**Department for Environment, Food and Rural Affairs**

# Disease risk considerations supporting the definition of Avian Influenza Higher Risk Areas in England, Scotland and Wales

## November 2018

## Contents

# Issue

Defining an approach to determining higher risk areas for introduction of avian influenza virus into poultry or captive birds due to contact with infected wild birds to comply with Commission Decision (EU) 2018/1136 of 10 August 2018.

# Summary

Great Britain (GB) has a variable risk of incursion (in wild birds and/or poultry) of notifiable avian disease throughout the year and the risk for avian influenza is generally heightened in the winter season when migratory wild waterfowl are arriving at their over-wintering sites across GB. A range of species, including, ducks, geese, swans and gulls are considered to act as reservoirs of avian influenza viruses (AIV). The heightened probability of GB poultry contact with wild birds in autumn/winter means we consider there may be a corresponding heightened risk of AIV exposure to poultry, but this would depend on the level of infection in the wild birds and the nature of the virus itself, which may not “jump” readily into poultry. Therefore and in accordance with the EU legislation (Commission Decision (EU) 2018/1136) we have conducted an analysis of higher risk areas across GB where the probability of finding wild birds infected with avian influenza viruses is greater at certain times of the year.

Expert analyses have taken place of 1) the disease introductions into the UK and across Europe, 2) the evidence from the widespread surveillance to date across Europe, 3) the wild bird species where infection has been identified and 4) the risk factors associated with spread from wild birds to domestic poultry identified. This has led to an understanding that “higher risk areas” may be identified within the country. Typically these are close to inland or coastal bodies of water, where large numbers of wild birds collect, with wild waterbirds, specifically duck species, being highlighted.

The presence of virus in the environment surrounding a poultry farm means it can be carried into the farm by various means, bridging species (birds visiting both poultry farms and waterbird areas), such as gulls and corvids, humans, equipment, rodents etc. Therefore the closer a poultry premises is to locations where high numbers of potentially infected wild birds are present, the greater is the risk that disease will be carried into it by one of these pathways. The level of risk reduces as the distance from wild bird resting places increases, as the likelihood of somehow bringing contamination into the farm is considered to decline.  Hence whilst best practice biosecurity must be practised in all areas of the country, in these higher risk areas, biosecurity protective measures may need to be enhanced at certain times of the year.

Housing or covering areas with netting where domestic poultry are kept or range should therefore continue to protect farms in these higher risk areas. Published studies indicate that a distance of 5km from such bodies of water would exceed the likely maximum daily foraging distance of most duck species and therefore be the proposed edge for Higher Risk Area, however 2km foraging distance would cover the majority of the spatial risk. The risk of contact with bridging species, such as gulls and corvids, exists for all areas of GB and therefore general biosecurity awareness for poultry keepers are necessary in all areas of GB.

# Background

Since October 2016, a highly pathogenic strain of avian influenza, H5N8 HPAI, has circulated in wild birds in Europe and caused high mortality in a wide range of species and lead to introductions into poultry holdings. In 2017 / 2018 a related but new virus strain (H5N6 HPAI) started to circulate in wild birds and caused widespread wild bird cases in Northern Europe, but only very few cases in poultry or captive birds. As a result, the European Commission asked all Member States to consider the definition of higher risk areas for their territories in which certain additional biosecurity and surveillance measures could be taken, if deemed appropriate (Commission Decision (EU) 2018/1136)

In view of concerns from the extraordinary situation in Europe in 2016/2017 the European Commission agreed an Implementing Decision[1] for risk mitigation and reinforced biosecurity measures, based on a scientific opinion from the European Food Safety Authority (EFSA)[2]. This decision required Member States to identify higher risk areas and put in place additional biosecurity measures within them. The new Decision amends the original legal text and this document addresses that requirement.

The European Implementing Decision recommends identifying: 1) areas with a history of previous outbreaks or positive surveillance results; 2) areas with detections in wild birds; 3) areas with a high density of poultry farms; and 4) areas with large wild water bird assemblages (ie mixed species) or aggregation (ie same species). To define those areas within GB at increased risk we have used these identifying factors above to develop the evidence base. These factors were originally included in the 2005/734/EC Directive for early warning systems for avian influenza (EC, 2005) and have been repeated in the new Implementing Decision.

The evidence for housing providing a preventive effect against infection with avian influenza in poultry is not extensive and is not unequivocal. Indeed it is difficult to define without case control studies. In 2014, in the USA there was a large epizootic of H5N2 HPAI in poultry which culminated in the culling or death of 7.5 million turkeys and 42.1

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[1] European Implementing Decision on risk mitigating and reinforced biosecurity measures and early detection systems in relation to the risks posed by wild birds for the transmission of highly pathogenic avian influenza viruses to poultry (EC/1044/2017).

