



Animal &
Plant Health
Agency

Highly Pathogenic Avian Influenza H5N1 Outbreaks in Great Britain

October 2022 to September 2023



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Abbreviations

ABP:	Animal by-products.
AIPZ:	Avian Influenza Prevention Zone
APHA:	The Animal and Plant Health Agency.
BTO:	British Trust for Ornithology.
CBMCZ:	Captive Bird (Monitoring) Control Zone.
C&D:	Cleansing and disinfection.
DAERA:	Department of Agriculture, Environment and Rural Affairs (Northern Ireland).
Defra:	The Department for Environment Food and Rural Affairs.
FAO:	The Food and Agriculture Organisation.
GBPR:	Great Britain Poultry Register.
HAIRS:	UK Human Animal Infections and Risk Surveillance (HAIRS) group.
HPAIV:	High pathogenicity avian influenza virus.
IP:	Infected Premises.
NAD:	Notifiable Avian Disease.
NEEG:	National Emergency Epidemiology Group.
PPE:	Personal protective equipment.
PZ:	Protection Zone.
RPE:	Respiratory protective equipment.
SZ:	Surveillance Zone.
WOAH:	The World Organisation for Animal Health.
WWT:	Wildfowl and Wetlands Trust.

Definitions

Kept birds are all poultry and other captive birds.

Commercial premises are any premises with more than 1,000 birds that:

1. rears or keeps birds in captivity for the production of any commercial products, or
2. for breeding birds for the above purpose, includes birds used for restocking supplies of game, or for breeding for this purpose, until they are released from captivity.

Small commercial premises are any premises with 1,000 birds or less that:

1. rears or keeps birds in captivity for the production of any commercial products, or
2. for breeding birds for above purpose, includes birds used for restocking supplies of game, or for breeding for this purpose, until they are released from captivity.

Note that this definition includes household/backyard flocks that sell, barter or give away products.

Non-commercial and pet premises are non-commercial flocks:

1. producing only for own consumption (no selling, bartering or giving away of products), or
2. are pets/hobby birds (showing, racing, captive birds of prey), or
3. rearing and selling for these purposes.

Note that these non-commercial and pet premises usually had fewer than 50 birds, but there were a few such premises that had more than 50 birds.

Sanctuaries/rehabilitators: premises taking in animals on a regular basis, whether companion, farmed, wild, protected or other species, with a view to rehabilitating and either rehoming or releasing (back to the wild), or for the aim of providing long-term care.

Wildlife centre: wildlife centres and nature reserves.

Zoo: licenced zoological collections.

Stakeholder: In this context, external stakeholders are individuals or groups outside government, who can affect or be affected by the disease control policies implemented for HPAI. They include representatives of the main commercial poultry sectors, as well as hobbyists, the Poultry Club (pedigree birds and the show sector), birds of prey, racing pigeons and waterfowl groups.

Species

The species on site is listed, however if more than one species is kept on the premises, they are summarised as follows:

Mixed domestic: chickens, turkeys, ducks or geese.

Mixed gamebird: pheasants, partridges, quails or ducks (if kept as gamebirds).

Mixed captive wild species

Mixed aviary birds: canaries, budgerigars, parrots, parakeets, etc.

Mixed other: premises keeping a mixture of domestic, gamebirds, aviary birds or captive wild species.

Indicator species and non-indicator species:

1. indicator species are species known to usually exhibit clinical signs or mortality with the virus strain in question. In this outbreak indicator species were chickens, turkeys, pheasants, partridges, and quail.

2. non-indicator species are those which appear to be more resistant and do not usually exhibit readily apparent clinical signs or mortality with the virus strain in question. In this outbreak non-indicator species were ducks and geese.

Poultry: all birds reared or kept in captivity for the production of any commercial animal products. or for breeding for this purpose, fighting cocks used for any purpose, and all birds used for restocking supplies of game or for breeding for this purpose, until they are released from captivity.

Birds that are kept in a single household, the products of which are used within the same household exclusively, are not considered poultry, provided that they have no direct or indirect contact with poultry or poultry facilities.

Birds that are kept in captivity for other reasons, including those that are kept for shows, racing, exhibitions, zoological collections and competitions, and for breeding or selling for these purposes, as well as pet birds, are not considered poultry, provided that they have no direct or indirect contact with poultry or poultry facilities.

Kept birds: all poultry and other captive birds.

Seabird: Generally cliff or island nesting colonial species; Auks, Suliforms, Procellariiforms, most gulls and terns where most of the populations mix or spend most of their year on the coast or at sea.

Executive summary

Great Britain experienced its largest outbreak of HPAI H5N1 during the two year period starting in October 2021, and unusually persisting over the summers of 2022 and 2023. For ease of reporting, the outbreak has been split into administrative seasons from 01 October to 30 September each year.

This report summarises the epidemiological investigations carried out in order to describe and explain the continuation of the outbreak in Great Britain of highly pathogenic avian influenza (HPAI) disease that occurred between 01 October 2022 and 30 September 2023 (the “2022 to 2023 season”).

The report on the 2021-2022 season is available here: [October 2021 to September 2022: Highly Pathogenic Avian Influenza H5N1 outbreaks in Great Britain](#)

It is important to note that the HPAI event, as reported to the World Organisation of Animal Health (WOAH), was a United Kingdom event, and a separate epidemiological report describing any cases of avian influenza in Northern Ireland is produced by the Department of Agriculture, Environment and Rural Affairs (DAERA www.daera-ni.gov.uk).

During the 2022 to 2023 administrative season, a total of 206 high pathogenicity avian influenza virus infected premises were confirmed across England (160), Scotland (38) and Wales (8) (see Figure 1 and Figure 2).

154 of these were in commercial flocks, of which 133 held over 1000 birds. 46 were in non-commercial flocks, with one zoo, two wildlife conservation centres and three animal rescue sanctuaries/rehabilitation centres also infected.

Figure 1: HPAI H5N1 infected premises 2022 - 2023 season.

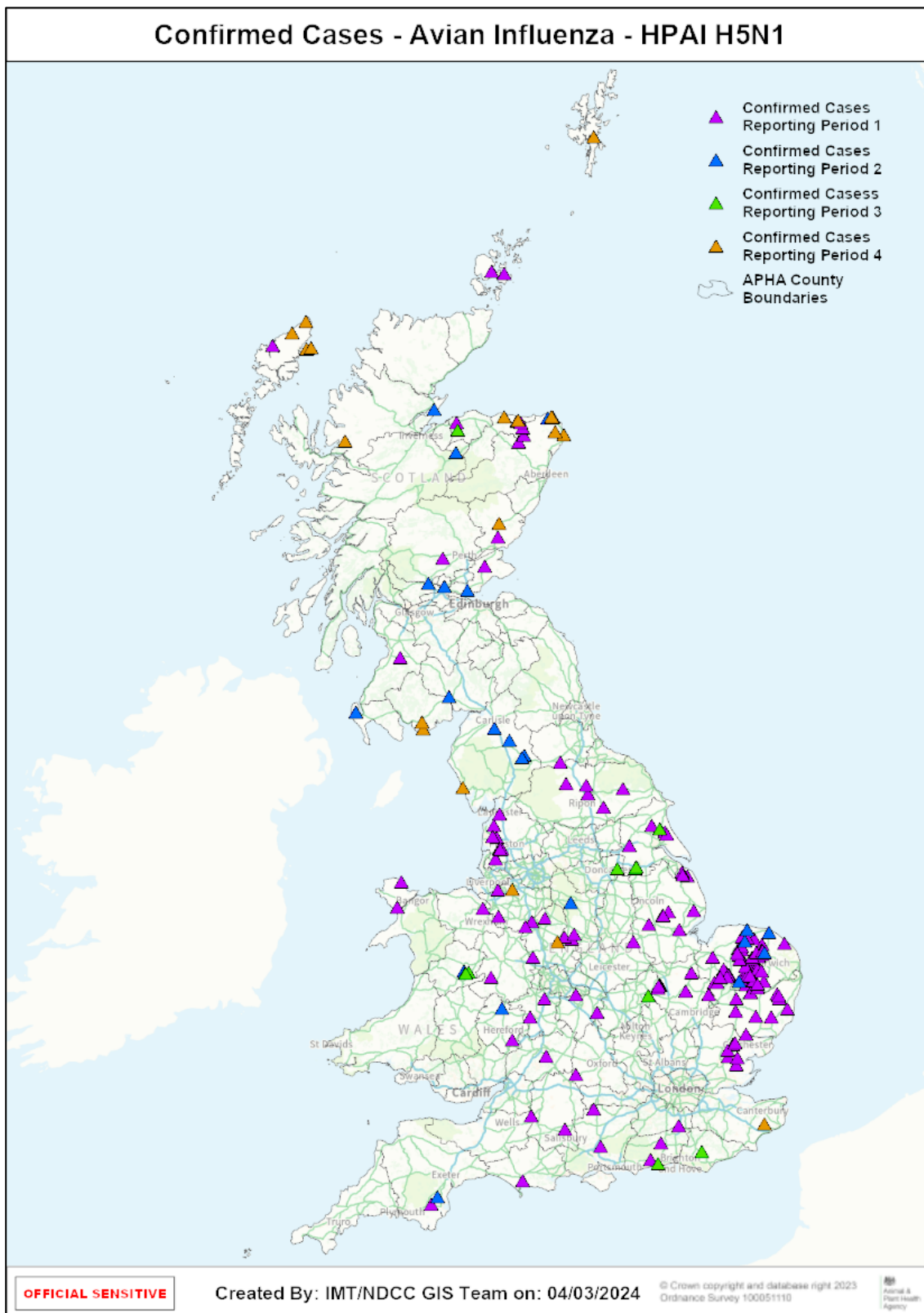
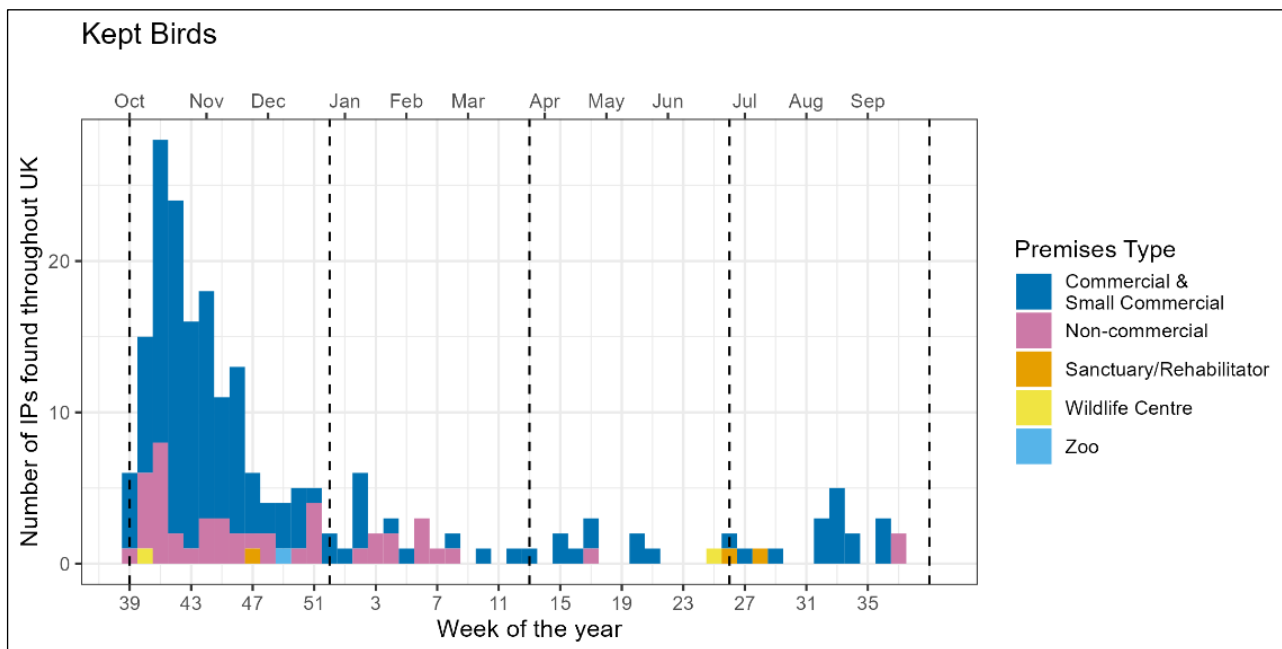
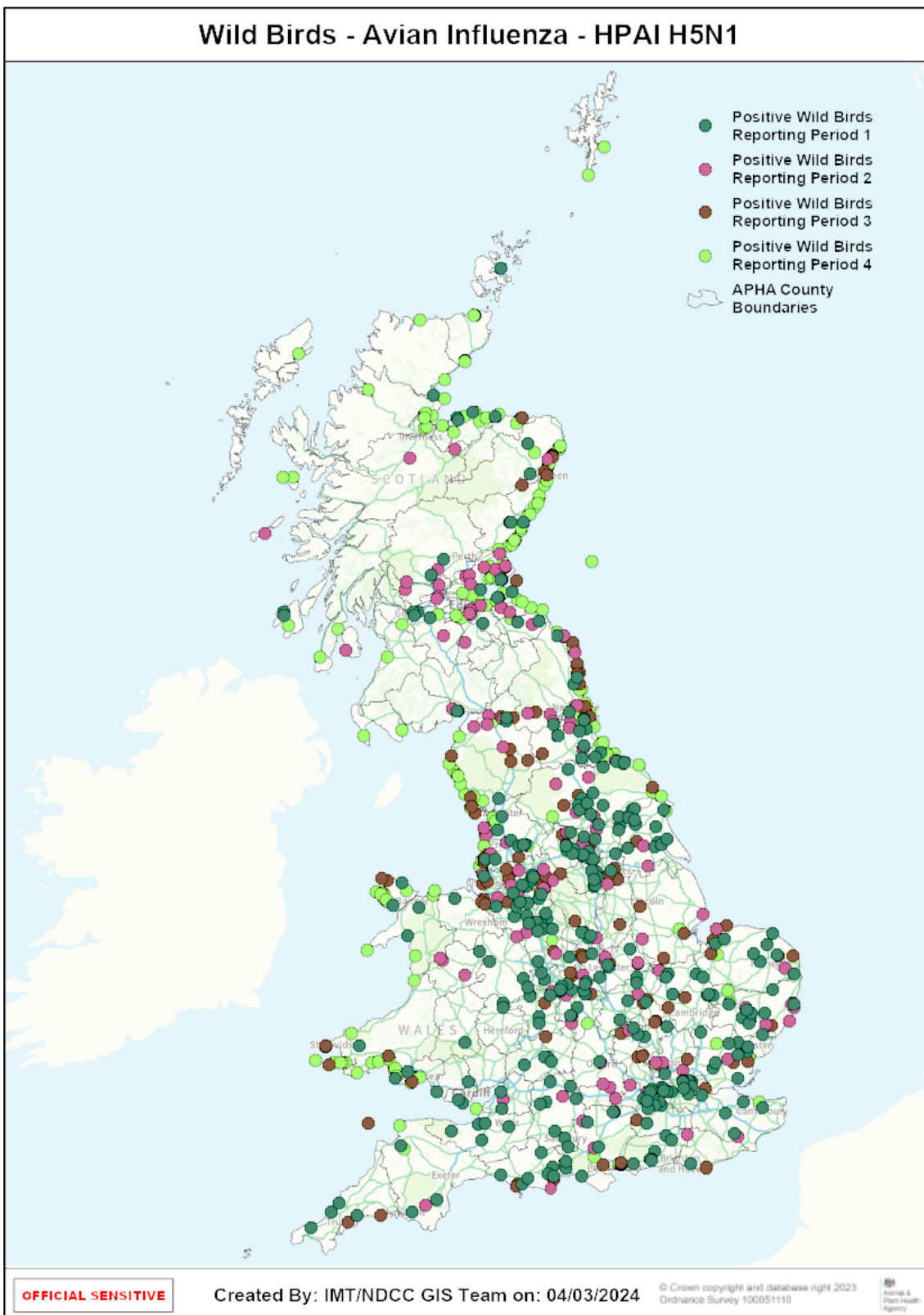


Figure 2: HPAI H5N1 Epidemic curve by date of confirmation by premises type



Through wild bird surveillance (Appendix 2) a total of 1,592 high pathogenicity avian influenza virus positive wild birds were identified across England (1,120), Scotland (346) and Wales (126) (see Figure 3). Although virus was detected in birds from a total of 14 different orders, the most common were waders, gulls, and auks (Charadriiformes 45%) wildfowl (Anseriformes 37%) and certain diurnal birds of prey (Accipitriformes 8%)

Figure 3: Cases of H5N1 avian influenza in wild birds 2022 - 2023 season



Due to the extent and intensity of infection seen in wild bird species, a high level of environmental contamination and infected wild bird carcasses, led to the potential for infection with HPAIV in free-living wild mammals. Further, through triage of mammalian samples held in frozen storage by conservation groups, samples that had been collected from the wild prior to 01 October 2022 were occasionally received for diagnostic evaluation.

