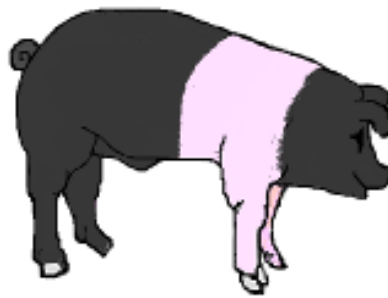




Animal &  
Plant Health  
Agency



## GB pig quarterly report

### Disease surveillance and emerging threats

Volume 23: Q2 – April to June 2019

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## Introduction and overview

This quarterly report reviews disease trends and disease threats for the second quarter of 2019, April to June. It contains analyses carried out on disease data gathered from APHA, SRUC Veterinary Services division of Scotland's Rural College (SRUC) 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

<https://www.gov.uk/government/publications/information-on-data-analysis>.

### Pig disease surveillance dashboard April to June 2019 output

Diagnoses made in the second quarter of 2019 compared to the second quarter of 2018 through the GB scanning surveillance network are illustrated in Figures 1a and 1b. These can be interrogated further using the interactive pig disease surveillance dashboard which was launched in October 2017 and can be accessed from this link:

<http://apha.defra.gov.uk/vet-gateway/surveillance/scanning/disease-dashboards.htm>

Figure 1: GB scanning surveillance diagnoses

1a: 223 diagnoses in Q2-2019

Number of diagnoses and/or undiagnosed cases, depending on selections	
Brachyspira pilosicoli	20
Proliferative enteropathy (Lawsonia sp.)	18
Pneumonia -PRRS	15
Streptococcus suis	15
Rotavirus	14
PRRS - systemic	11
Swine influenza	9
Colibacillosis - enteric	7
Meningitis -streptococcal	7
Brachyspira hyodysenteriae (swine dysentery)	6
Streptococcal infection	6
Yersiniosis	6
Not listed - digestive	5
Trueperella pyogenes infection	5
Gastric ulceration	4
Hypogammagloblinaemia	4
Inclusion body rhinitis	4
Not listed - systemic	4
Coccidiosis	3
Erysipelas	3
Meningitis/encephalitis	3
Mulberry heart disease	3
Pneumonia - Actinobacillus pleuropneumoniae	3

