



Animal &  
Plant Health  
Agency

# National epidemiology report Highly Pathogenic Avian Influenza H5N8: December 2016 to March 2017

Situation at 16:00 on Tuesday 2 May 2017

## Change control

Change date	Version	Change
02/05/2017	V1.0	First published.
16/07/2017	V2.0	The description of IP9 on p24 has been changed from grandparent broiler-breeder unit to broiler-breeder unit, in order to more accurately reflect the nature of the business



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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, distributed across six distinct geographical areas of England and Wales: Lincolnshire, Lancashire, Suffolk, Carmarthenshire, Yorkshire and Northumberland.

Three of the outbreaks, in Carmarthenshire, Yorkshire and Northumberland were on single smallholder premises. The three infected premises (IPs) in Lincolnshire were engaged in turkey production and the three infected premises in Lancashire were involved in gamebird production; and were all associated with one business enterprise. The single premises in Suffolk was a broiler breeder unit involved in the production of chickens for meat.

This report has been arranged in sections devoted to individual geographical clusters, which coincidentally also correspond to different production systems. The three smallholder premises are described as a production system cluster, although these outbreaks were not connected in any way, and the premises are widely distributed across the country.

All the outbreaks, apart from those at the game bird premises in Lancashire, are considered to have arisen as independent events, resulting from direct or indirect primary incursions from wild birds. The IPs in Lancashire are considered to have originated as the result of a direct or indirect primary incursion of HPAI H5N8 from wild birds, with subsequent spread between related premises, taking place as a result of business activities.

Extensive epidemiological investigations 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).

Although the epidemiological investigation concludes that the most likely route of introduction of virus onto the majority of the IPs was direct or indirect contact with wild birds, an 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 analysis of the whole genome of H5N8 HPAI of all the GB viruses both poultry and wild birds reveals a very close relationship. It is possible to detect some closer associations phylogenetically i.e. IP5, 7, & 8 and possibly between IP3 and IP10 that might either infer a direct relationship in the former cases, or from a common wild bird progenitor in the latter. The levels of genetic similarity, principally in excess of 99.4% at full genome level, between all viruses indicate that following the emergence of these viruses and spread through multiple wild bird species, there was been very limited opportunity for divergent evolution.

The virus is showing to date limited genetic diversity which reduces the power and reliability of molecular epidemiology in providing evidence supporting virus origins and associated pathways for spread. This evidence therefore confirms a high homogeneity in European wild bird H5N8 HPAI viruses currently, which makes assumptions about specific origins unreliable, other than most probably from a 'wild bird' source, including consideration of other epidemiological factors. Furthermore the absence of any sustained transmission in the GB poultry cases is supported by the high level of genetic similarity in the viruses, which would mutate following sustained transmission especially in galliforme hosts. The virus genotype, determined by mapping all eight viral genes, indicates the GB strains are of a single genotype, but might marginally cluster differently to other European viruses, indicating the GB strains were as a result of an independent introduction pathway, but there are levels of uncertainty.

All the GB viruses were assessed for zoonotic potential using previously applied genetic analyses and it can be concluded that all viruses are still essentially avian viruses, with no specific increased affinity for mammalian species including humans.

# Introduction and overview of the ten infected premises

The 2016-2017 outbreak of H5N8 highly pathogenic avian influenza in the UK consisted of ten IPs, distributed across six distinct geographical regions of England and Wales: Lincolnshire, Lancashire, Suffolk, Carmarthenshire, Yorkshire and Northumberland (see Figure 1).

Three of the outbreaks, in Carmarthenshire, Yorkshire and Northumberland were on single smallholder premises. The three infected premises in Lincolnshire were engaged in turkey production and the three infected premises in Lancashire were involved in gamebird production and were all associated with one business enterprise. The single premises in Suffolk was a broiler breeder unit involved in the production of chickens for meat.

This report has been arranged in sections devoted to individual geographical clusters, which coincidentally also correspond to different production systems. The three smallholder premises are described as a production system cluster although the outbreaks in these were not connected in any way and are widely distributed across the country.

All of the outbreaks, apart from those at the game bird premises in Lancashire, are considered to have arisen from independent events resulting from direct or indirect primary incursions of virus from wild birds. The infected game bird premises in Lancashire are considered to have originated as the result of a direct or indirect primary incursion of HPAI H5N8 from wild birds, with subsequent spread between the related premises as a result of business activities. An updated report will follow describing the small-holder chicken premises recently disclosed in Lancashire (on 04/05/2017 and 06/05/2017)

Figure 1: Map showing the location of the ten infected premises with associated PZ and SZ

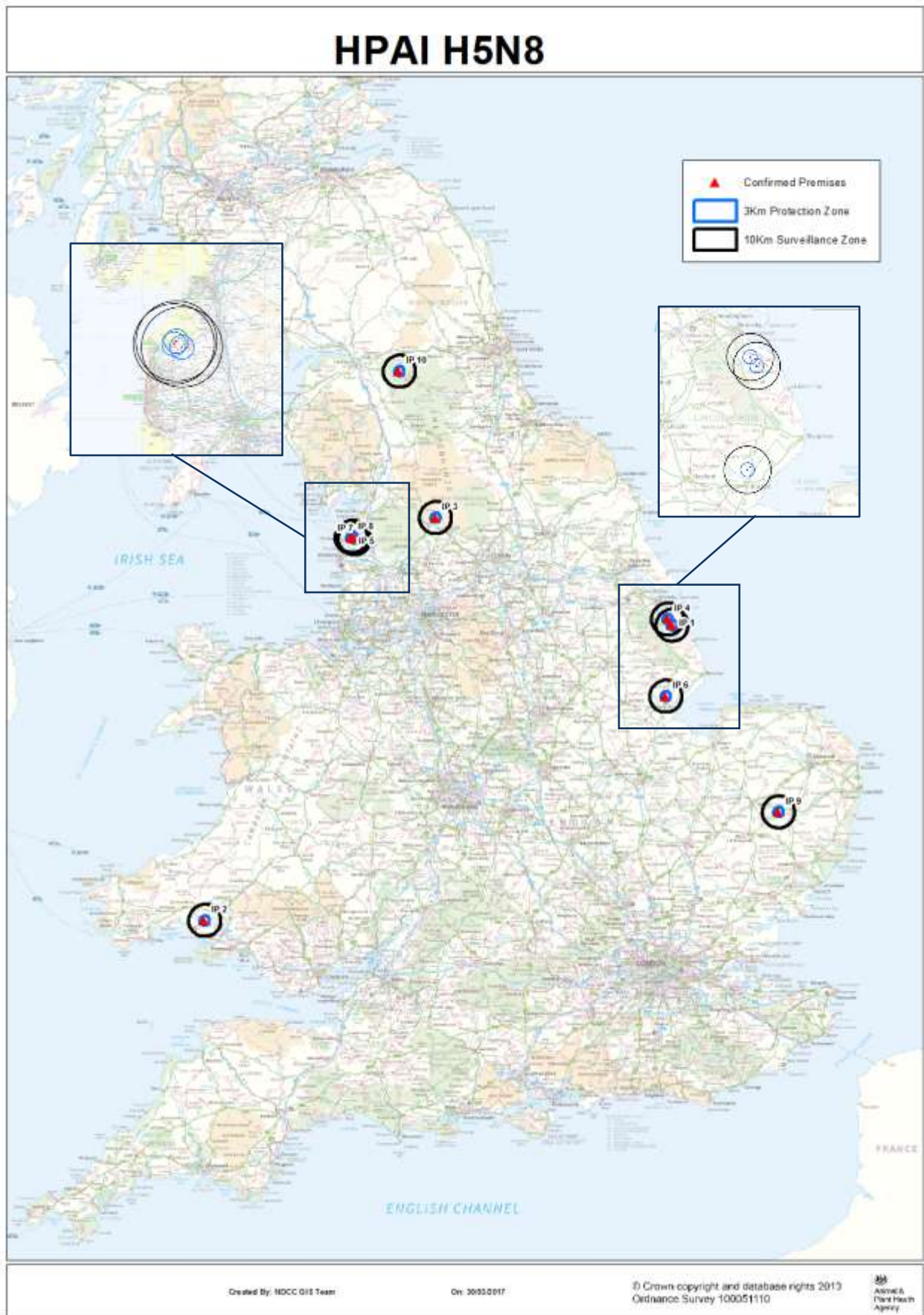
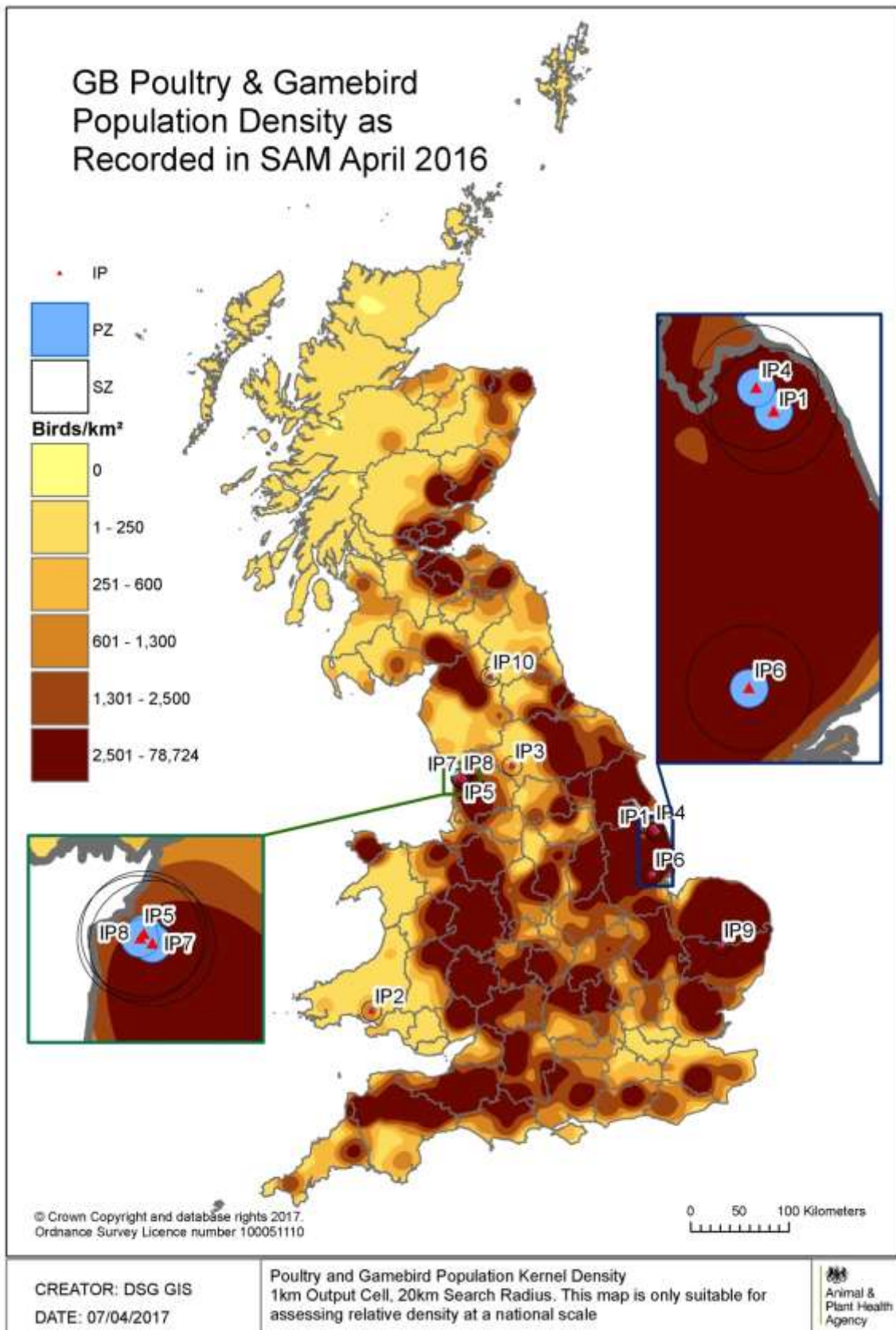