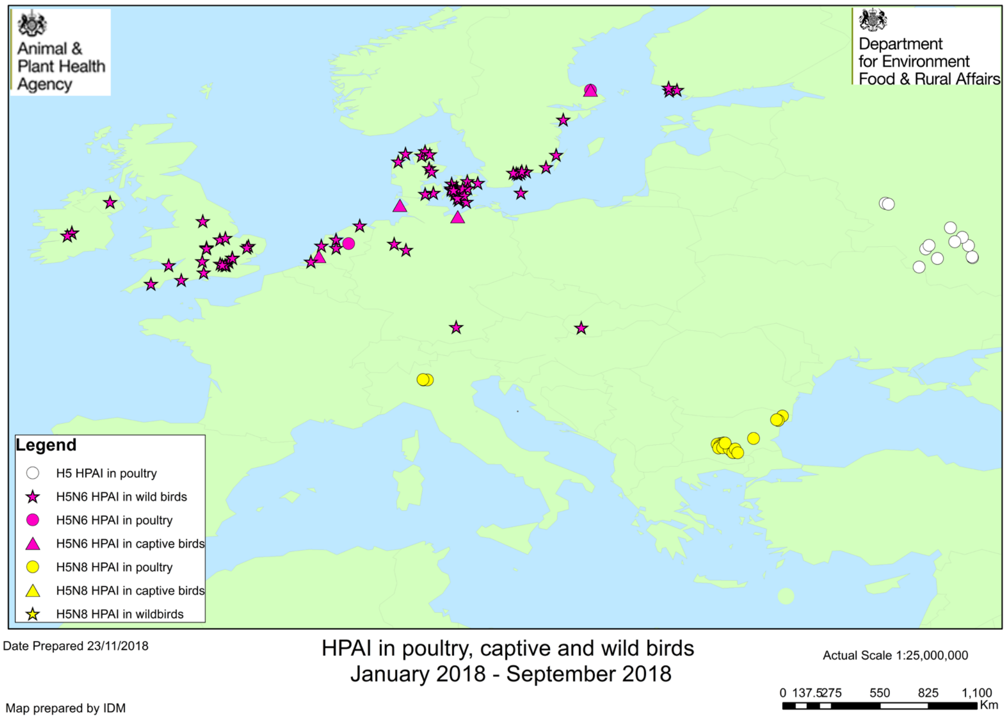
[2] EFSA(2016) Urgent request on avian influenza. https://www.efsa.europa.eu/sites/default/files/4687.pdf

million chickens, however broilers (which were housed) were rarely infected despite the proximity to other outbreaks. Epidemiological analyses of the EU epizootic in 2016/2017 however did not show any statistical relationship between infected commercial premises with or without outdoor access, as 53% had no outdoor access and 47% reported access for part of the day, although there is a tendency for smaller commercial holdings to be outdoors, unlike the larger (>10.000 birds) holdings. However of the non-commercial holdings, only 10% of the affected holding kept birds indoors all day (EFSA, 2017). Experimental evidence suggested this low incidence in broilers was not a feature of the genetic background of the different breeds of chicken used, but was a feature of the housing and husbandry, where broilers, kept for only a few weeks, have a faster turnover, with fewer contacts with workers, equipment and supplies, and better biosecurity practices (Bertran et al. 2016). In the Netherlands, in 2003, during a large epizootic of H7N7 HPAI, leading to 255 outbreaks, no single control measure could be identified which caused the epidemic to stop, except for reducing the number of susceptible stock in the area and speed of culling infected flocks. Other measures, such as compartmentalisation, tracing and improving biosecurity only served to slow down the spread to new regions (Stegeman et al. 2004).

The prevalence of HPAIV in wild birds is the parameter of fundamental importance to our estimated risk level, however it is variable and can only be inferred from incomplete surveillance data. If the prevalence is reduced, because there is no longer circulating virus and therefore there are fewer infectious birds, then the risk level to poultry within the UK would be expected to also be reduced. Higher temperature and longer daylight hours will reduce viral persistence and therefore environmental contamination which will in turn reduce the virus circulation in the wild birds, but if infected wild birds are present at the site all year round the contamination can remain. Bird migration patterns vary by season and towards spring and summer, different migratory species will arrive in the UK for breeding. These species include more passerine species which are not typically associated with transmission of HPAIV.

Similarly, the risk level to GB poultry will go up as the prevalence and rate of reporting of HPAI cases increases in Europe with new cases being detected in GB. The risk will be affected by changes in the weather particularly in the Baltic and Eastern Europe which influences wild water bird movement. Hence the extent of the higher risk areas will change with a number of factors external to GB. We will therefore need to keep the risk assessment under constant review. The results of the assessment will be made available to the public on an interactive map at http://www.gisdiseasemap.defra.gov.uk/intmaps/avian/map.jsp

**Map1: Outbreaks of H5N2[3], H5N6 and H5N8 HPAI in poultry and captive birds and cases in wild birds in 2018 in Europe**



# Risk pathways to poultry

There are multiple pathways by which a commercial or backyard poultry flock (including game birds and “pet” chickens and ducks) may become infected and all of these have been observed in recent outbreaks across Europe. These include:

- movement of infected live poultry
- exposure to contaminated poultry by-products
- exposure to contaminated people or objects (fomites)
- direct or indirect exposure to infected wild birds (most significantly their secretions and excretions)

This paper only considers the latter pathway in detail since it is the one most influenced by a requirement to house poultry or otherwise keep them separate from wild birds. The pathways for indirect and direct exposure are set out in Figure 1. Table 1 sets out the evidence and likelihood of different aspects of the risk pathway for indirect and direct exposure to infected wild birds.