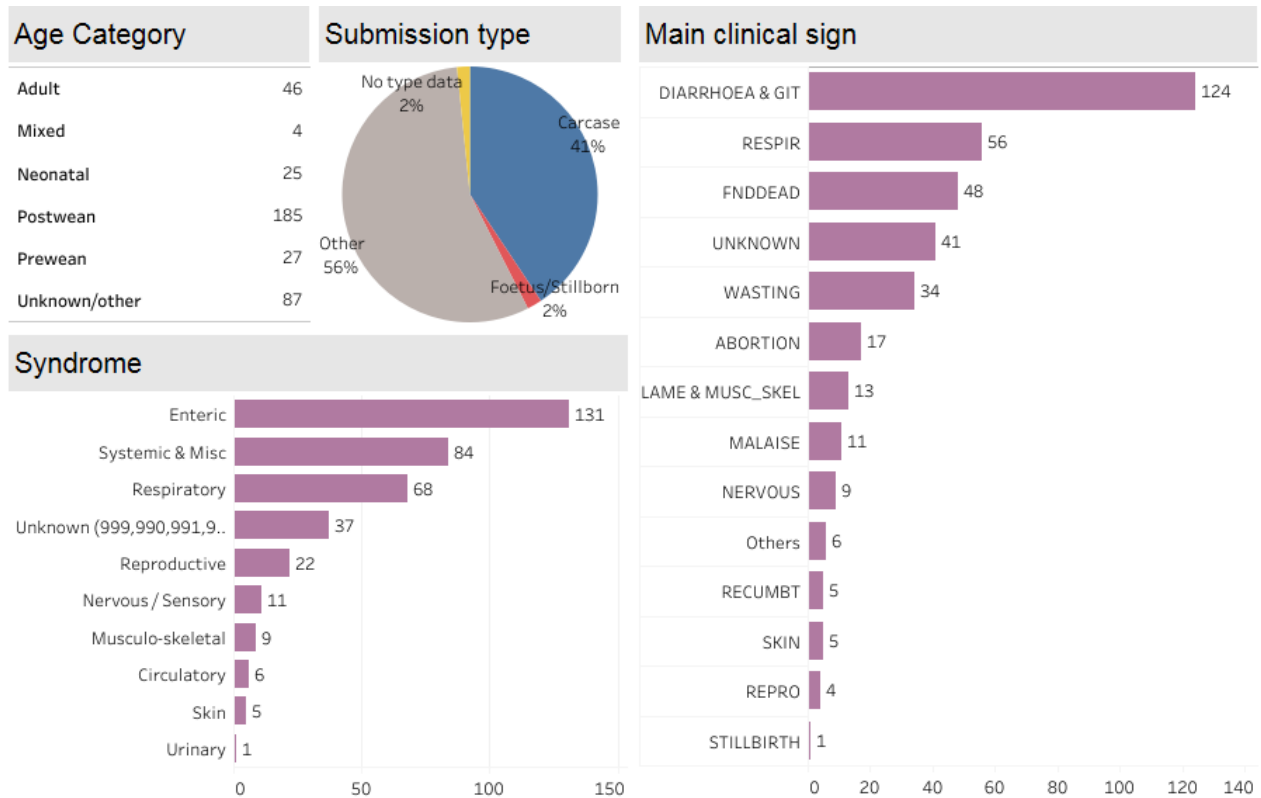
1b: 207 diagnoses in Q2-2018

Number of diagnoses and/or undiagnosed cases, depending on selections	
Streptococcus suis	17
Pneumonia -PRRS	12
PRRS - systemic	12
Proliferative enteropathy (Lawsonia sp.)	10
Hypogammagloblinaemia	9
Pneumonia - Pasteurella multocida	8
Pneumonia -other cause	8
Rotavirus	8
Swine influenza	8
Colisepticaemia	7
Arthritis - other cause	6
Gastric ulceration	6
Meningitis -streptococcal	6
Brachyspira pilosicoli	5
Pneumonia - Actinobacillus pleuropneumoniae	5
Mulberry heart disease	4
Trueperella pyogenes infection	4
Colibacillosis - enteric	3
Endocarditis	3
Helminthosis	3
Not listed - digestive	3
Not listed - systemic	3
Pneumonia -Mycoplasma hyopneumoniae	3

Note that diagnoses made in low numbers are not shown and that further diagnoses may be added if records for submissions made in Q2-2019 are finalised at a later date. The

surveillance data for all diagnostic submissions to the GB scanning surveillance network in the second quarter of 2019 from an enhanced pig disease surveillance dashboard are summarised in Figure 2.

Figure 2: Summary data for 374 submission records in Q2-2019 (325 in Q2-2018)



These diagnostic submissions are voluntary and subject to several sources of bias. The profile of submissions for the second quarter of this year is broadly similar to those in Q2 of 2017 and 2018 in that systemic, respiratory and enteric syndromes are consistently the most commonly submitted and diagnosed. However, in Q2-2019, enteric was the dominant syndrome which aligns with the most common main clinical sign reported in Q2-2019 which was “diarrhoea & GIT”. It is possible that the current concern about swine dysentery is prompting more investigation of diarrhoea in pigs and increased enteric diagnostic submissions. Total GB diagnostic submissions for the quarter were similar to those recorded in the same quarter in 2012 and were at least as high as each Q2 since then. Non-carcase (postal) submissions to APHA in Q2-2019 have been partially restored to levels received in Q2-2016, following the downward trend during 2017-18 described in previous APHA disease surveillance reports. Total APHA carcass submission throughput has been maintained and in Q2-2019 represented 44% of APHA diagnostic submissions. Changes in the profiles of sample type can influence diagnostic rates for certain diseases if they are more likely to be diagnosed in carcass submissions, in which more complete diagnostic investigation is possible. The number of diagnoses recorded in Q2-2019 (223) is above the average (199) for the same period in 2014-18 (range 182-212). The geographical areas where free carcass collection is offered to post-mortem examination

sites within the APHA network were expanded in 2017 (APHA, 2017) and the availability of this service is regularly publicised resulting in some increase in uptake.

## New and re-emerging diseases and threats

Please refer to the annexe on Gov.UK for more information on the data and analysis.

