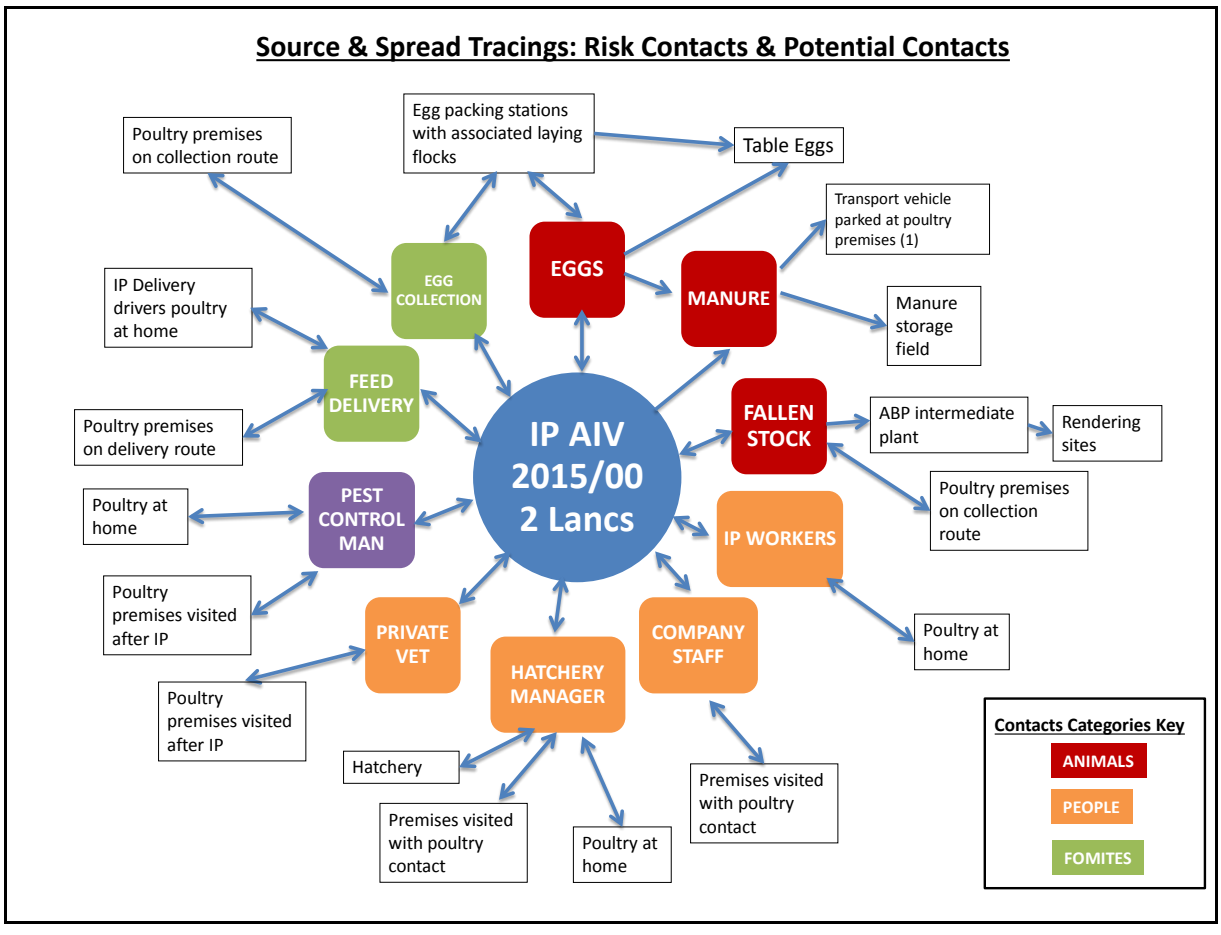
Animal & Plant Health Agency

Highly Pathogenic Avian Influenza H7N7
(AIV2015/02; *formerly AIV SOS2015/0001*),
In Table-egg Laying Hens

Preston, July 2015

Situation at 11:00 on Friday 28 August 2015



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1. Executive Summary

Description of premises: The Infected Premises (IP - designated as AIV 2015/02) is owned by a family-run business based in the administrative territory of Lancashire, England. The company owns seven linked premises, two of which rear pullets to supply the five other commercial laying premises, including the IP, which produce table eggs for human consumption.

Description of the virus: HPAI H7N7 was confirmed as the outbreak's causative agent on 13 July 2015. Laboratory results indicate that the incident is likely to have resulted from an incursion of LPAI virus that mutated to HPAI virus within the IP. The H7N7 virus is closely related to contemporaneously circulating strains in wild birds and poultry in Northern Europe. However the virus has probably derived from genetic reassortment in nature of two or more progenitor strains. This is a different strain to that seen in the LPAI outbreak in broiler breeders in Hampshire, England (AIV 2015/01 - February, 2015).

Source and spread windows: The most likely time that LPAI infection is estimated to have entered the IP is between the end of May 2015 and mid-June 2015. The high risk spread window for LPAI virus opened on 19/06/2015,, The mutation event from LPAI to HPAI is likely to have taken place at the end of June 2015 (most likely on 29 or 30 June 2015), with the spread window for HPAI virus extending until the completion of statutory preliminary cleansing and disinfection of the infected premises on 16 July 2015 following the sanitary slaughter of the birds.

Hypothesis for the source: There is uncertainty as to the most likely source of LPAI infection for the IP. However, the available evidence suggests that the source was the wildfowl present on the ponds on the premises, followed by an incursion into one group of free-range birds as a result of indirect contact, with subsequent spread to other epidemiological groups. In the case of the HPAI infection the evidence strongly suggests an initial mutation event in one of the sheds.

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 are no relevant industry related national or international source tracings, (iii) the presence of wild waterfowl close to the first shed which could have been infected, (iv) production records, and (v) strong laboratory evidence based on genetic analysis of the virus which indicate a recent introduction from wild birds to domestic poultry.

Assessment of potential spread: Following extensive investigations, no evidence of avian influenza virus infection has been found in other domestic poultry premises in the country. At this time the outbreak appears to have arisen as the result of an LPAI to HPAI mutation event on the IP and to be limited to the single IP.

2. Introduction

This report summarises the epidemiological investigations carried out in order to describe and explain the outbreak of H7N7 Highly Pathogenic Avian Influenza (HPAI) infection in layer chickens on a premises in the administrative territory of Lancashire, England.

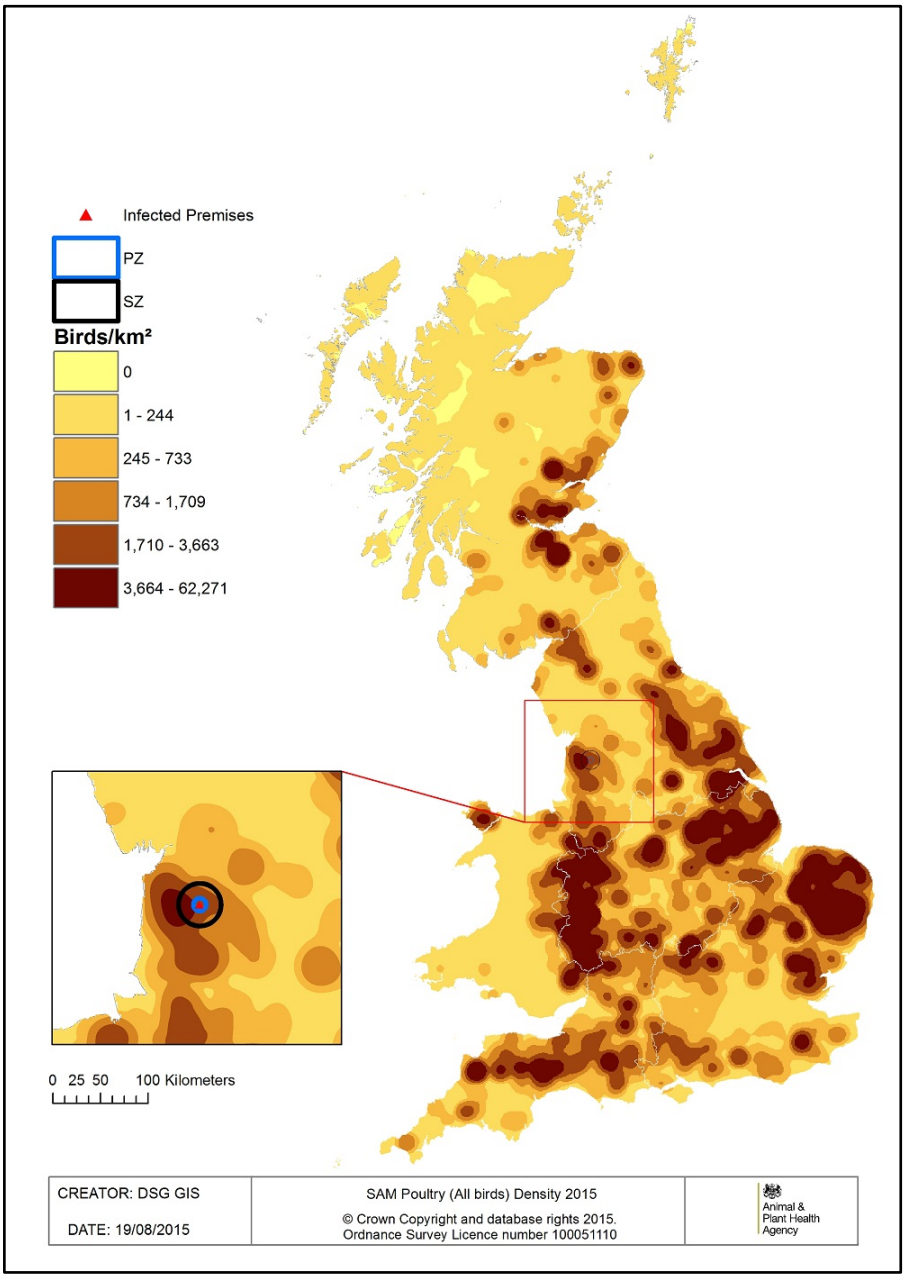
The report will be used to (i) provide evidence to support the UK's position on successfully controlling the outbreak and a declaration of freedom from H7N7 HPAI to both the EU and OIE and to inform trading partners in full transparency with a view to facilitate trade; (ii) to provide source material for the technical annex for UK co-financing claims to the EU; (iii) to record logistics and technicalities of investigation and control to inform future resource planning, contingency plans and training requirements; and (iv) to highlight gaps in our understanding of notifiable avian influenza and so identify areas for further research or other needs.