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[3] Only in Russia

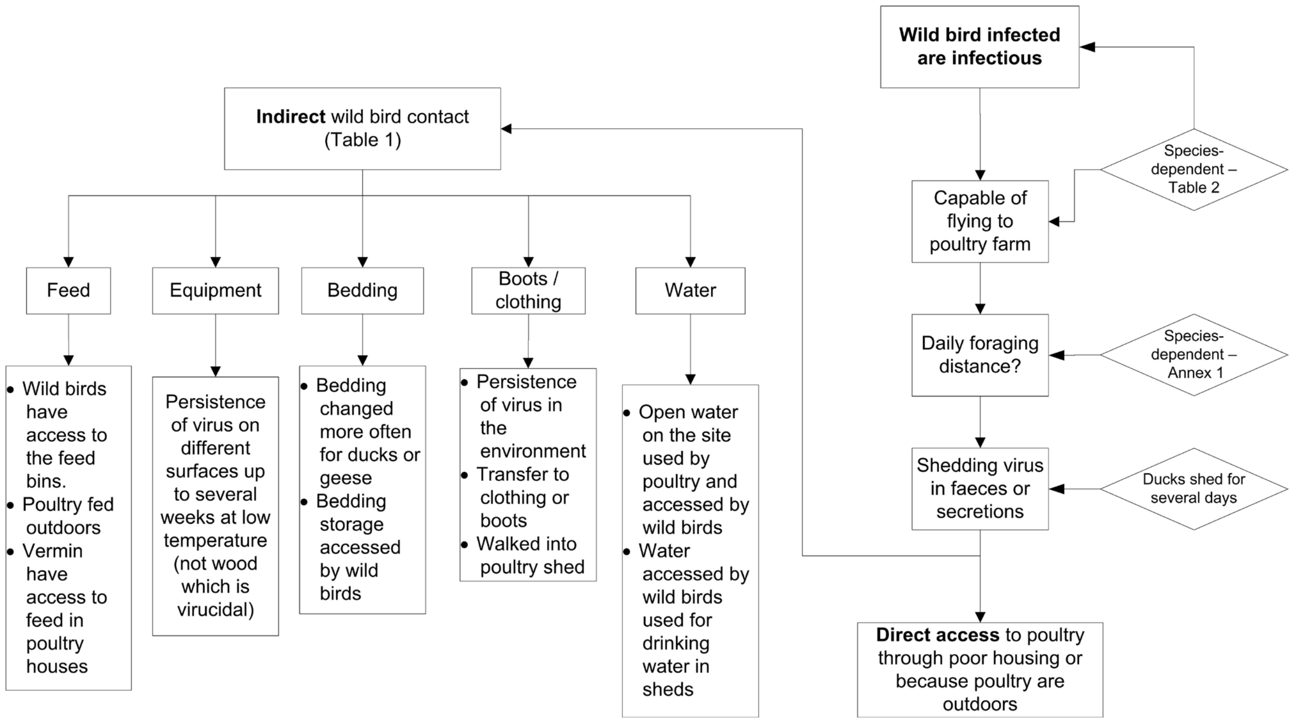

**Figure 1: Direct and indirect pathways for exposure of poultry to HPAIV in wild birds**

## Table 1 – Evidence and uncertainty for indirect pathways

| Indirect wild bird contact | Evidence | Uncertainty / assumptions | Risk factors or risk mitigations |
|---|---|---|---|
| Feed | Direct contamination of feed from contact with wild birds through opportunistic feeding in feed bins or troughs. Indirect contamination through vermin in contact with infected material and having access to feed or to the poultry houses themselves [Tejeda et al. (2015)].<br>USDA (2014) Risk of contaminated feed. | Assumed survival of virus in feed is several weeks at low temperatures. Grain which is used for feed and harvested locally may be higher risk from local contamination and for not going through processing. Commercial feed containing preservatives (formaldehyde for example, is used in the USA) is lower risk. No dilution effect in feed as it is all eaten by poultry | Feed stored in vermin proof bins – very difficult to have complete vermin-free poultry farms. Wild birds can be prevented from access. Indirect contamination of feed at site with wild bird faeces (e.g. through workers' hands and equipment) depends on the cleanliness of the site and workers. Direct contact depends on the physical barriers between wild birds and feeding sites |

| | | | |
|---|---|---|---|
| Bedding | Certain species of poultry, the Anseriformes, require bedding to be changed more frequently due to the problems with wet faeces. In the 16/17 H5N8 epizootic, 65% of outbreaks (where the species is known), were in Anseriformes. | Of outbreaks in France, Hungary and Bulgaria (in Anseriforms) many were secondary outbreaks due to poor biosecurity during transport (pers comm.) and through trade. | The use of other bedding material could be investigated but should not be used if it increases the risk of other infections, such as *Aspergillus*. |
| Water | Known to be the cause of an outbreak in commercial poultry in Spain. Using non-sanitised water from local reservoirs or ponds for drinking water is a potential risk for HPAIV transmission to poultry | | Poultry require regular access to water and should be sourced from treated mains water. |
| Equipment | Persistence of H5 viruses on wood is very short. On metal and plastic at low temperatures and in the dark is weeks | USA outbreaks in 2014 – investigations found fomite transmission was important in many outbreaks. While HPAI decay on surfaces is rapid, in the poultry house it will be protected by the organic matrix of the faecal pellet or secretion. Furthermore C&D may not be 100% efficient in terms of operational efficiency (due to by-pass) and also cross-contamination.<br>Wood resin is understood have some virucidal properties. | C & D |

| | | | |
|---|---|---|---|
| Clothing and footwear | Persistence in faeces of H5 HPAI viruses is several weeks at low temperatures and poor sunlight. At 20 ºC, for duck faeces, could be several days. | Contamination of clothing and boots depends on the level of faecal contamination | Washing in detergent for clothing and cleaning boots with approved disinfectant – including removing all the faeces, |