Figure 2: Map showing GB poultry and game bird population density relative to the location of the IPs



**Figure 3: Map to show the location of UK bird areas important for wintering gulls, geese or waterfowl**



# The Lincolnshire turkey cluster (IP 1, IP 4 and IP 6)

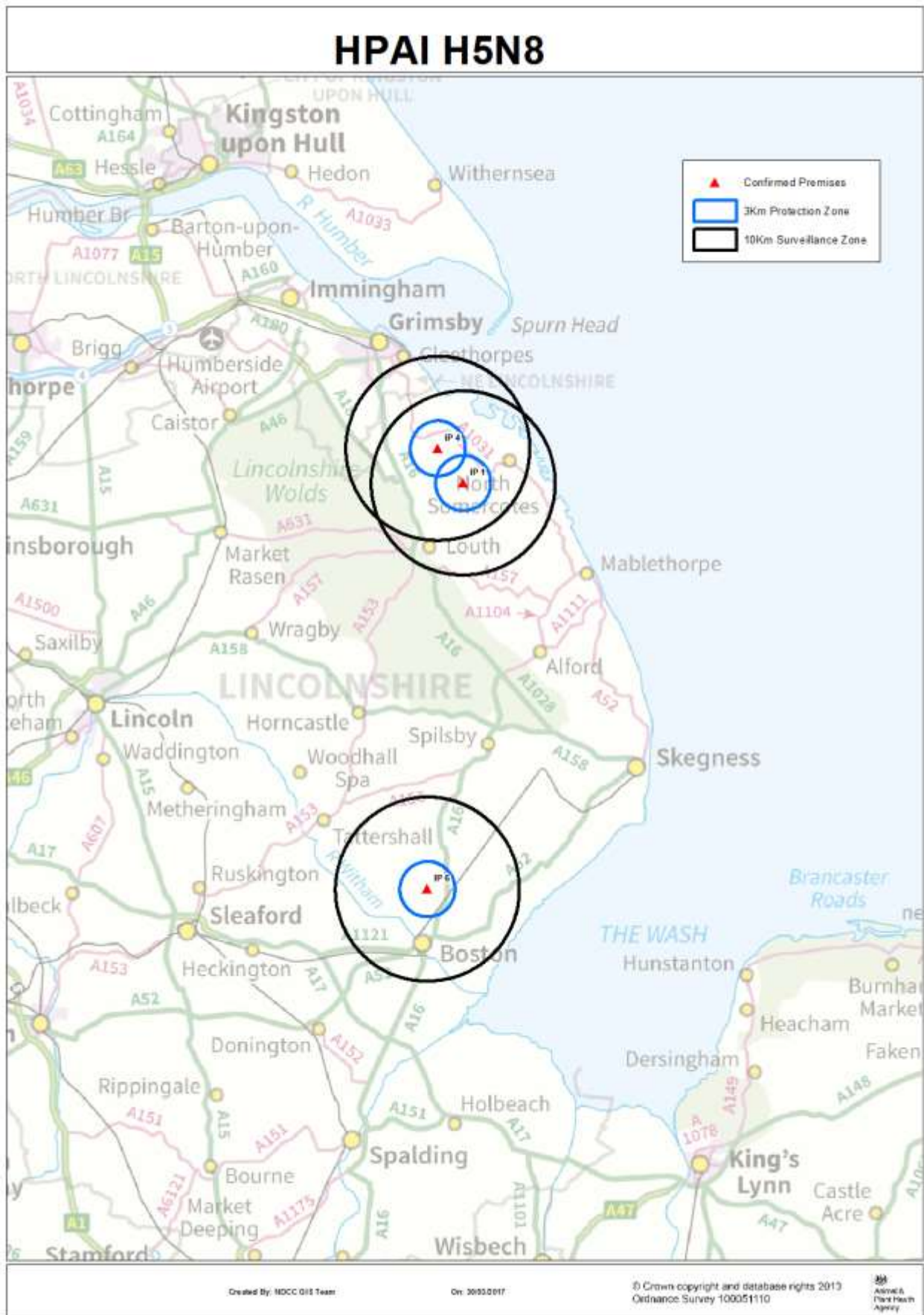
## Description of the Lincolnshire cluster

The cluster in Lincolnshire consisted of three premises:

1. IP1, confirmed on 16/12/2016 - an independent, seasonal, commercial turkey fattener, located close to Louth.
2. IP4, confirmed on 16/01/2017 - a commercial turkey fattening premises, located close to Fulstow.
3. IP6, confirmed on 26/01/2017 - a commercial brooding and fattening turkey premises, located close to Boston.

The location of the premises can be seen in Figure 4. In each case, infection is considered to have resulted from separate independent incursions of virus from both direct and indirect contact (via fomite) with infected wild birds, on the basis that no plausible source or spread tracings linking the three premises were identified.