3. Description of the Infected Premises

The Infected Premises (IP designated as AIV 2015/02) is owned by a family-run business based in Lancashire. The company owns seven linked premises, two of which rear pullets to supply the five other commercial laying premises, including the IP, which produce table eggs for human consumption. Two of the laying premises also have co-located egg packing stations.

The IP is located within a poultry dense area in the north-west of England – the numbers of poultry premises within the 3 km Protection Zone (PZ) and 10km Surveillance Zone (SZ) are provided at Appendix 3. There are also three Royal Society for the Protection of Birds (RSPB) reserves and one Wildfowl & Wetlands Trust (WWT) bird reserve within 30 km of the IP, in addition to which a large number of captive and wild gamebirds were reported to be present in the surrounding area.

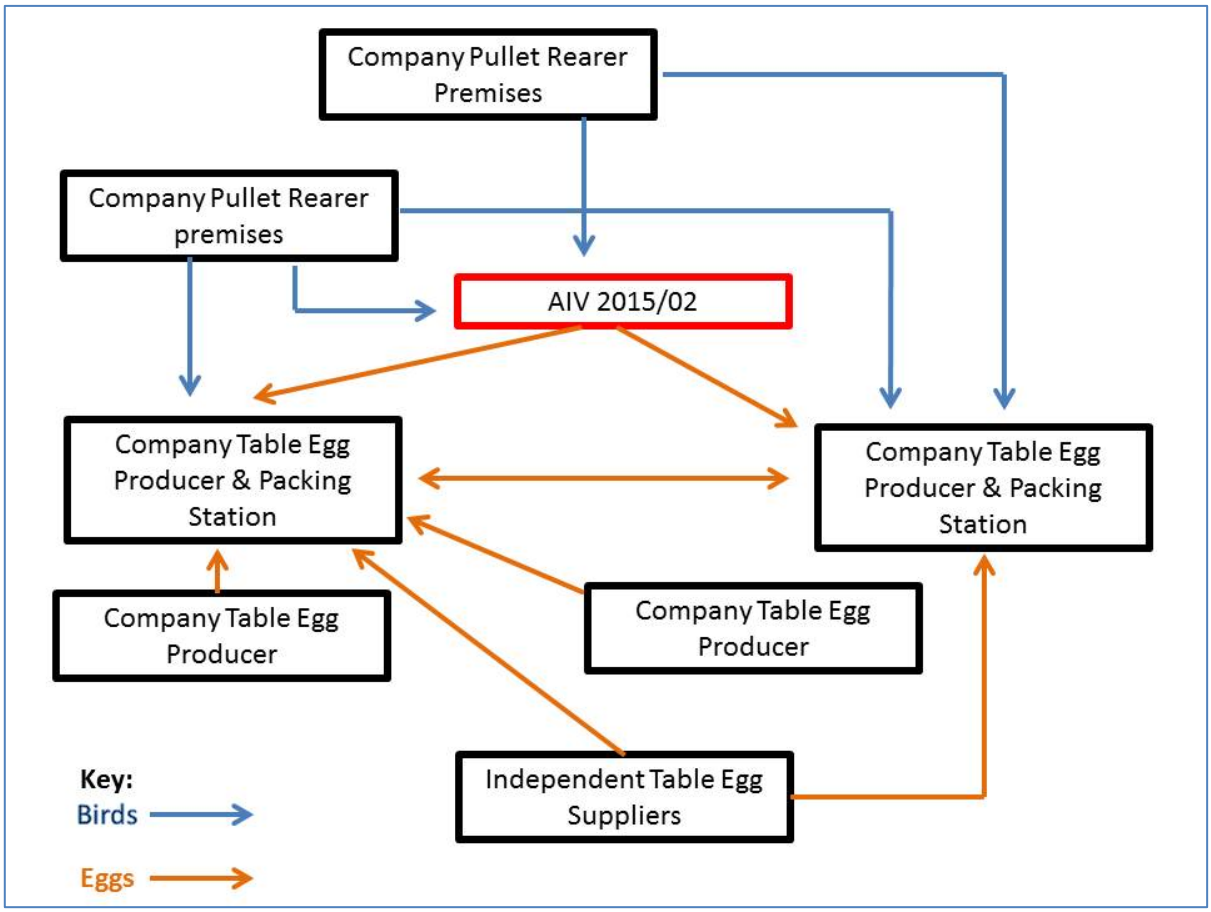
Figure 1: Map to show location of the IP and density of poultry



Note: The map was created using an extract of APHA's Sam database as at April 2015. Premises with less than 50 birds are likely to be under-represented as poultry registration is only mandatory for premises with 50 or more birds. Premises with less than 50 birds are encouraged to register and so a proportion of these premises will be included within the Sam extract. In the event of an outbreak, additional premises may be identified as a result of intensive foot patrols. The density of birds in GB was performed using the kernel density function in ArcGIS using a 15km search radius and output cell size of 1km. The data is classified into six quartiles and the map is suitable only for demonstrating relative density across GB.

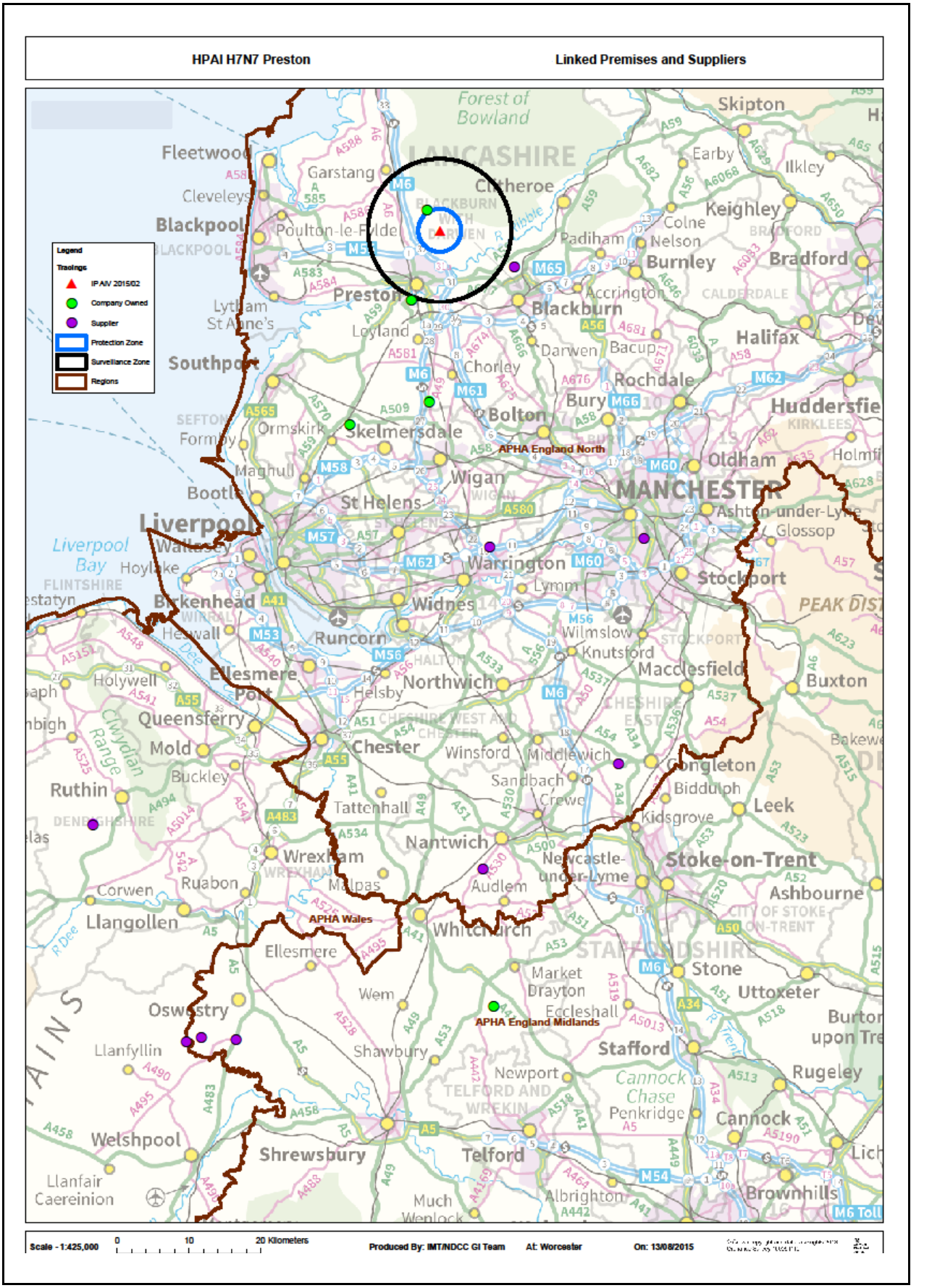
Eggs produced at the IP are collected daily by a dedicated vehicle and transported to two egg packing stations where they are graded and packaged for onward supply to predominantly commercial retailers. The vehicle used is parked on the IP when not in use. However, smaller quantities of eggs are also packed and supplied direct from the IP for sale to smaller private retail outlets.

Figure 2: Company premises links indicating the movements of pullets and eggs



In addition to eggs supplied by the company-owned premises, the egg packing stations also receive table eggs from six other commercial free-range laying premises located in Lancashire, Cheshire, Shropshire and Denbighshire. These eggs are also graded and repackaged at the packing stations before being distributed for retail sale within the UK.