In total, during this period, from 267 mammalian samples submitted for testing, 21 samples tested positive for H5Nx HPAIV (20xH5N1 and 1xH5Nx) and a single sample was positive for a non-H5, non-H7 influenza virus. Sequencing was attempted on all mammalian samples and sequence data was successfully generated for nine samples. From this sequence data, no genetic markers associated with significant adaptation to mammalian infection were detected. (See Appendix 3).

In addition to HPAIV detections in kept birds, a single low pathogenicity avian influenza virus (LPAIV) was detected in Scotland on 20 March 2023 (AIV 2023/21) and was characterised as an H7N3 subtype.

Some apparent clustering of infected premises was identified through the use of genomic, quantitative data, spatial and network analysis methods and also through routine outbreak and tracings investigations that flagged potential epidemiological links between cases. These apparent clusters and any infected premises that may have shared common factors or risk pathways with the same event, were considered in more detail as described in Appendix 1.

The main finding, in line with other countries, was that HPAI H5N1 continued to be an epizootic in wild birds with spill over to kept birds. In only two cases (1.0%) was the most likely source of infection identified to be from direct domestic contact, with high likelihood.

In two other cases (1.0%), the most likely source was identified as equally likely to be from direct or indirect wild bird contact or contaminated products or indirect domestic contact: (see analysis on page 42).

Several risk factors for the introduction of infection were identified during epidemiological investigations and this led to detailed biosecurity advice and guidance being provided to all keepers. See Appendix 4.

Background

Since 2020, the United Kingdom (UK) and Europe have experienced annual epizootics of high pathogenicity (HPAIV). The first during autumn/winter 2020 to 2021 involved the detection of 6 H5Nx subtypes, although H5N8 HPAIV dominated in the UK. Whilst genetic assessment of the H5N8 HPAIVs within the UK demonstrated relative homogeneity, there was a [background of other subtypes circulating](#) at a lower degree with different neuraminidase and internal genes.

Following a small number of summer detections of H5N1V in wild birds over the summer of 2021 ([Detection of Highly Pathogenic Avian Influenza Virus H5N1 Clade 2.3.4.4b in Great Skuas: A Species of Conservation Concern in Great Britain - PMC \(nih.gov\)](#)), the autumn/winter 2021 to 2022 saw another European H5 HPAIV epizootic that dwarfed the previous epizootic.

Disease circulation in wild birds continued through the summer of 2022 with substantial mortality in multiple seabird species ([Falchieri et al., 2023](#)). As the H5N1V then started to significantly affect kept birds again during October 2022, genetic assessment demonstrated that further genetic reassortment had occurred with 7 distinct genotypes being defined during the 2022-2023 season, each containing a high level of sequence identity in the haemagglutinin (HA) and neuraminidase (NA) glycoproteins, but with altered constellations of internal genes.

This summer circulation in wild birds continued to put infection pressure on kept birds as demonstrated by the fact that 15 of the IPs confirmed from 01 October 2022 had, following epidemiological investigations (see Appendix 1) been estimated to have become infected during the last week of September and before the first definitive migratory wildfowl were found to be positive in the 2022-2023 reporting season (a barnacle goose in Gloucestershire on 04 October and a pink footed goose in Lancashire on 05 October). For more information see wild bird surveillance system in Appendix 2

The genomic assessment of H5 HPAIVs (see Appendix 3) detected in the UK over the last two winter seasons (from 2021) has demonstrated the utility of in-depth genomic analyses of viral isolates in defining:

- The diversity of H5 HPAIVs circulating in avian species.
- The potential for zoonotic risk.
- Whether incidents of lateral spread between IPs (through for example, shared contaminated staff or equipment) could be defined in addition to independent incursion of infection from wild birds.

Further, the emergence of infection in free-living wild mammals, most likely through scavenging activities, has led to an increased interest in HPAIV H5N1 as a potential zoonotic agent.

As detailed in [previous epidemiological reports](#), the ancestral virus for the UK H5Nx viruses that emerged in 2020 is likely to be similar to that responsible for spread across the Middle East and Central Asia ([Investigating the Genetic Diversity of H5 Avian Influenza Viruses in the United Kingdom from 2020–2022 \(nih.gov\)](#)).

Avian influenza disease control legislation

Great Britain Poultry Register

Premises where 50 or more poultry (including game birds and poultry kept as pets) are kept, must legally be registered on the GB Poultry Register (GBPR). The aim of the GBPR is to provide information regarding the location and density of poultry populations in GB. In a disease outbreak, it provides essential information which assists government in the delivery of avian disease control measures.

Upon confirmation of disease, the register allows the initial location of premises containing poultry within the infected area to be identified.

Owners/occupiers of premises with less than 50 poultry (including those with significant populations of other captive birds) are also encouraged to voluntarily register their flock on the GBPR.

In the event of a disease outbreak, text alerts are also sent to all those on the register.

Movement records

Owners/keepers of flocks of poultry (including game birds and poultry kept as pets) of over 250 birds are required to keep records of poultry leaving or entering their premises. Similarly, any person involved in the transport or marketing of any poultry or eggs must keep a record of all poultry or eggs they transport or market. These records must be kept for 12 months and are vital in cases where a notifiable avian disease (NAD) is suspected or confirmed, so that contact premises can be identified rapidly.

In addition to these legal requirements, all keepers of poultry or other captive birds are encouraged to consider and implement record keeping measures that would assist APHA in carrying out tracings in the event of an outbreak of a NAD.

Reporting suspicion of disease

Keepers of poultry and other captive birds are legally required to report any suspicion of a NAD to the APHA who then place movement restrictions on the premises and conduct a veterinary investigation. These are referred to as report cases.

Risk mitigation

When risk assessments, containing the latest scientific and ornithological evidence and veterinary advice indicated that there was a high risk of transmission of avian influenza to poultry and other captive birds from wild birds or any other source, the government declared an Avian Influenza Prevention Zone (AIPZ). This specified all or part of Great Britain, and imposed a legal requirement on poultry, or other captive bird keepers, to follow additional protective measures to prevent direct or indirect contact between wild and kept birds. Exceptionally, the enforced housing of poultry and other captive birds, or their separation from wild birds was required.

A regional AIPZ in the counties of Norfolk, Suffolk and parts of Essex was imposed on 27 September 2022. This was in addition to a regional AIPZ in Cornwall, Devon, Isles of Scilly and part of Somerset, which remained in place from 31 August 2022. Both of these were extended to the whole of Great Britain on 17 October 2022.

Housing measures were added to the Norfolk, Suffolk and parts of Essex regional AIPZ on 12 October, to England on 07 November and Wales on 02 December 2022. No housing measures were imposed in Scotland during the 2022-2023 HPAI season.

Biosecurity advice

An epidemiological investigation was undertaken on each IP to determine when infection was introduced (see Appendix 1). This also investigated all possible sources of infection including possible movements of susceptible animals and their products, people, vehicles, equipment, feedstuffs, bedding material etc, together with any biosecurity failings. These findings were used to provide advice on potential biosecurity improvements to keepers and the wider industry, and a photo library of observed examples of both good and suboptimal biosecurity from a variety of poultry premises was compiled and shared (see Appendix 4).

Detection of infected premises

Early detection of NAD in kept birds is vital to reduce the extent of disease spread.

During the veterinary investigations into report cases, APHA veterinarians examined the birds and other records (for example, production records). If disease could not be ruled out, blood samples and swabs were taken from an epidemiologically appropriate selection of birds and submitted for testing at the national reference laboratory (NRL) at Weybridge. Housing, movement controls of birds and their products, together with strict biosecurity measures were enforced.

If HPAIV was confirmed on laboratory testing, all susceptible birds were culled, a full epidemiological investigation was undertaken (Appendix 1), and the premises were appropriately cleansed and disinfected.

If HPAI could be ruled out on clinical grounds, or if the samples taken were negative for HPAIV, the restrictions were lifted. These negated report cases were however used to provide additional surveillance evidence. See 'Reassurance that no infection remains undetected' section on page 35.

On six occasions, the relevant CVO took a decision to cull the flock before laboratory confirmation of the presence of HPAIV. These were known as "Slaughter on Suspicion" cases (SOS) and were culled to pre-empt any potential onward spread of disease. This option is only used during a known confirmed disease outbreak, where the clinical signs and observed production changes in a flock (for example, exponentially increasing mortality) are highly consistent with a suspicion of infection with HPAI and/or there is a known epidemiological link to a previously confirmed case (for example, via shared staff or equipment). Of the six cases, four were subsequently confirmed as IPs and two were negated.

Descriptive epidemiology

Overview of the epidemic

Introduction of infection

Historically, the arrival of HPAIV in Great Britain (GB) has been linked with the autumnal arrival of migratory wildfowl (Anseriformes) to the UK – in particular, those which breed across continental Eurasia and acquire exotic HPAIVs enroute. The risk of disease in these species is amplified by their general sensitivity to HPAIVs and their behaviour once in the UK, forming large and diverse overwintering aggregations on wetlands and waterbodies inland, as well as mud flats in estuaries. They are often joined by resident wildfowl at this time, as well as other susceptible species (for example gulls, waders).

Epidemiological investigations (Appendix 1) have strongly suggested that over the course of the 2022 –2023 season, infection of kept birds was largely the consequence of the independent introduction of virus directly or indirectly from wild birds. In only two cases (1.0%) was the most likely source of infection identified to be from direct domestic contact, with high likelihood.

In two other cases (1.0%), the most likely source was identified as equally likely to be from direct or indirect contact with wild birds, or contaminated products. or indirect domestic contact (see analysis on page 11).

The epidemiological processes at play changed as the ecology and behaviour of wild birds and the management systems of kept birds changed seasonally so we have sub-divided this report into three-month reporting periods (reporting periods 1 to 4) to better characterise the overarching trends in wild and kept bird infection throughout the 2022 –2023 season.

Infection in kept birds

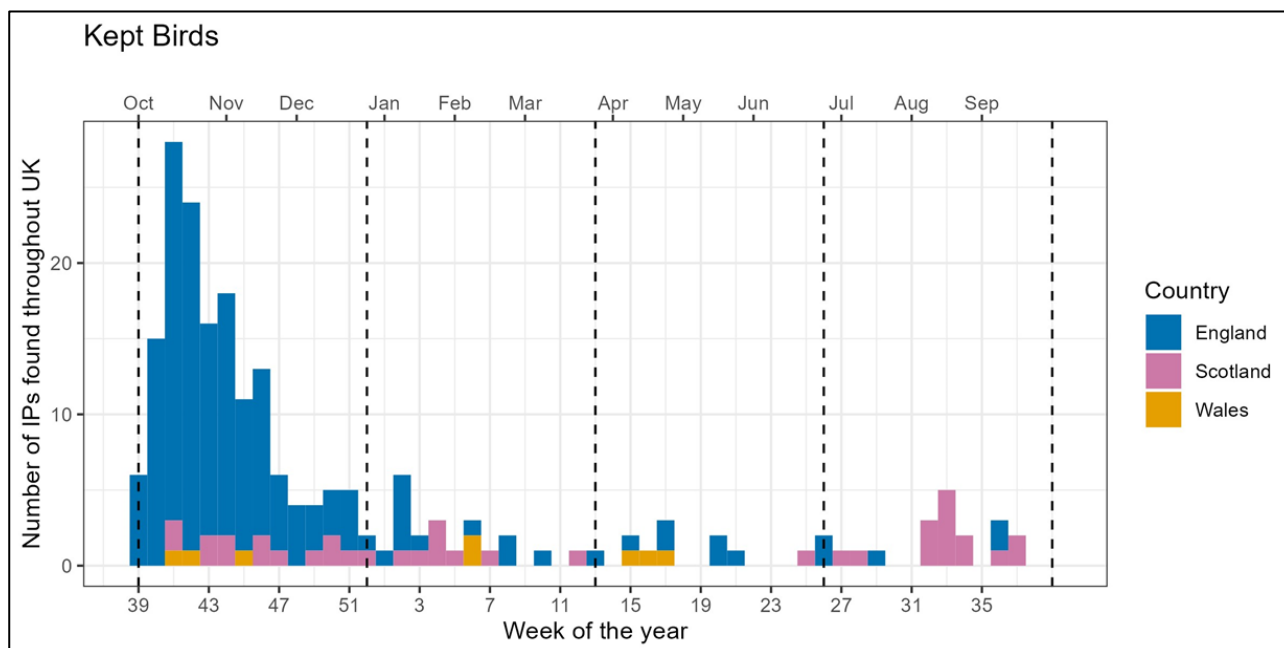
During the 2022 to 2023 administrative season, a total of 206 HPAIV infected premises were confirmed across England (160), Scotland (38) and Wales (8) (see distributions by date of confirmation in Figure 4).

154 (75%) of these were in commercial flocks, of which 133 held over 1000 birds.

46 (22%) were in non-commercial flocks, with one zoo, two wildlife conservation centres and three animal rescue sanctuaries/rehabilitation centres (3%) also infected.

Overall, this represented 0.36% of premises in the Great British Poultry Register (GBPR).

Figure 4: HPAI H5N1 Epidemic curve by date of confirmation by country



Species

Among the 206 IPs, the greatest proportion were holdings with only chickens present (66 IPs, 32%), followed by holdings with only turkeys (45 IPs, 22%), holdings with a mixture of two or more domestic species (40 IPs, 20%), and holdings with only ducks (24 IPs, 12%).

For the different species types, a higher proportion of IPs occurred among holdings with captive wild species (25.0%), turkeys only (6.0%), birds of prey (2.5%), ducks only (2.4%) and geese only (1.0%).

Table 1: Number and percentage of HPAI Infected Premises by species occurring 1st Oct 2022 to 30th Sept 2023 in Great Britain and in each country, and the number and percentage of holdings by species in Great Britain and in each country.