Figure 4: Map showing the distribution of IPs in the Lincolnshire cluster



**Table 1: Timeline of key events in the Lincolnshire turkey cluster**

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

Date:	IP 1		IP 4		IP 6	
	Turkeys	Louth Lincs	Turkeys	Fulstow Lincs	Turkeys	Boston Lincs
	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window
20/11/2016						
21/11/2016						
22/11/2016						
23/11/2016						
24/11/2016						
25/11/2016						
26/11/2016						
27/11/2016						
28/11/2016						
29/11/2016						
30/11/2016						
01/12/2016						
02/12/2016						
03/12/2016						
04/12/2016						
05/12/2016						
06/12/2016						
07/12/2016						
08/12/2016	Infection					
09/12/2016						
10/12/2016						
11/12/2016						
12/12/2016						
13/12/2016						
14/12/2016						
15/12/2016						
16/12/2016		Confirmation				
17/12/2016						
18/12/2016		1° C&D				
19/12/2016						
20/12/2016						
21/12/2016						
22/12/2016						
23/12/2016						
24/12/2016						
25/12/2016						
26/12/2016						
27/12/2016						
28/12/2016						
29/12/2016						

	IP 1		IP 4		IP 6	
	Turkeys	Louth Lincs	Turkeys	Fulstow Lincs	Turkeys	Boston Lincs
Date:	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window
30/12/2016						
31/12/2016						
01/01/2017						
02/01/2017						
03/01/2017						
04/01/2017						
05/01/2017						
06/01/2017						
07/01/2017						
08/01/2017						
09/01/2017						
10/01/2017						
11/01/2017			Infection			
12/01/2017						
13/01/2017						
14/01/2017						
15/01/2017						
16/01/2017				Confirmation		
17/01/2017					Infection	
18/01/2017						
19/01/2017						
20/01/2017				1° C&D		
21/01/2017						
22/01/2017						
23/01/2017						
24/01/2017						
25/01/2017						
26/01/2017						Confirmation
27/01/2017						
28/01/2017						
29/01/2017						
30/01/2017						
31/01/2017						1° C&D
01/02/2017						
02/02/2017						
03/02/2017						

## IP 1 – Louth (AIV 2016/02)

**Description of the premises:** The infected premises (designated as AIV 2016/02) was on a site rented out by an independent, seasonal, commercial turkey producer. The birds were housed in one naturally ventilated house, which was divided internally into three areas, with shared air space and no biosecurity measures applied when moving between the different partitions.

**Description of the virus:** High pathogenicity avian influenza virus (HPAI) H5N8 was confirmed as the outbreak’s causative agent on 16 December 2016.

**Source and spread windows:** The most likely time that HPAI infection is estimated to have entered the IP is between 27 November and 10 December 2016. The most likely

time for hypothetical spread of HPAI infection off the IP is estimated as being between 28 November and 15 December 2016.

**Hypothesis for the source:** All the available evidence suggests that the incident resulted from direct and/or indirect contact via a primary incursion of HPAI virus into the turkey house on the IP, via infected wild birds.

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

- (i) No poultry were brought on to the premises in the source window.
- (ii) There was no evidence of HPAI infection in poultry in the local area at that time.
- (iii) There are no relevant, industry-related, national or international source tracings.
- (iv) Strong laboratory evidence, based on sequencing results of the virus that are consistent with HPAI H5N8 strains found in the 2016 European epizootic in poultry and wild birds.
- (v) The time of year that this outbreak occurred with respect to wild bird migratory movements, 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, together with the tracings of contacts from the IP demonstrated 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 was found on any other UK premises linked to this IP. At this time, the outbreak appears to have arisen as the result of direct and/or indirect introduction of HPAI H5N8 infection into the IP via infected wild birds. Preliminary cleansing and disinfection (C&D) of the IP was completed on 18 December 2016.

## IP 4 – Fulstow near Louth (AIV 2017/03)

**Description of the premises:** The infected premises (designated as AIV 2017/03) was a commercial turkey fattening business, located in Fulstow near Louth, Lincolnshire. The turkeys were housed in two permanent poly-tunnels with concrete floors (and straw litter), a steel frame covered with metal and mesh sheeting, and PVC.

**Source and spread windows:** The most likely time that HPAI infection is estimated to have entered the IP is between 31 December 2016 and 13 January 2017. The most likely time for hypothetical spread of HPAI infection off the IP is estimated as 01-15 January 2017.

**Hypothesis for the source:** All the available evidence suggests that the incident is likely to have resulted from direct and/or indirect contact as primary incursion of HPAI virus into the turkey housing on the IP via infected wild birds.

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

- (i) No poultry were brought on to the premises in the source window.
- (ii) This IP is located within 5 km of the first IP detected in the H5N8 HPAI outbreak in the UK (designated as AIV 2016/02) and it had undergone a veterinary investigation at the time without any significant findings (N.B. other than that there was no evidence of other HPAI infection in poultry in the local area).
- (iii) There are no relevant industry-related international source tracings.
- (iv) There was good biosecurity on the IP and personnel tracing activities, feed deliveries, ABP collections, water, bedding and veterinarian visits were assessed as very low or low risk, with no potential contact premises requiring a visit identified.
- (v) Strong laboratory evidence based on sequencing results of the virus consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds.
- (vi) The time of year that these outbreaks occurred with respect to wild bird migratory movements and 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 the tracings of contacts with the IP indicates there has not been spread of infection from the IP into the local area or more widely. On 26 January 2017, H5N8 HPAI was confirmed in a turkey fattening holding, owned by the same company as this IP. In spite of extensive epidemiological investigations, there has been no evidence so far of spread of infection between these two premises.

**Summary:** Following extensive investigations, no HPAI H5N8 infection has been found on any other UK premises linked to the IP. At this time the outbreak appears to have arisen as the result of introduction of HPAI H5N8 infection into the IP via direct and/or indirect contact with infected wild birds. Preliminary cleansing and disinfection (C&D) of the IP was completed on 20 January 2017.

## IP 6 - Boston (AIV 2017/05)

**Description of the premises:** The infected premises (designated as AIV 2017/05) is an intensive brooding and fattening commercial turkey site, belonging to a large integrated company, located in Lincolnshire. At the time of the report case visit the IP contained approximately 19,000 96 days old white turkey stags, housed in three conventional, controlled environment houses.

**Description of the virus:** HPAI H5N8 was confirmed as the outbreak's causative agent on 26 January 2017. Sequence results suggested that this was still predominantly an avian-adapted virus, without any specific increased affinity for humans.

**Source and spread windows:** The most likely time that HPAI infection is estimated to have entered the IP is between 06 January 2017 and 19 January 2017. The most likely time for spread of HPAI infection off the IP is estimated as 07-25 January 2017.



**Hypothesis for the source:** All the available evidence suggests that the incident is likely to have resulted from a primary incursion of HPAI virus into the IP via indirect contact with fomites from infected wild birds.

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

- (i) No poultry were brought onto the premises in the source window.
- (ii) There are no relevant industry related, national or international source tracings.
- (iii) Strong laboratory evidence based on sequencing results of the virus consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds.
- (iv) The time of year of these outbreaks occurred with respect to wild bird migratory movements and 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, together with the tracings of contacts from 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 this IP. At this time, the outbreak appears to have arisen as the result of indirect introduction of HPAI H5N8 infection into the IP via indirect contact with fomites from infected wild birds. Preliminary cleansing and disinfection (C&D) of the IP was completed on 31 January 2017.