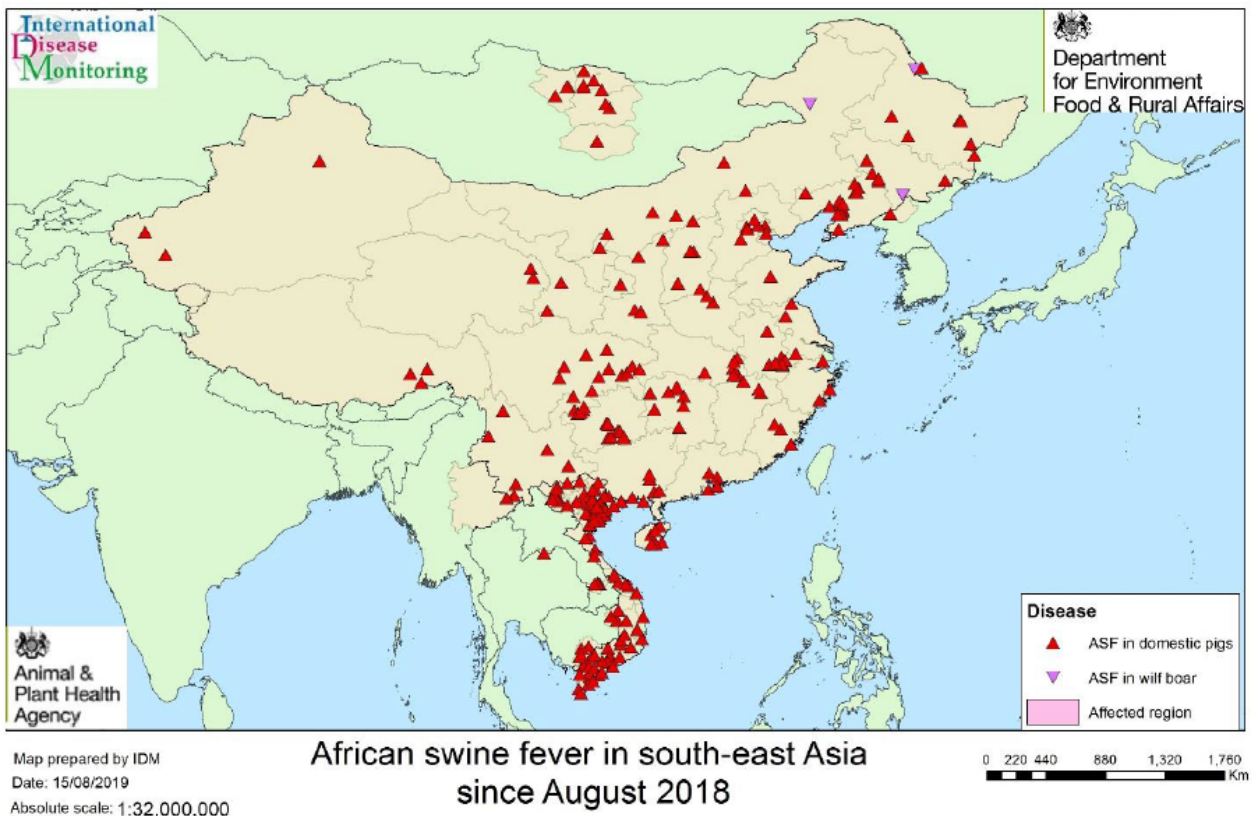
### Summary update of African swine fever in South East Asia and Europe

Updated assessments continue to be published on African swine fever (ASF) in South East Asia and Europe including Belgium:

<https://www.gov.uk/government/collections/animal-diseases-international-monitoring#outbreak-assessments-2019>.

In South East Asia, outbreaks of ASF in domestic pigs have now been reported in China, Vietnam, Cambodia, Mongolia, Hong Kong, North Korea and Laos, as illustrated in Figure 3. Media reports of pigs dying, possibly due to ASF, in Myanmar have been followed by the first official report to OIE confirming disease. The disease is likely to present particular risk to small-scale Myanmar pig keepers where farm biosecurity may be weak and kitchen waste is fed to pigs.

Figure 3: ASF cases reported in South East Asia since August 2018 (map as on 15-08-19)



The first ASF report in China was on 3<sup>rd</sup> August 2018 and 151 outbreaks were officially reported up to 15<sup>th</sup> August 2019 with the recent slowing of the rate of reporting raising some concern that disease is being under-reported. Outbreaks have been detected at highway checkpoints for animal health supervision in China, showing that illegal pig

movements are occurring, some involving ASF-infected pigs with obvious adverse effects on disease control.

New developments since the Q1-2019 pig surveillance report include Hong Kong, North Korea, Laos and Myanmar reporting their first detections of ASF on 10<sup>th</sup> May, 30<sup>th</sup> May, 20<sup>th</sup> June and 9<sup>th</sup> August respectively. Following its first reported case, Laos has seen several outbreaks in domestic pigs in the south of the country and one in Laos' capital Vientiane, close to the Thai border. The outbreaks are unsurprising given the current disease situation in Vietnam. In Myanmar, cases have been reported in an eastern district, close to the Thai border. ASF virus is suspected to have entered Laos and Myanmar most likely through the import of infected pigs and pork products, rather than a wild boar source, given the cross-border trade routes that may facilitate entry into new areas and countries. Further details are available on: <https://www.gov.uk/government/publications/african-swine-fever-in-pigs-in-china>

The FAO and Swine Health Information Centre (US) are both providing regular updates: [http://www.fao.org/ag/againfo/programmes/en/empres/ASF/Situation\\_update.html](http://www.fao.org/ag/againfo/programmes/en/empres/ASF/Situation_update.html); <https://www.swinehealth.org/global-disease-surveillance-reports/>