Species	Number of IPs in England (%)	Number of holdings in England	Number of IPs in Scotland (%)	Number of holdings in Scotland	Number of IPs in Wales (%)	Number of holdings in Wales	Number of IPs in GB (%)	Number of holdings in GB
Chicken	45 (0.2)	28,407	19 (1.1)	1,681	2 (0.1)	2,161	66 (0.2)	32,249
Turkey	45 (6.5)	697	0	21	0	39	45 (6.0)	757
Mixed domestic*	27 (0.3)	8,265	8 (1.4)	578	5 (0.6)	840	40 (0.4)	9,683
Duck	24 (2.7)	897	0	42	0	53	24 (2.4)	992
Mixed other**	8 (0.2)	4,893	1 (0.3)	330	0	368	9 (0.2)	5,591
Pheasants	2 (0.1)	1,706	5 (1.4)	364	1 (1.2)	82	8 (0.4)	2,152
Captive wild species	3 (16.7)	18	2 (100.0)	2	0	0	5 (25.0)	20
Geese	4 (1.0)	386	0	13	0	26	4 (1.0)	425
Mixed gamebird***	2 (0.1)	1,606	1 (0.4)	236	0	54	3 (0.2)	1,896

Species	Number of IPs in England (%)	Number of holdings in England	Number of IPs in Scotland (%)	Number of holdings in Scotland	Number of IPs in Wales (%)	Number of holdings in Wales	Number of IPs in GB (%)	Number of holdings in GB
Birds of prey	1 (1.3)	75	1 (33.3)	3	0	3	2 (2.5)	81
Other birds****	0	834	0	48	0	70	0	952
Pigeon	0	788	0	59	0	45	0	892
Aviary birds	0	627	0	14	0	21	0	662
Psittacines	0	299	0	14	0	16	0	329
Quail	0	193	0	13	0	13	0	219
Partridge	0	101	0	10	0	4	0	115
Guinea fowl	0	38	0	0	0	2	0	40
Rhea	0	7	0	1	0	1	0	9
Ostrich	0	7	0	1	0	0	0	8
Emu	0	6	0	0	0	0	0	6
Poultry unknown****	0	2	0	0	0	0	0	2
Total	161 (0.32)	49,852	37 (1.08)	3,430	8 (0.21)	3,798	206 (0.36)	57,080

Poultry population data extracted from the Great Britain Poultry Register, December 2022.

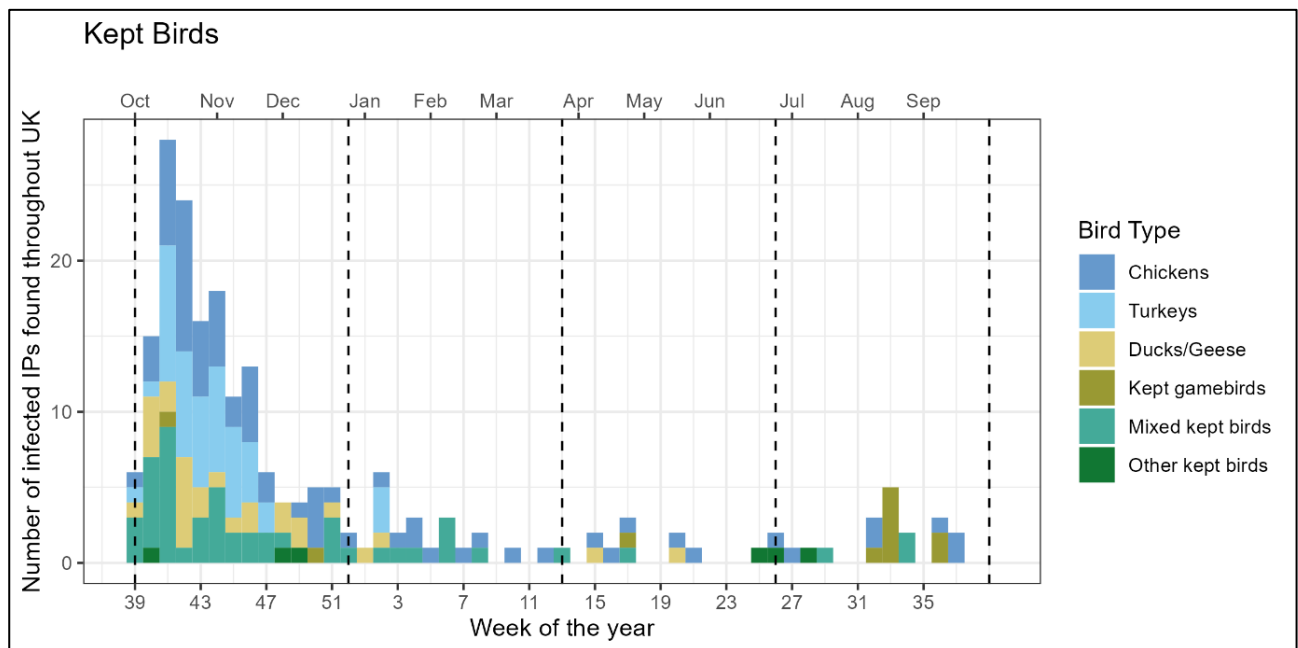
*holdings keeping two or more domestic bird species

**holdings keeping domestic bird species and other kept bird species

***gamebirds in captivity

****species not specified

Figure 5: HPAI H5N1 Epidemic curve by date of confirmation by species



Production type

When considering the production type of Infected Premises, IPs most frequently occurred in commercial rearer-fattener holdings (63 IPs, 31%), followed by non-commercial (46 IPs, 22%), commercial layer (41 IPs, 20%) commercial breeder (20 IPs, 10%) and commercial gamebird holdings (12 IPs, 6%) (Table 2).

When considering the number of holdings of each production type, rearer-fattener holdings had the greatest proportion of holdings affected (9.5%), followed by breeder holdings (1.3%) and broiler holdings (0.6%) (Table 2).

Table 2: Number and percentage of IPs and holdings by production type in Great Britain and in each country.

Production type	Number of IPs in England (%)	Number of holdings in England	Number of IPs in Scotland (%)	Number of holdings in Scotland	Number of IPs in Wales (%)	Number of holdings in Wales	Number of IPs in GB (%)	Total Number of holdings in GB
Rearer-fattener *	62 (10.2)	606	0	28	1 (3.0)	33	63 (9.5)	667
Non-commercial **	34 (0.2)	20,571	8 (0.7)	1,131	4 (0.3)	1,527	46 (0.2)	23,229
Layer	20 (0.2)	13,383	19 (2.1)	916	2 (0.2)	1,167	41 (0.3)	15,466
Breeder	18 (1.3)	1,347	2 (1.9)	103	0	101	20 (1.3)	1,551
Gamebird	5 (0.2)	3,191	6 (1.0)	582	1 (0.8)	129	12 (0.3)	3,902
Broiler ***	8 (0.7)	1,237	0	60	0	94	8 (0.6)	1,391
Mixed domestic ****	8 (0.2)	3,834	0	228	0	329	8 (0.2)	4,391
Other	6 (0.1)	5,683	2 (0.5)	382	0	418	8 (0.1)	6,483
Total	161 (0.32)	49,852	37 (1.08)	3,430	8 (0.2)	3,798	206 (0.36)	57,080

*ducks, geese, turkeys kept for rearing and fattening

**birds kept as pets, showing or production for household consumption only

***broiler chickens

****holdings with two or more different production types for example, layer and broiler

Figure 6: HPAI H5N1 Epidemic curve by date of confirmation by production type

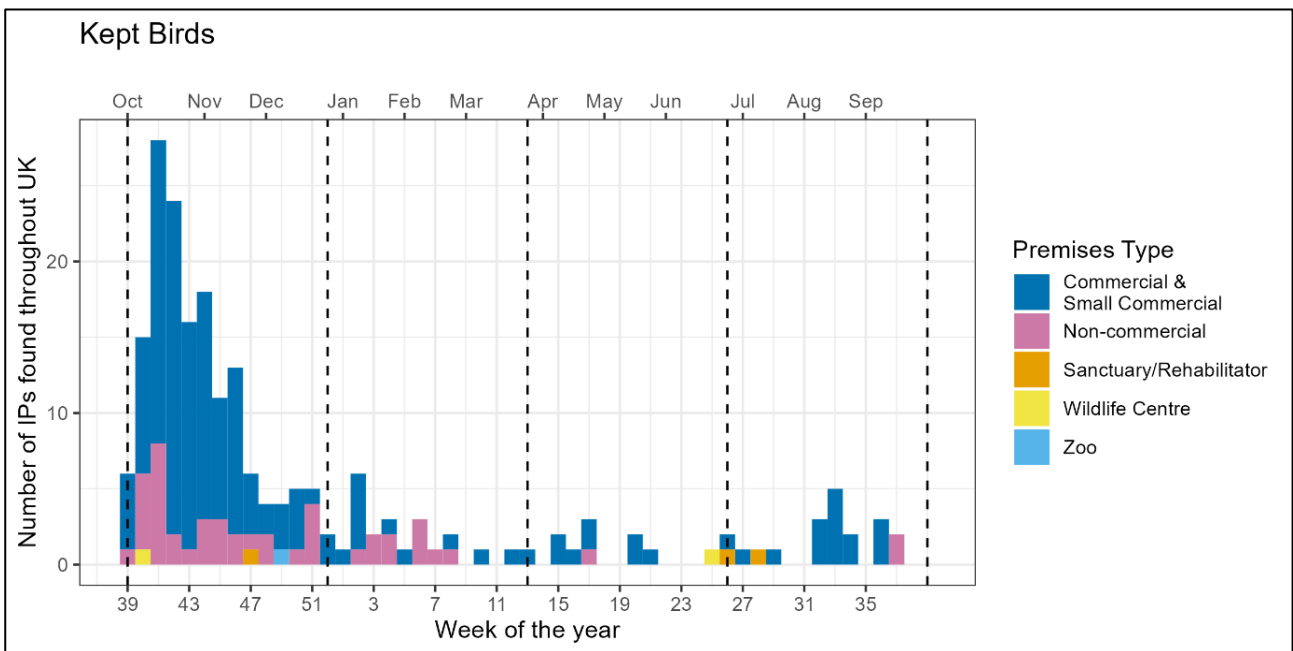
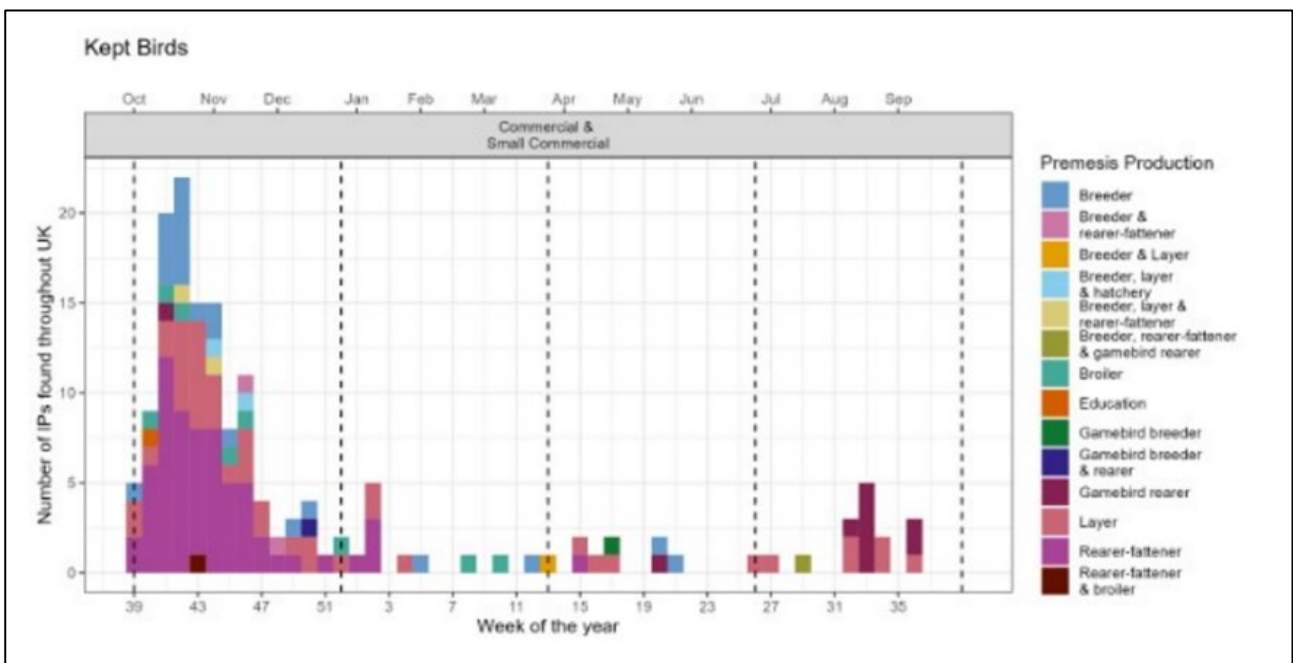


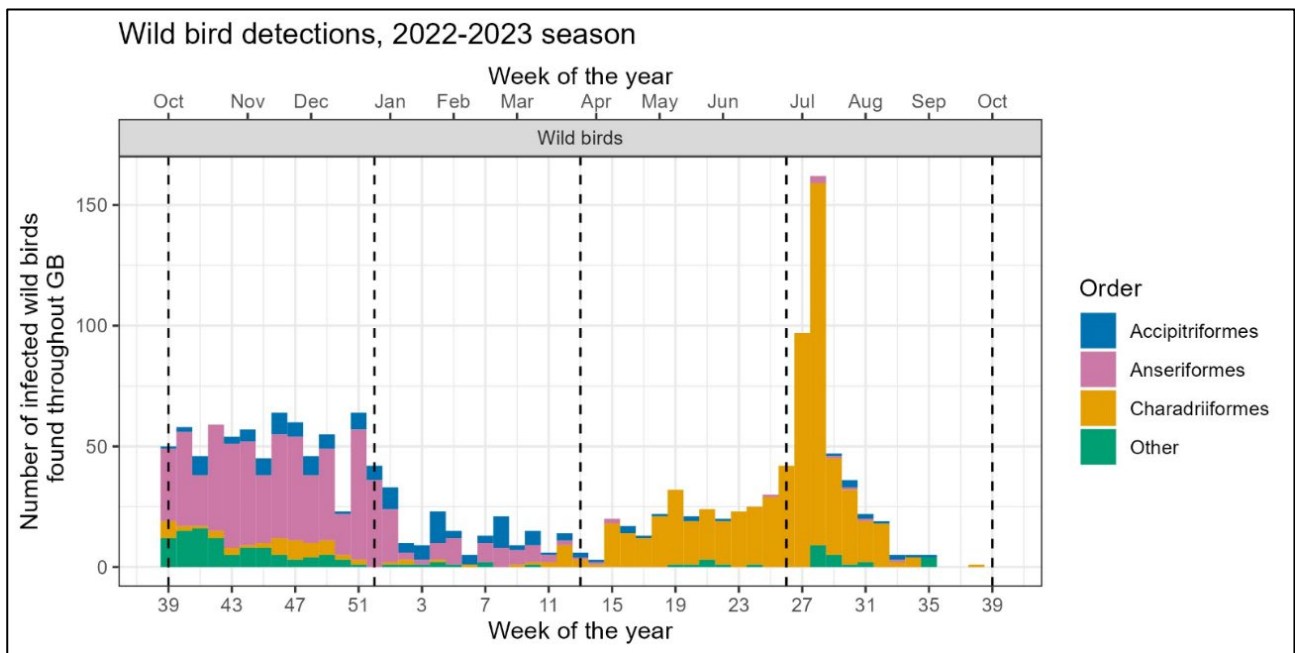
Figure 7: Epidemic curve by date of production as above, with commercial premises broken down by production type.