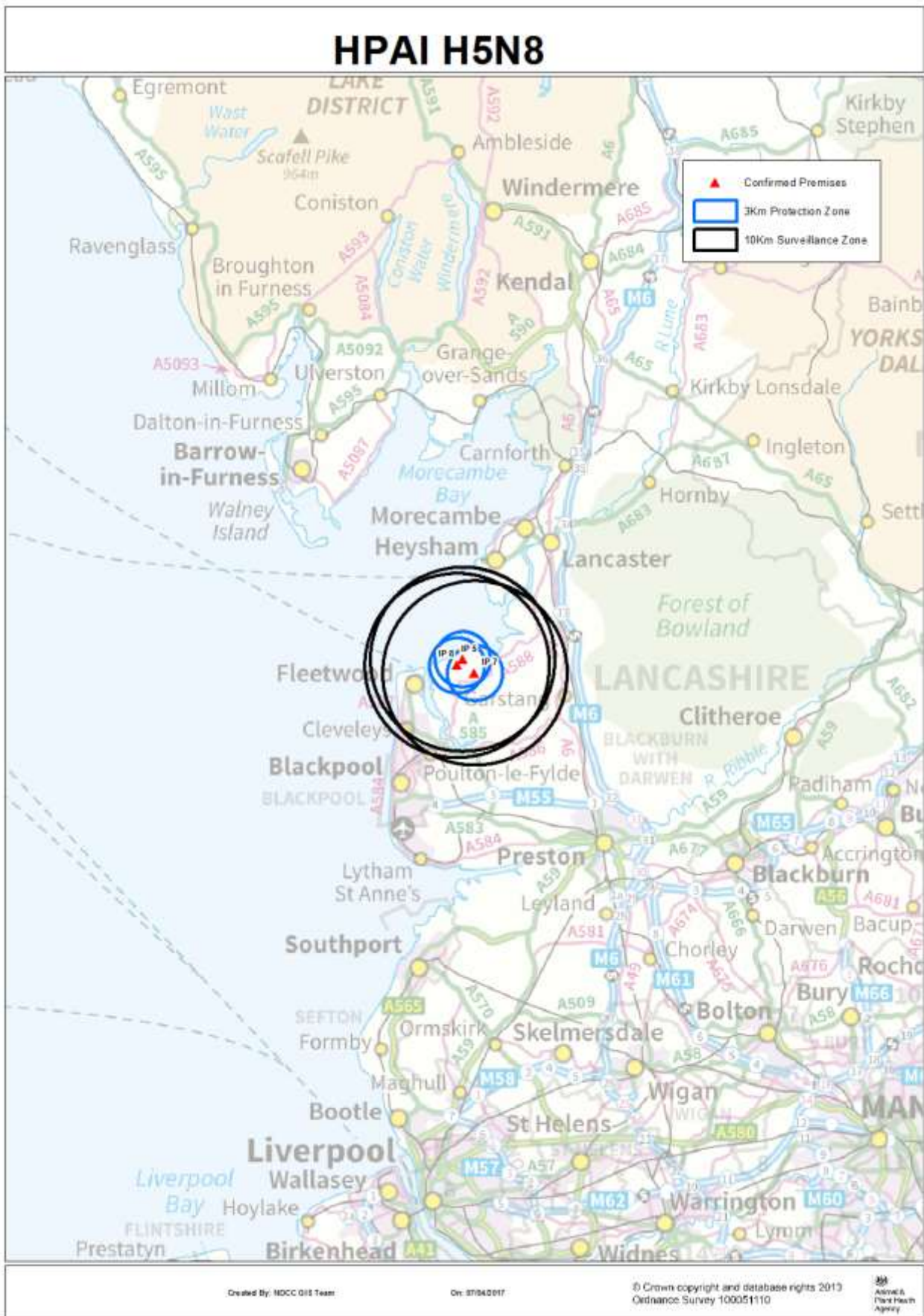
# The game-bird cluster (IP 5, IP 7 and IP 8)

## Description of the game-bird cluster

The game-bird cluster consisted of three premises in Lancashire that were part of the same commercial enterprise:

1. IP5, confirmed on 24/01/2017 – a large game-rearing premises, with over-wintering fields close to Morecambe Bay. It is part of a large, commercial, multi-site, game bird breeding and rearing enterprise.
2. IP7, confirmed on 27/01/2017 - a commercial, contract pheasant breeding premises, located close to IP5, which breeds pheasants for the company that owns IP5 and IP8.
3. IP8, confirmed on 30/01/2017 – is the main site of the large, commercial, game bird breeding and rearing enterprise, and is located close to IP5 and IP 7, with large numbers of pheasants, partridges, ducks and other species.

Figure 5: Map showing the distribution of IPs in the game bird cluster



**Table 2: Timeline of key events in the Lancashire game-bird cluster**

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

	IP 5		IP 7		IP 8	
	Game birds	Pilling Lancs	Game birds	Pilling Lancs	Preesall Lancs	Game birds
Date:	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window
24/12/2016						
25/12/2016						
26/12/2016						
27/12/2016						
28/12/2016						
29/12/2016						
30/12/2016						
31/12/2016						
01/01/2017						
02/01/2017						
03/01/2017						
04/01/2017						
05/01/2017						
06/01/2017						
07/01/2017						
08/01/2017						
09/01/2017						
10/01/2017						
11/01/2017						
12/01/2017	Infection				Infection	
13/01/2017						
14/01/2017						
15/01/2017						
16/01/2017						
17/01/2017						
18/01/2017			Infection			
19/01/2017						
20/01/2017						

	IP 5		IP 7		IP 8	
	Game birds	Pilling Lancs	Game birds	Pilling Lancs	Preesall Lancs	Game birds
Date:	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window
21/01/2017						
22/01/2017						
23/01/2017						
24/01/2017		Confirmation				
25/01/2017						
26/01/2017						
27/01/2017				Confirmation		
28/01/2017						
29/01/2017		1° C&D		1° C&D		
30/01/2017						Confirmation
31/01/2017						
01/02/2017						
02/02/2017						
03/02/2017						
04/02/2017						
05/02/2017						
06/02/2017						
07/02/2017						
08/02/2017						
09/02/2017						
10/02/2017						
11/02/2017						
12/02/2017						
13/02/2017						1° C&D
14/02/2017						
15/02/2017						

## IP 5 – Pilling (AIV 2017/04)

**Description of premises:** The infected premises (IP designated as AIV 2017/04) is a large game breeding and rearing premises with over-wintering fields, and is part of a complex multi-premises game farming company, located in Lancashire. The IP contained approximately 10,000 nine-month old, unhoused pheasants with clipped wings kept in two fields in pens with no overhead netting.

**Description of the virus:** HPAI H5N8 was confirmed as the outbreak's causative agent on 24 January 2017. Sequence results suggest that it is predominantly an avian-adapted virus, without any specific increased affinity for humans.

**Source and spread windows:** The most likely time that HPAI infection is estimated to have entered the IP is between 02 January 2017 and 15 January 2017. The most likely time for spread of HPAI infection off the IP is estimated as 3-23 January 2017.

**Hypothesis for the source:** All the available evidence suggests that the incident is likely to have resulted from a primary incursion of HPAI virus into the pheasant fields on the IP via infected wild birds.

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

- (i) No poultry were brought onto the premises in the source window.
- (ii) The IP did not comply with the Prevention Order requirements.
- (iii) There are no epidemiologically linked industry related international source tracings
- (iv) Feed deliveries, water and bedding were assessed as low risk with no potential contact premises requiring a visit identified.
- (v) Strong laboratory evidence based of sequencing results of the virus consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds
- (vi) Morecambe Bay is a world-renowned, over-wintering site for wild water fowl.
- (vii) The time of year of these outbreaks occurred with respect to wild bird migratory movements and 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 indicated there had been spread of infection from the IP to two premises belonging to the same company and with direct epidemiological links with the IP, which were later confirmed as IP7 and IP8.

**Summary:** In summary, following extensive investigations, associated HPAI H5N8 infection has been found only on two other UK premises with direct epidemiological links to the IP. At this time, the outbreak appears to have arisen as the result of introduction of HPAI H5N8 infection into the IP via infected wild birds. Preliminary cleansing and disinfection was completed on 29 January 2017.

## IP 7 – Pilling (AIV 2017/06)

**Description of premises:** The infected premises (IP designated as AIV 2017/06) was a commercial premises with approximately 1,000 breeding pheasants (36 weeks old) present at the time of the report case. The site began to be populated on 17/01/2017 with pheasants from IP8 (AIV 2017/07), prior to that it had been depopulated since the summer of 2016. The owner of the premises did not own the birds, but bred them for IP8, which is part of a large game farming company. At the time of the report visit there was one epidemiological group present, distributed over thirty pens (separated by netted fences and covered with net roofs).

**Description of the virus:** HPAI H5N8 was confirmed as the outbreak's causative agent on 27 January 2017. Sequence results suggest that it is predominantly an avian-adapted virus, without any specific increased affinity for humans.

**Source and spread windows:** The most likely time that HPAI infection is estimated to have entered the IP is between 17-21 January 2017. The most likely time for spread of HPAI infection off the IP is estimated as 17-26 January 2017.

**Hypothesis for the source:** All the available evidence suggests that the incident is likely to have resulted from an incursion of HPAI virus into the IP (either directly or indirectly) via infected pheasants from IP5 via IP8. Genomic analysis conducted confirms the potential for transmission of the virus between these IPs.

