Preliminary Outbreak Assessment

Highly Pathogenic Avian Influenza H5N1 in poultry in France

26 November 2015

Disease Report

France has reported an outbreak of highly pathogenic avian influenza, H5N1 in backyard poultry (broilers and layer hens) in the Dordogne (OIE, 2015; see map). An increase in mortality was reported with 22 out of 32 birds dead and the others destroyed as a disease control measure. Samples taken on the 19th November confirmed HPAI. Other disease control measures have been implemented including 3km protection and 10km surveillance zones in line with Directive 2005/94/EC.

This is an initial assessment and as such, there is still considerable uncertainty about the source of virus and where or when a mutation event occurred. However the French authorities have confirmed by sequence analysis that this is a European lineage virus (European Commission, 2015) and as such control measures are focussed on poultry.

Situation Assessment

The preliminary sequence of the strain indicates it is closely related to LPAI strains detected previously in Europe which are clearly distinguishable from contemporary strains associated with transglobal spread since 2003. H5N1 LPAI was last reported in France in 2009 in Calvados department in northern France in decoy ducks (ie tethered by hunters, and often in contact with wild birds). H5N1 LPAI viruses of the ‘classical’ European lineage have been isolated from both poultry and wild birds sporadically in Europe, but mutation to high pathogenicity of these strains is a rare event. The last known such event was in 1991 in the UK when mutation occurred in a single commercial flock. H5N1 HPAI viruses detected in Europe since 2005 have been characterised by the fact they all derived from a common progenitor (Goose/Guandong/1/96) and have been classified into several clades.
(WHO 2014) three of which (clades 2.2, 2.3.2.1, 2.3.4.4) have reached Europe (Salzburg et al 2007; Reid et al 2011; Adlhoch et al 2014). This group of viruses can be transmitted as HPAI by wild birds and also have different biological properties to the ‘classical European strains’ which arise through conventional pathways ie introduced to galliforme poultry as LPAI and can mutate to HPAI, and which has been detected in this outbreak. These events are moderately rare given that in Europe detections of H5/H7 LPAI in domestic poultry are relatively frequent. Importantly the HPAI derived forms of this group of viruses have not been shown to be maintained and spread by wild birds.

The poultry sector in France has some clearly defined sectors: the commercial sector which may include the highly valued Bresse brand and red label poultry, the organic and free range poultry sector and then the backyard sector, the vast majority of which do not belong to farmers but which still represent a large number of premises and diversity of breeds (FAO, 2010). The Dordogne region is not one of the highest poultry-dense regions but nevertheless, this time of year always sees a seasonal increase in production, as is true for most of Europe. There is no indication that H5N1 HPAI is present in the commercial poultry sector, although naturally at this stage in investigations, some uncertainty still remains.

The peak autumn bird migration for the East Atlantic flyway, which would link France to the UK, has passed for this year, and most birds would have migrated south into Spain to cross into Africa over the Strait of Gibraltar. The risk from migratory wild birds bringing H5N1 from the affected area in France into the UK is therefore very low, if not negligible, at present further supported with knowledge that the risk of carriage by wild birds of HPAI viruses of this putative type is not known to occur. Furthermore, the affected area in France does not appear to have the appropriate habitats for staging posts of migratory waterfowl. Of greater concern is that the virus spreads into the free-range geese flocks in the area, and what this could mean for undetected spread.

According to Traces, the EU electronic trade notification system, there have been no recent traded consignments of live poultry or hatching eggs / Day Old Chicks from the affected areas to the UK. Trade in poultry related products is not subject to certification in the EU, but is considered a much lower risk pathway, provided this outbreak remains confined to the non-commercial poultry sector.

**Conclusion**

This is only an initial report and at present there are still many unknowns, but the risk to the UK as a result of this outbreak is not significantly increased at this time but we will keep under close review. At the moment, it is not known whether the mutation from LPAI to HPAI occurred in the backyard poultry farm itself or was introduced by some other transmission pathway from another source. There may not be high significance attached to the knowledge that this LPAI virus has mutated: indeed this is the reason behind our disease control measures for LPAI, so that early detection and elimination reduces the
likelihood of mutation events occurring, and can therefore be quickly identified and controlled.

We will continue to monitor the situation closely. We would like to remind all poultry keepers to maintain high standards of biosecurity, remain vigilant and report any suspect clinical signs promptly and in addition using the testing to exclude scheme for avian notifiable disease where appropriate for early safeguard. For more information, please see Gibbens et al. (2014) and www.defra.gov.uk/ahvla-en/disease-control/nad

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References


notice that notifiable avian influenza A H5N1 viruses from clade 2.3.2 into European poultry. 
Transboundary and Emerging Diseases, Vol. 58 Issue 1 pages 76-78.

Salzberg, A.L., Kingsford, C., Cattoli, G., Spiro, D.J., Janies, D.A., Mehrez Aly, M., Brown, I.H., 
Couacy-Hymann, E., Mario de Mia, G., Huu Dung, D., Guercio, A., Joannis, T., Alo, A.S.A, 
Osmani, A., Padalino, I., Saad, M.D., Savic, V., Sengamalay, N.A., Yingst, S., Zaborsky, J., 
Zorman-Rojs, O., Ghedin, E. & Capua, I. (2007) Genome analysis linking recent European and 
African Influenza (H5N1) viruses. Emerging Infectious Diseases 13: 713-718.

WHO (2014) World Health Organization/World Organisation for Animal Health/Food and 
Agriculture Organization (WHO/OIE/FAO) H5N1 Evolution Working Group (2014) Revised and 
updated nomenclature for highly pathogenic avian influenza A (H5N1) viruses. Influenza and 

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