Infection in wild birds

Through wild bird surveillance (Appendix 2) a total of 1,592 HPAIV-positive wild birds were identified across England (1,120), Scotland (346) and Wales (126) (see Figure 8). Although virus was detected in birds from a total of 14 different orders, the most common were waders, gulls, and auks (Charadriiformes 45%) wildfowl (Anseriformes 37%) and certain diurnal birds of prey (Accipitriformes 8%)

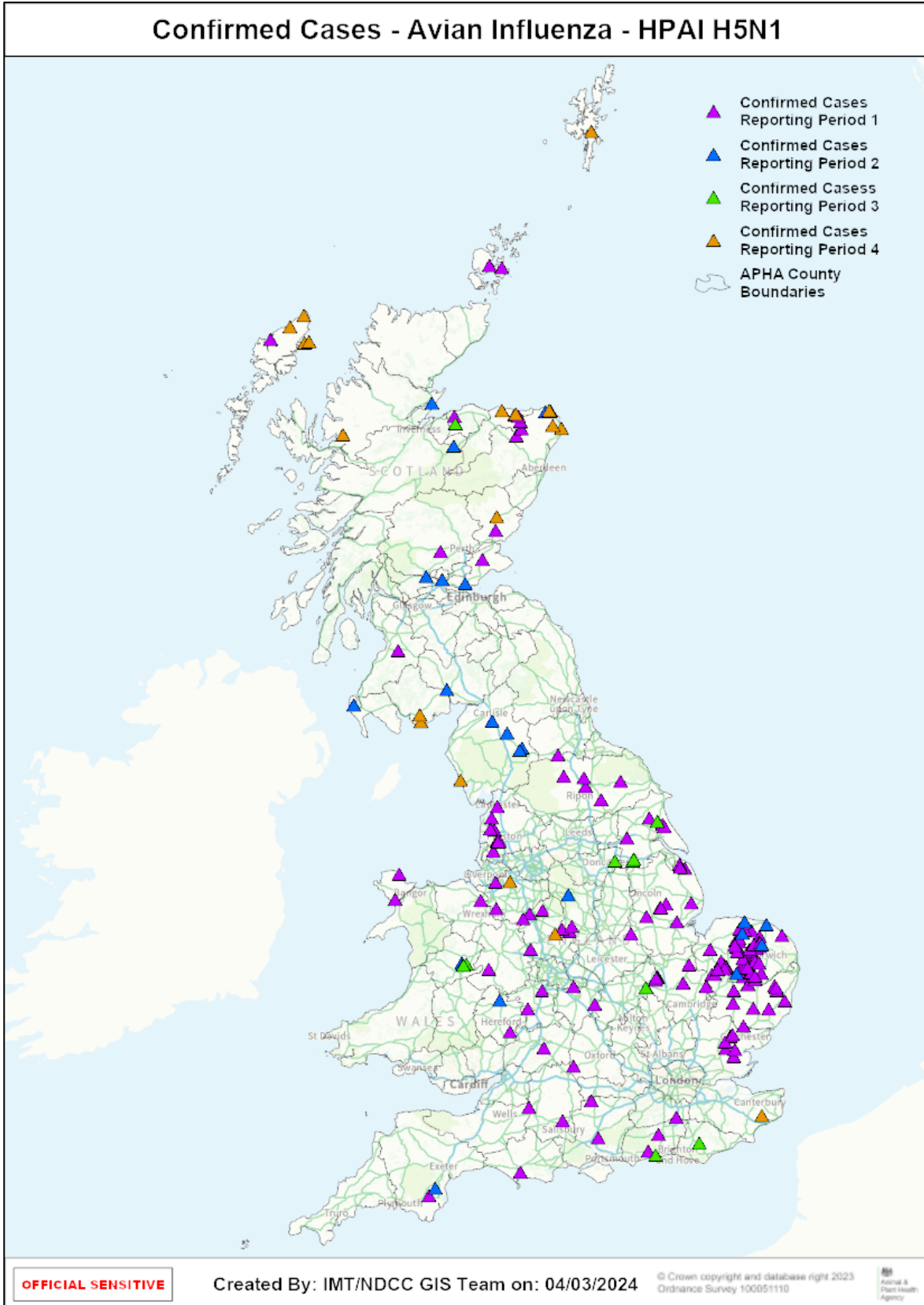
Figure 8 HPAI H5N1 detections in wild birds by order



Geographic distribution

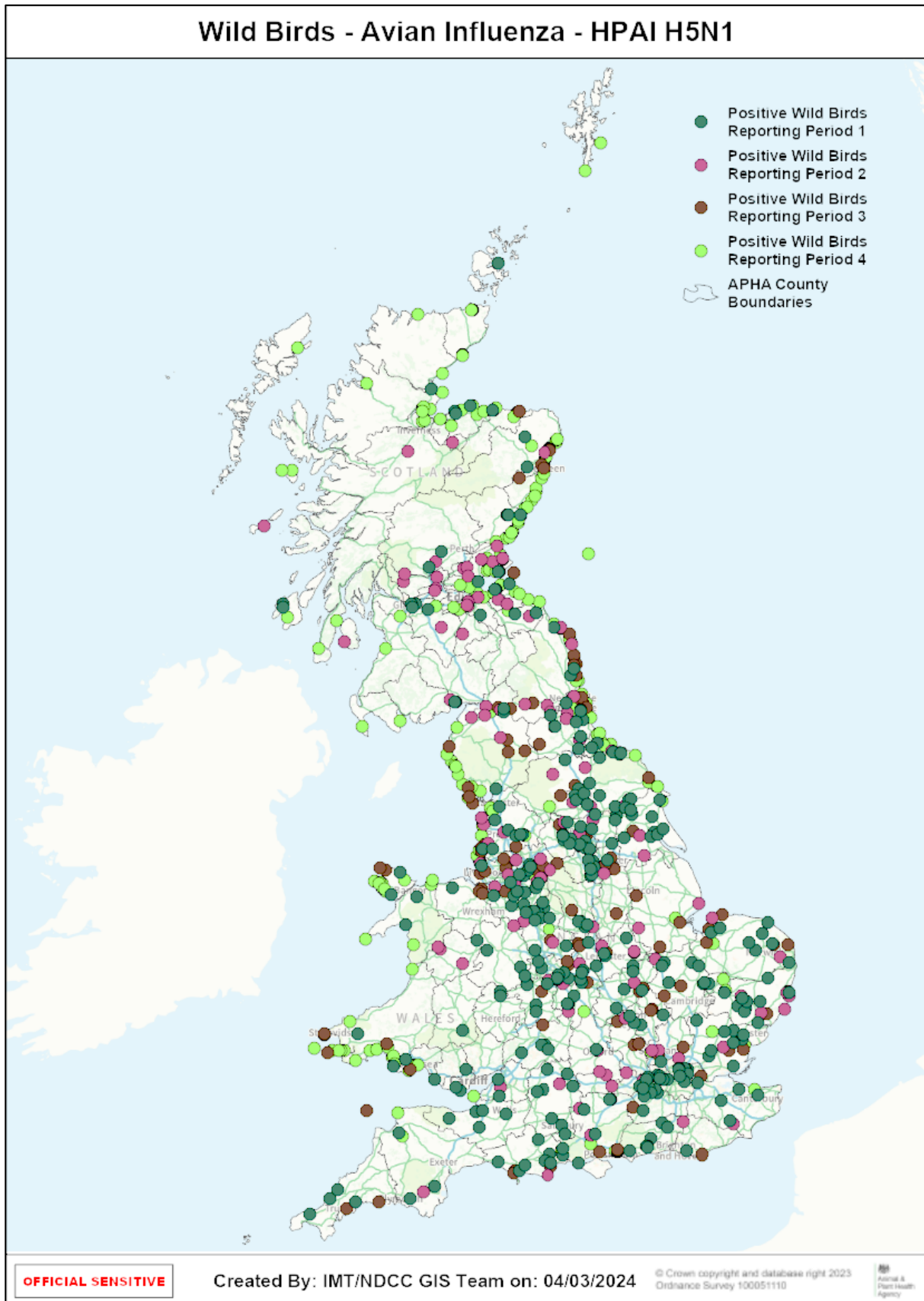
Kept birds infected premises

Figure 9 Location of IPs colour coded by reporting periods



Wild bird confirmed positive cases

Figure 10 Location of wild bird detections colour coded by reporting periods



In addition to HPAIV detections in kept birds, a single low pathogenicity avian influenza virus (LPAIV) was detected in Scotland on 20 March 2023 (AIV 2023/021) and was characterised as an H7N3 subtype.

Some apparent clustering of infected premises was identified through the use of genomic, quantitative data, spatial and network analysis methods and also through routine outbreak and tracings investigations that flagged potential epidemiological links between cases. These apparent clusters and any infected premises that may have shared common factors or risk pathways with the same event, were considered in more detail, as described in Appendix 1.

Analysis of likely source on infection of kept bird IPs

In the 2022-2023 season, the most likely source of infection, based on the outbreak investigation and subsequent tracing investigations, was in the majority of cases identified as direct and/or indirect contact with wild birds, and/or wild bird contamination of bedding or feed (92.7% of IPs).

In two cases (1.0%), the most likely source was identified as equally likely to be from direct or indirect wild bird contact, or contaminated products, or indirect domestic contact: in one case the premises shared staff and vehicles with another infected premises belonging to the same company that was located in close proximity, and in the second case, egg collection was identified as a possible source of introduction.

In only two cases (1.0%) was the most likely source of infection identified to be from direct domestic contact, with high likelihood.

One IP was a small commercial mixed domestic and gamebird premises, where the birds had outdoor access. A batch of chickens was purchased two days prior to the onset of clinical signs, during the high risk spread window of a premises that subsequently also became an infected premises.

The second IP was a large indoor commercial duck layer premises that was part of a company group that had other IPs. The ducks had moved onto the infected premises from another premises that subsequently reported clinical signs and became an IP shortly afterwards. Based on serological and genomic results it was likely that these birds were infected on the source premises.

In 5.3% cases, the most likely source of infection was not fully determined, but direct or indirect domestic contact was not considered to be likely.

Several risk factors for the introduction of infection were identified during epidemiological investigations and this led to detailed biosecurity advice and guidance being provided to all keepers. See Appendix 4.

Reporting period 1 (October to December 2022)

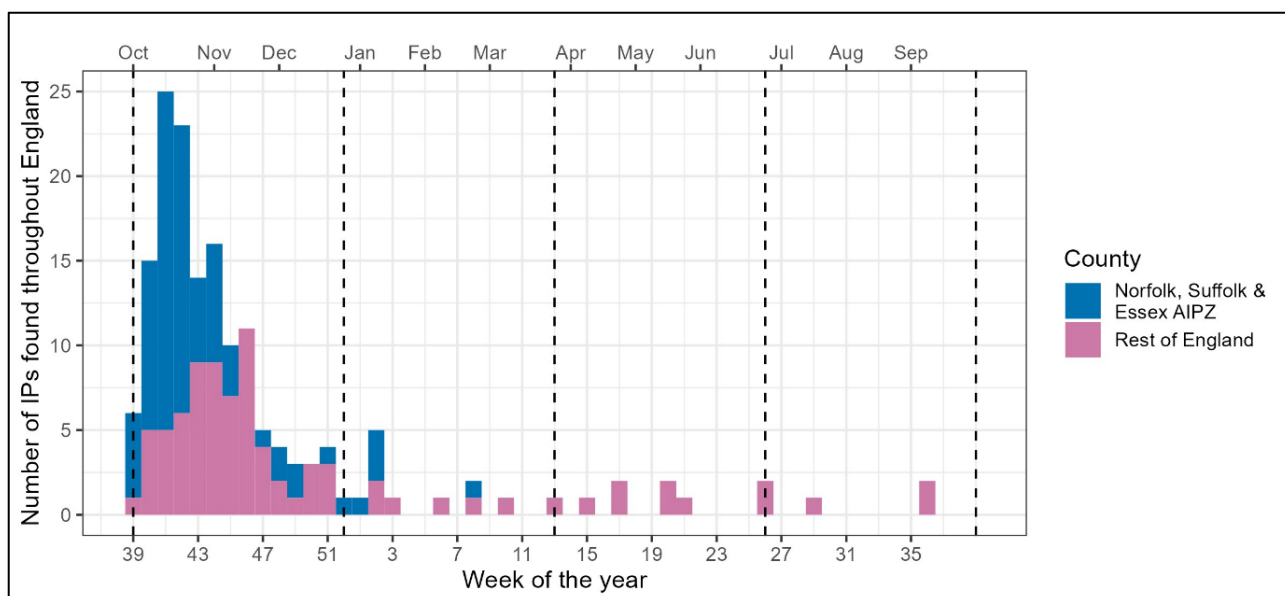
Wild birds: The majority (70%) of the 677 positive detections of HPAIVs in wild birds came from wildfowl, of which approximately 10% were in species which are considered migratory). Regular virus detections were also made from gull species, free-living pheasants and raptors – with the common buzzard the most severely affected raptor.

It is not clear if there was any significant importation of exotic HPAIV and the epizootic appeared to be a continuation of the outbreak from the summer of the previous season 2021-2022.

The first virus detections of the 2022-2023 season in migratory waterfowl occurred earlier than in previous years – on 04 and 05 October. These were from a barnacle goose in Gloucestershire and a pink footed goose in Lancashire.

Kept birds: the reporting period started with confirmation of infection in two commercial premises in Norfolk on 01 October and one non-commercial premises in Suffolk. Over the following three months, 154 infected premises were confirmed in GB – 137 in England, 14 in Scotland and three in Wales. Of the 137 in England, 72 were concentrated in three neighbouring counties – 55 in Norfolk, 11 in Suffolk and 6 in Essex.

Figure 11 HPAI H5N1 Epidemic curve by date of confirmation location in England



Of these affected premises, the relative proportions of commercial to non-commercial were similar to the proportions overall (77% commercial to 21% non-commercial plus one zoo, one sanctuary and one wildlife holdings).