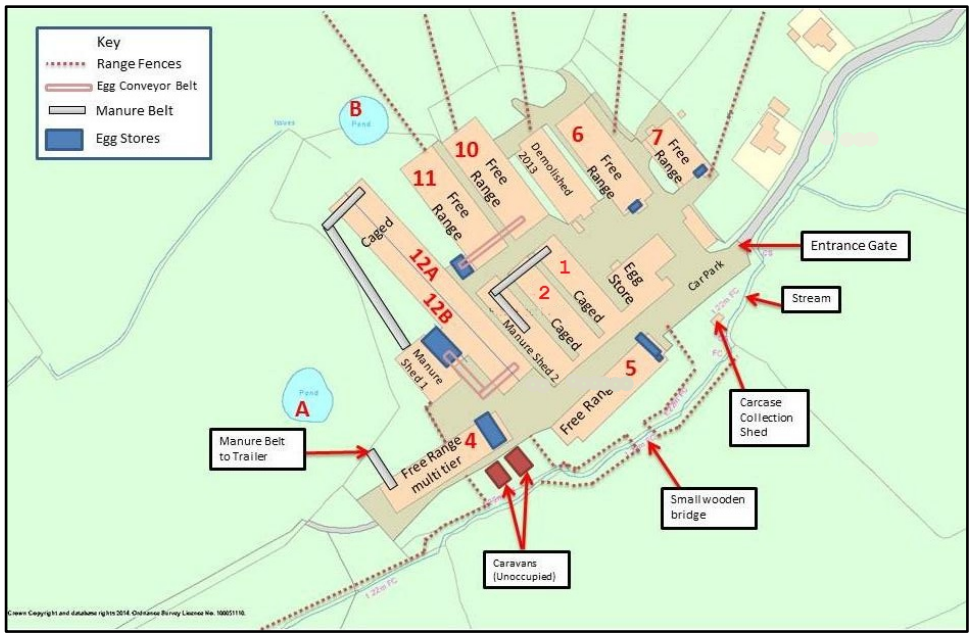
Figure 3: Locations of company-owned and non-company table egg supplier premises



At the start of the current outbreak there were 170,000 laying hens on the IP housed in ten sheds. Four of the sheds housed a total of 120,000 birds in enriched cages. The remaining six sheds housed a total of 50,000 free-range birds, which had access to ranges associated with each shed during the daytime.

The location and boundaries of individual ranges are shown in Figure 4 below. None of the ranges are fenced off completely as individual units, but mixing of poultry from different sheds is considered to be unlikely. All fences are chicken wire and permanent. At the end closest to the housing, the fence is six feet high, reducing to four feet high at the end of the range. As is normal in the UK, the ranges are not covered and so are open to access by wild birds.

Figure 4: Site plan of the IP



Management: The site operates an 'all-in/all-out' policy; with all of the birds present being 67 weeks of age at the time disease was confirmed. The current flock was placed on the site in July 2014 at 16 weeks of age and no movement of live birds onto or off the site has taken place since then.

4. Timeline of key events

Day	Date	Event
Friday	03/07/2015	• Drop in egg production in sheds 1 and 12a on the Suspect Premises (SP).
Saturday Sunday	04/07/2015- 05/07/2015	• Increased mortality.
Monday	06/07/2015	• Sudden increase in mortality rate. • Farm manager highlighted the problem in the afternoon and private vet was called. • The company restricted the movement of eggs and vehicles due to the sudden increase in mortality (no eggs left the farm after this date) Biosecurity was increased.
Tuesday	07/07/2015	• The private veterinary surgeon (PVS) visited and starts antibiotic treatment (tetracycline). Mortality approximately 2500 birds. Post mortem by PVS: petechial haemorrhages in spleen and liver. Carcases sent to APHA Lasswade.
Wednesday	08/07/2015	• Mortality increases to >3000 birds. • Two of the six free range sheds (i.e. sheds 10 & 11) and three of the four sheds with caged birds (i.e. sheds 1, 2 and 12a) present on the SP are clinically affected. • Notification of suspicion of avian notifiable disease received from the PVS. • Official veterinary investigation commenced and restrictions served.
Thursday	09/07/2015	• Follow up official visit and official sampling of SP.
Friday	10/07/2015	• H7 AI virus identified in samples submitted by the PVS • Deteriorating clinical picture. • Slaughter on suspicion authorised by the UK CVO. • 10km radius Temporary Control Zone (TCZ) imposed.
Saturday	11/07/2015	• Culling of poultry on SP commenced.
Sunday	12/07/2015	• Visit by expert ornithologist.
Monday	13/07/2015	• H7N7 HPAI confirmed. • Premises declared to be an Infected Premises (IP). • 10km TCZ replaced with 3km Protection Zone (PZ) and 10km Surveillance Zone (SZ).
Saturday Sunday Monday	11/07/2015- 13/07/2015	• Pre-culling samples collected from nine sheds on the IP for epidemiological purposes.
Tuesday	14/07/2015	• Culling completed. Environmental sampling undertaken
Thursday	16/07/2015	• Carcase disposal completed • Statutory Preliminary C&D completed

Day	Date	Event
Friday	17/07/2015	• Statutory Preliminary C&D considered to be effective
Friday	07/08/2015	• PZ merged with SZ
Sunday	16/08/2015	• SZ lifted

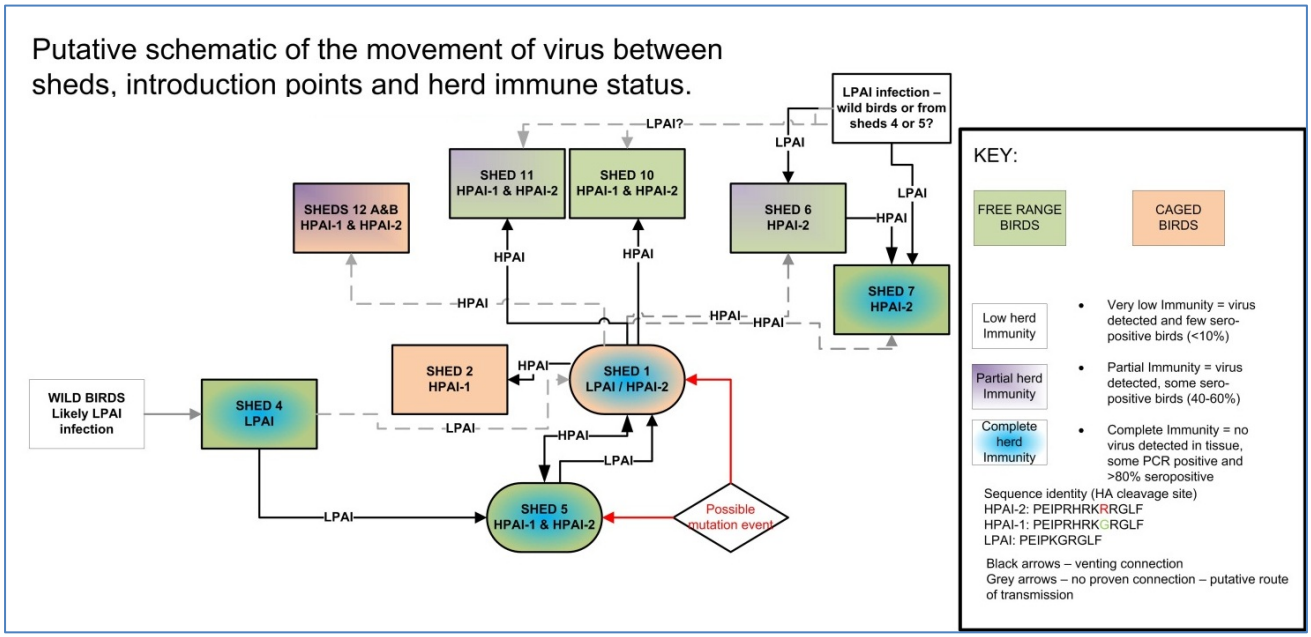
5. Investigations on the Infected Premises

The investigations and analyses conducted used the following:

1. Clinical and production data from farm records;
2. Laboratory results on standard samples (oropharyngeal and cloacal swabs plus blood) collected:

    i. At official sampling on 09/07/2015
    ii. More extensive sampling at cull (11/07/2015 &12/07/2015) or
    iii. Environmental samples consisting of litter from free-range sheds (10, 11, 6, 7, 4, 5), feather/egg debris/dust from caged bird sheds (1, 2, 12A), and feathers and faeces from pond A (adjacent to shed 4).

Figure 55: Disease transmission events within the IP.



Clinical signs: An increase in mortality rate preceded by a drop in egg production was seen from 03/07/2015 onwards in two cage sheds, i.e. sheds 1 & 12A, and then three more sheds from 06/07/2015 cage shed 2, and free range sheds i.e., 10 & 11. The pattern of increased mortality continued until 08/07 when notification of suspicion of avian notifiable disease was received from the PVS and restrictions were served.

Official investigation: An official veterinary investigation was instigated on 08/07 and official samples taken from Sheds 1, 2 and 10, 11, 12a the following day. On 10/07 H7 AI virus was identified by PCR in samples that had been previously submitted by the PVS. Based on those results and the deteriorating clinical picture, the UK CVO authorised slaughter on suspicion and a 10km temporary control zone (TCZ) was imposed.

Confirmation of infection: On 13 July H7N7 HPAI was confirmed by sequencing the haemagglutinin (HA) gene of detected virus in the official samples collected on 09/07. Initially virus was recovered from a single bird and identified as H7N7 HPAIV. All epi groups were PCR and antibody positive, with 50-90% of the birds shedding and 5-45% were H7 antibody positive (levels of variation within groups reflecting different and evolving time course for infection with LPAI/HPAI). Based on molecular sequencing work of the HA gene of the HPAI H7N7 virus, two forms (genetic variants) were identified; one of them believed to be an early form, and the other a derivative of the

early form. Both forms co-existed once the HPAI virus was established in the flock.

Results: Further samples were collected from 11/07/2015 to 13/07/2015 from birds selected in a random manner from 9 out of 10 sheds on the site before slaughter, in order to determine whether AI virus infection was present in each of the clinically unaffected sheds and, if so, whether it was of high or low pathogenicity, to estimate prevalence of AI virus infection in each of the clinically affected sheds and to help estimate the likely date of introduction of the virus and the tracing window. Results of this official testing revealed that H7N7 HPAI virus was detected in birds in all sheds, except shed 4 where only H7N7 LPAI virus was detected. Sheds 1 & 2 were the only sheds where both HPAI and LPAI viruses were detected in birds. Furthermore from this wider sampling it was possible to conduct detailed analyses at bird level to provide further insights into possible timelines and routes of entry for the LPAI virus while enabling an assessment of virus mutation to HPAI and subsequent spread within the IP. The assessment evaluated individual bird status as immune or infected or both and took into account the level of H7 specific and quantity of virus being shed.

