



Animal &
Plant Health
Agency

National epidemiology report

Highly Pathogenic Avian Influenza H5N8

Annex 1: Three additional infected small-holder premises - April to May 2017

Situation at 16:00 on Friday 22 June 2017



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Executive summary

The initial phase of the 2016-2017 outbreak of H5N8 highly pathogenic avian influenza in the UK consisted of ten infected premises (IPs), distributed across six distinct geographical areas of England and Wales: Lincolnshire, Lancashire, Suffolk, Carmarthenshire, Yorkshire and Northumberland.

Shortly after the resolution of this initial phase of the outbreak, a cluster of two non-commercial, small-holder premises infected with H5N8 highly pathogenic avian influenza virus, were disclosed in Lancashire, and one single small-holder premises in Norfolk. The two infected premises in Lancashire were located within 700 metres of each other and seven kilometres from the three infected premises in the earlier Lancashire cluster involved in gamebird production, which were situated close to Morecombe Bay, an important area for the over-wintering of wild birds.

Epidemiological investigations did not disclose any tracings linking the two IPs in Lancashire, with each other, nor with the single IP in Norfolk. Tracings investigations did not identify any links with any other premises in Great Britain, including the three nearby IPs that formed the recent Lancashire gamebird cluster.

Extensive follow-up epidemiological investigations and surveillance activities did not detect the presence of infection in any further premises investigated in connection with the IPs, either by known contacts (source and spread tracings), or as a result of proximity (protection and surveillance zones).

On this basis, these three IPs are considered to have arisen as individual independent events, resulting from direct or indirect primary incursions of HPAI H5N8 virus from wild birds.

Although the epidemiological investigation concludes that the most likely route of introduction of virus onto these IPs was either direct or indirect contact with wild birds, any incursion such as these, onto an individual premises, remains a low likelihood event and is largely influenced by the effectiveness of biosecurity measures that have been implemented.

Assessment of potential spread: Introduction / background

This report summarises all the epidemiological investigations carried out in order to describe and explain the outbreak of H5N8 highly pathogenic avian influenza (HPAI).

The report will be used to:

- (i) Provide evidence to support the UK's position in successfully controlling the outbreak and as a declaration of freedom from H5N8 HPAI to both the EU and OIE.
- (ii) Inform trading partners, with a view to facilitate international trade.
- (iii) Provide source material for the technical annex for UK co-financing claims to the EU.
- (iv) Record the logistics and technicalities of the investigation and disease control in order to inform future resource planning, contingency plans and training requirements.
- (v) To highlight gaps in our understanding of notifiable avian influenza and so identify areas for further research or other needs.

Analysis of the virus

Genetic analyses – similarities and differences:

The H5N8 HA gene of viruses from the infected premises (IP) IP11 and IP12 are identical, almost certainly implying that birds on the two premises were infected by a virus from a common wild bird source (taking into account epidemiological data showing no direct linkage between premises), which is all the more likely given the relatively close geospatial and temporal proximity. A cautionary note should be stated however that, as with other viruses in these related outbreaks, there are extremely high levels of similarity amongst the poultry viruses in particular, but also close relationships to the wild bird strains. Furthermore, the IP11 and 12 viruses show close relationships to other viruses i.e. IP3 and probably derive from a common ancestor to the pheasant case cluster nearby (IP5, 7 & 8) that supports limited genetic diversity in the wild bird strains within the region.

Whole genome molecular analyses – similarities and differences:

Phylogenetic analysis of the whole genome reveals a very close association with poultry isolates from other UK IPs. The H5N8 genome from IP11 and IP12 shows extremely high levels of similarity, greater than 99.29% to all other H5N8 viruses

detected in poultry in the UK, including selected wild bird strains. These viruses show even higher similarity to viruses from contemporary UK poultry outbreaks, in the range of 99.6% to 99.7%. They are also highly similar to each other at 99.91% across the full genome.

The H5N8 genome from IP13 shows extremely high levels of similarity, greater than 99.25% to all other H5N8 viruses detected in poultry in the UK, including selected wild bird strains. This virus shows even higher similarity to viruses from contemporary UK poultry outbreaks, in the range of 99.4% to 99.7%.