## Wild bird species:

The OIE/FAO International Reference Laboratory (IRL) at Weybridge collates HPAI infection data from wild bird findings across Europe. It is not a comprehensive overview as not all countries will report to the same degree of confidence or sensitivity, but passive surveillance of dead wild birds still has utility across the EU. Testing of dead wild birds in areas where disease is already present is not always done; some areas may not be part of surveillance programmes; predation of dead birds may mean samples are not tested. Nevertheless, the range and number of wild birds found dead in the H5N8 HPAI epizootic of 2016/2017 was greater than seen in recent years. The H5N6 HPAI epizootic in 2017/2018 saw many wild raptors and swans reported, but this could have been an ascertainment bias – these are large birds readily reported by the public.

According to the EURL and EU Animal Disease Notification System (ADNS), duck species were the most frequently reported wild birds infected with H5N8 HPAI, with Tufted ducks (*Aythya fuligula*) and Eurasian wigeon (*Anas penelope*) being two such species. An increasing feature became detection of infection in several species of Charadriiformes, such as Herring gulls (*Larus argentatus*), Black-headed gulls (*Chroicocephalus ridibundus*) and Great black-backed gulls (*Larus marinus*) have also tested positive. These species were not generally considered target species for wild bird surveillance but it would appear the host range for H5N8/H5N6 HPAIV has changed. Their exact role in the transmission of avian influenza is not known but they may act as bridging species between wild waterbirds and poultry because their behaviour favours roosting on large water bodies that may also be frequented by waterfowl and feeding on agricultural land, domestic waste tips or scavenging feed from poultry farms.

It should also be noted however, that current surveillance systems are not perfect – in GB our system is based on warden and wildlife officer patrols in wetland areas or nature reserves, to identify and collect dead wild waterbirds. There is little surveillance being undertaken across Europe at present systematically to determine which species are acting as reservoir species, where there is little mortality or morbidity, but still virus shedding. Nevertheless, it is important to recognise that targeted surveillance in areas of known high wild bird density will be more efficient than a non-targeted survey.

Many findings have been made in swans, but these birds are very site-loyal once they have arrived in an area, so it is difficult to extrapolate the importance of this observation as they may well be acting as local sentinel populations rather than key reservoir species. Faecal shedding of virus from mallards or pekin ducks (*Anas platyrhynchos var domestica*; a species for which most evidence is available) can occur over a period of 14 days post infection. The highest viral titres in faeces are generally seen at 4 days post infection. After an inoculation of $10^6$ 50% Egg Infectious Dose ($EID_{50}$) with a H5 HPAI virus (Clade 2.3.2.1b which is relevant for H5N8 and H5N6), virus titres in ducks faeces were in the range of $10^2$ to $10^8$ log $EID_{50}$ per gram of faeces (Data from Defra-funded APHA project). A duck is estimated to produce 7.5 to 10kg of faeces per annum (geese produce around 12.5 to 15 kg faeces per annum). Although the infectivity to different wild bird species (in terms of number of $EID_{50}$ per oral $ID_{50}$) may vary viral contamination of the environment where wild birds are exposed could be important, particularly if there is feed or open water making the area more attractive resulting in congregation of large numbers of wild birds.

## Table 2: Wild bird families and their involvement in the 2016/2017 H5N8 HPAI epizootic

| **Direct wild bird contact** | **Evidence (percentage of wild bird cases by species)** | **Uncertainty / assumptions** |
|---|---|---|
| Anseriformes | 42% in duck species; 6% in geese species; 19% in swan species (increasing in the recent weeks) | Almost all of the birds reported in the surveillance have been found dead or moribund, therefore this does not represent the actual infection rate. Some duck species have tested positive for H5N8 HPAI, yet were clinically normal. (Netherlands and Germany surveillance of shot wild wigeon and teal). Will not defecate while flying and therefore the faecal or other secretion contamination will be areas where they roost or forage. |
| Charadriiformes | 19% in gull species | Most of the species which have been found infected in this epizootic are on the target species list of the European Commission Decision 2010/367/EEC and the new list published by EFSA, 2017. Several gull species exhibit behaviour which would make them efficient bridging species between waterfowl and poultry farms. Will defaecate as they fly, so areas below their flight lines as well as roosts and forages sites are potential areas of contamination. |
| Other waterfowl | 6% including coots, moorhens, herons, grebes | Other species are known to be susceptible to avian influenza viruses but generally do not shed the same level of virus into the environment as the Anseriformes. Most of these birds are solitary and exhibit different behaviour |
| Passerines | <1% | A handful of passerines have tested positive – most likely as a spill-over host rather than a reservoir species |
| Corvids | 2% | Rooks, magpies and hooded crows have tested positive. Corvids feed primarily on worms, leatherjackets and other invertebrates, as well as seeds, fruits and other vegetable matter. They will scavenge, but this is a small part of their diet (especially Rooks). They will often visit poultry units both to feed on waste poultry food and to search for invertebrates in bare ground or grassland on free range poultry sites. |
| Columbiformes | <1% | Very small number has tested positive and as with |