Further insights into the clinical and pathological course of infection have been provided by the gross pathology observations on birds collected from sheds at cull. Specified lesions including splenomegaly, multifocal splenic necrosis and haemorrhagic ovarian follicles (all typical of HPAI) were observed in birds from sheds 6, 11 and 12. In other epi groups the pathological severity was less well defined consistent with presence of some specific protective immunity in birds following prior exposure to H7 LPAIV thereby reducing systemic infection. PCR analyses on the necropsied tissues (brain, lung and trachea, viscera, intestine) confirmed systemic spread of H7 virus in affected birds

Environmental sampling: Environmental samples were collected from a range of locations from the IP on 14 July (i.e. before statutory preliminary C&D began). These consisted of litter from free-range sheds (10, 11, 6, 7, 4, 5), feather/egg debris/dust from caged bird sheds (1, 2, 12A), and duck feathers and faeces from pond A (adjacent to shed 4). HPAI genome (but no infectious virus) was detected in samples from all sheds except shed 5. The results support the rapid inactivation of infectious virus in the environment especially in litter. Negative results for samples collected from around the pond cannot definitively rule this out as a potential source of the initial LPAI virus.

Summary: a progenitor LPAI virus is postulated to have entered the IP somewhere between 29 May and 19 June. This is based on analysis primarily of production data but also serological profiles from nine out of ten of the epidemiological groups present on the site. It is believed that a mutation event to HPAI virus occurred somewhere around 29 June to 30 June and this is based on clinical indices increasing for HPAI in the days leading up to the formal reporting of a clinical suspicion (8 July). Putatively, it is possible to plot a time course of events by epidemiological group present on the infected premise, taking into account different modalities of spread in free range and caged birds. This is based on the analysis of samples collected from birds at cull (11-13 July) and (approximately 14 days after the mutation event), through the use of serological and virological tools to determine both immune and active infection status with respect to presence of virus,.

This indicates that the LPAI virus entered shed 4. This is further supported by the close proximity of this shed to a pond (Pond A) frequented by wild ducks, providing clear opportunity for introduction of LPAI. The virus then spread to both free range and caged birds. It would appear that the mutational event occurred either in shed 1 or shed 5 and this is based on the criterion of a significant proportion of immune birds to provide selection pressure for an HPAI variant emerging but also a significantly large susceptible population of naïve birds to ensure amplification of such virus.

Following mutation to virulence, the HPAI spread to other sheds which had had no prior exposure to LPAI (i.e. shed 12), or to other groups with variable levels of prior immunity to H7 virus and this resulted in a variable clinical presentation in affected groups. Furthermore, the HPAI virus was able

to spread back into groups that had high levels of immunity to LPAI (i.e. sheds 4 and 5). The relatively open connectivity through the on farm activities and the ineffective separation of distinctive epidemiological groups presumably enabled the virus to spread relatively easily between all the groups.

6. Overview of tracing activities

Evidence based on the clinical picture, laboratory results, epidemiological investigations and expert advice; together with the OIE requirement for a precautionary assumption of a 21 day incubation period prior to first clinical signs being observed gave the following source and spread time windows:

The source and spread window is complicated by the presence of LPAI virus on the IP since potentially late May/early June, but the date for the likely mutation event into a HPAI virus strain has been given as 29 - 30 June according to molecular epidemiology studies. Therefore:

- Most likely date of introduction of HPAI infection is 29/06, with a maximum precautionary source period over which HPAI tracings were investigated from 11/06 to 01/07, a day before clinical signs were apparent.
- Most likely potential for spread of HPAI infection from the premises is from 29/06 to 08/07, when preliminary C&D started, with a maximum precautionary spread period over which tracings were investigated extended back to 12/06.

There have been a large number of personnel and other contacts within the company and with other businesses. In total 108 source and 123 spread tracing tasks were generated with 103 premises identified as potential contact premises via tracings. Investigations have been completed on all premises including clinical inspection, checks of production records and testing where indicated, with negative findings. This included investigation of the premises most closely associated with the infected premises within the company structure.

Figure 66: Source and spread tracing windows

Source Tracing Window	Spread Tracing Window	Date	
		29/05 – 19/06/15	A low pathogenic avian influenza virus is postulated to have entered the infected premise somewhere between 29 May and 19 June.
Day 21		**11/06/15**	Start of precautionary clinical signs incubation period for OIE (21 days) 11/06/2015
Day 20		12/06/15	
Day 19		13/06/15	
Day 18		14/06/15	
Day 17		15/06/15	
Day 16		16/06/15	
Day 15		17/06/15	
Day 14		**18/06/15**	Most likely start of tracing window (non-precautionary) 18/06/2015
Day 13	Day 1	19/06/15	
Day 12	Day 2	20/06/15	
Day 11	Day 3	21/06/15	
Day 10	Day 4	22/06/15	
Day 9	Day 5	23/06/15	
Day 8	Day 6	24/06/15	
Day 7	Day 7	25/06/15	
Day 6	Day 8	26/06/15	Visit by veterinary technician to IP.
Day 5	Day 9	27/06/15	
Day 4	Day 10	28/06/15	

Source Tracing Window	Spread Tracing Window	Date	
Day 3	Day 11	29/06/15	Most likely date for the LPAI-HPAI mutation event (29 or 30 June 2015)
Day 2	Day 12	30/06/15	Most likely date for the LPAI-HPAI mutation event (29 or 30 June 2015)
Day 1	Day 13	01/07/15	Start of oxytetracycline treatment by PVS (evening)
	Day 14	**02/07/15**	**Most likely precautionary date of FIRST CLINICAL SIGNS**
	Day 15	03/07/15	Drop in egg production noted in sheds 1 and 12a on the Suspect Premises (SP).
	Day 16	04/07/15	Increased mortality
	Day 17	05/07/15	Continuing pattern of raised mortality
	Day 18	06/07/15	Sudden mortality increase to ≅ 1800 birds in five sheds
	Day 19	07/07/15	PVS involved and starts antibiotic treatment (tetracycline). Mortality approx. 2500 birds. PM by PVS: petechial haemorrhages in the spleen and liver. Carcases sent to APHA Lasswade.
	Day 20	**08/07/15**	**Mortality: >3000 birds. Report case initiated at 18:30. RESTRICTIONS SERVED 08/07/2015 (DPR2015/21)**
		09/07/15	Follow-up report case visit and sampling of suspect premises carried out. Deteriorating clinical picture. Private samples received evening and processed overnight.
		10/07/15	**Preliminary (unofficial/private samples) results H7 pos. and deteriorating clinical signs. SOS declared. 10 km TCZ (TCZA 3 km and TCZB 10 km). Four hot tracings restricted and three of them inspected (clinically and production records).**
		11/07/15	**CULLING STARTED at around 13:00. Foot patrols in 3km also started. Additional hot tracing visited today.**
		12/07/15	Foot patrols finished by COP today. Visit by BTO ornithologist.
		13/07/15	**AIV 2015/02: HPAI H7N7 PRESTON DECLARED**
		14/07/15	**Culling finished 21:00 14/07/2015**
		15/07/15	**Preliminary C&D started 15/07/2015**
		16/07/15	**Completion of preliminary C&D 18:00 16/07/2015**
		17/07/15	**Preliminary C&D effective 18:00 17/07/2015**

	Purple colour reflects source tracing window. Increased intensity of colour reflects increased possibility of introduction on these dates.
	Yellow colour reflects spread tracing window. Increased intensity of colour reflects increased possibility of spread from the IP on these dates.
	The pale yellow shading reflects the very low risk of spread from the IP, which is under official control following the service of legal restrictions; this is consistent with the normal precautionary approach followed until statutory preliminary C&D is considered to be effective (24 hours after it is completed).

7. Source investigations - hypotheses for source

For any outbreak of avian notifiable disease the source of infection may be related to contact with infected wild birds (directly or via fomites), introduction of live birds from infected flocks, introduction of infected or contaminated products, or contact with contaminated equipment (fomites) including bedding. A summary of the sources of infection considered is shown in Table 1; definitions of qualitative risk terms are given in Appendix 4.

Indirect contact with wild birds has been postulated as the most likely route for the introduction of the disease into the infected premises. A rapid risk assessment was carried out to assess this possible route of entry and spread using (i) evidence obtained from expert ornithologists during meetings convened following detection in the UK, (ii) a site assessment of the UK infected premises and (iii) data from the EU Reference Laboratory (EURL) at APHA Weybridge.

The risk assessment addressed three specific risk questions:

1. What is the risk of introduction of LPAI into the UK, specifically the infected premises, through direct or indirect contact with wild birds?
2. What is the risk of introduction of HPAI into the UK infected premises through contact with wild birds (either migratory or UK resident)?
3. What is the risk of further outbreaks in poultry in the UK occurring through contact with potentially infected wild birds in the UK, either LPAI or HPAI?

1 - The risk of introduction of LPAI through contact with migratory and UK-resident wild birds: It was concluded that there are no significant movements of migratory birds during the source window of the outbreak. Most waterfowl will be sedentary at this time of year, due to breeding and moulting (flight feathers are lost). Although there are some wild waterfowl reserves within 20-30 km of the IP, there was no evidence of large flocks of migratory waterfowl in this area. In addition, there were no flyways over the IP as most birds would be more attracted by the River Ribble estuary. Nearby reservoirs are not conducive to migratory wild waterfowl nesting sites. The peak of migration is in early autumn through to January from North West Europe. However, the low number of wild birds observed, particularly around and within the IP and reports of the presence of wild waterfowl species (Mallards, *Anas platyrhynchos*) suggested **wild birds pose a medium risk** (between “occurs regularly or as likely to occur as not” and “occurs very often”) of being the source of introduction.