These results provide further confirmation of the extremely high similarity but also of the limited genetic diversity amongst this group of viruses in general, meaning that meaningful genetic relationships to inform pathways of origin and precise relationships are problematical and uncertain.

Introduction and overview of the three infected premises

The two IPs in Lancashire were non-commercial, small-holder premises located within 0.7 kilometres of each other (see **Error! Reference source not found.**) and seven kilometres from the three earlier infected premises involved in gamebird production, situated close to Morecombe Bay, which is an important area for the over-wintering of wild birds.

The infected premises in Norfolk was a non-commercial, small-holder premises. All three have similar characteristics to the other UK small-holder IPs disclosed in this outbreak.

The Lancashire small-holder cluster (IP 11 and IP 12)

Description of the “cluster”

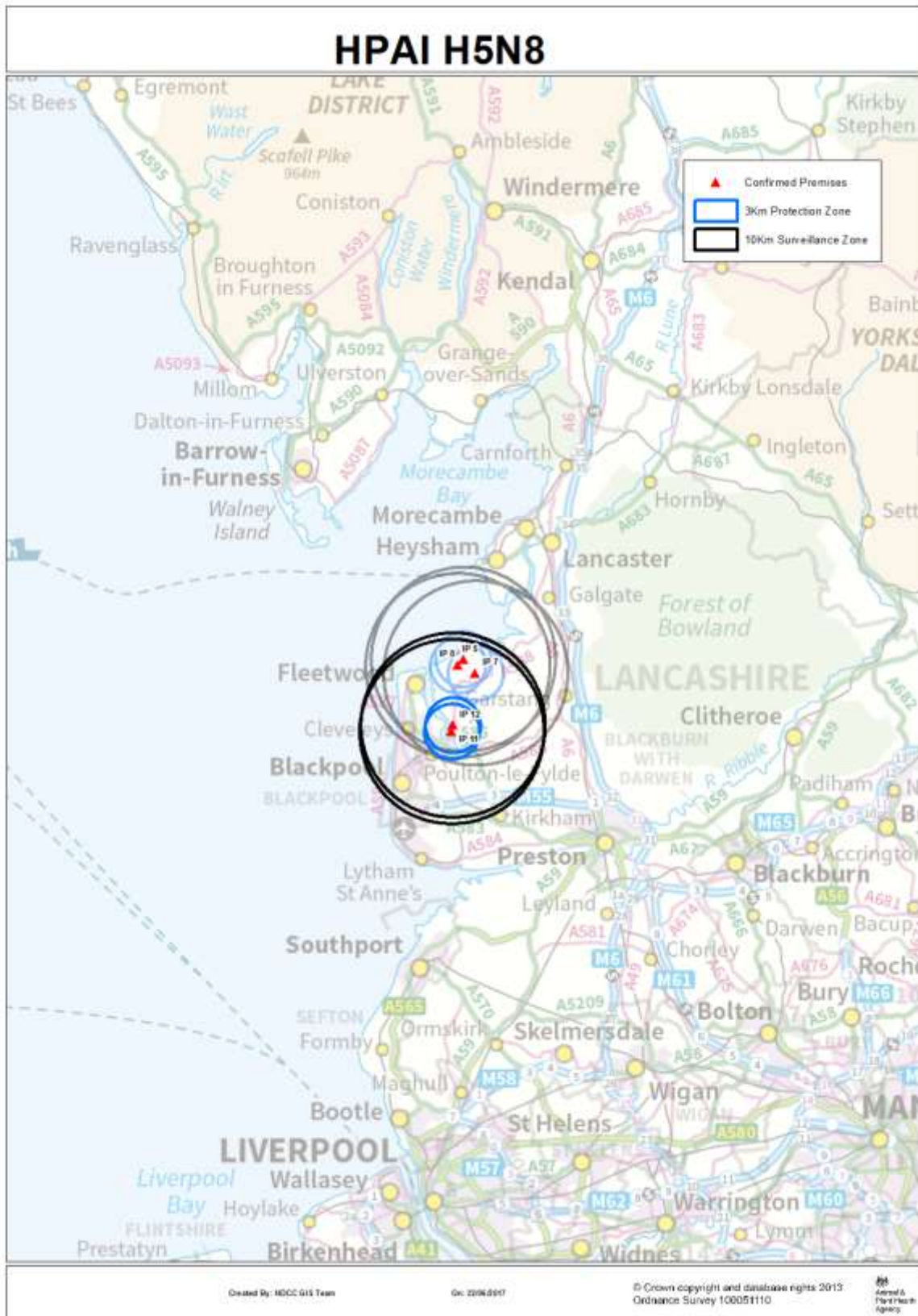
The cluster consisted of two small-holder premises, 700 metres apart.