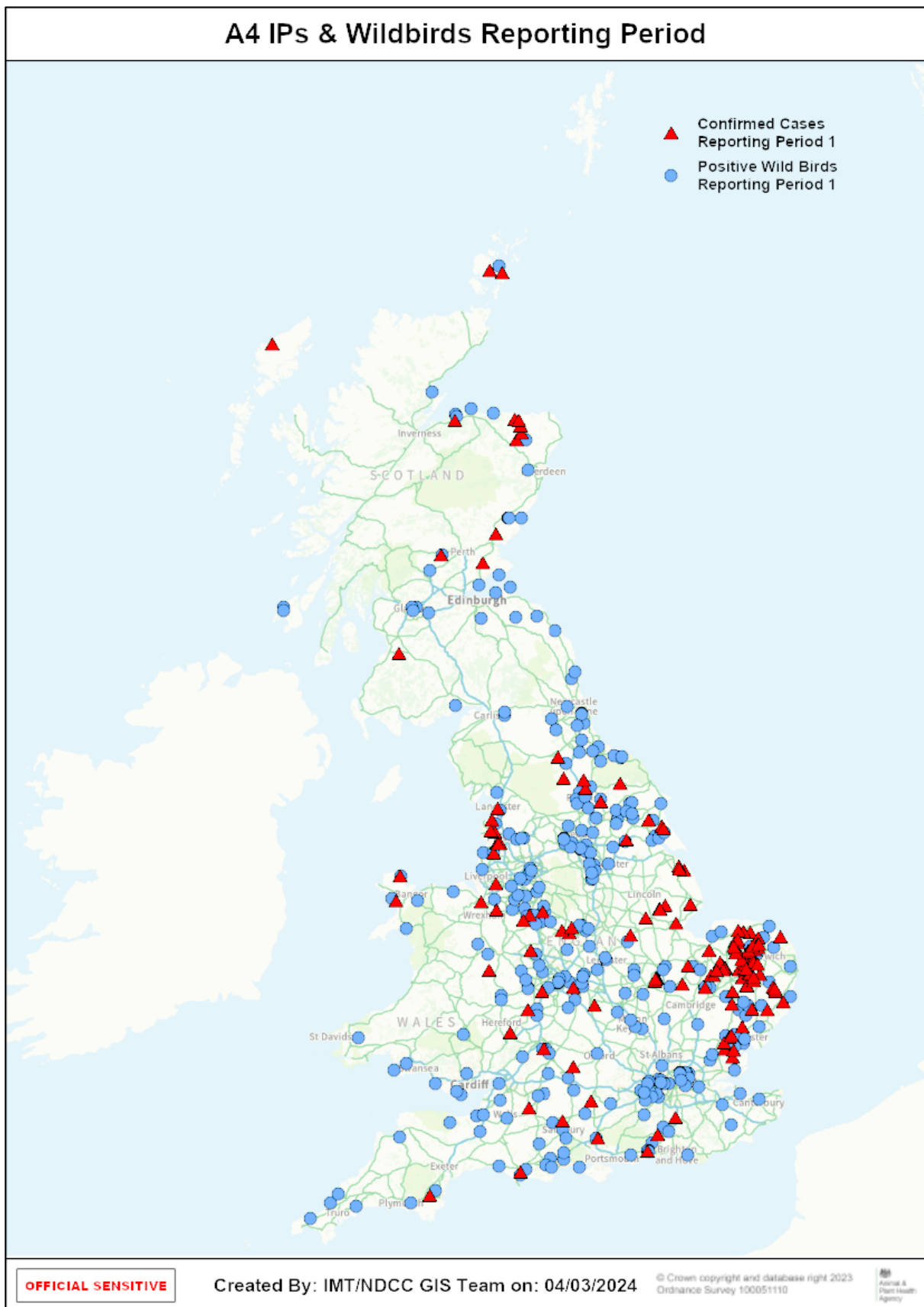
With regard to species, 51% were rearers (compared to 31% of IPs overall). 33% held turkeys, 26% held chickens, 21% held ducks and 1.4% held geese, (compared to 22%, 32% and 12% and 0.5% of IPs overall). These differences indicate that there were likely to have been different epidemiological risk factors in this area and time period.

An Ornithological Expert Panel (OEP) was convened on 05 October and identified the Norfolk and Suffolk area as having:

- A particularly high-risk combination of large numbers of kept birds and sensitive premises (for example, free-range production systems), exacerbated by increased numbers of birds intended for the seasonal Christmas market (turkeys and ducks).
- The area also had large numbers of outdoor pig farms and seasonal ploughing activities which may have attracted wild birds (gulls, pheasants, and both resident and migratory wildfowl) bringing the virus into close proximity to kept birds.

Housing measures were added to the Norfolk, Suffolk and parts of Essex regional AIPZ on 12 October (see risk mitigation section at page 14).

Figure 12 Location of IPs and wild bird cases in reporting period 1

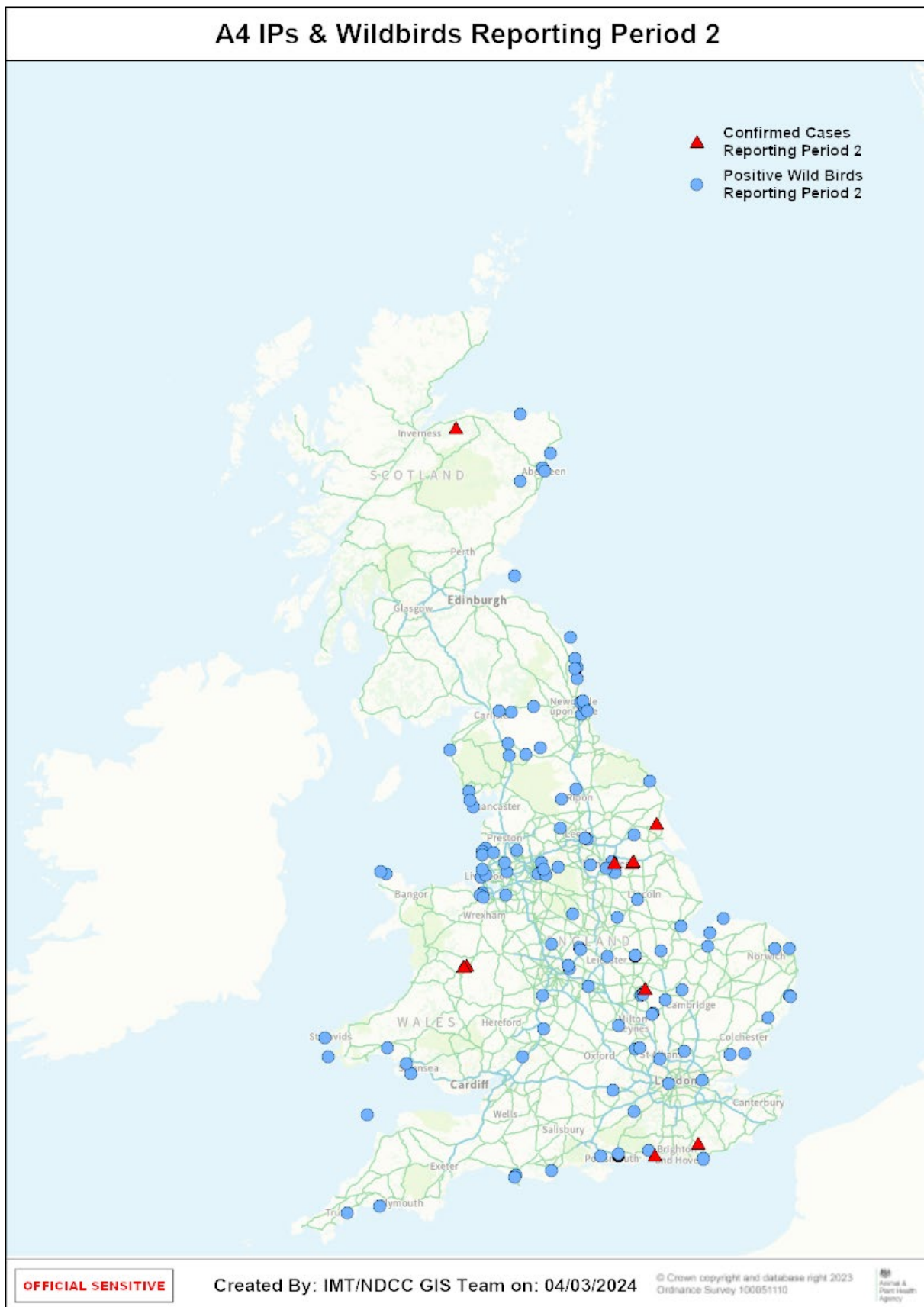


Reporting period 2 (January to March 2023)

Wild birds: The number of confirmed cases in wild birds dropped substantially from the previous reporting period, with a total of 181 detections. 45% of these came from wildfowl, of which 53% were in species considered to be migratory. The numbers of detections from gull species also dropped. Confirmed cases in raptors remained at similar levels again with the majority being from buzzards.

Kept birds: Outbreaks in kept birds also decreased with 21 IPs confirmed (12 in England, five of which were in Norfolk). The numbers of IPs in Scotland did not fall to the same degree – with a total of eight IPs in this period and two in Wales. Eleven (52%) were in commercial premises and 10 (48%) in non-commercial premises, which differed from the proportion during the overall season of 75% to 22%. Chickens were the most commonly affected species being present on 16 premises (76%). Only three IPs (14%) were turkey rearers – likely reflecting the lower numbers of these in production at this time of year and demonstrating the impact of seasonality in kept birds as well as wild birds on infection risk.

Figure 13: Location of IPs and wild bird cases in reporting period 2.



Reporting period 3 (April to June 2023)

Wild birds: The number of confirmed cases in wild birds increased to 282 over this reporting period. 92% of these were from gulls and terns, a noticeable switch from previous majority detections being in wildfowl. Of these, 68% were from Black-headed gulls, most of which were reported as mass-mortalities in May. Cases reported to the surveillance scheme most likely underestimated the effects of disease on Black-headed gulls as many colonies were inaccessible, severely limiting opportunities to collect carcasses. In contrast, detections from wildfowl and raptors were much lower than the previous two reporting periods, and no detections were made from seabirds.

Kept birds: The numbers of IPs declined further from the previous reporting period, with a total of 11 IPs identified. One premises in Scotland, three were in Wales and seven in England. Of the 11 IPs, eight premises (73%) were commercial, one was non-commercial (9%) one was a sanctuary and one a wildlife premises. The species on the commercial and non-commercial premises were chickens (63%), ducks (25%) and gamebirds (12%).

This reporting period saw the end of winter behaviour in wildfowl, with aggregations on inland waterbodies and estuaries dispersing. The last of the migrant species departed for their breeding grounds in the north or east, and resident birds re-occupied their breeding sites scattered across the wider landscape and formed pairs which interacted with others much less regularly (an important change in population contact structure) which reduced the potential for virus spread.

Figure 14: Location of IPs and wild bird cases in reporting period 3.



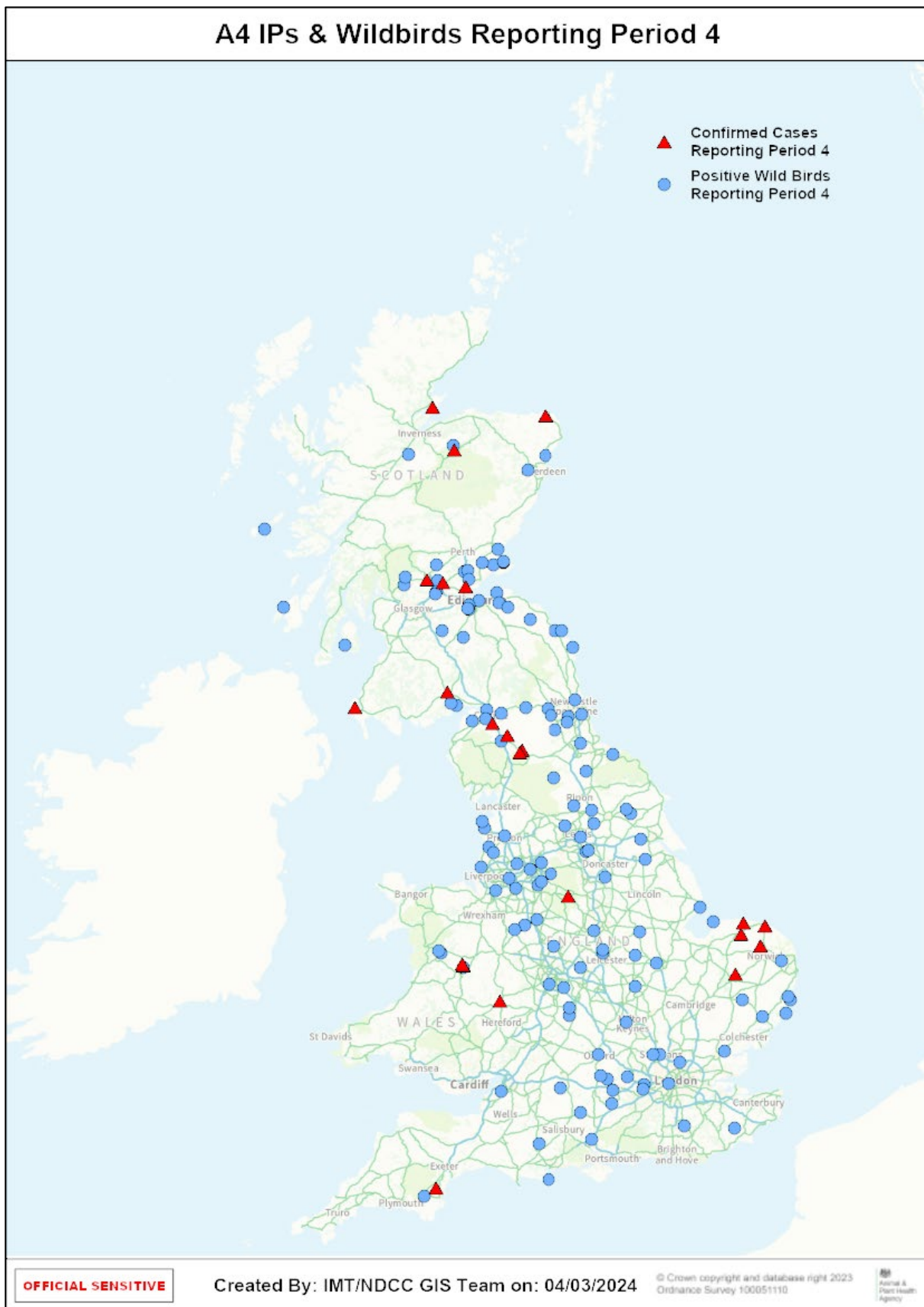
Reporting period 4 (July to September 2023)

Wild birds: The number of confirmed cases in wild birds increased during this reporting period with a total of 416 detections. Again, the majority (89%) were from gulls, terns and auks. Of these, 59% were from gulls and terns, with the remainder from auks, mainly guillemots. This represented the first signs of disease in these colonial cliff-nesting species during the 2022-2023 season. This pattern of cases occurring in cliff-nesting seabirds continued with a shift from the Black-headed gull (which generally breed away from cliffs) to Kittiwakes and Herring gulls. Associated with this were also a few cases reported in Gannets (not a charadriiform but cliff-nesting). Detections amongst wildfowl and raptors remained at similarly low levels to those observed in the previous reporting period.

Further from the coast, a total of nine detections were made from free-living pheasants – representing the first-time detections had been made from this species (as a wild bird) since (4 December 2022) reporting period 1.

Kept birds: There were 20 IPs in this reporting period and there was also a pronounced shift in the geographic distribution of these, with all except for one IP located within 25 km of either coastal or estuarine areas, and 16 located in Scotland. 17 (85%) were commercial premises, 2 (10%) non-commercial and one was a sanctuary. Of the commercial premises, 47% were gamebird premises and 53% held chickens.

Figure 15 Location of IPs and wild bird cases in reporting period 4



This reporting quarter was characterised by a dramatic shift in the geographic distribution of infection risk for both wild and kept birds, due to high levels of infection amongst coastal breeding seabirds.

A number of gamebird premises in Scotland became IPs and although linked to a common supplier, further investigation found no evidence of infection in the supplier premises prior to detection of infection in the destination locations. It was considered likely that these cases represented independent infections directly or indirectly from wild birds rather than lateral spread between premises.

There were also 5 IPs on the Isle of Lewis, associated with birds housed very close to the coast. This was considered likely to represent a particularly pronounced example of the coastal risk, which in this landscape was compounded by the type of premises affected (small non-commercial premises), their coastal location, and the local geography which was considered to restrict and concentrate the activity of most species (especially foraging gulls and corvids) to a relatively thin coastal landscape including the premises.