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|---|---|---|
| | | the passerines, these are considered spill-over hosts rather than reservoirs. Feral pigeons in particular will frequent poultry houses to feed on spoiled food and will enter buildings if the biosecurity is poor. |
| Birds of prey | 5% including white tailed eagles, buzzards and peregrine falcons | These birds will either feed on carrion or will predate young/adult birds including wild waterfowl. High susceptible species but contribution to onward spread unclear but presumed limited for poultry |

As many waterbird species are gregarious and mobile, particularly towards the end of the wintering season, when food sources are scarce, they will often undertake daily flights from roosting to feeding areas as a flock rather than individuals. A literature review was carried out to ascertain the most likely maximum foraging distance for duck species (Annex) and this was supported by the expert opinion of ornithologists[4]. A distance of 2km was considered a sufficient buffer distance applied to the combined areas, to cover the majority of feeding flights and hence the majority of the risk to poultry premises.

## Risk factors for identifying areas at heightened risk

The following factors comply with the Commission Decision (EU) 2018/1136 on how to define the Higher Risk Areas for avian influenza.

1. **Areas with a history of previous outbreaks or positive surveillance results**: the UK has had relatively few outbreaks in the past few years to draw from, one of H5N8 HPAI (in Yorkshire, 2014/2015 season) 13 of H5N8 HPAI in 2016/2017 season (of which 3 were linked) and none in 2017/2018 season.

2. **Areas with detections in wild birds:** there have been multiple findings in wild birds infected with H5N8 HPAI and then H5N6 HPAI in GB during the last two seasons. However, it is acknowledged that these findings are heavily biased by our surveillance programme which is focussed on dead wild waterbirds, birds of prey or gulls, and therefore centres around wetland areas and national parks where wardens from NGOs or other agencies or authorities are patrolling and picking up dead wild birds. The above bird species tend to be quite large in size and live in open habitats, such that dead carcases may be more obvious than for example smaller birds or more secretive, skulking birds in denser habitats (although this may not apply to most waterbird species). In one area, (Abbotsbury, Dorset) a large wild bird die-off of mute swans was observed over a period of several weeks and with H5N6 HPAI there were just two large collections of mixed wild waterbirds including gulls in England.

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[4] The Ornithologists Expert Panel (OEP) is an APHA-chaired expert group consisting of members of the BTO, WWT, RSPB, JNCC, SNH, BASC, NE, CNC (NRW) and APHA.

3. **Areas of high density poultry:** Large parts of England have relatively high densities of poultry farms (see map 1a) and many of these farms are not free range or large commercial holdings. There are no specific areas where the distribution of a free range or non-commercial poultry holding is higher than a housed population. When current outbreaks and wild bird findings (map 1b) are compared on a map with poultry density, it is clear that poultry density is not the single driving factor.

4. **Areas with a high aggregations or known assemblages of wild waterbirds**: the data have been gathered from two sources: the Important Bird Areas (IBAs) which are predominantly coastal and wetland sites and the sites where there are high annual bird counts of wild waterbirds, carried out by the British Trust for Ornithology (BTO) as part of their wild wetland bird survey (WeBS). In addition, a map of inland gull roosts was provided by BTO.

A set of input data on wild-bird populations across the UK has been used to determine areas of high usage or over-flight by wintering waterbird species. The data used in this review are the BTO Wetland Bird Survey (WeBS) data, with the 5 year mean (up to 2015) taken for each site. For full details on the WeBS scheme, see Frost et al. (2017) [1]. Additional data from the historical winter gull survey (Banks et al. (2007) [2]) have been used for gull species, as these are not well covered by the WeBS dataset. The underlying unit for the HRA is a WeBS site (normally composed of several ‘sectors’ that are routinely surveyed for wetland birds during the winter months). It is assumed that the WeBS scheme provides sufficient national coverage of the most heavily used sites, and that, although gaps in coverage do exist, the sites with the highest populations and concentrations of wildfowl are consistently covered.

The sites with the largest bird populations are selected from the WeBS dataset, according to the criterion:

- all sites with 5000 or more birds (equivalent to the top 3.6% of sites (bird numbers))

All areas that match the above criterion have been mapped at the site level, with a 2km buffer applied to the site to account for typical foraging ranges for wild waterbird species. The 2km figure was agreed as a suitable foraging range for duck species during the 2016/17 outbreak, following an extensive literature search and consultation with the Ornithological Expert Panel (see Guillemain, Mondain-Monval [3], Legagneux, Blaize [4]).

Any additional WeBS sites that fall within the 2km buffer were incorporated into the site, and re-buffered by a further 2km. This process was repeated until no further sites were captured. The rationale behind this iterative buffer process was that any sites within a foraging flight distance from a major site are likely to host some inter-site mixing of birds, and may act as satellites areas for the larger population. Once the buffering process can find no further outliers within the forage distance, a site can be considered isolated.