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

- (i) Pheasants were brought onto the premises from IP5 through IP8 within the high risk source window, and serology results indicated that they had been infected before the movement took place.
- (ii) There were no effective biosecurity procedures in place between IP5, IP7 and IP8.
- (iii) There are known business links between this IP and IP5 and IP8.
- (iv) There are no relevant, industry-related international source tracings.
- (v) Strong laboratory evidence based on sequencing results of the virus consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds.

**Tracings:** Evidence from local surveillance completed in the protection zone, together with the tracings of contacts from 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, IP7 is part of the cluster of IPs 5, 7 and 8 with transmission of infection to IP7 from IP5 via IP8. Transmission of infection between these IPs is also supported by genomic analysis results. Preliminary cleansing and disinfection (C&D) of the IP was completed on 29 January 2017.

## IP 8 – Preesall (AIV 2017/08)

**Description of premises:** The infected premises (IP designated as AIV 2017/07) is a large gamebird breeding and rearing site and was identified as a tracing premises prior to confirmation as IP, with direct business links with IP5 and IP7. It is located in Lancashire. The IP contained approximately 25,000 pheasants, 23,000 partridges, 14,000 ducks and 600 other birds at the time of the report case contained in various overwintering fields, pens and cages.

**Description of the virus:** HPAI H5N8 was confirmed as the outbreak's causative agent on 30 January 2017. Sequence results suggest that it is predominantly an avian-adapted virus, without any specific increased affinity for humans.

**Source and spread windows:** The most likely time that HPAI infection is estimated to have entered the IP is between 03 January 2017 and 27 January 2017. The most likely time for spread of HPAI infection off the IP is estimated as 4-29 January 2017.

**Hypothesis for the source:** All the available evidence suggests that the incident is likely to have resulted from incursion of HPAI virus into the IP via infected pheasants from IP5. Genomic analysis conducted confirms potential transmission of the virus between these IPs.

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

- (i) Pheasants were brought onto the premises from IP5 within the high risk source window.
- (ii) No effective biosecurity measures were implemented between IP5 and IP8.
- (iii) There are known business links between this IP and IP5.
- (iv) There are no relevant, industry-related international source tracings.
- (v) Strong laboratory evidence based on sequencing results of the virus consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds. Nevertheless, a wild bird introduction or indirect fomite transmission (via movements of vehicles and equipment, deliveries of feed and delivery of shot game bird to an onsite game bird larder) cannot be excluded as a potential source (assessed as of medium likelihood).

**Tracings:** Evidence from local surveillance completed in the protection zone indicates there has not been spread of infection from the IP into the local area, however tracings of contacts with the IP indicates there has been spread of infection from the IP to another premises (IP7) belonging to the same company and with direct epidemiological links with the IP.

**Summary:** In summary, following extensive investigations, HPAI H5N8 infection has been found on two other UK premises (IP5-source and IP7-spread) with direct epidemiological links to the IP. Preliminary cleansing and disinfection (C&D) of the IP was completed on 13 February 2017.

## The Suffolk chicken IP (IP9)

### IP 9 – Redgrave near Diss, Suffolk (AIV 2017/07)

**Description of premises:** The infected premises (IP designated as AIV 2017/08) is a broiler-breeder rearing premises, part of a fully integrated poultry group located in mid-Suffolk. The IP contained approximately 22,000 birds housed in three houses.



Figure 6: Map showing the location of the single Suffolk chicken IP



**Description of the virus:** HPAI H5N8 was confirmed as the outbreak's causative agent on 14 February 2017. Sequence results demonstrated that the virus was predominantly the same avian-adapted virus as in the other IPs in this outbreak, without any specific increased affinity for humans.

**Source and spread windows:** The most likely time that HPAI infection is estimated to have entered the IP is between 20 January 2017 and 2 February 2017. The most likely time for spread of HPAI infection off the IP is estimated as 21 January to 11 February 2017 (see Table 5).

**Hypothesis for the source:** All the available evidence suggests that the incident is most likely to have resulted from incursion of HPAI virus into the IP via indirect contact with wild birds. This hypothesis is supported by genomic analysis results.

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

- (i) No poultry were brought onto the IP within the source window.
- (ii) The low likelihood of introduction of infection into the IP via indirect contact with poultry.
- (iii) The very low likelihood of introduction of infection via contaminated products.
- (iv) The very low likelihood of introduction of infection via direct contact with infected wild birds.
- (v) There are no relevant industry related national or international source tracings.
- (vi) The strong laboratory evidence based on sequencing results of the virus consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds.

**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.

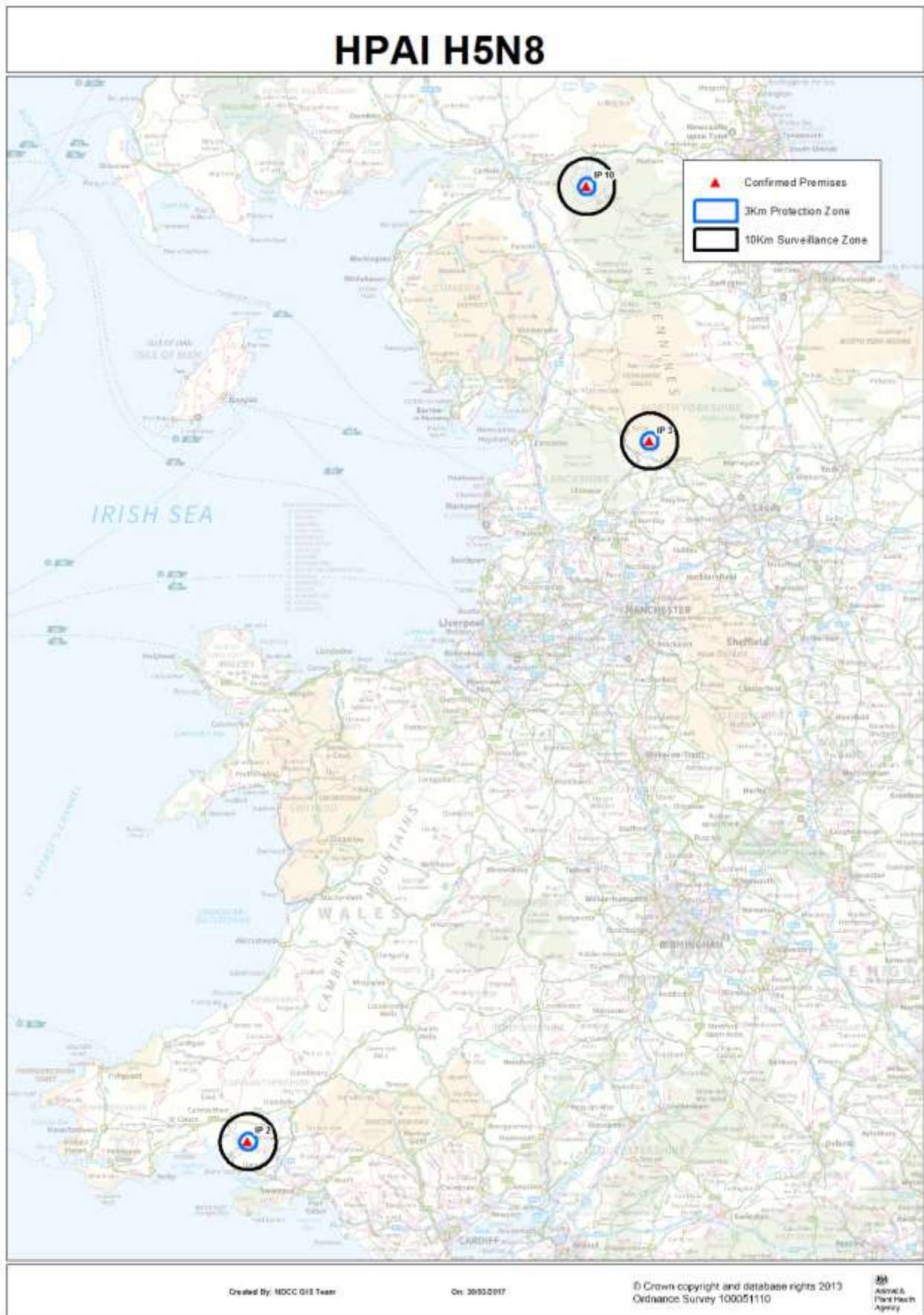
**Summary:** In summary, following extensive investigations, HPAI H5N8 infection has not been found on any other UK premises linked to this IP. At this time, the outbreak appears to have arisen as the result of indirect introduction of HPAI H5N8 infection into the IP via infected wild birds. Preliminary cleansing and disinfection (C&D) of the IP was completed on 17 February 2017.