Figure 16: Wild and kept bird detections (2022-2023 season)

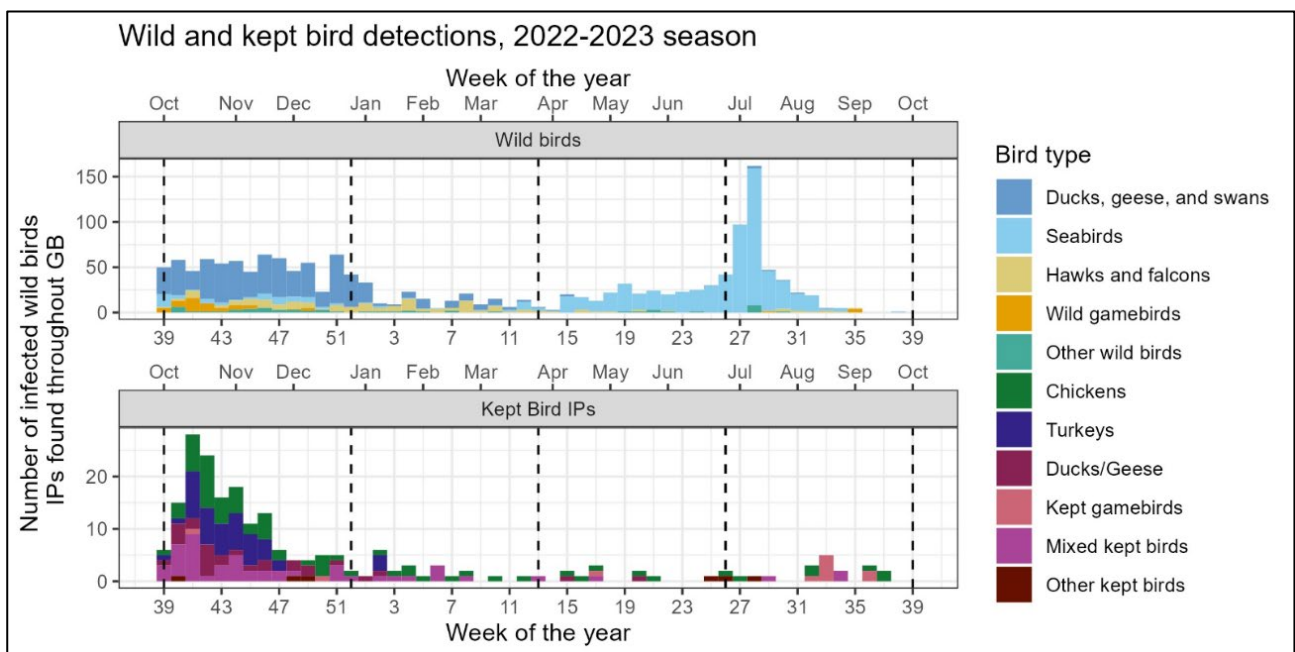
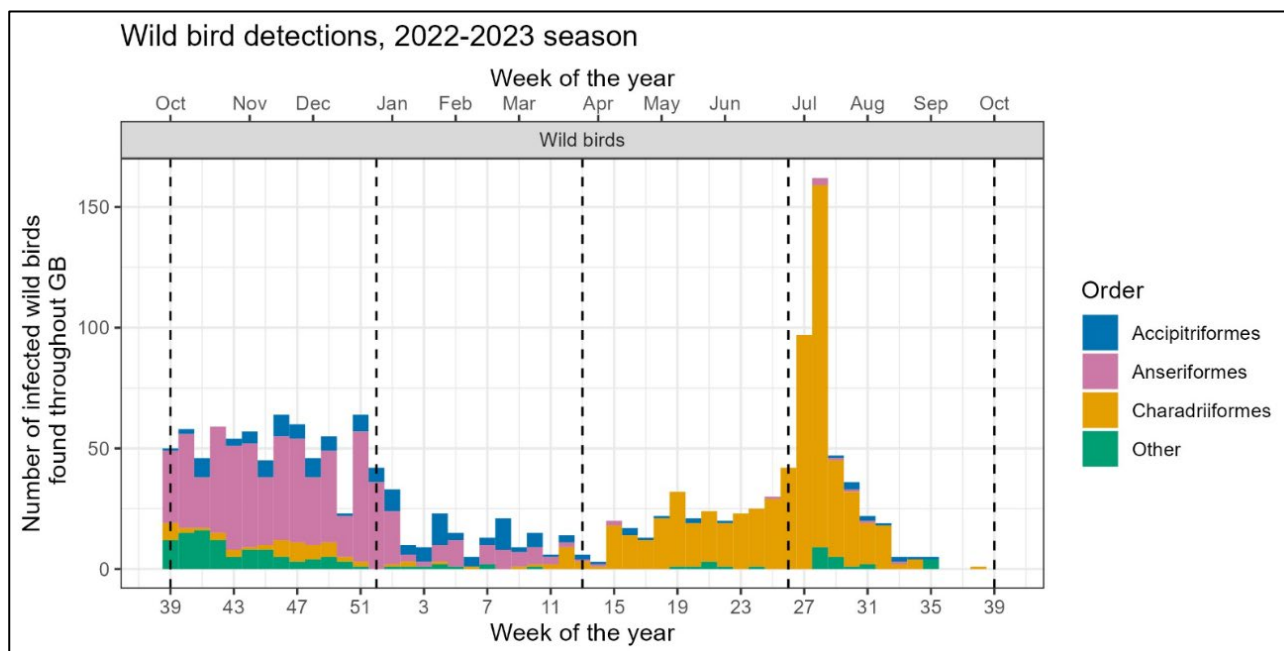


Figure 17: Wild bird detections (2022-2023 season)



Reassurance that no infection remains undetected.

For confirmed cases, surveillance was also carried out on potentially exposed premises in the 3 km protection zones (PZ). This comprised a clinical inspection of the poultry and other captive birds at each site for signs of disease typical of avian influenza and an examination of the records of water and feed intake, health and medicine records, egg production where applicable and daily mortality rates at each site. On commercial premises, non-indicator species were sampled and tested where they were the only species present or if they were kept separately from any indicator species.

Premises in the surveillance zone (SZ) (3-10 km around an IP) were not routinely visited as part of SZ surveillance. Keepers with at least 50 birds received a health census call or stock enquiry visit and at least 20 premises had surveillance visits with clinical inspection, record checks and sampling on commercial premises.

Avian influenza surveillance

In addition to investigation of report cases described above, APHA also carried out active surveillance through the national survey for avian influenza of subtypes H5 and H7 in domestic poultry (including game birds and poultry kept as pets). The aim of the survey was to identify the circulation of AI viruses in poultry (in particular, production ducks and geese) before they became widespread in the poultry population. Serological samples were taken from a random selection of premises and were tested for the presence of AIV antibodies. The premises eligible for selection were flocks over 50 birds for game birds, ducks or geese and flocks over 500 birds for turkeys or domestic fowl. It was not unusual for a small number of samples taken to test positive for H5 or H7 antibodies each year during the survey. These triggered further enquiries and further laboratory testing at the premises in question. If these tests showed that infection with AIV was present, the control measures described were applied. If not, restrictions were lifted.

Negated report cases

During the 2022-2023 season APHA investigated 365 report cases of NAD. Of these, 353 were reports of clinical signs of NAD and 12 were non-negative laboratory results after sampling as part of the process for issuing pre-movement licences (six) or during the national routine AI surveillance (six).

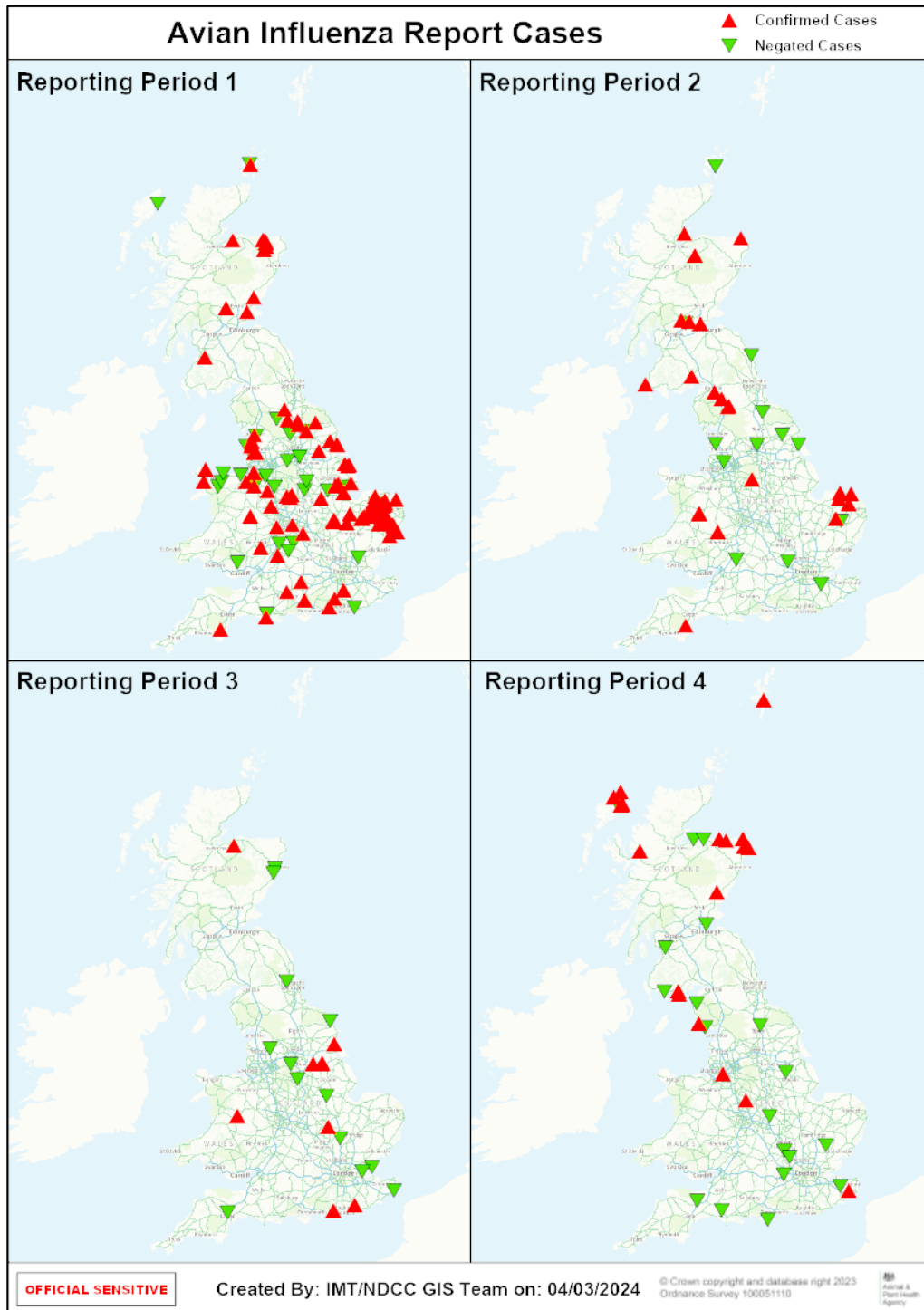
Following the investigations, 206 were confirmed as HPAIV H5N1 and one as LPAIV H7N3. 158 were negated, 66 on clinical grounds and 92 following negative laboratory testing results.

The negated report cases are shown in Table 3 and on the map at Figure 19 to show the geographical coverage.

Table 3: Outcome of negated report cases

Outcome of investigations	Negated on clinical grounds	Negated on lab results	Confirmed HPAI	Confirmed LPAI	Total
Reason for report cases: Clinical signs	66	86	200	1	353
Reason for report cases: Non-negative lab results (routine annual surveillance)	0	5	1	0	6
Reason for report cases: Non-negative lab results (sampling for licensing purposes)	0	1	5	0	6
Total	66	92	206	1	365

Figure 18: Geographical distribution and outcome of avian influenza report case investigations in 2022-2023



Public health impact

Food safety

Based on the current scientific evidence, the Food Standards Agency and Food Standards Scotland advise that avian influenza poses a very low food safety risk for consumers.

Properly cooked poultry meat and poultry meat products are safe to eat and the Agencies' advice on consumption of poultry meat and poultry products, including eggs, does not change during outbreaks of avian influenza.

H5N1 public health risk statement

The UKHSA considers the risk to the public as a result of contact with infected poultry to be very low for the general public and low for those who have prolonged contact with the contaminated environment or infected birds without the use of appropriate PPE. The UK Technical Advisory Group considers the overall risk for the current virus strain is Level 3, meaning some mammals have been infected, but there is no change in the virus indicative of adaptation to mammalian cell receptors. The UK Human Animal Infections and Risk Surveillance (HAIRS) group risk assessment for the likelihood of exposure from contact with infected free-living wild mammals is very low for the general public, and low for those in close contact. The impact for everyone is very low due to the small number of people and the available treatments or interventions, coupled with the lack of evidence for human-to-human transmission.

The risk assessment of 30 January 2023 remains appropriate. The risk to human health relates to the continued high levels of transmission in birds globally, increasing the opportunity for mammalian and human exposures, and the ability of the currently circulating clade to cause direct spill-over infection with opportunities therefore for adaptation and recombination. There is very limited evidence of aerosol transmission between mammals to date although in large mammal die-offs, direct prolonged close contact between the animals is likely to play a role, but this is a key gap to address with surveillance.

The global spread of this virus and the increased species range means there is an elevation of risk compared to the risk before the 2020 to 2021 emergence of the epidemic clade, but there is no evidence of currently increasing human health risk through genomic or epidemiological surveillance. The risk to the UK of human-to-human transmission emerging in the general population is likely to be greater from imported than domestic cases, however UK-based surveillance scenarios can be used to refine understanding of the human health threat.

The Great Britain viruses detected on poultry farms, wild birds and mammals were assessed for zoonotic potential by the WOA/FAO International Ref Lab (also the UK National Reference Laboratory), Weybridge UK using previously applied genetic analyses and it can be concluded that all the viruses are avian viruses, with no specific increased affinity for mammalian species including humans.

Genetic evaluation demonstrated that the H5N1 viruses were distinct from Asian H5N1 viruses historically associated with human infection.

Remaining uncertainty and risks

There remains some uncertainty around the risk posed by wild birds, and when and where further cases or outbreaks may occur. There is evidence of this AI strain still circulating in Europe, therefore we consider that there is an on-going risk of another outbreak occurring in poultry on individual premises. This likelihood will reduce over the summer months and is largely dependent on the level of biosecurity on the individual premises.

Concluding remarks

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

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

The Reference Laboratory at Weybridge is the WOAH/FAO International Reference Laboratory and the UK National Reference Laboratory for avian influenza, swine influenza and Newcastle disease. The laboratory undergoes continual fitness-for-purpose assessments on its frontline UKAS:17025 accredited diagnostic assays. It has the necessary ongoing proven diagnostic capability for these strains of virus, whether low or highly pathogenic avian influenza, and continually monitors changes in the virus.

Acknowledgements

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

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

Appendices

Appendix 1 Epidemiological investigations

Epidemiology is the study of the distribution, the determinants (risk factors) and causes of disease. Epidemiologists, using sophisticated statistical analyses, field investigations and complex laboratory techniques, investigate the cause of a disease, its distribution and method of spread and provide advice on measures for control and prevention. Epidemiology draws conclusions based on the evidence available and the balance of probabilities.

To effectively control a pathogen and stamp it out, it is important to understand the routes by which it spreads and any factors which make the disease more or less likely to occur.