There are numerous features about ASF in the pig industry media, speculating on the effects of ASF on global pig trade and the situation in China accessed by the links below:

Pig trade: [https://www.pigprogress.net/World-of-Pigs1/Articles/2019/7/Trade-wars-and-ASF-The-global-pork-market-mid-2019-444778E/?cmpid=NLC|pigprogress\\_focus|2019-07-01|Trade wars and ASF: The global pork market mid-2019](https://www.pigprogress.net/World-of-Pigs1/Articles/2019/7/Trade-wars-and-ASF-The-global-pork-market-mid-2019-444778E/?cmpid=NLC|pigprogress_focus|2019-07-01|Trade_wars_and ASF: The global pork market mid-2019);

China biosecurity: <https://www.wattagnet.com/articles/38271-china-pig-farmers-ramp-up-biosecurity-to-slow-asf-spread>

Spread in SE Asia and human involvement: <https://www.wattagnet.com/articles/38361-african-swine-fever-spreads-in-southeast-asia>; <https://www.wattagnet.com/articles/38147-researchers-chinese-asf-outbreak-most-likely-a-man-made-disaster>

In Europe, Slovakia and Serbia have reported their first ASF cases, in backyard pigs in both countries. In Slovakia this was in the east of the country, quite near Ukraine and a few kilometres from the border with Hungary where ASF has been found in wild boar. In Serbia, ASF has been confirmed in pigs on four backyard premises in early August. While wild boar cases have tended to reduce month on month recently in most affected European countries, the number of ASF outbreaks in domestic pigs has increased significantly in Bulgaria and Romania with some large pig units involved. More details are available on this link: <https://www.gov.uk/government/publications/african-swine-fever-in-pigs-and-boars-in-europe>.

With regular direct flights to the EU and UK from China and eastern Asia, there is a risk of entry of ASF virus in pork or wild boar meat or meat products from Asia in passenger luggage. Reports indicate that several countries have seized ASF virus-infected pork or pork products at their borders, illustrating the threat of spread posed by undisclosed ASF cases associated with human behaviour. In one instance ASF-infected pork was smuggled

from Vietnam to Japan, allegedly with intent to sell on-line. In June 2019, port authorities in Northern Ireland seized 300 kg of meat and dairy products illegally brought into NI by passengers during the month and ASF virus DNA fragments were detected in a sausage originating from Asia, which was tested at the Agri-Food and Biosciences Institute (AFBI). This underlines the potential risk to the UK from pork and pork products being brought illegally into the country. A UK border campaign has recently been launched which includes the introduction of new posters and screen graphics to UK airports and ports warning passengers not to bring meat or meat products into the country. This is being promoted by the four Chief Veterinary Officers and Minister for Biosecurity:

<https://www.gov.uk/government/news/new-uk-border-campaign-warns-of-threat-of-african-swine-fever>. The Veterinary Record included an item on this (Loeb, 2019); disseminating the campaign's messages is key to achieving its aims of raising awareness of ASF and reducing the risk of people bringing ASF-contaminated meat and products into the UK.

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:

<https://www.gov.uk/guidance/african-swine-fever> and

<http://apha.defra.gov.uk/documents/surveillance/diseases/african-swine-fever-images.pdf>

### ***Brachyspira hampsonii* detected in pig faeces in England**

Whole genome sequencing (WGS) of an unusual *Brachyspira* species cultured at APHA from pig faeces from one premises has identified *Brachyspira hampsonii*. This is the first detection of *B. hampsonii* in GB pigs by APHA. *B. hampsonii* was described as a new potentially pathogenic species in pigs in North America in 2012 (Chander and others, 2012) and experimental infection confirmed it as a potential cause of diarrhoea (Wilberts and others, 2014). One historic *Brachyspira* isolate (P280/1) from a pig with colitis, thought to have originated from a UK research group before 1994, has since been identified as *B. hampsonii* (Mirajkar and others, 2016).

*B. hampsonii* has been reported in Europe in pigs imported to Germany from Belgium (Rohde and others, 2013) and pigs imported to Belgium from the Czech Republic (Mahu and others, 2014). *B. hampsonii* has also been detected in wild waterfowl, some of which are migratory, in Europe (Martínez-Lobo and others, 2013) and North America (Rubin and others, 2013) and wild birds have been implicated in the transmission of infection which in *Brachyspira* species is via the oro-faecal route.

The infection was detected on a single indoor finisher unit in pigs showing uneven growth and loose faeces; the pigs were not imported. Antimicrobial sensitivity testing showed that the isolate was susceptible to antimicrobials licensed to treat *Brachyspira* spp. infections in pigs. The contribution of the *B. hampsonii* to the clinical disease is uncertain in this case; it was detected in one pooled pig faeces sample and other enteric pathogens, including *B. pilosicoli* and *Lawsonia* species, were identified in the group. There is currently heightened surveillance for swine dysentery and whole genome sequencing is being used to analyse isolates; no further *B. hampsonii* isolates have been identified in pigs by APHA to date. *B. hampsonii* is not a notifiable or reportable disease. It is not zoonotic and

transmission through pork/pork products is not a recognised route of transmission for enteric *B. hampsonii*.