## The small-holder cluster (IP 2, IP 3 and IP 10)

### Description of the “cluster”

This is not a cluster in the conventional epidemiological sense. These three IPs are separated both spatially and / or temporally, as can be seen in Figure 7 and Table 3, and resulted from entirely separate primary introductions of virus from wild birds. They have been grouped together in this report purely on the basis that they are of the same production system type.

Figure 7: Map showing the distribution of IPs in the small-holder cluster



**Table 3: Timeline of key events in the small-holder “cluster”**

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

Date:	IP 2		IP 3		IP 10	
	Small-holder	Carmarthen Carmarthens hire	Small-holder	Skipton Yorkshire	Small-holder	Haltwhistle, North humberland
	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window
20/11/2016						
21/11/2016						
22/11/2016						
23/11/2016						
24/11/2016						
25/11/2016						
26/11/2016						
27/11/2016						
28/11/2016						
29/11/2016						
30/11/2016						
01/12/2016						
02/12/2016						
03/12/2016						
04/12/2016						
05/12/2016						
06/12/2016						
07/12/2016						
08/12/2016						
09/12/2016						
10/12/2016						
11/12/2016						
12/12/2016						
13/12/2016						
14/12/2016	Infection					
15/12/2016						
16/12/2016						

Date:	IP 2		IP 3		IP 10	
	Small-holder	Carmarthen Carmarthens hire	Small-holder	Skipton Yorkshire	Small-holder	Haltwhistle, North humberland
	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window
17/12/2016						
18/12/2016						
19/12/2016						
20/12/2016						
21/12/2016			Infection			
22/12/2016						
23/12/2016						
24/12/2016						
25/12/2016						
26/12/2016						
27/12/2016						
28/12/2016						
29/12/2016						
30/12/2016						
31/12/2016						
01/01/2017						
02/01/2017						
03/01/2017		Confirmation				
04/01/2017		1° C&D				
05/01/2017						
06/01/2017				Confirmation		
07/01/2017						
08/01/2017				1° C&D		
09/01/2017						
10/01/2017						
11/01/2017						
12/01/2017						
13/01/2017						
14/01/2017						
15/01/2017						
16/01/2017						
17/01/2017						
18/01/2017						
19/01/2017						
20/01/2017						
21/01/2017						
22/01/2017						
23/01/2017						
24/01/2017						
25/01/2017						

Date:	IP 2		IP 3		IP 10	
	Small-holder	Carmarthen Carmarthens hire	Small-holder	Skipton Yorkshire	Small-holder	Haltwhistle, North humberland
	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window	Source tracing window	Spread tracing window
26/01/2017						
27/01/2017						
28/01/2017						
29/01/2017						
30/01/2017						
31/01/2017						
01/02/2017						
02/02/2017						
03/02/2017						
04/02/2017						
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22/02/2017						
23/02/2017						
24/02/2017						
25/02/2017						
26/02/2017						

## IP 2 – Carmarthen (AIV 2017/01)

**Description of the premises:** The infected premises (IP designated as AIV 2017/01) is a smallholding in south-west Wales, which originally held six chickens and nineteen ducks, in addition to four horses and nineteen sheep. The premises has a small pond which was accessible to the domestic ducks and chickens, and also to wild birds. The chickens and

ducks were able to roam freely outside, with access to the farm and the pond. During the night the chickens were housed in one of the horse stables, while the ducks remained outside.

**Description of the virus:** HPAI H5N8 was confirmed as the outbreak's causative agent on 03 January 2017. The IP virus has been fully sequenced and sequence results are consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds. It is also highly similar to a strain recovered from a found-dead wild Eurasian Wigeon in Llanelli, SW Wales only days before this outbreak. Sequence results suggest that it is still predominantly an avian-adapted virus, without any specific increased affinity for humans.

**Source and spread windows:** The most likely time that HPAI infection is estimated to have entered the IP is between 03 and 17 December 2016. The most likely time for hypothetical spread of HPAI infection off the IP is estimated as 04 December 2016 to 31 December 2016.

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

**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 with access to the farm and pond where wild birds also had access.
- (ii) No poultry were brought on to the premises in the source window.
- (iii) There is no evidence so far of HPAI infection in poultry in the local area.
- (iv) There are no 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 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 the contacts with the IP, indicates that there has not been spread of infection from the IP into either 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 the IP. At this time, the outbreak appears to have arisen as the result of introduction of HPAI H5N8 infection into the IP via infected wild birds. Preliminary cleansing and disinfection (C&D) of the IP was completed on 04 January 2017.



## IP 3 – Settle near Skipton, Yorkshire (AIV 2017/02)

**Description of the premises:** The infected premises (IP designated as AIV 2017/02) is a residential premises in Settle near Skipton, Yorkshire, which had a back-yard flock of ten chickens and seven ducks. Chickens and ducks were free-range and shared a field adjacent to a stream with wild waterfowl. The chickens were housed at night, but the ducks were not housed at all. There are a number lot of shoots in the area, but no large commercial flocks nearby.

**Description of the virus:** HPAI H5N8 was confirmed as the outbreak's causative agent on 06 January 2017. The IP virus has been fully sequenced and sequence results are consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds. Sequence results suggest that it is predominantly an avian-adapted virus, without any specific increased affinity for humans.

**Source and spread windows:** The most likely time that HPAI infection is estimated to have entered the IP is between 10 and 23 December 2016. The most likely time for hypothetical spread of HPAI infection off the IP is estimated as 11 December 2016 to 04 January 2017 (see Table 3)

**Table 3 Hypothesis for the source:** There is some remaining uncertainty as to the source of infection for the IP, however all the available evidence suggests that the incident is likely to have resulted from introduction of HPAI virus into the IP via direct contact with infected wild birds.

- (i) **Evidence base for the source:** This assessment of the source is based on the evidence that:
- (ii) The chickens and ducks on the IP were freely roaming outside and shared a field adjacent to a stream with wild waterfowl.
- (iii) Three of the ducks were brought from another premises onto the IP within the high risk source tracing window but the ducks were considered unlikely to have introduced infection onto the IP as they originated from a premises where they had mixed with chickens and those chickens on the source premises remained alive and well.
- (iv) There is no evidence so far of HPAI infection in poultry in the local area.
- (v) There are no relevant premises related national or international source tracings.
- (vi) Wild birds (mallards) shot on the contiguous premises were found PCR positive for H5N8.
- (vii) Strong laboratory evidence based of sequencing results of the virus consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds.
- (viii) Genome sequencing analysis showed that the virus from the IP shares very high similarity with the virus isolated from a wild bird (wigeon) from Wales.
- (ix) The time of year of these outbreaks occurred with respect to wild bird migratory movements and 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 the IP. 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 08 January 2017.

## IP 10 – Haltwhistle, Northumberland (AIV 2017/10)

**Description of the premises:** The infected premises (IP designated as AIV 2017/09) is a commercial sheep farm (with 350 ewes) in Northumberland, where 32 hens were also being kept.

**Description of the virus:** HPAI H5N8 was confirmed as the outbreak's causative agent on 23 February 2017. The IP virus has been fully sequenced and sequence results suggest that it is still predominantly an avian-adapted virus, without any specific increased affinity for humans.

**Source and spread windows:** The most likely time that HPAI infection is estimated to have entered the IP is between 27 January 2017 and 9 February 2017. The most likely time for spread of HPAI infection off the IP is estimated as 28 January to 24 February 2017.

**Hypothesis for the source:** All the available evidence suggests that the incident is most likely (with low uncertainty) to have resulted from the incursion of HPAI virus into the IP, via direct or indirect contact with wild birds. This hypothesis is supported by genomic analysis results.

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

- (i) No poultry were brought onto the IP within the source window.
- (ii) Wild ducks regularly visited the field where the hens were located.
- (iii) There is a low likelihood of introduction of infection into the IP via indirect contact with poultry.
- (iv) There is a very low likelihood of introduction of infection via contaminated products.
- (v) There are no related national or international source tracings.
- (vi) Strong laboratory evidence based on sequencing results of the virus consistent with European HPAI H5N8 strains found in the 2016 epizootic in poultry and wild birds.