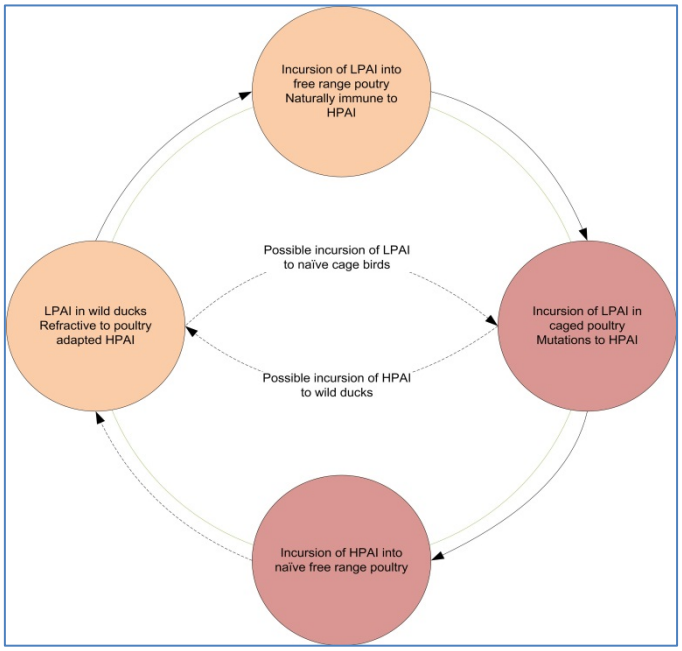
There is high uncertainty around the infection prevalence in wild birds, but H7 LPAI viruses are known to circulate continuously in waterfowl. Samples of duck feathers and faeces collected from around pond A gave negative results, but these negative findings cannot definitively exclude the possibility of the wild ducks being the source of the LPAI virus.

It should be noted that the current strategic objective for AI surveillance in wild birds in the EU is focussed on the early detection of HPAI H5N1 in wild birds (as defined by Commission Decision 2010/367/EU). The scanning (or passive) surveillance programme relies on detecting abnormal mortality in wild birds. There is no evidence in the literature for wild waterfowl mortality due to H7N7 LPAI.

2. The risk of introduction of HPAI through contact with wild birds at the premises: While it is accepted that there was a significant level of direct and indirect contact between wild waterfowl at the IP and free range poultry, the molecular epidemiology of the virus mutation and clinical progression of disease in the poultry sheds is very strong evidence of a mutation event occurring among chickens on the IP, which suggests the source of HPAI is not from wild birds,. H7 HPAI has not been previously reported from wild birds apart from two instances in close proximity to infected

poultry. This pathway is considered as being negligible, with some uncertainty.

Figure 77: Routes of incursion of HPAI and LPAI



3 - On the risk of spread, an expert ornithological field assessment was carried out at the infected premises on the 12th July 2015. There was a notable presence of mallards on the property and several small ponds that would be expected to hold a number of mallards (see Figure 4 of the IP). APHA Veterinary Officers on site soon after restrictions were served on the IP, reported seeing several mallards on the ponds (which flew away when disturbed) and the managers of the IP reported seeing wild ducks walking through the yard, occasionally. Occasional events where wild birds have become infected with H7 HPAI viruses as a result of a poultry outbreak are considered spill-over events, which do not result in further spread. Nevertheless, such wild birds can act as mechanical vectors, transferring infective material from one farm to another and it was concluded that for onward spread through the movement of wild birds (susceptible or bridge species) from the premises to other farms the risk was very low.

3 - On the risk of further outbreaks in poultry in the UK from infected wild birds potentially present in the UK: In February 2015, an outbreak of LPAI H7N7 was reported in Hampshire. The most likely route of introduction was through direct or indirect contact with wild birds, likely precipitated by a flooding episode. The virus sequence in the Lancashire outbreak suggests there is no direct link between the two outbreaks, however there is genetic sequence similarity with other contemporary European H7 viruses (see section 10 virus analysis); while the NA gene sequence show close relationship to not only the Netherlands H7N7 but also the Hampshire H7N7 virus). In GB, wild bird surveillance for AI is focused on investigation of target species of wild birds found dead, in high risk areas (i.e. where there are high density of poultry) or mass mortality incidents of any wild bird species. Interestingly, the region around the Lancashire outbreak is considered a high risk area and there are several warden patrol sites, where dead birds of target species are collected and tested for avian influenza. However there have been no recent die-offs of wild birds in the region at the sites testing positive for avian influenza.

It is therefore assumed that there is a low level of LPAI virus currently circulating in either indigenous or migrating wild birds, particularly waterfowl, and therefore the **risk of further incursions is considered low** (rare but could occur).

See also a list of the risk assessments carried out as part of investigations into further spread (see Appendix 5)

Table 1: Possible source of infection for the Infected Premises AIV 2015/02, source tracing window 11/06/15 – 01/07/15.

	Pathway	Comment	Assessment of likelihood of infection via this route
1	**Direct or indirect introduction from wild birds**	A few wildfowl present in small ponds (confirmed also during expert ornithological visit). Likely to have been there some time since they were raising ducklings. Environmental contamination possible. Analyses of virological and virus genetic data support a relatively recent introduction (weeks rather than months but some uncertainty) and a proven hypothesis that the virus was introduced as LPAI into one or more free range sheds in close proximity to one of the ponds on the IP (i.e. shed 4 and possibly also shed 5) and from it spread further, including to sheds 1 & 2 which house caged birds. The mutational event is likely to have occurred in sheds 1 or 5 (see section 5).	Medium likelihood Low uncertainty
2	**Undisclosed infection in the UK:** Direct introduction by purchased birds	The birds on the IP were placed as pullets 51 weeks prior to report case.	Negligible likelihood Low uncertainty
3	**Undisclosed infection in poultry in the UK:** Indirect contact with an infected flock	No evidence of active AI infection at any traced premises or within the surveillance zones. Some uncertainty regarding staff movements to other premises. Feed delivery – Transported in covered vehicles. External silo filled using feed delivery pipe and feed blown in. Silo enclosed so limited contact by wildlife. Bedding not moved onto the IP since April 2015. Any viral contamination from prior to April would not still be infectious Unknown whether potential for contamination by wild birds whilst stored on IP	Low likelihood Low uncertainty Very low likelihood Low uncertainty Very low likelihood Medium uncertainty
4	**Infection elsewhere in the world:** Direct	No recent trade into the IP of live birds or hatching eggs/day old chicks.	Negligible likelihood

	Pathway	Comment	Assessment of likelihood of infection via this route
	contact with an infected flock or wildfowl	Incursion via migratory birds is less likely as this is the bird breeding season so active migration is minimal and most migratory birds are sedentary at present.	Low uncertainty
5	**Infection elsewhere in the world:** Indirect contact with an infected flock or wildfowl	Incursion via trade in contaminated poultry products cannot be ruled out. H7N7 LPAI is present on the Continent, however, it is unlikely that poultry meat, feathers, table eggs etc. would have a high enough viral load to initiate infection. No evidence of contaminated product being brought onto the IP.	Very low likelihood Very low uncertainty

8. Assessment of likely source

The most likely source of the outbreak is direct or indirect contact with wild birds, particularly the wildfowl present on the small ponds on the IP. This assessment is based on the following key pieces of evidence:

1. Findings from the investigation suggest that there was high potential for fomite transfer of disease on the IP and direct wild bird contact with the free-range flock.

2. The genetic analyses of the virus which indicate a relatively recent introduction from wild birds to poultry, the circulation of H7 LPAI viruses in wild birds, particularly wild waterfowl, and the presence of wild waterfowl on the two ponds near the sheds on the IP, all support a hypothesis that the source was contamination via wild birds.

3. There have been no further cases of H7N7 identified in domestic poultry in the UK despite raised awareness following confirmation of disease, tracings investigations undertaken and the ongoing passive surveillance programme with a legal requirement to report suspicion of avian influenza to APHA.

4. There were no consignments of live birds or hatching eggs/day old chicks imported into the IP or associated neighbouring premises during the risk period. Neither was there any evidence of contaminated product being brought onto the IP during the risk period.

9. Spread investigations - Potential and probability of spread

Potential routes of onward transmission both within and outside the company structure are shown in Table 2, together with comment on the probability of transmission and the action taken.

Evidence does not suggest that there has been any spread of infection from the Infected Premises.

Table 2: Possible spread of infection from the Infected Premises AIV 2015/02

	Spread Pathway	Comment	Assessment of likelihood of infection via this route
1	**Movement of poultry hatching eggs or day old chicks off the IP**	None, including no international trade	Negligible risk Low uncertainty.
2	**Movements of poultry products off IP - table eggs**	All table eggs which had left the IP and not entered retail were traced and restricted / destroyed. No eggs were sent for export or EU trade.	Very low risk High likelihood that table eggs and trays / trolleys may be contaminated, but mitigated by the packing / grading process and the lack of exposure to poultry.
3	**Movement of contaminated substrate off IP - manure, straw, carcasses**	Risk of undetected spread of H7N7 HPAI and LPAI to other poultry premises as a result of carcase removal in the 21 days prior to restrictions being served – risk is greatest for farms visited within 7-10 days of the restrictions and within 24 hours of the carcase removal. Last carcase collection 01/07/15 (previously twice weekly). Removal of manure/litter on 02/07/15 and 07/07/15 – litter could have come from infected sheds and was removed in high risk spread window. It was traced, restricted (stacked in a field) and sprayed with disinfectant, covered to prevent wildlife access and left to heat/compost for at least 42 days.	Low likelihood Medium uncertainty - based on worst case scenario of poor biosecurity for all the steps in the pathway. Manure high risk but risk mitigated by control measures implemented. , Medium uncertainty