Once the isolated waterbird clusters were drawn up, additional areas for gulls were added to this. Gull roost information has been provided for all gull roosts that host a minimum of 5000 birds (taken from those sites where gulls have been covered by the WeBS scheme, in addition to roosts covered by the BTO Winter Gull Roost Survey (WinGS) (2003-2006)[5]). Each of the gull roosts has been buffered by a distance of 2km to account for the highest density areas of overflight and foraging, and these buffers have been merged with the isolated areas generated as described above.

The process above creates a relatively complex set of shapes, and steps have been taken to attempt to reduce the complexity of the HRA. Any internal gaps that exist within each area have been filled to create closed regions. These regions have then been processed to close gaps or ‘kinks’ less than 500m wide, with any resulting gaps eliminated in order to ensure that each zone remains enclosed.

In addition to the simple area mapping which will form the basis of the published Higher Risk Areas, the boundaries have been intersected with the 10km grid for GB, with each square that contains a section of a HRA unit included in the refined output. In order to provide a degree of smoothing to this gridded approach, grid squares that are less than 2.5% ‘high risk’ have been flagged for exclusion (i.e. grid squares containing areas less than 500m² of risk area).The grid square map will be used by APHA to target wild bird surveillance.

In the case of Scotland, the above analysis has been carried out, but the species included in the analysis have been restricted in order to remove those that are considered to be lower risk in terms of their behaviours and likelihood to transmit AI.

A desk based study carried out by APHA summarised in Table 3 has highlighted those species that are likely to be relatively low risk in Scotland. The assessment is based on two factors:

1) the geographical origin of the birds prior to their autumn migration. Thus species/populations moving into Scotland from populations summering in Greenland and/or Iceland, are unlikely to have come into contact with AIV or AIV-infected birds. This compares to population wintering further south in England that migrate from continental Europe/Eurasia); and

2) the general feeding behaviour/habitat preference of the species. Thus some species, for example Common eider (*Somateria mollissima*) - spend all of their time out at sea where they feed exclusively on molluscs and although abundant around Scottish coasts are very unlikely to contact poultry let alone transmit AI viruses to them.

On this basis, each of the selected species was categorised qualitatively according to its relative risk in the Scottish context. A summary of the species and their risk categories for Scotland is given in Table 3.

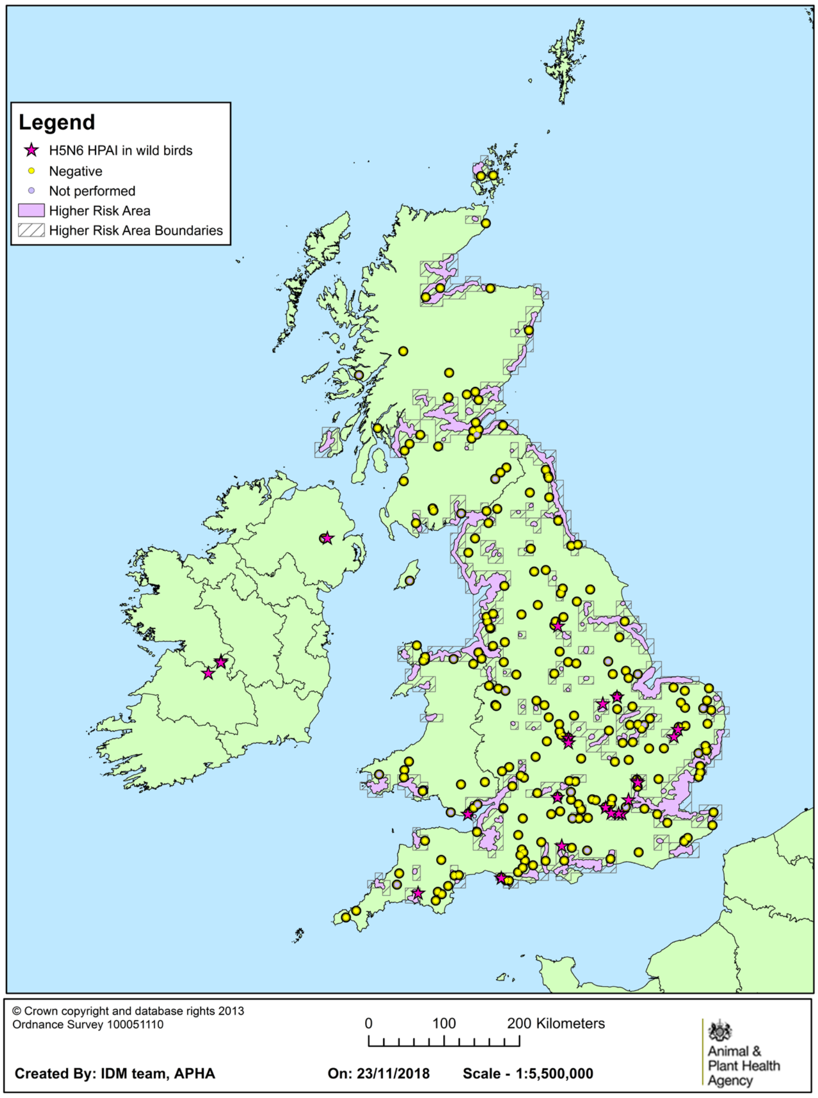
### Table 3: Relative risk assigned to species for highly pathogenic avian influenza (HPAI) in Scotland.