An epidemiological investigation was undertaken each individual infected premises (IP) to estimate when infection was introduced to each infected premises by assessing the clinical history and the results of laboratory testing of epidemiological samples. It also investigated all likely sources of infection including movements of susceptible animals and their products, people, vehicles, equipment, feedstuffs, bedding material etc, together with any biosecurity failings (Appendix 4). In this outbreak there has been specific involvement of experts in virology, ornithology/disease ecology and biomathematics.

Investigations for source and spread of infection are described as 'tracings', and were based on the estimated incubation period, statutory requirements and period over which virus was likely to be excreted by infected birds. A timeline was estimated from the earliest likely date of introduction of infection to the latest date for potential spread. Source tracings were assessed from 1 to 21 days prior to notification of suspicion of disease; spread tracings were assessed from one day after the start of source tracings until the imposition of movement restrictions. Tracings visits were carried out for contacts during the high-risk source and spread windows. See Figure 20.

For indicator species, defined as species that exhibit clinical signs or mortality with the virus strain in question, these were the three days prior to clinical signs for source tracings and two days before for spread tracings. For non-indicator species defined as those that do not exhibit readily apparent clinical signs or mortality with the virus strain in question, which were not mixing with indicator species, epidemiological sampling was carried out and tracing windows were calculated based on laboratory testing results.

For the virus involved in this outbreak, chickens, turkeys, pheasants were considered to be indicator species, and ducks and geese were considered to be non-indicator species.

Following the epidemiological investigation, each IP case was reviewed to assess the likely sources of infection, based on likelihood and level of uncertainty in the relevant evidence base.

The source hypotheses included direct or indirect introduction by wildlife, direct or indirect introduction by domestic flock/animal or animal products with known or undisclosed infection, introduction from contaminated product(s), for example, feed, water or bedding, and infection from an international source.

The review also assessed hypotheses for spread of infection and included direct or indirect introduction by domestic flock/animal or animal products, local spread in the PZ or SZ, onward transmission through wildlife and onward transmission through international trade/connections.

Based on these outbreak investigations and subsequent tracing investigations, the most likely source of infection in the majority of cases (92.7% of IPs) was identified as direct and/or indirect contact with wild birds and/or wild bird contamination of bedding or feed

In two cases (1.0%), the most likely source was identified as equally likely to be from direct or indirect wild bird contact or contaminated products or indirect domestic contact: in one case the premises shared staff and vehicles with another infected premises belonging to the same company, and in the second case, egg collection was identified as a possible source of introduction.

In only two cases (1.0%) was the most likely source of infection identified to be from direct domestic contact, with high likelihood.

One IP was a small commercial mixed domestic and gamebird premises where the birds had outdoor access. A batch of chickens was purchased two days prior to the onset of clinical signs during the high risk spread window of a premises that subsequently also became an infected premises.

The second IP was a large indoor commercial duck layer premises, part of a company group that had other IPs. The ducks had moved onto the premises from another premises that subsequently became an IP and clinical signs occurred shortly afterwards. Based on serological and genomic results it was likely that the birds were infected on the source premises.

In 5.3% cases, the most likely source of infection was not fully determined, but direct or indirect domestic contact was not considered to be likely.

Cluster detection and analysis

In addition to individual IP investigations, groups of infected premises were also identified. Sometimes these were multiple premises under the same ownership. In these cases, the field epidemiology team reported a potential 'company' cluster and carried out additional analyses to determine if there was any evidence of lateral spread between the infected premises through the movement of people, equipment or products. Alternatively, some groups were of multiple premises in the same geographic area which became infected around the same time. These were initially identified by eye (with a notable example being the various large clusters of infected premises in East Anglia at the very start of the season).

At the end of 2022, the analytical epidemiologists in the National Emergency Epidemiology Group (NEEG) employed a statistical method for detecting clusters of cases, such as those that occurred near each other in space and time, "geographic clusters". In these cases, all the potential links between the infected premises and between the premises and the surrounding environment were explored. Each week (or more frequently as needed), current and recent cases were mapped, and a spatiotemporal scan statistic (implemented in the

software 'SaTScan[®]') was used to identify any clusters of cases (which could be as few as two cases in a 2,800 km² area (a circular window of 30 km radius) over the previous 30 days).

When a geographic cluster was detected, a decision was made as to whether this warranted a more comprehensive discussion. All new statistically significant clusters underwent further discussion, as did previous significant clusters containing new IPs. In some cases, clusters which were not statistically significant, but which reflected a potential future focus of infection (for example, those involving coastal premises in the summer months).

In the case of either company or geographic clusters of interest, a working group of relevant experts was convened to discuss the situation.

Field epidemiologists sought information regarding all the movements of people, animals, vehicles, products, and equipment to and from each infected premises prior to confirmation, together with information regarding any biosecurity measures in place, husbandry practices and geographic features of the surrounding area, such as proximity to lakes, rivers, or coastline. They also produced an aggregated timeline that estimated the most likely dates of infection and described source and spread windows for each IP compared. Importantly, field epidemiologists provided a valuable link with bird owners on the ground, allowing them to capture both important local considerations and the bigger picture amongst different groups of bird keepers.

An ornithological expert was able to provide information regarding the species of wild birds that would be expected in the area at that time, as well as general comments on their expected behaviours and movements, and how this might affect some infection pathways. Results from APHA's wild bird surveillance (see page 47) were analysed to understand if there had been any wild birds confirmed as positive for HPAI in the vicinity of the cluster, as well as the broader scale patterns of wild bird mortality and detections.

The virologists and bioinformaticians were able to provide genomic analysis of the viral isolates taken from each IP, and advised on their genetic similarity and the probability that the isolates in the cluster were epidemiologically linked, based on the genomic analyses of the viral isolates involved.

Through discussion the group determined the most likely routes of transmission for the IPs in the cluster (including whether there was any evidence to suggest lateral transmission between premises) and considered whether there was any need to gather further information. This also allowed a prospective estimate of the potential for future cases in the area to be made. If the group considered air borne transmission to be a plausible explanation for the cluster, meteorologists were invited to the group to advise on further analysis to understand if carriage of particles in the wind between premises was likely to have occurred.

In field conditions studies have demonstrated that HPAI viral RNA can be identified in air samples collected 1000 m from infected premises; however, infectious virus was only detected at a maximum of 70 m from the shed.

In 2023 APHA carried out on farm testing to detect viral RNA and infectious viruses in air on infected premises, and this study found that airborne particles harbouring infectious virus could only be found a short distance from the poultry houses (<10 m) even when sampled at a time of maximum risk, when sheds with clinically infected birds, showing high levels of morbidity and mortality, were being culled. [The Role of Airborne Particles in the Epidemiology of Clade 2.3.4.4b H5N1 High Pathogenicity Avian Influenza Virus in Commercial Poultry Production Units \(nih.gov\)](#)

Appendix 2 Ornithological overview

Wild bird activity is an important risk factor in the epidemiology of the current avian influenza outbreaks and assessments of likely infection pressure were carried out by APHA Wildlife ornithologists.

Limited ornithological resource prevented a full assessment for every case. Each IP was risk assessed for prioritisation and the majority were considered in one form or another, including important contributions to case investigations and reporting. Similar analyses were carried out for each outbreak cluster.

Assessments were rapid, desk-based opinions of the type, abundance, and aggregation of wild birds that might support a plausible source of infection close to an IP, and the potential for species specific wild bird behaviours that might give rise to infection pathways onto the premises. This case specific assessment was particularly helpful in cases when infection pressure might be dynamic (reflecting seasonal variation produced by migration or weather), in certain geographical contexts, or in complex or novel cases involving kept birds.

Assessment of the potential infection pathways by 'bridge species' was more complex. Bridge species are defined as bird species which bridge the gap between outbreaks of H5N1 among populations of wild birds and the human environment (human settlements, poultry farms) or vice versa. In this context we reserve the term 'bridge species' for those species that pose significant risks, meaning those most likely to acquire virus at geographic sources where they occur (generally waterbodies, wetland, and estuarine features where sufficient susceptible wild species might aggregate and maintain a prolonged disease process), and transmit it to poultry premises because of their behaviour (including gulls, corvids, and starling), without necessarily succumbing to the infection themselves.

In winter, these three bridge species were of particular interest because they aggregate themselves in night roosts, as well as whilst foraging. All are comfortable visiting poultry houses and are likely to exploit forage provided by farming operations, thus contaminating surfaces. Finally, corvids and gulls are regular scavengers and some fly relatively long distances as part of their daily movements in winter, increasing the likelihood that infection from local wild bird cases might find its way onto a farm.

The main finding, in line with other countries, was that HPAI H5N1 continued to be an epizootic in wild birds with spill over to kept birds. In only two cases (1.0%) was the most likely source of infection identified to be from direct domestic contact, with high likelihood.

In two other cases (1.0%), the most likely source was identified as equally likely to be from direct or indirect wild bird contact or contaminated products or indirect domestic contact: (see analysis on page 11).

Apart from these four cases, extensive epidemiological tracings and genome sequencing investigations revealed no evidence of spread between the infected holdings, either within the United Kingdom, nor to trading partners.

Wild bird surveillance

Surveillance of wild birds – background surveillance

Wild bird populations are monitored for HPAIV through passive surveillance of dead wild birds of certain priority species (BTO). Dead wild birds are identified for virological testing through public reporting and warden patrols. Numbers and species tested can be changed depending on the sensitivity of surveillance required. The threshold number of dead birds required for laboratory testing has recently been updated (ref). Currently, 1 or more dead bird of prey, gull, swan, goose or duck in the same place, or 5 or more dead wild birds of any other species in the same place, are reportable ([Report dead wild birds – GOV.UK \(www.gov.uk\)](https://www.gov.uk/guidance/report-dead-wild-birds)).

These data only represent cases where birds have tested positive for avian influenza. During the 2022 to 2023 season, 1,592 cases of HPAI were identified in 81 species of dead wild birds, including 14 where there was an unidentified 'bird type', such as goose or swan. (See Figure 17)

During the period, H5N1 HPAIV was frequently detected in both UK resident bird species as well as more typical migratory species. However, continual assessment of infection status across different seasons has not suggested endemicity within UK bird populations.

Ornithological Expert Panels

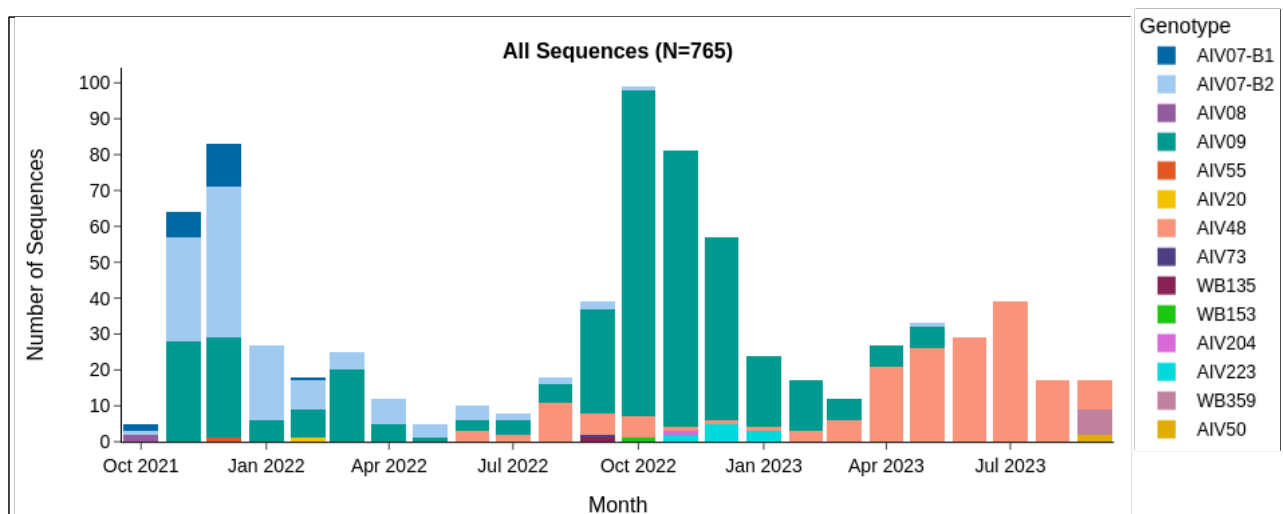
The Ornithological Expert Panel (OEP) is an APHA-chaired expert group established in 2004. Membership is drawn from individuals who bring unique knowledge and expertise of the area. Members are typically associated with, but not limited to, the APHA, the British Trust for Ornithology (BTO), British Association for Shooting and Conservation (BASC), Game and Wildlife Conservation Trust (GWCT), NatureScot, NE, NRW, the Royal Society for the Protection of Birds (RSPB) and Wildfowl & Wetland Trust (WWT). However, members are invited to join the OEP as individuals with specific expertise, and are free to share their expert opinions which may not necessarily be those of the organisation they are affiliated to.

The OEP is an advisory group, it does not have decision-making powers. Its role is to provide veterinary technical and scientific evidence or insight in response to specific questions on a developing policy issue. The OEP does not advise on disease control strategy, although the evidence it gives should support a policy team in identifying options. Throughout the 2022 to 2023 season, the OEP was called upon six times to provide information regarding migration routes, timings, behaviours and any variance.

Appendix 3 Description of the virus – H5N1

Since autumn 2022, the H5N1 clade 2.3.4.4b HPAIV has undergone further genetic reassortment events with other circulating viruses since the preceding year. However, the H5N1 subtype has remained dominant across this period. From a genotype perspective, genetic diversity has increased with a number of novel genotypes being detected and the emergence of a new dominant H5N1 genotype (AIV48/EURL: BB) during the year.

Figure 19: A schematic overview of the waves of genotypes detected across each of the 2021-22 and 2022-23 seasons demonstrating emergence of dominant genotypes from samples where genetic characterisation was possible.



Alongside defining the emergence of novel genotypes, each virus that could be characterised, according to strength of molecular signal, had its internal gene cluster assessed and typed according to UK detections from the previous seasons. Further, with the release of genetic data from laboratories across the European Union (EU), and the defining of European genotypes by the EURL, an alignment between UK genotype classifications and EU detections was made. The genetic reference strains (Table 4) and schematic composition of the genotypes detected in the UK since 2020 is detailed Figure 22, with, where possible alignment with EURL schema.

Table 4: Alignment of the UK and EURL schema for H5 HPAIV clade 2.3.4.4b genotype nomenclature.

UK H5 2.3.4.4b Genotype	UK Genotype Representative	EURL Equivalent Genotype
	H5N1	
AIV07-B1 ^a	<i>A/chicken/England/053052/2021</i>	C
AIV07-B2 ^a	<i>A/greylag goose/England/054503/2021</i>	C

UK H5 2.3.4.4b Genotype	UK Genotype Representative	EURL Equivalent Genotype
AIV07-B2 ^b	A/turkey/England/057679/2021	AL
AIV08	A/chicken/Wales/053969/2021	AH
AIV09	A/chicken/Scotland/054477/2021	AB
AIV20	A/turkey/England/016515/2022	AM
AIV48	A/chicken/England/085598/2022	BB
AIV55	A/chicken/England/069816/2021	AA
AIV73	A/chicken/England/118935/2022	CQ
AIV204	A/chicken/England/152082/2022	CP
AIV223	A/Humboldt penguin/England/161651/2022	CC
WB135 ^c	A/herring gull/England/324803/2022	BB
WB153	A/pheasant/England/251536/2022	CR
WB359	A/Pheasant/England/113701/2023	TBC ^d
AIV50	A/Chicken/Scotland/114160/2023	TBC ^d
	H5N3	
H5N3 HPAIV	A/peregrine falcon/Northern Ireland/AI102021-2/2021	G
	H5N5	
H5N5.1	A/Brent goose/England/095684/2020	D
H5N5.2	A/mute swan/Wales/048068/2020	E
H5N5.3	A/herring gull/England/123277/2023	I
	H5N8	
H5N8	A/greylag goose/England/032698/2020	A

^a Under the UK genotyping scheme the AIV07-B1 and AIV07-B2 are described as distinct genotypes due to divergence in the HA gene ([Pohlmann et al. 2022](#) and [Byrne et al. 2023](#)), however under the EURL scheme such a distinction is not made.