A visit to the pig unit will investigate risk factors for the presence of *B. hampsonii* and undertake sampling of pig/wild bird faeces as appropriate. Testing for *Brachyspira* has been offered if diarrhoea occurs in subsequent batches of pigs.

Interestingly, *B. hampsonii* was also recently identified by APHA in a captive rhea (*Rhea* sp.) with severe typhlocolitis, similar to lesions reported with *B. hyodysenteriae* infection in this species (APHA, 2019a). This represents the first detection of *B. hampsonii* in a rhea, or any other bird, in GB. The source of the *B. hampsonii* infection was not established but wild waterfowl had access to a pond in the field where the rheas were kept. The *B. hampsonii* isolated from the pigs and rhea differed from each other genetically. The possibility of future surveillance of wild birds for *Brachyspira* infection is under discussion.

This finding highlights the importance of carrying out cultures for *Brachyspira* species in tandem with PCR testing and maintaining laboratory expertise. This dual approach facilitates detection of new or emerging *Brachyspira* species, atypical *B. hyodysenteriae* isolates, or strains with altered characteristics.

## Porcine circovirus 3-associated disease

Porcine circovirus 3 (PCV3) is distinct from PCV2 and has been reported in pigs since 2016 in a growing number of countries globally, including the US, China, Poland, Italy, Spain and the UK (Palinski and others, 2016; Collins and others, 2017). In these, it has been detected in samples from healthy pigs and in samples from pigs with a variety of disease presentations, including PDNS-like disease. No zoonotic concern is reported. Information from an increasing number of countries indicates that PCV3 is widespread in pigs globally and publications suggest that this virus, although newly discovered in pigs, has been present in the pig population for a number of years. Experimental infection of weaned pigs with PCV3 induced disease which in some respects resembled PDNS (Jiang and others, 2019).

A recent publication from the US (Arruda and others, 2019) reported findings from diagnostic investigations which demonstrated PCV 3 within lesions of diseased pigs by *in situ* hybridization, with high viral loads. These cases included fetuses with myocarditis and weak-born neonatal piglets with encephalitis and myocarditis and thus bear similarity to an incident involving a single farm investigated in 2018 in England in which stillborn and preweaned piglets had multi-systemic inflammation associated with high PCV3 viral loads in the same tissues (APHA, 2018b). There are other reports in the literature of PCV3 detection with high viral loads in stillborn and aborted piglets (Palinski and others, 2016; Faccini and others, 2017) and in semen (Ku and others, 2017; Li and others, 2018) indicating that vertical transmission can occur; although histopathological findings in PCV3-positive fetuses or stillbirths were not described. Multisystemic inflammation has also been described in growing pigs which were PCV3-positive (Phan and others, 2016).

The APHA Pig Expert Group is interested to hear of any similar clinical presentations or findings and surveillance is in place for similar cases by use of myocardial histopathology on foetal and stillborn piglets submitted in which no diagnosis has been established. Those found to have non-suppurative myocarditis are investigated further. The APHA case was presented at the 2019 European Symposium for Porcine Health Management in May 2019 and has stimulated useful collaboration.

There have been a number of other informative publications on PCV3; Klaumann and others (2019a) report results of a longitudinal study on the infection dynamics of PCV3 on four farms with Zhai and others (2019) providing editorial comment. PCV3 was found to be widespread in clinically healthy pigs and, in these, PCV3 loads were low, suggesting that subclinical infection may be how PCV3 is maintained in herds. PCV-3 was detected by PCR in pigs at all ages that were tested and in all four farms. A small number of pigs were positive at several time points during their growing period raising the possibility of persistent infection in these individuals. PCV3 has been detected in wild boar in Spain (Klaumann and others, 2019b) and Germany (Prinz and others, 2019), in both cases at high prevalence and the Spanish data indicates virus was present in the earliest samples in the study from 2004.

## Unusual diagnoses or presentations

### Clostridial myositis and cellulitis in finisher pigs

Clostridial disease in pigs most commonly manifests as clostridial enterotoxaemia (*Cl. perfringens*) in young piglets or clostridial hepatitis (*Cl. novyi*) in breeding sows. Outbreaks of clostridial myositis seen in ruminants, particularly cattle as blackleg or malignant oedema, are unusual in pigs and usually relate to contaminated injection sites or skin trauma (Stalker and others, 2007; Bidewell, personal communication). This outbreak was diagnosed on a well-managed indoor pig unit without ruminant contact. Eleven pigs in a group of 160 well-grown finishers were acutely affected over approximately 36 hours and six died. Affected pigs had well-defined haemorrhagic patches on the skin of the ears, flanks, ventral abdomen or ventral neck, some with associated swelling (Figure 4a). The pigs became lethargic and those dying did so within 36 hours. Affected pigs were scattered across the three strawed pens within one shed.