**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, HPAI H5N8 infection has not been found on any other UK premises linked to this IP. At this time, the outbreak appears to have arisen as the result of direct or indirect introduction of HPAI H5N8 infection into the IP via infected wild birds. Preliminary cleansing and disinfection (C&D) of the IP was completed on 26 February 2017.

## Overview of tracing activities

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.

Contact premises were identified in the following categories:

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

## Surveillance in the protection and surveillance zones

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

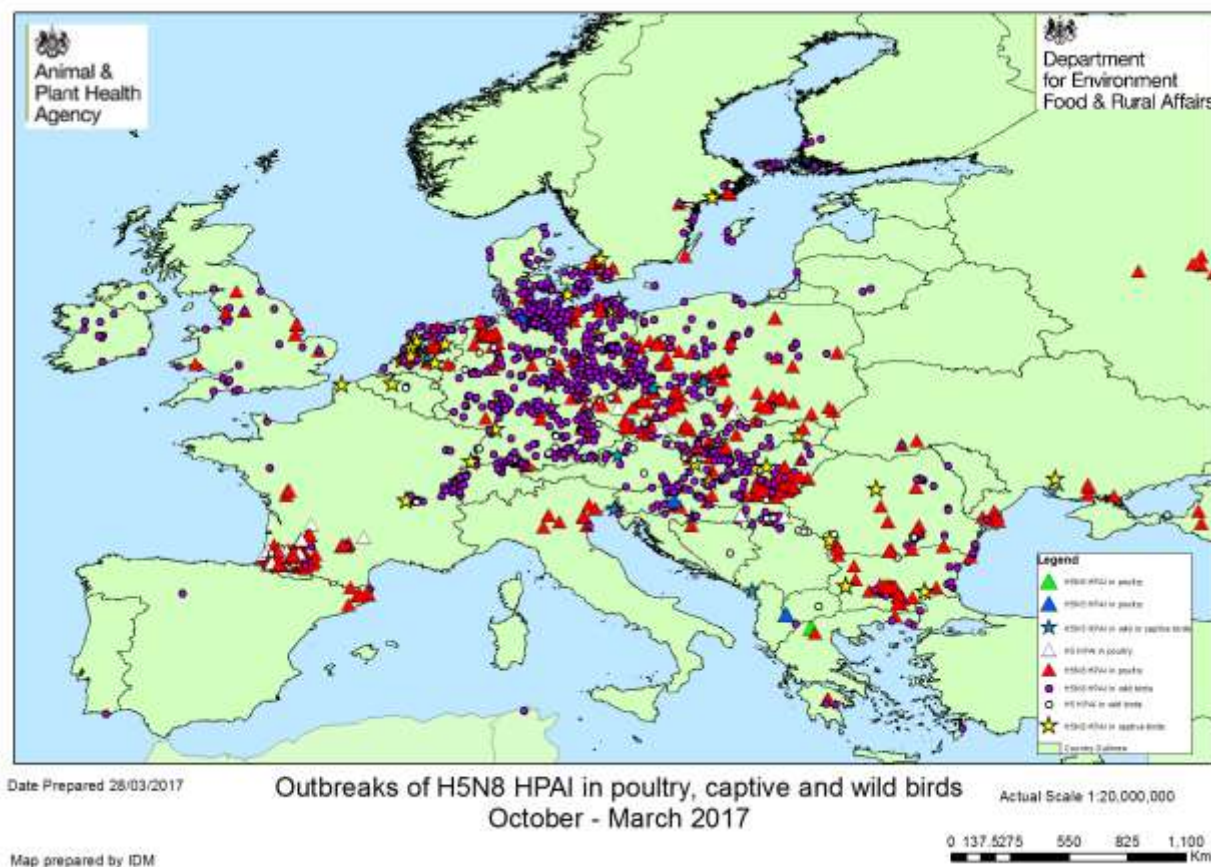
Guidance notes were sent to all holdings within the PZ to raise awareness and remind keepers of the restrictions applying in this zone.

The poultry on these premises, together with their production and medicine records were also clinically inspected by APHA personnel (and sampled and tested where relevant of 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.

## International context

Figure 8: Outbreaks of H5N8 in poultry, captive and wild birds (October 2016 - March 2017)



In late October 2016, H5N8 HPAI was first detected in the Eastern EU in wild birds and poultry and, given the migration patterns of wild migratory waterfowl, the risk level to the UK was increased from low to medium on the 11<sup>th</sup> November. In mid-November, wild bird cases were detected in western EU Member States and on the 1<sup>st</sup> December the risk for incursions to poultry was raised to low but heightened. Outbreaks in poultry and findings in wild birds continued over the coming months in most Member States as well as neighbouring countries in the Middle East, North Africa and East Europe. To date, over a thousand poultry outbreaks have been reported and nearly 1,500 wild bird findings (see Table 4 below). This is an unprecedented level of highly pathogenic avian influenza, even more so than the epizootic of H5N1 HPAI in 2005-6. The wider range of wild bird species (including gulls, birds of prey and a small number of corvids) and high pathogenicity were also unusual and the risk level for the UK was such for a wild bird incursion that the CVO put in place an Avian Influenza Prevention Zone on the 7<sup>th</sup> December and this is still in place. Under this order, poultry keepers must take all possible provisions to prevent wild bird contact and the risk level for poultry was raised to low to medium. Sequence data suggests there have been two incursions into Europe, one across Central Europe from Hungary and as far as SW France, while the other route encompasses the Baltic region and NW Europe including the UK.

**Table 4: Total number of findings of H5N8 HPAI since November 2016**

	H5N8 in domestic poultry	H5N8 in captive birds	H5N8 in wild birds	H5N5 or H5N6 – all birds
European Member States*	1070	51	1378	16
Rest of Europe	46	4	94	2
North Africa, Middle East, East and West Africa	3	1	2	0
Asia	59	0	21	72

In terms of international trade, there were no links to other Member States or third countries in terms of imports of live poultry, hatching eggs, day old chicks or other poultry products which could have been the source of infection or given rise to any spread off the IPs, for any of the UK outbreaks.

### Wild Bird Context

The migration season for wild waterfowl arriving for wintering starts in August / September and birds continue to arrive through to December. Cold weather in the north of Europe can influence further movements through winter. The birds generally inhabit wetland areas and estuaries over winter, are gregarious and mobile, particularly when foraging for food. They will visit poultry ranges when foraging for food but are less likely to enter into poultry sheds.

Ornithological field assessments were carried out around each of the commercial poultry farm outbreaks: IPs 1 and 4; IPs 5, 7 and 8; IP6 and IP9. At IPs 1, 4, 5, 7, and 8, wild water fowl were seen very close to the properties either on the actual range or alongside close waterways. The wild waterfowl were less apparent around IP 6 and IP9, but there were plenty of potential bridging species, such as corvids, gulls and starlings.

Wild bird surveillance of found dead target species (such as waterfowl) across GB has detected 33 wild birds in different regions testing positive. Fifty-five known species have been submitted for AI testing in GB to date. Some birds were unclassified due to various factors but these remain in the analysis as a proportion were H5N8 positive. Of 581 birds tested, the highest proportions tested were mallard ducks (64) and Black headed gulls (62). However the highest ratio of H5 positives were found in Pochard (diving duck) (100%,  $n = 2$ ); Wigeon (grazing/dabbling ducks) (71%,  $n = 14$ ); Canada Geese (10%;  $n$

=19) and Whooper Swans (4%;  $n = 43$ ). There are parallels with other member states who have reported a high incidence of positive wildfowl; although further evaluation of the temporal pattern of submission versus positive detection for GB and EU is required. In MSs the mute swan was the highest indicator (21% of all H5N8 detections). In GB, 1.7% of all H5N8 detections were found in Wigeon.