1. IP11 - confirmed on 04 May 2017.
2. IP12 - confirmed on 06 May 2017. .

These two IPs were closely situated both spatially and temporally, as can be seen in **Error! Reference source not found.**Figure 1 and Table 1, but resulted from entirely separate, direct or indirect, primary introductions of virus from wild birds.

The IPs are within the former Surveillance Zone (SZ) of the Lancashire gamebird cluster (IP5, IP7 & IP8) (see Figure 1**Error! Reference source not found.**). No links with these IPs were established, despite extensive tracings investigations.

Figure 1: Map showing the location of IP11 and IP12 in relation to the gamebird cluster (IP 5, IP 7 & IP 8), together with the associated PZs and SZs.



IP 11 – Near Thornton, Lancashire (AIV 2017/10)

Description of the premises: The infected premises (IP11 designated as AIV 2017/10) is a small-holding, located approximately 0.5 km from the tidal estuary of the River Wyre. Only chickens were kept on the holding, and these were kept for non-commercial domestic consumption. The land around the Wyre estuary has a significant wild waterfowl population, and there are numerous ponds and ditches in the locality.

Prior to the start of mortality there were approximately thirty, twelve months-old chickens present on the holding. The chickens were kept indoors in a stable from December 2016 until mid-March 2017, following the lifting of the local SZ for IP5, IP7 and IP8, after which they were allowed to range free across the property. The birds were fed mixed grain indoors and corn, which was scattered over the pasture surrounding the buildings. Wild mallard ducks were reported to visit the premises regularly looking for food.

Source and spread windows: The most likely time that HPAI infection is estimated to have entered IP 11 (the high-risk source tracings window) is between 24 and 26 April 2017. The most likely time for hypothetical spread of HPAI infection from IP 11 is estimated as being between 25 April and 03 May 2017.

Hypothesis for the source: All the available evidence suggests that the incident is likely to have resulted from introduction of HPAI virus onto the IP, via direct or indirect contact with infected wild waterfowl.

Evidence base for the source: This assessment of the source is based on the evidence that:

- (i) The chickens on the IP were freely roaming outside, with access to the pasture where wild waterfowl, and other birds, also had access.
- (ii) No poultry were brought on to the premises in the source window.
- (iii) There is evidence of HPAI infection in waterfowl and gamebirds in the local area.
- (iv) A contiguous premises with emus, rheas and chickens was visited and the birds clinically examined and sampled. All the birds were found to be clinically normal and the rheas and emus that were sampled tested negative for avian influenza.
- (v) No other linked infected premises have been identified through national and international source tracings.

- (vi) There is strong laboratory evidence from sequencing the virus that shows it is consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds, and a strain found in a wild bird in Wales.
- (vii) The time of year of these outbreaks occurred with respect to wild bird migratory movements and the observations by expert ornithologists of wild waterfowl and other birds, together with the finding of this strain of virus in poultry and wild birds in multiple countries are both supportive of a wild bird-mediated introduction.

Tracings: Evidence from local surveillance completed in the Protection Zone and tracings of all contacts with the IP, indicates that there has not been any spread of infection from IP 11 into either the local area, or more widely.

Summary: Following extensive investigations, no HPAI H5N8 infection has been found on any other UK premises linked to IP 11. At this time, the outbreak appears to have arisen as the result of the introduction of HPAI H5N8 infection into the IP via direct or indirect contact with infected wild waterfowl or other birds. Preliminary cleansing and disinfection (C&D) of the IP was completed on 06 May 2017.