	Spread Pathway	Comment	Assessment of likelihood of infection via this route
4	**Indirect contact via personnel, equipment or vehicles**	Documented contacts: 1. Company personnel 2. Egg collection staff, egg trays/trolleys and vehicles 3. Private Vet and technical advisor 4. Feed delivery staff and vehicles **5.** Straw delivery dealer 6. Pest controller There is a biosecurity protocol at the feed mills: all lorries go through a Virkon spray wash underneath upon entrance. Drivers have footbaths at reception, with Virkon. Feed Lorries are externally washed daily but with water only. Single loads delivered to IP with return to mill subsequently. Some routine biosecurity was in place for vehicles / personnel. Dedicated site staff, with minimal visitors. Spray disinfectant point at entrance used on all visitors that have been to other poultry sites. Unregulated access to the site and poor visitor records.	High likelihood of contact, but subsequently assessed as low risk, following completion of tracing investigations Tracing investigations showed no evidence of spread via these contacts
5	**Local spread into PZ and SZ**	Visits and clinical inspections were completed on all premises within the PZ and there is no evidence of local spread of HPAI virus.	Low risk. Moderate uncertainty
6	**Direct or Indirect contact with wild birds**	The resident Mallard ducks are able to leave the site and may come into contact, direct or indirect, with other wild birds/their faeces; they are good amplifiers of this virus. The pond on-site is open and it is not possible to rule out other non-resident ducks visiting. The ornithological field	Medium risk Low uncertainty

	Spread Pathway	Comment	Assessment of likelihood of infection via this route
		assessment noted little in the way of presence of gulls, migratory birds etc. on fields adjacent to the property. Wild birds (which could act as bridge vectors) were scarce at the IP except the resident mallards which lived on the ponds and were raising ducklings. The ducklings are believed to have fledged and were not observed again once culling started. Wild birds could enter the ranges and free range sheds via pop-holes	
7	**Mechanical spread by other wildlife species**	Foxes, badgers and occasionally feral cats are reported to be seen near the site. Mechanical transmission e.g. by scavenging and removal of carcases may be possible, but is unknown. The range of spread by such means is covered by the implementation of restriction zones around the IP and is generally not considered a higher risk for areas outside the zones than for other environmental contamination already present.	Very low risk Medium uncertainty

There was no trade of live poultry, hatching eggs, day-old chicks, poultry meat or other poultry products from the IP to other EU Member States, or third countries, in the previous two months.

10. 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.

Premises containing poultry identified within the 3-km radius of the outbreak (Protection Zone).

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 inspected by APHA personnel (and tested where relevant) with no evidence of AI virus being present.

Premises with susceptible stock identified in the area between the 3km-10km radius of the outbreak (Surveillance Zone).

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

11. Analysis of the virus

Virus characteristics

The HPAI virus was conventional in its viral characteristics, disease presentation (in a partially immune population), pathology, tropism and infection kinetics. Samples from five epidemiological groups (Table 3: Bird level H7 serology and PCR/shedding results for report case samples) were submitted to the laboratory on Thursday 9th of July for analyses (20 oropharyngeal swabs/20 cloacal swabs/20 bloods). The index virus named A/chicken/England/26352/2015 (exAV868/15, EPI D-House 2) was identified as H7N7 HPAIV based on molecular analyses using H7 HA2 RRT-PCR (Slomka *et al* 2009)] and conventional virus typing (HAIT and NI) using isolated virus, together with intravenous pathogenicity index assay (IVPI, 2.52). The haemagglutinin (HA) gene cleavage site motif (CSM) was unique PEIPR**HRKG**RGLF (3/5 Houses - 2, 10, 11). A second HPAI CSM motif (PEIPR**HRKR**RGLF) was also detected during the investigations, (2/5 Houses – 1 and 12) and is indicative of viral evolution as the virus transmitted through the flock on the IP. Both CSM are characteristics of HPAI. Further investigations revealed that viruses carrying both motifs were maintained on the IP after their emergence from a common LPAI progenitor. It should be noted that the sample size per epi group fully analysed from pathotype was moderately small providing some level of uncertainty i.e. failure to detect LPAI or HPAI in a given epi group needs to take this into account. In some epi groups this was influenced by the relatively low level of virus shedding in sampled birds both at disease report and cull (see below). Importantly in addition an LPAI progenitor H7 virus was detected in birds sampled at report in houses 1 and 2.

Infection dynamics

During the initial investigation of the IP the levels of virus genome detected in the oropharyngeal (OP) and cloacal (C) swabs were similar, with one route of shedding not being favoured over the other at the time of the first collection. These report case sample swab and blood results are summarised in Table 3, all epi groups were virus and antibody positive, with 50-90% of the birds shedding and 5-15% were H7 antibody positive (Epi A-E).

At cull the number of positive birds ranged from 90% in Houses 11 to 0% in Houses 4 and 7 (Table 4: Bird level H7 serology and PCR/shedding results for Cull samples:). Detailed analyses at bird level has provided further insights into possible timelines and routes of entry for the LPAI virus while enabling an assessment of virus mutation to HPAI and subsequent spread within the IP. The assessment evaluated individual bird status as immune or infected or both. To understand this infection status four categories were defined: i) antibody positive consistent with exposure at least 7-10 days prior/virus negative therefore cleared; ii) low or no antibody consistent with no reliability of prior exposure/virus positive and therefore actively infected; iii) antibody positive consistent with exposure at least 7-10 days prior/virus positive and therefore still actively infected; iv) low or no antibody consistent with no reliability of prior exposure/ virus negative therefore no active infection. Results are summarised in Table 5: Bird level H7 serology and PCR/Shedding for Cull Samples – Exposure/infection status.

Overall only infectious HPAI virus was recovered by virus isolation on multiple sample sets collected at report and cull. The presence of LPAI has been confirmed by a) presence of antibody positive birds consistent with LPAI infection b) detection of LPAI genome. These results confirm at the time of sampling (8/7/15 onwards) there was no active infection with LPAI virus which had been replaced by HPAI virus following mutation.

Detailed examination of samples taken at cull

The second set of enlarged sampling from the IP were collected just prior to the cull on 10th and 11th of July (60/60/60, 2 carcases per Epi group), in order to further investigate the precise epidemiology

to understand the infection course within the premises and inform source and spread investigations, this included samples from nine epidemiology groups (A-I from Houses – 10, 11, 1, 2, 12, 6, 7, 4, 5). The results obtained supported the results from the official sampling but also provided greater insights into the sequence of events on the IP (An LPAIV potential progenitor virus (CSM – PEIPKGRGLF), was detected in birds from three Houses (1, 2 and 4).

Phylogenetic analyses

Analysis of the full genome of the HPAI index virus isolate revealed highest levels of similarity (98.3-99% at nucleotide level) in six gene segments (PB2, PB1, PA, HA, M, NA) to A/chicken/Netherlands-Barneveld/15004745-001-005/2015 a recent H7N7 LPAI virus. The NP gene was more distantly but most closely related to that of an H7N7 HPAI virus from Italy in 2013 A/chicken/Italy/13VIR4527-11/2013), whilst the NS gene was much more divergent and derived from a third strain likely of wild bird origin. Interestingly the virus (A/chicken/England/2830/2015) detected in broiler breeders in Hampshire earlier in 2015 could be clearly differentiated in all gene segments, demonstrating that this incursion was an unrelated event. Furthermore the results indicate that H7N7 HPAI virus concerned with this outbreak most probably derived from more than one progenitor strain (contemporaneously circulating in Europe) through genetic reassortment.

Genetic analyses of the H7N7 HPAI virus to understand zoonotic potential

In order to define the publish health risk and inform the RA for staff operationally involved in the outbreak response we assessed the full genome for specific mutations that increase the affinity for human infection. Full genome sequencing was completed by Next Generation Sequencing for the highly pathogenic H7N7 avian influenza virus isolated.

Sequences were analysed for the molecular determinants that may confer enhanced transmissibility or severe disease for highly pathogenic avian influenza (HPAI) viruses in mammals as defined by the Centre for Disease Control (CDC) (http://www.cdc.gov/flu/avianflu/h5n1/inventory.htm).

Several mutations were identified in PB2, PB1-F2, NA, HA, M1 and NS1. The mutations identified in PB2, PB1=F2, M1 and NS1, have been reported to enhance virus replication and virulence or reduce the antiviral response in mouse models. The three mutations identified in HA – Ser128Ala, Thr151Ala and GLy177Val – have been reported to increase the binding efficiency of HA to human receptors. The single mutation identified in NA – His274Arg – has been reported to confer a reduced susceptibility to antiviral products oseltamivir and peramivir. However, a number of other mutations reported to affect zanamivir and oseltamivir susceptibility were not found.

There are substantial levels of uncertainty regarding the cumulative contribution these residues make to risk for zoonotic infection. Some of the critical genetic correlates for increased human affinity e.g. PB2E627K, appear lacking in this virus, and so the risk for human infection was assessed as low. The data was shared with PHE (see section 14).