## Public health impact

The European Centre for Disease Prevention and Control (ECDC) published a risk assessment on the H5N8 strain of virus in November 2016. The assessment concludes that *“To date, no human infections with this virus have ever been reported world-wide and the risk of zoonotic transmission to the general public in EU/EEA countries is considered to be very low. The full genome sequences of several recent HPAI A (H5N8) viruses showed that these viruses to date are still essentially bird viruses without any specific increased affinity for humans.”* <http://ecdc.europa.eu/en/publications/Publications/risk-assessment-avian-influenza-H5N8-europe.pdf>

## 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 the 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, an 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

02 May 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 5: Composite source and spread timelines for the outbreak

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

Date:	IP1 - Turkeys	Louth Lincs	IP2 - Small-holder	Carmarthen shire	IP3 - Small-holder	Skipton Yorks	IP4 - Turkeys	Fulstow Lincs	IP5 - Game birds	Pilling Lincs	IP6 - Turkeys	Boston Lincs	IP7 - Game birds	Pilling Lincs	IP8 - Game birds	Preesall Lincs	IP9 - Chickens	Diss Suffolk	IP10 - Small-holder	Haltwhistle Northland	
	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	
20/11/2016																					
21/11/2016																					

	Haltwhistle North'land	IP10 - Small-holder	Diss Suffolk	IP9 - Chickens	Preesall Lancs	IP8 - Game birds	Pilling Lancs	IP7 - Game birds	Boston Lincs	IP6 - Turkeys	Pilling Lancs	IP5 - Game birds	Fulstow Lincs	IP4 - Turkeys	Skipton Yorks	IP3 - Small-holder	Carmarthen shire	IP2 - Small-holder	Louth Lincs	IP1 - Turkeys	
	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Date:
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	IP1 - Turkeys	Louth Lincs	IP2 - Small-holder	Carmarthen shire	IP3 - Small-holder	Skipton Yorks	IP4 - Turkeys	Fulstow Lincs	IP5 - Game birds	Pilling Lincs	IP6 - Turkeys	Boston Lincs	IP7 - Game birds	Pilling Lincs	IP8 - Game birds	Preesall Lincs	IP9 - Chickens	Diss Suffolk	IP10 - Small-holder	Haltwhistle North'land
Date:	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread	Source	Spread
14/12/2016			Inf																	
15/12/2016																				
16/12/2016		Conf																		
17/12/2016																				
18/12/2016	1° C&D																			
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	Haltwhistle North'land	IP10 - Small-holder	Diss Suffolk	IP9 - Chickens	Preesall Lancs	IP8 - Game birds	Pilling Lancs	IP7 - Game birds	Boston Lincs	IP6 - Turkeys	Pilling Lancs	IP5 - Game birds	Fulstow Lincs	IP4 - Turkeys	Skipton Yorks	IP3 - Small-holder	Carmarthen shire	IP2 - Small-holder	Louth Lincs	IP1 - Turkeys	Date:
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	Haltwhistle North'land	IP10 - Small-holder	Diss Suffolk	IP9 - Chickens	Preesall Lancs	IP8 - Game birds	Pilling Lancs	IP7 - Game birds	Boston Lancs	IP6 - Turkeys	Pilling Lancs	IP5 - Game birds	Fulstow Lancs	IP4 - Turkeys	Skipton Yorks	IP3 - Small-holder	Carmarthen shire	IP2 - Small-holder	Louth Lancs	IP1 - Turkeys	Date:	Spread	Source
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29/01/2017								1° C&D															
30/01/2017																							
31/01/2017										1° C&D													
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Haltwhistle North'land	Spread		
IP10 - Small-holder	Source		
Diss Suffolk	Spread		
IP9 - Chickens	Source		
Preesall Lancs	Spread		
IP8 - Game birds	Source		
Pilling Lancs	Spread		
IP7 - Game birds	Source		
Boston Lincs	Spread		
IP6 - Turkeys	Source		
Pilling Lancs	Spread		
IP5 - Game birds	Source		
Fulstow Lincs	Spread		
IP4 - Turkeys	Source		
Skipton Yorks	Spread		
IP3 - Small-holder	Source		
Carmarthen shire	Spread		
IP2 - Small-holder	Source		
Louth Lincs	Spread		
IP1 - Turkeys	Source		
	Date:	18/02/2017	
		19/02/2017	
		20/02/2017	
		21/02/2017	
		22/02/2017	
		23/02/2017	
		24/02/2017	
		26/02/2017	

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## Appendix 2: Details of tracings and stock numbers in zones

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 6: Number of locations investigated**

<b>Method of investigation</b>	<b>IP 1</b>	<b>IP 2</b>	<b>IP 3</b>	<b>IP 4</b>	<b>IP 5</b>	<b>IP 6</b>	<b>IP 7</b>	<b>IP 8</b>	<b>IP 9</b>	<b>IP 10</b>
Locations investigated and ruled out by non-exposure to susceptible animals	43	6	37	15	40	22	9	40	17	16
Locations investigated and ruled out by clinical inspection	24	3	2	1	13	2	0	19	2	1
Locations investigated ruled out by production data analysis	0	0	0	0	0	0	0	0	0	0
Locations investigated and ruled out by individual VRA	3	0	5	2	0	2	0	5	7	3
Locations identified as contact premises	2	3	0	0	2	0	0	2	1	0
<b>Total number of locations</b>	<b>70</b>	<b>9</b>	<b>44</b>	<b>18</b>	<b>55</b>	<b>26</b>	<b>9</b>	<b>66</b>	<b>27</b>	<b>20</b>



**Table 7: Outcome of tracing investigation visits**

<b>Number of locations</b>	<b>IP 1</b>	<b>IP 2</b>	<b>IP 3</b>	<b>IP 4</b>	<b>IP 5</b>	<b>IP 6</b>	<b>IP 7</b>	<b>IP 8</b>	<b>IP 9</b>	<b>IP 10</b>
Locations requiring a tracing visit	28	3	2	2	15	7	0	21	2	1
Locations where restrictions were issued	25	3	2	1	15	5	0	19	2	1
Locations where restrictions were lifted at the conclusion of the tracing investigation	25	3	2	1	13	5	0	17	1	0
Locations containing susceptible animals <sup>(1)</sup>	24	3	2	1	15	2	0	21	2	1
Locations identified as contact premises	2	3	0	0	2	0	0	2	1	0
Locations negated as contact premises	2	3	0	0	0	0	0	0	0	0
Locations remaining under investigation	0	0	0	0	0	0	0	0	0	0

## Appendix 3: Definitions of qualitative risk terms for likelihood and uncertainty

Table 8: Definitions for the qualitative risk terms based on EFSA (2006) and OIE (2004) with expanded descriptions adapted from NHS (2008), IPCC (2005), and Kahn et al., (1999)

Risk level	Definition	Expanded description
Negligible	Event is so rare, does not merit consideration	The chance of the event occurring is so small it does not merit consideration in practical terms (i.e. < 0.1% probability)
Very low	Event is very rare, but cannot be excluded	The event is not expected to occur (very rare) but it is possible (i.e. >0.1-1% probability)
Low	Event is rare, but does occur	The event may occur occasionally (rare) (i.e. >1-10% probability)
Medium	Event occurs regularly	The event occurs regularly (i.e. >10-66% probability)
High	Event occurs very often	The event will happen more often than not (i.e. ≥66-90% probability)
Very high	Event occurs almost certainly	The event will undoubtedly happen (i.e. >90% probability)

**Table 9: Qualitative categories for expressing uncertainty given the available evidence; based on definitions within the literature (EFSA, 2006; ECDC, 2011, Spiegelhalter & Riesch, 2011).**

Uncertainty category and definition	Type of information/evidence to support uncertainty category
<p><b>Low</b></p> <p>Further research is very unlikely to change our confidence in the assessed risk</p>	<ul style="list-style-type: none"> <li>• Solid and complete data available (e.g. long term monitoring results)</li> <li>• Peer reviewed published studies where design and analysis reduce bias (e.g. systematic reviews, randomised control trials, outbreak reports using analytical epidemiology)</li> <li>• Complementary evidence provided in multiple references</li> <li>• Expert group risk assessments, specialised expert knowledge, consensus opinion of experts</li> <li>• Established surveillance systems by recognised authoritative institutions</li> <li>• Authors report similar conclusions</li> </ul>
<p><b>Medium</b></p> <p>Further research is likely to have an important impact on our confidence in the risk estimate</p>	<ul style="list-style-type: none"> <li>• Some but no complete data available</li> <li>• Non peer-reviewed published studies/reports</li> <li>• Observational studies/surveillance reports/outbreak reports</li> <li>• Individual (expert) opinion</li> <li>• Evidence provided in a small number of references</li> <li>• Authors report conclusions that vary from one another</li> </ul>
<p><b>High</b></p> <p>Further research is very likely to have an important impact on our confidence in the risk estimate</p>	<ul style="list-style-type: none"> <li>• Scarce or no data available</li> <li>• No published scientific studies available</li> <li>• Evidence is provided in grey literature (unpublished reports, observations, personal communication)</li> <li>• Individual (non-expert) opinion</li> <li>• Authors report conclusions that vary considerably between them</li> </ul>