IP 12 – Near Thornton, Lancashire (AIV 2017/11)

Description of the premises: IP12 is a private dwelling in a residential area of a village in Lancashire. There were six laying hens, one cockerel and three ducks, all of which were kept for non-commercial purposes. The birds were kept together in one large pen, partially enclosed, in the back garden of the house. Located 0.7 km to the south west of this IP is IP11 and 0.7 km to the west is the large tidal estuary of the River Wyre, the mouth of which is located approximately 8 km from the internationally important, wild bird over-wintering area of Morecambe Bay. There are also numerous ponds and ditches spread across the local area.

The IP is in a high poultry density area and was in the SZ of the game-bird cluster (IP5, IP7 & IP8) (see Figure 1 **Error! Reference source not found.**). There is a significant degree of overlap of the PZs and SZs for IPs 11 and 12

Source and spread windows: The most likely time that HPAI infection is estimated to have entered the IP (the high risk source tracing window) is between 25 April and 28 April 2017. The most likely time for hypothetical spread of HPAI infection off the IP is estimated as 26 April to 05 May 2017 (see Table 1).

Hypothesis for the source: The available evidence suggests that the incident is likely to have resulted from introduction of HPAI virus into the IP via indirect contact with infected wild waterfowl.

Evidence base for the source: This assessment of the source is based on the evidence that:

- (i) The chickens and ducks on the IP were freely roaming outside and shared a field adjacent to a stream with wild waterfowl.
- (ii) Four hens were brought from another premises onto the IP, but outside the high risk source tracing window.
- (iii) There is evidence of HPAI infection in waterfowl and gamebirds in the local area.
- (iv) There are no other linked infected premises that have been identified through national and international source tracings.
- (v) There is strong laboratory evidence from sequencing the virus that shows it is consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds, and a strain found in a wild bird in Wales.
- (vi) The time of year of these outbreaks occurred with respect to wild bird migratory movements and the observations by expert ornithologists of wild waterfowl and other birds, together with the finding of this strain of virus in poultry and wild birds in multiple countries are both supportive of a wild bird-mediated introduction.

Tracings: Evidence from local surveillance completed in the Protection Zone and tracings of all contacts with the IP indicates there has not been spread of infection from the IP into the local area or more widely.

Summary: Following extensive investigations, no HPAI H5N8 infection has been found on any other UK premises linked to IP 12. At this time the outbreak appears to have arisen as the result of introduction of HPAI H5N8 infection into the IP via direct contact with infected wild birds. Preliminary cleansing and disinfection (C&D) of the IP was completed on 07 May 2017.

The single infected premises in Norfolk (IP 13)

IP 13 - Near Diss, Norfolk (AIV 2017/12)

Figure 2: Map showing the location of IP 13 in relation to IP 9, together with the associated PZs and SZs.



Description of the premises: IP13 is a smallholding with chickens and geese, which were kept for non-commercial purposes. The IP is in south-central Norfolk, near the Suffolk border and is more than 20 km away from the East Anglian coastline, but near the confluence of the Rivers Dove and Waveney. It is located approximately 3 km outside the Surveillance Zone of IP9 (see Figure 2).

Twenty-four chickens and seven geese were present on the holding before the onset of mortality. The chickens had been housed in poultry hutches with access to a small solid-roofed enclosure and the geese were kept separately in a netted livestock trailer, until the AI Prevention Zone was lifted on 13 April. After that, the chickens continued to be housed separately at night, but had access to outside ranges, which they shared with the seven geese.

There are also two pigs and two sheep on the IP, all of which remain healthy. The two pigs were sampled on 05 June 2017 and tested negative for avian influenza.

Source and spread windows: The most likely time that HPAI infection is estimated to have entered the IP (the high risk source training window) is between 09 May and 11 May 2017. The most likely time for hypothetical spread of HPAI infection off the IP is estimated as 10 May to 02 June 2017 (see Table 1).

Hypothesis for the source: All the available evidence suggests that the incident is likely to have resulted from introduction of HPAI virus onto the IP, via direct or indirect contact with infected wild waterfowl.