Four pigs were submitted to the APHA Thirsk VIC where, in view of the throat swelling in some pigs which can occur in the pharyngeal form of anthrax in pigs, smears were examined for *Bacillus anthracis* but with negative results. There were accumulations of gas (emphysema) and oedema within the subcutaneous tissue and the musculature was oedematous or emphysematous and dry (Figure 4b) with dark red-black discolouration. The suspicion of clostridial myositis and cellulitis was confirmed by the detection of *Clostridium septicum* by direct fluorescent antibody testing of lesioned tissues from the two most freshly dead pigs. Histopathology confirmed acute, necrotising myositis and cellulitis consistent with clostridial disease.



Factor(s) that may have precipitated this outbreak were not identified. The group had not received recent injections, there was no visible associated skin trauma and their diet and water was the same as that provided to unaffected groups. The affected group was promptly treated with amoxicillin in the water and paracetamol and no further pigs developed signs suggesting that there was a transient unidentified point source of infection, such as ingested spores. This case was described in the July 2019 APHA monthly surveillance report in the Veterinary Record (APHA, 2019b).

Figure 4: Clostridial myositis and cellulitis:

(a) Well-demarcated skin discoloration and swelling, image courtesy of the unit's private practitioner



(b) Emphysematous muscle with dark red central discoloration



## Changes in disease patterns and risk factors

Please refer to the annexe on Gov.UK for more information on the data and analysis.

### PRRS diagnosed in negated notifiable disease investigation

Aujeszky's disease (AD) and swine fevers were ruled out on clinical grounds and by testing respectively following an official APHA investigation into a report of suspect notifiable disease in June 2019. The report was prompted by widespread lethargy and inappetance across the breeding herd, with the deaths of eight sows from a group of 90 which had recently farrowed and high mortality of piglets in the litters born to this group. Severely affected sows were described by farm staff as having hindlimb ataxia and appearing drunk, with some goose-stepping. The case was first reported to APHA as suspect AD and the investigation was extended to include swine fevers following the finding of splenic infarcts (Figure 5a) and enlarged lymph nodes with haemorrhages

(Figure 5b) in a dead sow. Splenic infarcts are uncommon, even more so in an adult sow, and can be caused by classical swine fever. However, notifiable disease (ND) was ruled out within 48 hours in this case and restrictions were then lifted. Diagnostic testing confirmed porcine reproductive and respiratory syndrome (PRRS) due to PRRS virus-1 (PRRSV-1) as the cause of the outbreak and immunohistochemistry detected PRRSV antigen in association with spleen and lung lesions. Histopathology confirmed vasculitis and thrombosis in the spleen which resulted in the infarction; vasculitis is reported in the literature on the pathology of PRRS. Histopathology on the brain and spinal cord, and calcium estimation on aqueous humour, were undertaken to investigate the apparent nervous signs but the findings were unremarkable. It is thus considered likely that those signs reflected marked weakness in the sows. Whenever splenic infarcts are seen in pigs, the possibility of classical swine fever should be considered and, if suspected, must be reported immediately by calling the Defra Rural Services Helpline on 03000 200 301 in England, if in Wales, contact 0300 303 8268 and in Scotland, contact the local [Field Services Office](#).

Figure 5: Systemic PRRS in sow:

a) Splenic infarcts



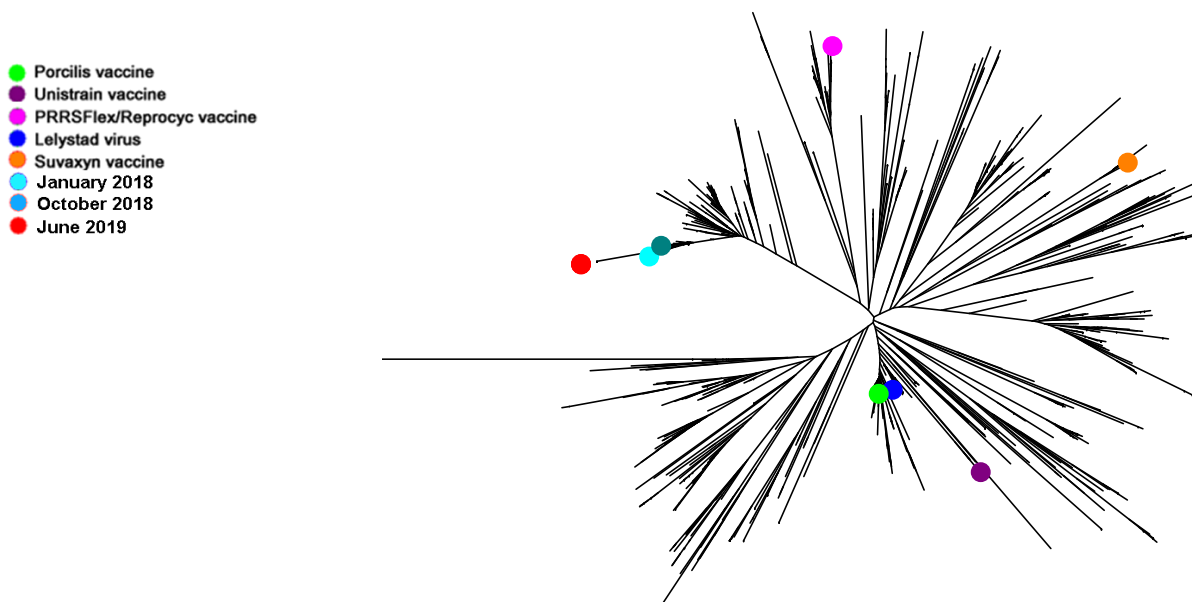
b) enlarged lymph node with haemorrhages



Additional testing for PCV2 by immunohistochemistry and PCV3 by PCR did not provide evidence of their involvement. The ORF 5 sequence of the infecting PRRS virus showed that it was a PRRSV-1 virus within the GB cluster (Figure 6). The virus was not similar to any of the four live PRRS vaccine viruses licensed in GB. The viruses with closest similarity showed 97% homology in ORF5 sequence. It is interesting to note that three official investigations into suspect ND in commercial pigs in 2018-19 (of which this incident is one), in which ND was ruled out, were subsequently diagnosed as involving PRRS and its secondary effects (APHA, 2018). Unlike the other two incidents, the affected pigs on this occasion were PRRSV-vaccinated and this was reported to the Veterinary Medicines Directorate as a possible failure of vaccine efficacy. The phylogenetic tree based on the

ORF5 gene sequence (Figure 6) shows the PRRS viruses in these three incidents. Although not closely related to each other (i.e. none >98.5% similar), they belong in the same small cluster along with about 30 other sequences from the UK, and may have evolved from a common ancestor. The virus has been isolated and will be used for further analyses, including whole genome sequencing, and comparison with other viruses. Virulence factors are poorly understood in PRRSV; the three incidents involved disease of sufficient concern to result in suspect ND being reported, however other incidents in which PRRSV in this cluster was identified did not raise similar concern and other factors may have been involved in the disease severity, such as naivety, concurrent disease, and stage of production. Approximately 60 further PRRSV have been sequenced from 2019 incidents and these fall into at least 16 individual clusters. All are PRRSV-1 and fall within the overall GB cluster, and there is no evidence of novel introductions.

Figure 6: Phylogenetic analysis of ORF5 gene sequences from UK PRRSV strains – legend indicates viruses detected in three negated ND incidents alongside live vaccine viruses



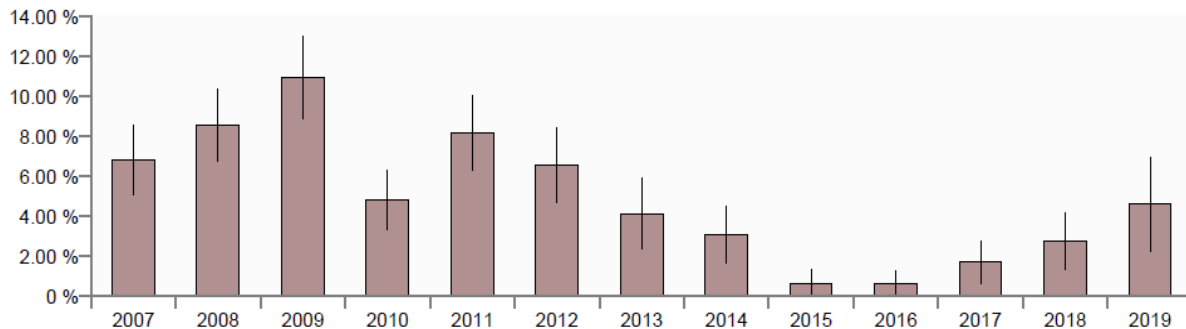
### ***Brachyspira hyodysenteriae* MLST in swine dysentery incidents**

Further diagnoses of swine dysentery were made in several regions including Scotland and Wales in the second quarter of 2019 and, although annual data for 2019 are incomplete, the diagnostic rate for this year to date has continued the increase which began in 2017 as illustrated in Figure 7.

