini and others, 2023).

Tissues were obtained from pigs in the same geographic area. Those from rural (backyard) farms were collected from healthy pigs at slaughter, tissues from pigs on commercial farms were provided from clinical cases and were already confirmed as being PCV2-positive by prior testing.

Phylogenetic analysis of ORF-2 gene detected PCV-2e only in pigs from five of 45 rural farms, and no PCV2e was detected in pigs from the 65 commercial farms, while genotypes PCV-2a, 2b and 2d were found in pigs in both types of herd. Whether PCV2e is actually present in commercial pigs in the region at a lower prevalence or whether results were affected by the different sampling strategy is not clear, however, the study reveals PCV2e presence in backyard pigs in northeastern Italy where there is potential for transfer of pathogens between them and commercial pigs and/or wild boar.

The degree of surveillance for different PCV2 genotypes varies in different countries and it is possible that PCV2e is more widespread but unrecognised due to lack of surveillance or under-reporting. As described in the item above, APHA monitors the genotype of PCV2 in disease-associated submissions periodically, this work has confirmed PCV2b and PCV2d as being involved (and PCV2a identified in the past) and has not found PCV2e to date.

## Contact

Editor: Susanna Williamson

Address: APHA, Bury St Edmunds

Telephone: + 44 (0) 2080 264990

Email: [susanna.williamson@apha.gov.uk](mailto:susanna.williamson@apha.gov.uk)

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