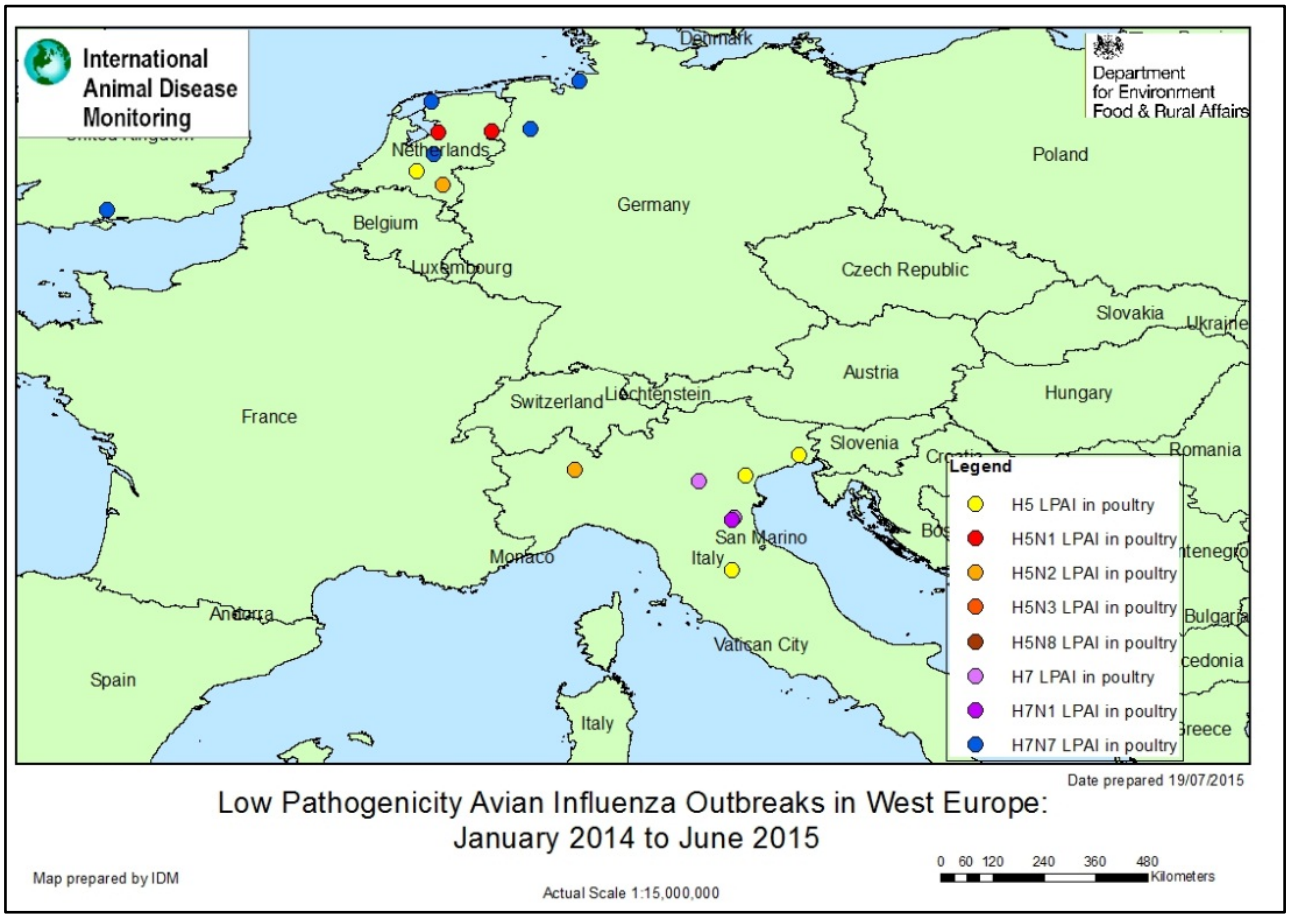
12. International context

Spread from Europe:

Outbreaks of H7N7 LPAI virus have recently been reported in poultry in Germany (March 2015 and June 2015), the Netherlands (two outbreaks in March 2015), and the UK (February 2015) and H7N7 HPAI in Germany in July 2015 (see Figure 8). Control measures were put in place on all affected holdings. In the case of the UK and Netherlands outbreaks, the restrictions were lifted following surveillance, including sampling where appropriate. All outbreaks have affected different poultry species and production systems. It is widely considered that H7 LPAI viruses circulate continuously year round in wild birds, particularly in wild waterfowl.

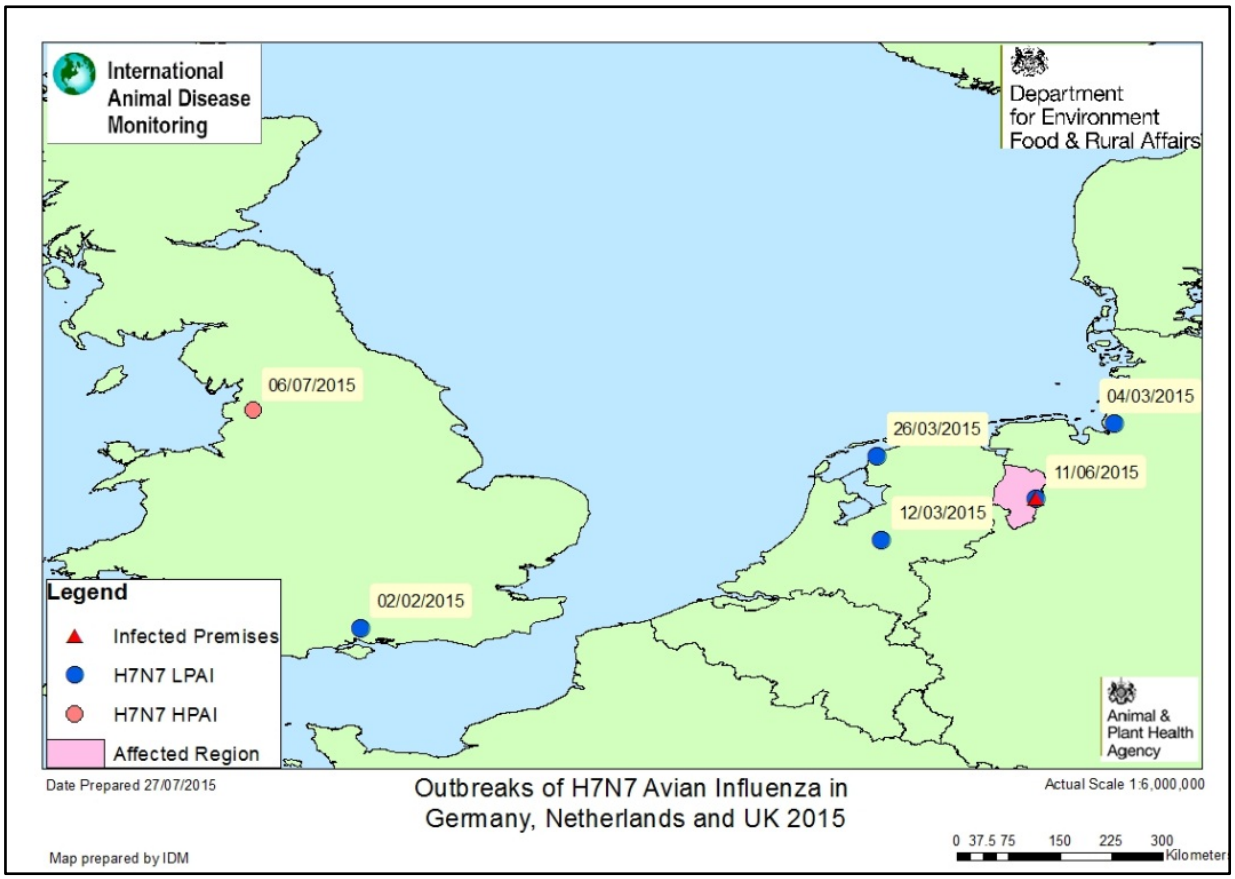
It should be noted that Germany and the Netherlands both have early warning systems in place for avian influenza virus and the current situation provides evidence that incursions of H7N7 LPAI are infrequent, but occurrences are possible. Early detection is vital to prevent the mutation into HPAI strains that is more likely to occur in dense poultry populations, especially chicken layers.

Figure 88: Locations of recent AI outbreaks in Europe



In addition, a short time after the UK outbreak, Germany reported an outbreak of H7N7 HPAI in a commercial poultry farm. In this case, the farm had been tested earlier in the year during surveillance around a LPAI outbreak and had tested negative. At some stage an LPAI incursion occurred and the virus consequently mutated to HPAI. This is again further evidence of the constant risk of avian influenza outbreaks occurring and how mutation events are not unusual occurrences (see Figure 11).

Figure 11: Location of H7 outbreaks (LPAI and HPAI) in Northern Europe in 2015



13. Public health impact

Public Health England (PHE) undertook a risk assessment following confirmation of H7N7 LPAI and concluded that the risk to the general public was very low – given there have been no reported cases of human infection with H7N7 LPAI and the low probability of exposure to infected birds. PHE determined the risk to persons occupationally exposed to H7N7 HPAI (i.e. workers on the IP) to be slightly higher than the general public but still low. PHE provided antiviral prophylaxis and health surveillance to those directly involved in handling and culling the affected flock and at the identified rendering plant, and provided advice on the need for appropriate PPE.

Some of the critical genetic correlates for increased human affinity e.g. PB2E627K, appear lacking in this HPAI virus, and so the risk for human infection was assessed as low.

Both PHE and the Food Standards Agency (FSA) advised that on the basis of current scientific evidence avian influenza does not pose a food safety risk for UK consumers (http://www.food.gov.uk/news-updates/news/2014/13230/fsa-advice-about-avian-bird-flu).

14. Remaining uncertainty

- The source of the progenitor LPAI virus.
- The route of introduction onto the IP.
- The earliest likely date that LPAI was introduced onto the IP.
- The precise date that the mutation event from LPAI to HPAI occurred.

There is a continually present, global risk of further outbreaks of avian influenza as a result of the ongoing presence of AI viruses within the wild bird population. There is ongoing AI surveillance (both active and passive) in the UK aimed at early detection of such an incursion.

15. Concluding remarks

The most likely source of infection is the introduction of LPAI virus from wildfowl present on the ponds on the infected premises. Genetic analysis of the HPAI virus identified on the holding and other epidemiological/laboratory data gathered from all groups on site indicate that this originated as the result of a mutation from LPAI virus that occurred within the IP. This mutation has made this a complex investigation.

Investigation of tracings from other premises identified as potential sources, via tracings of personnel and vehicle movement, have revealed no other premises that could have been the origin of the HPAI infection on this premises. Investigations of similar spread tracings have not revealed any spread of HPAI virus from the IP to other premises.

Although our investigations suggest that the most likely route of introduction of virus onto this infected premises was direct or indirect contact with wild waterfowl, an incursion such as this remains a low likelihood event.

National Emergency Epidemiology Group
28 August 2015

Acknowledgements

The views expressed in this report are those of the National Emergency Epidemiology Group (NEEG). However, we wold like to express our thanks to the members of the Ornithological expert Panel and the many colleagues who have assisted with this on-going investigation.