Diarrhoea and wasting continue to be the main clinical signs reported with disease occurring mainly but not exclusively in pigs of grower to finisher age. As described under “Pig disease surveillance dashboard April to June 2019 output” on page 1, enteric syndrome submissions have been prominent which is likely to reflect, at least in part,

increased diagnostic investigations following concern about swine dysentery. An increase in *Brachyspira pilosicoli* and *Lawsonia intracellularis*-associated diagnoses has also occurred, which may reflect the increased throughput of enteric submissions and will be kept under review.

Figure 7: GB incidents of swine dysentery as % of diagnosable submissions



Whole genome sequence (WGS) results for *Brachyspira hyodysenteriae* isolates obtained at SAC-CVS or APHA from 2016 to June 2019 have been issued to the submitting vets. This sequencing has been part funded by Huvepharma together with Defra funding from the “Scanning surveillance for diseases of pigs in England and Wales” project.

The WGS reports confirm the isolate as *B. hyodysenteriae* and indicate the multilocus sequence type (MLST ST) that the isolate groups with. They also indicate those *B. hyodysenteriae* isolate(s) showing closest similarity (if any) and identify which antimicrobial resistance genes are present, which complements the minimum inhibitory concentration (MIC) test results. Work is in progress to determine the best means of sharing WGS results more widely to assist epidemiological investigations without compromising confidentiality, possibly through the development of an on-line dashboard.

WGS of isolates from incidents from 2017 to June 2019 has detected eight MLST STs (ST52, ST 88, 229, 242, 251, 252, 254, 255) with two additional isolates of “new” MLST ST but which align with ST52 or ST251. Four of these MLST groups (ST229, ST251, ST254, ST255) do not feature amongst sequenced isolates which derive from submissions earlier than 2017. This information confirms that the outbreaks since 2017 do not derive from spread of a single *B. hyodysenteriae* type.

Isolates continue to be tested for their antimicrobial susceptibility by MIC under funding from the ‘Monitoring of Antimicrobial Resistance in Bacteria from Animals and their Environment Project’ within APHA. No Q2-2019 isolates examined had an MIC greater than the clinical breakpoint for tiamulin against *Brachyspira hyodysenteriae*, thus none appeared tiamulin-resistant. As indicated in the last quarterly report (APHA, 2019c), some recent isolates have been sensitive to all the antimicrobials tested (tiamulin, valnemulin, tylvalosin, lincomycin, tylosin and doxycycline).

The “#MuckFreeTruck” lorry wash campaign launched by the National Pig Association and AHDB Pork, and endorsed by the four Chief Veterinary Officers remains active. This promotes the need for pig producers, processors and hauliers to ensure livestock lorries

are properly cleaned. It was launched in response to the threat posed by ASF and other livestock diseases, including swine dysentery. Further information on swine dysentery and its control is provided through these links:

<http://apha.defra.gov.uk/documents/surveillance/diseases/swine-dysentery.pdf>

<https://pork.ahdb.org.uk/health-welfare/health/swine-dysentery/>;

<http://www.nadis.org.uk/disease-a-z/pigs/swine-dysentery/>; <https://pork.ahdb.org.uk/health-welfare/health/significant-diseases-charter>

## Horizon scanning

### Porcine epidemic diarrhoea surveillance

No suspect incidents of porcine epidemic diarrhoea (PED) were reported in England or Scotland during Q2-2019. Enhanced surveillance for PED continues and diagnostic submissions from cases of diarrhoea in pigs (non-suspect) submitted to APHA are routinely tested for PED virus (PEDV) on a weekly basis. None have tested positive for PEDV in 890 diagnostic submissions tested under AHDB Pork funding between June 2013 and June 2019.

Since the emergence of virulent PED from mid-2013 in the USA and elsewhere, the virulent PEDV strain has only been reported on the European continent in Ukraine (Dastjerdi and others, 2015). However, reportedly less virulent strains (known as INDEL strains) have been reported in pigs on several continents, including countries in mainland Europe. These INDEL strains have both an insertion and a deletion in the PEDV S gene and the first INDEL strain, named OH851, was described in the US in 2014 (Wang and others, 2014). PED is now endemic in the US where the numbers of diagnoses are no longer tracked weekly. Sixty PED cases have been diagnosed in Manitoba in 2019 (24 finisher, 11 nursery, 24 sow, one in quarantine): this Canadian Province had a significant outbreak (80 cases) in 2017. The continuation of active PED elsewhere supports the testing requirements of the National Pig Association import protocol when live pig imports are planned (NPA, 2019).

PED due to any strain remains notifiable in England and Scotland and suspicion of disease, or confirmation of infection, must be reported (Defra, 2015). Further information on PEDV is available on this link: <https://pork.ahdb.org.uk/health-welfare/health/emerging-diseases/pedv>.

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