| Species | HPAI priority for Scotland |
|---|---|
| Bean Goose | Very low |
| Bewick’s Swan | Very low |
| Dark-bellied brent Goose (bernicla) | Very low |
| Eurasian white-fronted goose (albifrons) | Very low |
| Goldeneye | Very low |
| Graylag Goose | Very low |
| Greenland white-fronted goose (flavirostris) | Very low |
| Lesser white-fronted goose | Very low |
| Light-bellied brent goose (hrota) | Very low |
| Mute swan | Very low |
| Pink-footed goose | Very low |
| Red-breasted goose | Very low |
| Whooper swan | Very low |
| Barnacle goose | Low |
| Common eider | Low |
| Greater scaup | Low |
| Pochard | Medium |
| Tufted Duck | Medium |
| Common Teal | Medium |
| Eurasian Wigeon | Medium |
| Mallard | Medium |

The scavenging behaviour of gulls, like the herring gull and the black-headed gull and their daily commute between roost sites near waterfowl and feeding sites on farm land make them potential bridging species. Free range poultry units, where gulls may forage amongst the poultry, will be at particular risk and because gulls will defecate in flight, farms under a flight line or which are attractive to gulls (because of ploughing nearby or where animal feed is in the open) could also be at increased risk. Because the gull roosts and flight lines could encompass all the country, it is not possible to identify specific areas of higher risk so the measures to mitigate it should apply across the whole country. For gull movements in general, these seem to be up to 40 km per day, but longer distances are also reported. If daily movements of all the birds tagged and tracked in research projects are taken together, 50% of daily movements are 2.3 km or less and 75% 7.5 km or less.

# Results

**Wild bird surveillance for Dec 2017 to November 2018 and positive findings of H5N6 HPAI in wild birds,**



## Map 2: Higher Risk Areas (HRAs) for England, Scotland and Wales

Map 2 is the result of the combined Important Bird Areas for overwintering migratory waterfowl, the annual abundance of wild waterfowl (by a finer scale of 2x2 km rather than the larger 10x10 km of the original BTO data and where more than 5,000 wild waterfowl are counted within this smaller area), with a buffer zone of 2km to account for the daily flight distances of relevant duck species. These are the regions considered to be at a higher risk of direct or indirect contact with waterbirds, particularly ducks, according to their behaviour. Because this relies on bird behaviour and other external factors such as weather, it is not always possible to predict the most likely areas where wild water birds will forage. Therefore the risk may change and the map and the need for control measures may also change.

Nevertheless, the final risk factor which the EU Implementing Decision recommends also includes where historical outbreaks or positive surveillance data are reported and therefore this can mean some areas may also be designated with this in mind.

This process will be kept under review as the situation is changing on regularly. The HRAs will be published on the Interactive Map on GOV.UK.

## Potential causes of increase in risk

An increase in risk is possible in the following circumstances if:

- there is a prolonged cold spell in Continental Europe, such that wild birds make short migrations from NW Europe to the UK
- there is increased incidence with more cases in wild birds in Continental Europe, then the increased incidence of infected wild birds may mean more infected birds entering the UK
- novel wild bird species become reservoirs, such as passerines or waders, which we have not considered previously in our risk mapping
- new clusters of cases occur in “lower risk” areas and where investigations conclude that there is a relatively high risk of exposure to infected wild birds in the locality

## Decrease in risk

There is a year round risk of any notifiable avian disease being introduced into poultry or captive birds from the contact with wild birds, but this is not a constant level. The highest risk period will usually be winter, and the risk may decrease according to the following circumstances:

- Case reporting rate in Europe decreases
- If a high proportion of cases being reported are due to lateral spread from an index premises
- Increased temperature and sunlight to reduce environmental contamination
- Wintering waterfowl returning from the UK to northern latitudes to breed in the spring.
- Dispersion of gulls from inland wintering sites to coastal areas to breed.

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# Annex 1: Literature review to ascertain the most likely maximum foraging distance for duck species

## Bird foraging distances

### Table 4. (Adapted from Table 2, Johnson et al. 2014 for UK and France) "Distances flown (flight distance) between roost site to feeding site for waterfowl. When significant differences between age cohorts or year were reported, we included them as independent foraging flight distance values in our review and subsequent analyses."

For all entries in the table, the survey period was the winter and the foraging area surveyed was wetland

| **Species (subspecies)** | **General location** | **Year/How Followed** | **Mean flight distance** | **Source** |
|---|---|---|---|---|
| Mallard | North (Seine) France | 2002-03/T | 0.7 | Legagneux et al., 2009 |
| | North (Seine) France | 2003-04/T | 1.1 | Legagneux *et al.* 2009 |
| | Central (Brenne) France | 2001-02/T | 0.5 | Legagneux *et al.* 2009 |
| | Central (Brenne) France | 2002-03/T | 1.2 | Legagneux *et al.* 2009 |
| | Central (Brenne) France | 2003-04/T | 1.3 | Legagneux *et al.* 2009 |
| Northern Pintail | West (Moeze) France | 2004 and 05/T | 1.3 | Legagneux *et al.* 2009 |
| Eurasian Wigeon | West (Saint-Denis-du-Payre) France | 2003-04/T | 2.8 | H. Fritz *personal communication* |
| | Camargue, France | 1926-04/R | 2.5, (2-3) | Guillemain et al., 2008 |