Evidence base for the source: This assessment of the source is based on the evidence that:

- (i) The chickens and geese on the IP were able to roam freely outside and shared a field adjacent to ponds on site, including a large pond with resident wild water fowl (approximately thirty-two wild mallard ducks and four moorhens).
- (ii) The domestic geese are known to have interacted with the wild waterfowl on the pond, and whilst the chickens were rarely seen near the pond they had direct contact with the geese (and indirect contact via the environment). It is therefore a plausible hypothesis that infection was transmitted from wild waterfowl to the geese, and then from the geese to the chickens (and subsequently chicken-to-chicken transmission once the geese had seroconverted and cleared virus)..
- (iii) There is evidence of HPAI infection in waterfowl and gamebirds in the local area.
- (iv) There are no other linked infected premises that have been identified through national and international source tracings.

- (v) There is strong laboratory evidence from sequencing the virus that shows it is consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds, and a strain found in a wild bird in Wales.
- (vi) The time of year of these outbreaks occurred with respect to wild bird migratory movements and the observations by expert ornithologists of wild waterfowl and other birds, together with the finding of this strain of virus in poultry and wild birds in multiple countries are both supportive of a wild bird-mediated introduction.

Tracings: Evidence from local surveillance completed in the Protection Zone and tracings of contacts with the IP indicates there has not been spread of infection from the IP into the local area or more widely.

Summary: In summary, following extensive investigations, no HPAI H5N8 infection has been found on any other UK premises linked to IP 13. At this time the outbreak appears to have arisen as the result of introduction of HPAI H5N8 infection into the IP via direct or indirect contact with infected wild birds. Preliminary cleansing and disinfection (C&D) of the IP was completed on 04 June 2017.

Overview of tracing activity for IP11, IP12 and IP13

Evidence based on the clinical picture, laboratory results and expert advice, together with the OIE requirement for a precautionary assumption of a 21 day incubation period prior to clinical signs, gave the source and spread time windows which informed tracing activities.

Expert advice from the APHA OIE / FAO / EU Reference Laboratory, based on a 48-72 hour incubation period for this particular H5N8 HPAI virus, resulted in the definition of the high risk tracing window.

Multiple telephone and email enquiries were generated to confirm information about the different tracing investigations linked to the various IPs and to inform the risk assessments.

Potential contact premises were identified in the following categories:

1. Movements of live poultry and eggs.
2. People.
3. Animal by-products.
4. Feed deliveries.
5. Bedding deliveries.

Surveillance in the protection and surveillance zones of IP11, IP12 and IP13

A census to identify all premises containing poultry was undertaken in both the Protection and Surveillance Zones, in line with EU legislative requirements.

Guidance notes were sent to all holdings within the PZ to raise awareness and remind keepers of the restrictions applying in this zone.

The poultry on these PZ premises, together with their production and medicine records were also clinically inspected by APHA personnel (and sampled and tested where relevant if non-mixing waterfowl) with no evidence of HPAI virus being identified. This surveillance was repeated prior to the merging PZ into the SZ.

Owners of premises within the SZ were sent guidance notes to raise awareness and also remind keepers of the restrictions applying in this zone.

Remaining uncertainty

There remains some uncertainty around the risk posed by wild birds, and when and where further cases or outbreaks may occur. There is evidence of this AI strain still circulating in Europe, therefore we consider that there is an increased risk of another outbreak occurring in poultry on individual premises depending on the level of biosecurity (the level of risk is “low to medium” where “low” is defined as an event that is rare, but could occur; and “medium” is an event which occurs regularly).

Concluding remarks

Extensive epidemiological investigations did not detect the presence of infection in any further premises investigated in connection with these three IPs, either by known contact (source and spread tracings), or as a result of proximity (protection and surveillance zones).

Although the epidemiological investigation concludes that the most likely route of introduction of virus onto this IP was direct or indirect contact with wild birds, any incursion such as these onto an individual premises, remains a low likelihood event and is influenced by the effectiveness of biosecurity measures that have been implemented.

National Emergency Epidemiology Group

22 June 2017

Acknowledgements

The views expressed in this report are those of the National Emergency Epidemiology Group (NEEG). However, we would like to express our thanks to the avian virology experts within APHA, members of the Ornithological Expert Panel, the Cardiff Specialist Service Centre Tracings Team and the many other APHA colleagues who have assisted with this investigation.