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

16. Appendices

Appendix 1: Tables summarising selected lab analyses:

Table 3: Bird level H7 serology and PCR/shedding results for report case samples (these were diagnostic samples collected at the time of the veterinary inquiry into suspicion of disease)

EPI group	House number	Type	Bird Level Serology / Shedding N=20			
			H7 Ab+	% Pos	+ PCR	% Pos
A	10	Free range	3	15	14	70
B	11	Free range	9	45	18	90
C	1	caged	6	30	10	50
D	2	caged	1	5	15	75
E	12	caged	1	5	12	60

Table 4: Bird level H7 serology and PCR/shedding results for samples collected at the time of culling:

EPI group	House number	Type	Bird Level Serology / Shedding N=60			
			H7 Ab+	% Pos	+ PCR	% Pos
A	10	Free range	49	82	33	55
B	11	Free range	36	60	54	90
C	1	caged	29	48	27	45
D	2	caged	5	8	49	82
E	12	caged	1	2	23	28
F	6	Free range	53	88	2	3
G	7	Free range	24	40	0	0
H	4	Free range	60	100	0	0
I	5	Free range	55	92	26	32

Table 5: Bird level H7 serology and PCR/Shedding for samples collected at time of culling – Exposure/infection status

EPI group	House number	Type	PCR-virus / Antibody (Ab) status N=60			
			Hi virus	Lo/No virus	Hi virus	Low/No virus
			Hi Ab	Low/No ab	Low/no ab	Hi Ab
A	10	Free range	20 (33%)	0	11 (18%)	29 (48%)
B	11	Free range	30 (50%)	0	24 (40%)	6 (10%)
C	1	caged	6 (10%)	8 (13%)	17 (28%)	23 (38%)
D	2	caged	3 (5%)	8 (13%)	47 (78%)	2 (3%)
E	12	caged	0	36 (60%)	23 (38%)	1 (2%)
F	6	Free range	1 (2%)	5 (8%)	0	53 (88%)
G	7	Free range	1 (2%)	35 (58%)	0	23 (38%)
H	4	Free range	0	6 (10%)	0	54 (90%)
I	5	Free range	19 (32%)	0	0	41 (68%)

Infection status four categories were defined:

i. low/no virus; high antibody- consistent with exposure at least 7-10 days prior/virus negative therefore cleared;
ii. HI virus; low or no antibody- consistent with no reliability of prior exposure/virus positive and therefore actively infected;
iii. HI virus; HI antibody- consistent with exposure at least 7-10 days prior/virus positive and therefore still actively infected;
iv. Low / no antibody; low / no virus - consistent with no reliability of prior exposure/ virus negative, therefore no active infection.

Appendix 2: Details of tracings and stock numbers in zones

Table 6: Total number of locations linked by tracings by region

	Source only	Spread only	Both	Total
England	8	12	77	97
Scotland	0	2	2	4
Wales	0	0	2	2
Total	8	14	81	103

Table 7: Number of locations with tracings by level of risk

Risk rating	Source only	Spread only	Both	Total
High	0	3	7	10
medium	7	9	71	87
Low	1	2	3	6
Total	8	14	81	103

Table 8: Number of source tracing tasks

Risk rating	ABP collections	Egg collections	Feed delivery	Manure collections	Personnel	Visitors to the IP	Total
High	2	5	0	1	2	2	12
Medium	60	16	1	0	3	11	91
Low	0	1	3	0	0	1	5
Total	62	22	4	1	5	14	108

Table 9: Number of spread tracing tasks

Risk rating	ABP collections	Egg collections	Feed delivery	Manure collections	Personnel	Visitors to the IP	Total
High	2	5	0	3	2	3	15
Medium	60	16	1	2	2	15	96
Low	6	1	4	1	0	0	12
Total	68	22	5	6	4	18	123

Note: Numbers have been calculated from the records of the tracings team at close of play 06/08/15. The total number of traced locations shown above is lower than the sum of source and spread tracing tasks, because a number of locations and tasks were both source and spread tracings and additionally some locations were investigated as a result of more than one contact type.

Table 10: Summary of stock and holdings in zones

	Chicken	Duck	Goose	Guinea Fowl	Partridges	Pheasant	Pigeon	Turkey	Quail	Other Birds	Other Exotic Species	Total
Number of holdings with that species in the PZ	79	15	19	5	0	0	3	1	1	3	2	87*
Number of animals of that species in the PZ	43507	19074	1371	3011	0	0	258	2	2	212	8	67445
Number of holdings with that species in the SZ	96	17	13	1	4	7	2	3	0	3	0	105*
Number of animals of that species in the SZ	277917	12026	181	3	19400	61712	160	1253	0	98	0	372750

Notes: Premises and stock numbers have been calculated from an extract of CORE2 taken on 28/07/15. The data is only accurate as of this date and may have altered as further visits where completed. The table has been produced to summarise the number of premises and stock in each control zone surrounding the IP. It contains only the susceptible stock present. None of the following species are present in the zones; Aviary Birds, Birds of Prey, Cassowary, Emu, Kiwi, Ostrich, Other Domestic Species, Rhea.

* The total number of premises in the PZ and SZ is not the sum of the premises within each species type column as a premises may have more than one species type associated with it.

Appendix 3: Risk mitigation measures taken

Restriction of the suspected premises on 8th July, 2015. Following notification of suspicion of a suspect Avian Notifiable Disease to the local APHA office on the 8th of July, 2015, statutory disease control restrictions were imposed on the premises – prohibiting the movement of birds, eggs, animals, people vehicles, and any other things which may transmit avian influenza , requiring records to be kept of numbers of birds present and number of deaths numbers of apparently affected birds, and requiring disinfection points to be set up and maintained at all entrances to and exits from the premises and the poultry housing on the premises.

Implementation of Temporary Control Zones (TCZ). TCZ A (3km radius from affected premises) and TCZ B (10km radius from affected premises) on 10th July, 2015 which required enhanced poultry record keeping in the zones and restricted animal/bird/product movements unless under authority of a licence issued by APHA.

Foot patrols to identify unregistered poultry premises in Temporary Control Zone A were undertaken by Local Authority officials, starting on the 10th July, 2015 and completed by the 12th July, 2015. This returned a census of other poultry in a 3km radius from the affected premises and provided opportunity for rapid feedback of any flocks with suspected clinical signs.

Culling of birds on the Affected Premises commenced on 11 July, 2105 following CVO authorisation to slaughter on suspicion. Culling was completed on 14 July 2015

Expert Ornithological Field Assessment of the site was carried out on July 12th by members of the British Trust for Ornithology, under contract to Defra. The report looked at movements and populations of wild birds on the IP, in the restriction zones, and wider afield at local wild bird roosts and breeding sites. This information fed into the qualitative risk assessment on the risk of incursion and onward spread of H7N7 from wild birds.

Secure disposal of all carcasses and stored ABP (already dead birds and eggs), transported in leak proof vehicles to a rendering plant – all completed under official supervision by the 16 July, 2105.

Following **official confirmation of existence of Highly Pathogenic Avian Influenza (HPAI) virus** on the affected premises on 13th July, 2015, the suspect premises was confirmed as an infected premises (IP).

This enabled a **declaration of a Protection Zone (PZ) and Surveillance Zone (SZ)** to be made on the 13th July, 2015.

Commercial poultry holdings within the Protection Zone were subject to a veterinary inspection and surveillance sampling (where appropriate) to be completed within 14 days from the date of completion of preliminary cleansing and disinfection, specific requirements being differentiated as follows: in the 1km radius from the IP all commercial poultry holdings required a veterinary inspection and surveillance sampling, and in the remainder of the PZ all holdings were subject to a veterinary inspection, with sampling as above only if the holding comprised either only non-indicator species (e.g. waterfowl) or mixed species where there was no co-mingling or direct contact.

Non-commercial poultry holdings within the Protection Zone were subject to a veterinary inspection, with sampling only if there were twenty or more non-indicator species present which did not mix with indicator species. All visits to be completed within 14 days of preliminary cleansing and disinfection of the IP.

Public awareness was raised by the issue of guidance notes to all livestock keepers in the

Protection and Surveillance Zones and an **APHA helpline** was set up to address queries from livestock keepers and stakeholders.

Statutory preliminary **cleansing and disinfection of the IP** started on 16 July, 2015 and was completed on the same day. This was considered to be complete and effective 24 hours after application of the approved disinfectant .

Identification of all known contacts with the IP within the 21 day tracing window before and after the most likely precautionary date of first clinical signs. The infection pathway was considered and an assessment was made of the inherent risk of disease spread/source of each contact. Based on the available intelligence, prioritisation of premises for tracings visits was completed.

Veterinary visits were undertaken to traced premises according to the assigned priority and risk, and following veterinary clinical inspection of domestic poultry and waterfowl on the premises, inspection of the production records, assessment of pre-existing biosecurity measures and premises biosecurity protocols, a **veterinary decision was made regarding the need for restriction and sampling of birds on the premises**.

Rapid risk assessments were completed in order to assess the risk of highly pathogenic H7N7 undetected spread to other poultry premises from the infected premises via 1) animal-by-products - collection vehicles/personnel 2) feed - delivery vehicles/personnel 3) manure containing broken eggs - collection vehicle/personnel/manure heap. These assessments informed the decisions regarding degree of restriction applied to each traced premises and the movements which required licensing by APHA.

A **veterinary risk assessment** was completed in order to assess the risk of highly pathogenic H7N7 undetected spread to other poultry premises from the infected premises via 1) live day old chicks 2) animal-by-products (primarily dead male day old chicks collected by a company retailing those for raptor and reptile feeding) from a commercial hatchery in the Surveillance Zone producing day old chicks for table egg producers. This hatchery had contact with the infected premises via the hatchery manager.

A gate officer was in place on the IP after restrictions were served, and all movements on and off the premises were controlled and recorded.

Appendix 4: Definitions of qualitative risk terms

Table 11: 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); it is not expected to happen for years;
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); it is expected to occur at least annually
Low	Event is rare, but does occur	The event may occur occasionally (rare) (i.e. >1-10% probability); expected to occur at least monthly
Medium	Event occurs regularly	The event occurs regularly (i.e. >10-66% probability); expected to occur at least fortnightly
High	Event occurs very often	The event will happen more often than not (i.e. ≥66-90% probability); expected to occur at least weekly
Very high	Event occurs almost certainly	The event will undoubtedly happen (i.e. >90% probability); expected to occur at least daily

Appendix 5: List of risk assessments and other measures carried out as part of investigations into further spread:

1. Emergency Ornithology Field Assessment (EOFA) carried out by the British Trust for Ornithology.

2. The list of rapid risk assessments is as follows:

   i. Wild bird incursion and spread.
   ii. Carcases removed from the IP 21 days prior to restrictions being served.
   iii. Inclusion of egg waste in manure.
   iv. Feed lorries delivering feed to the IP.
   v. Risk assessment of the hatchery premises.