| | | | | |
|---|---|---|---|---|
| Gadwall | Camargue, France | 1926-04/R | 2.5, (2-3) | Guillemain *et al.* 2008 |
| Northern Shoveler | Camargue, France | 1926-04/R | 2.5, (2-3) | Guillemain *et al.* 2008 |
| Teal | North (Seine) France | 2002-03/T | 3.8 | Legagneux *et al.* 2009 |
| | North (Seine) France | 2003-04/T | 2.3 | Legagneux *et al.* 2009 |
| | Central (Brenne) France | 2002-03/T | 0.8 | Legagneux *et al.* 2009 |
| | Central (Brenne) France | 2003-04/T | 8.4 | Legagneux *et al.* 2009 |
| | West (Moeze) France | 2004-05/T | 1.0 | Legagneux *et al.* 2009 |
| | Camargue, France | 1926-04/R | 2.5, (2-3) | Guillemain *et al.* 2008 |

T = telemetry; R = marked with leg ring/band.

### Table 5. Overall mean foraging flight distances (km) and standard errors for goose and duck studies used in Johnson et al. (2014) that were located in the UK or France

| | **Average of mean foraging flight distance taken from relevant goose studies (km)** | **Average of mean foraging flight distance taken from relevant duck studies (km)** |
|---|---|---|
| Mean | 6.56 | 2.20 |
| Standard error of the mean | 0.85 | 0.47 |
| Number of studies (n=) | 13 | 16 |

## Virus persistence rates

In general, moisture and temperature are the two main determinants of viral persistence. At temperatures of 17 to 25 °C most AI viruses will not survive longer than a few days, even under moist conditions. In general, higher humidity and cooler temperatures permit virus survival in moist substrates over longer periods of time.

**Table 6. Viral persistence rates for AI virus in different media**

| Strain | Media | Persistence | Conditions* | Reference |
|---|---|---|---|---|
| H7N2 HPAI | Duck faeces | 7 days | 20 °C, high humidity when kept out of direct sunlight | Webster et al, 1978 |
| H5N1 HPAI | Duck feathers | 15 days | 20 °C, high humidity | Yamamoto et al., 2010 |
| H5N1 HPAI | Drinking water | no virus identified after 3 days | 20 °C | Yamamoto et al., 2010 |
| H7N2 LPAI | chicken manure | 6 days, 2 days | 15 to 20 °C, and at 28 to 30 °C | Lu et al., 2003 |
| H5N1 HPAI | Faeces | killed in 30 minutes | 32-35 °C, in sunshine | Songserm et al., 2006 |
| H5N1 HPAI | Chicken manure | no virus identified after 24 hours | 25 °C | Chumpolban chorn et al 2006 |
| H13N7 LPAI | Cotton | 24 hrs. | Dark at room temperature | Tiwari et al., 2006 |
| H13N7 LPAI | Latex | 6 days | Dark at room temperature | Tiwari et al., 2006 |
| H13N7 LPAI | Feathers | 6 days | Dark at room temperature | Tiwari et al., 2006 |
| H13N7 LPAI | Wood | 2 days | Dark at room temperature | Tiwari et al., 2006 |
| H13N7 LPAI | Truck tyre | 3 days | Dark at room temperature | Tiwari et al., 2006 |

## Limitations

This approach represents a best estimate of wild bird density across GB, and attempts to delineate areas of highest usage/density. There are some limitations in the available knowledge and data presented here that should be acknowledged.

Data availability and counts are restricted to areas covered by the WeBS scheme. Whilst this is likely to capture the most intensively used areas, some waterbird sites may be missed (for example, if a local WeBS counter cannot be found to cover a site), and more dispersed waterbird populations are not covered by the survey [6]. The WeBS coverage is geographically variable, as some areas have more limited resources in terms of available WeBS counters- these areas in general, have a lower poultry density, so although the wild bird populations are not well covered by the data, they are also likely to pose a lower risk in terms of AI infection.

Data on gull populations is not routinely captured as part of the WeBS scheme, and the WinGS dataset is now over 10 years out of date, so a more recent dataset would be of benefit in understanding the current over-winter structure of the GB gull population, particularly as there is evidence to suggest that gull populations are undergoing significant structural changes [7].

It should be noted that although the focus of this analysis is wintering populations, the UK does host significant breeding populations of some risk species (particularly gulls). However the breeding populations are more concentrated in coastal areas, and the foraging and ranging behaviours of the birds are less likely to result in high levels of AI infection.

The focus of this definition is on areas where we have comprehensive abundance data. Other areas of ornithological significance may play a role in the definition of risk but are not captured by systematic survey, and have therefore been excluded. One such example is landfill sites, which are well documented as foraging resources for gulls, but are not covered by this assessment [8, 9].

A further issue with incorporating data on gulls is that winter behaviours and foraging are not well studied, therefore approximating a suitable foraging risk threshold has proven difficult, and further research on this would be of benefit.

Not included in this analysis is additional ranging information for populations of wintering geese. Typical foraging radii for wintering geese have been shown to be in the order of 20km, with the birds having been observed to disperse widely to feed on lowland agricultural areas [10]. The radii used in this study will help to capture the areas that experience the most overflight by geese on their commute to and from foraging areas, but do omit some of the wider foraging areas, as these are likely to represent a transient resource, with the birds widely dispersed within the area.

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