The NEEG is comprised of staff from APHA's Veterinary, Operations and Science Directorates

Appendices

Appendix 1: Composite source and spread timelines for the outbreak

Table 1: Composite source and spread timelines for the outbreak

KEY	Date of confirmation	Conf	Most likely date of infection	Inf	Date of primary C&D	
Source tracing window	Precautionary as per OIE (-21 days)		Likely (-14 days)		High-risk (-3 days)	
Spread tracing window	Precautionary (source +24 hrs)		Likely (source +24 hrs)		High risk (source +24 hrs)	

	IP11 - Small-holder	Lancashire	IP12 - Small-holder	Lancashire	IP13 - Small-holder	Norfolk
Date:	Source	Spread	Source	Spread	Source	Spread
06/04/2017						
07/04/2017						
08/04/2017						
09/04/2017						
10/04/2017						
11/04/2017						
12/04/2017						
13/04/2017						
14/04/2017						
15/04/2017						
16/04/2017						
17/04/2017						
18/04/2017						
19/04/2017						
20/04/2017						
21/04/2017						
22/04/2017						

	IP11 - Small-holder	Lancashire	IP12 - Small-holder	Lancashire	IP13 - Small-holder	Norfolk
Date:	Source	Spread	Source	Spread	Source	Spread
23/04/2017						
24/04/2017	Inf					
25/04/2017			Inf			
26/04/2017						
27/04/2017						
28/04/2017						
29/04/2017						
30/04/2017						
01/05/2017						
02/05/2017						
03/05/2017						
04/05/2017		Conf				
05/05/2017						
06/05/2017		1o C&D		Conf		
07/05/2017				1o C&D		
08/05/2017						
09/05/2017						Inf
10/05/2017						
11/05/2017						
12/05/2017						
13/05/2017						
14/05/2017						
15/05/2017						
16/05/2017						
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24/05/2017						
25/05/2017						
26/05/2017						
27/05/2017						
28/05/2017						
29/05/2017						

	Norfolk	IP13 - Small-holder	Lancashire	IP12 - Small-holder	Lancashire	IP11 - Small-holder	
Date:	Spread	Source	Spread	Source	Spread	Source	
30/05/2017							
31/05/2017							
01/06/2017							
02/06/2017							
03/06/2017							
04/06/2017		1o C&D					Conf
05/06/2017							

Appendix 2: Details of tracings and stock numbers in the protection and surveillance zones of IP11, IP 12 and IP 13.

The tables below are calculated from data taken from APHA Cardiff Specialist Services Centre (SSC) Tracing Team records. This data describes the pathways and tracing locations investigated by the outbreak tracing team to identify premises from where the infection may have arrived into the IP (back-tracing for source) and identify premises where there may have been onward spread of infection (forward-tracing for spread) from the IP, thus preventing further spread. In the text, the word “location” is used as a catch-all encompassing term that includes poultry premises, premises where there was no susceptible stock or linked-locations that could potentially spread the pathogen.

Veterinary risk assessments were carried out to determine the level of risk associated to the different risk pathways either for source and/or spread. These were supported by tracing activities involving data gathering and data verification (record checks, telephone interviews, emails, declarations). The outcome of the VRAs indicated which locations required follow-up for action.

Table 2: Number of locations investigated

Method of investigation	IP 11	IP 12	IP 13
Locations investigated and ruled out by non-exposure to susceptible animals	20	6	28
Locations investigated and ruled out by clinical inspection	2	0	3
Locations investigated ruled out by production data analysis	0	0	0
Locations investigated and ruled out by individual VRA	1	0	1
Locations identified as contact premises	0	0	0
Total number of locations	23	6	32

Table 3: Outcome of tracing investigation visits

Number of locations	IP 11	IP 12	IP 13
Locations requiring a tracing visit	2	0	3
Locations where restrictions were issued	2	0	3
Locations where restrictions were lifted at the conclusion of the tracing investigation	2	0	3
Locations containing susceptible animals ⁽¹⁾	2	0	3
Locations identified as contact premises	0	0	0
Locations negated as contact premises	0	0	0
Locations remaining under investigation	0	0	0