^b A/turkey/England/057679/2021 is classified as distinct from other AIV07-B2 sequences by the EURL genotyping scheme due a divergent NP gene segment based on phylogenetic analysis.

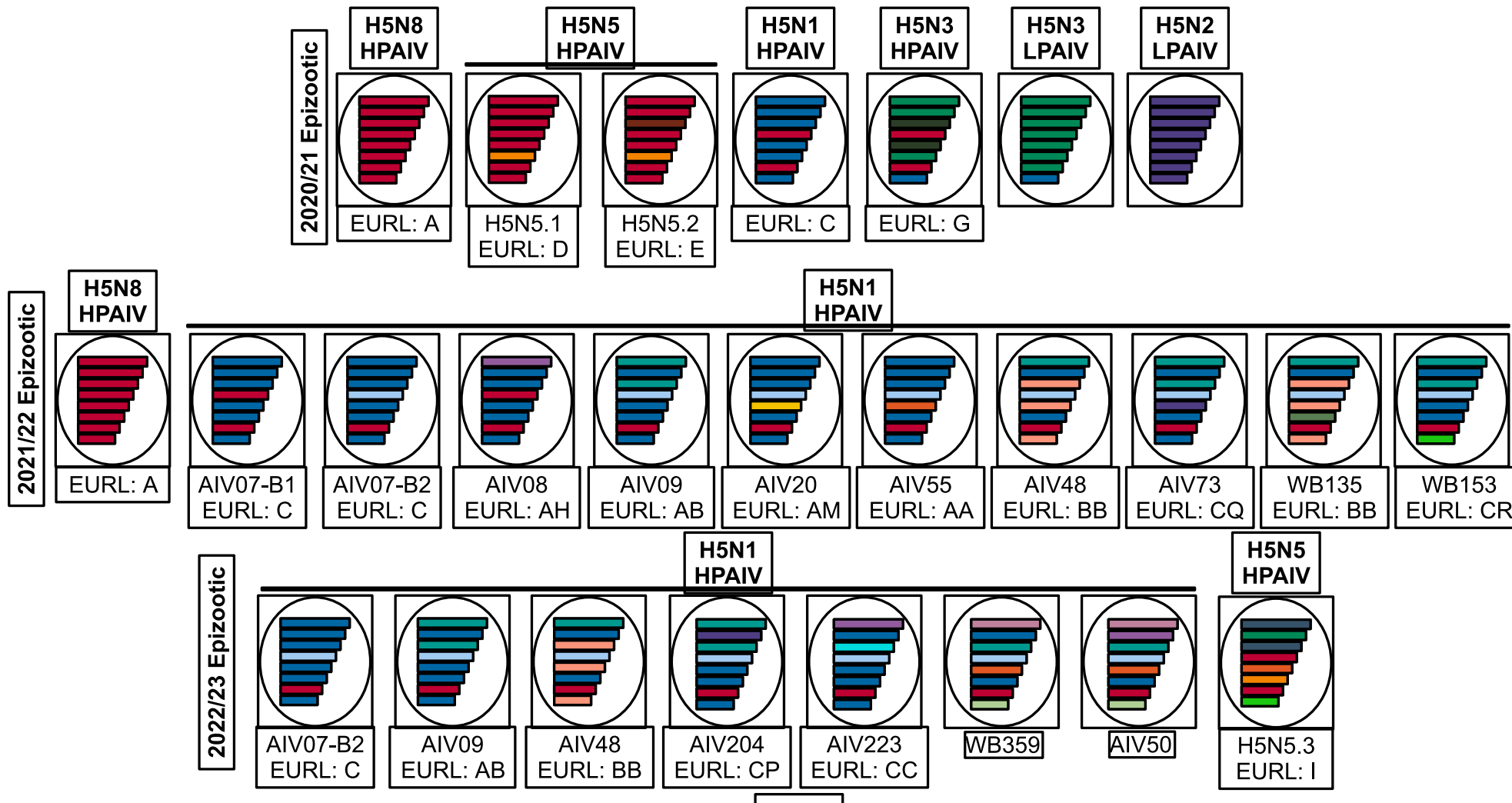
UK H5 2.3.4.4b Genotype	UK Genotype Representative	EURL Equivalent Genotype
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However, under the UK genotyping scheme, this does not constitute a new genotype as it shares >97% nucleotide identity to NP segments observed within AIV07-B2 sequences.

^c The UK genotyping scheme differentiates between the AIV48 and WB135 genotypes due to differences within the NA gene segment, however, this is not observed within the EURL scheme meaning both are considered to be of the AIV48/BB genotype.

^d The WB359 and AIV50 genotypes have not yet been described by the EURL, however, work is ongoing to determine the appropriate designation for these genotypes.

Figure 20: Genetic composition of genotypes detected across the 2020-2023 period according to each wave of infection.



From a genotype perspective, several genotypes detected and described for the 2021-2022 season continued to be detected during the 2022-2023 season. This included: AIV07-B2 (EURL: C), ([avian influenza epidemiology reports on GOV.UK](#)); AIV09 (EURL: AB), a genotype initially detected in Scotland in November 2021, but has since been detected across the UK in poultry and wild birds; and AIV48 (EURL: BB), a genotype initially detected in June 2022, being linked to disease in gulls and other wild birds, as well as poultry report cases. The AIV48 genotype is the result of reassortment between contemporary H5N1 viruses and AIVs with internal genes being most closely related to sequences from H13 and H16 viruses which are most commonly associated with gulls and have a different evolutionary ancestor to the Goose/Guangdong lineage H5 HPAIVs. The sequences from AIV48 viruses possess the same PB2 as the AIV09-like viruses that have been observed through the epizootic, with the PB1, NA and MP genes being shared with AIV07-like viruses, and the HA grouping within the AIV07B2 sub-lineage. For the PA, NP and NS, these sequences cluster with gull H13/H16 sequences obtained from Europe, Asia, and North America between 2007 and 2022. The closest relative across all gene segments is a H5N1 sequence collected from an unspecified gull in France during May 2022, followed by a H13N8 sequence obtained from a Black-headed gull in Belgium in December 2021 for the PA, NP, and NS segments only. Interestingly during the 2022-2023 season we also detected a non-notifiable H16N3 virus in a cloacal swab from a herring gull collected on 16 August 2023. Although we were unable to gain a virus isolate for the H16N3 virus we were able to generate partial sequence data for the virus and compared it to the AIV48 reference sequence. The comparison demonstrated that the AIV48 virus and the H16N3 had high genetic similarity to those segments which are derived from H16-gull viruses (PA:98.17%, NP:98.26% and NS:99.31%), whilst the other segments were more disparate (PB1:88.81% and MP:89.42%) and were more closely related to other H16/H13 viruses.

AIV204, detected in a chicken flock from Gloucestershire is an AIV09-like virus with a different PB1 (most closely related to European H5N2 and H5N5 viruses from 2021). Only a single instance of this genotype has been detected and it aligns with the EURL genotype CP.

Genotype AIV223 was initially detected in samples from Humboldt penguins from a zoo in Hampshire in December 2022, with subsequent detections in kept (N=3) and wild birds (N=6) until January 2023. This genotype has a B2 sub-lineage HA, consistent with other recent European H5N1 sequences, but the PB2 and PA segments are different to any other B2 H5N1s detected in the UK. The PB2 has a high identity (>98%) to that observed in the AIV08 genotype detected in October 2021 (which had a B1 HA). The PA is novel compared to UK sequences and shows high identity (>98%) with H5N1 PA segments from wild birds and poultry from the Czech Republic, Poland, France and the Netherlands detected between 2021 and 2022, as well as Eurasian LPAIV sequences. There are also sequences from the Netherlands (the EURL: CC genotype) that share the same entire gene constellation as AIV223 from November 2022.

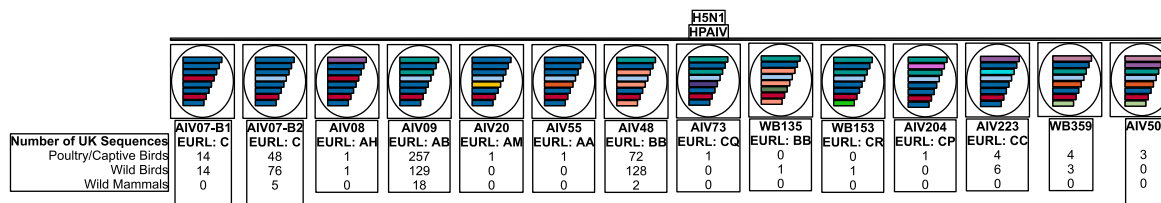
A further two H5N1 genotypes were detected at the tail end of the 2022-2023 season, namely AIV50 and WB363. Neither of these genotypes appear to have been detected elsewhere across the EU, based on publicly available data. WB359 was initially detected in sequences obtained from report case on a pheasant farm in Staffordshire (AIV2023 48) but has since been detected in pheasants (also from Staffordshire) that we received through wild bird passive surveillance. Based on previous nomenclature this genotype should be

called AIV2023-48. However, to avoid confusion in naming this genotype with AIV48 (EURL: BB) we have amended the name to WB359, the first wild bird detection with this genotype. This genotype appears to be derived from AIV09, but with a novel PB2, NP and NS segments. This PB2 has not previously been detected in UK AIV sequences during the epizootic but has been observed in sequences from Europe and is found in a number of the genotypes described by the EURL. An analysis of this segment demonstrates high genetic similarity to AIV sequences of various subtypes from Europe, including H5 HPAIVs detected since 2020, with the closest match being a H5N3 LPAIV from Italy in September 2023. The NP has a high degree of genetic similarity to that which detected the AIV55 genotype, which was a genotype that was only detected on a single occasion on a chicken farm in December 2021, and has also been observed in a number of EURL H5 HPAIV genotypes. The NS has also not previously been observed in our UK genotypes, or the European H5 HPAIV genotypes, and a genetic analysis against available sequence data demonstrates high sequence similarity to European AIVs, including H5 LPAIVs from before 2020, but also H5N1 HPAIVs from South Africa (wild bird and poultry) from 2021. AIV50 was initially detected in sequences from AIV2023 50, a chicken layer premises in Aberdeenshire, but has since also been detected in a pheasant from Scotland (wild bird surveillance) and AIV2023 –54, backyard chickens also from Aberdeenshire in October 2023. This genotype is very similar in sequence identity to WB359 but differs on the PB1 segment. This PB1 segment has not been detected in UK H5 HPAIV genotypes previously but has been observed in three EURL H5 HPAIV genotypes (H5N1: AF and AG; H5N2: CJ). Genetic analysis against available sequences shows this segment has high similarity to Eurasian AIVs of various subtypes including H5N1 LPAIVs and HPAIVs, but also H11N9 sequences detected in the US in 2020. However, it should be noted that this PB1 did not share any similarity to that observed in the current North American H5N1 HPAIVs. Further, the PB1 from this genotype appears to be very similar genetically to the new H5N1 genotype detected in the Netherlands during November 2023 ([New variant bird flu virus in Renswoude – WUR](#)), but that genotype still appears to be mostly AIV09(AB)-like.

Interestingly an H5N5 HPAIV has also been detected in the UK, initially in a Herring Gull from the Northeast of England during September 2023. The sequence recovered from this detection was found to possess a high genetic identity to H5N5 HPAIV from Norway and Romania and was consistent with the EURL I genotype, which is the sole H5N5 HPAIV genotype observed in Europe since late 2021, although detections have been limited. Analysis of the NA segment also revealed a stalk deletion, observed in sequences from Norway and Russia also. Assessment of wild birds that test positive for H5Nx will include assessment for N5 wherever N1 negative throughout the 2023-24 season.

The overall frequency of H5N1 HPAIV genotype detections across the entire epizootic period is detailed in Figure 3. In total 14 distinct genotypes of H5N1 have been detected since the beginning of the epizootic in 2020. As per Figure 21, the waves of genotypic dominance from both wild bird and report case detections have changed each season.

Figure 21: H5N1 HPAIV Genotype detection and distribution across poultry/captive birds, wild birds and wild mammals in the UK since October 2020.



The H5N1 AIV09 genotype was seen to dominate detections from the beginning of the 2022-2023 season and during the first month of the season an unprecedented number of report cases and wild bird positives were detected. As the outbreak reduced in intensity so did the number of report cases but AIV09 remained dominant into early 2023. However, during spring 2023 the AIV48 genotype that had first been detected during 2022 re-emerged causing a wave of gull mortality events both across the UK and Europe. AIV09 was last detected in May 2023. However, with a reduction in both wild bird positives and report cases towards the end of the season it is not clear what might dominate the coming season.

Detections of HPAIV in mammalian species

During the 2022 to 2023 administrative season a range of detections of HPAIV in mammalian species have also been reported. During the 2021-2022 outbreak period mammalian infection was detected in four otters and four foxes. Since then, a series of samples have tested positive across a range of species (Table 5).

Table 5: Mammalian samples tested under suspicion of infection with influenza A virus of avian origin 2022 – 2023 administrative season.

Species	Negatives	HPAIV H5N1	HPAIV H5Nx	Influenza A (non-H5 HPAIV)
Red fox (<i>Vulpes vulpes</i>)	27	6		
Otter (<i>Lutra lutra</i>)	55	5		
Badger (<i>Meles meles</i>)	1			
Grey seal (<i>Halichoerus grypus</i>)	48	5		
Harbour seal (common seal, <i>Phoca vitulina</i>)	53	2		1
Harp seal (<i>Pagophilus groenlandicus</i>)	1			
Unspecified seal	40			
Stoat (<i>Mustela erminea</i>)	2			
Common Dolphin (<i>Delphinus delphis</i>)	35	1	1	

Species	Negatives	HPAIV H5N1	HPAIV H5Nx	Influenza A (non-H5 HPAIV)
Harbour Porpoise (<i>Phocoena phocoena</i>)	4	1		
Pine marten (<i>Martes martes</i>)	1			
Total	267	20	1	1

Due to the extent of infection detected in wild bird species, a high level of environmental contamination most likely led to increased potential for infection with HPAIV in free-living wild mammals. Further, through triage of mammalian samples held in frozen storage by conservation groups, samples that had been collected from the wild prior to 01 Oct 2022 were occasionally received for diagnostic evaluation. In total, during this period, from 267 mammalian samples submitted for testing, 21 samples tested positive for H5Nx HPAIV (20xH5N1 and 1xH5Nx) and a single sample was positive for a non-H5, non-H7 influenza virus. Sequencing was attempted on all mammalian samples and sequence data was successfully generated for nine samples. From this sequence data, no genetic markers associated with significant adaptation to mammalian infection were detected. I

Of interest, an outbreak of influenza A of avian origin was also detected in a group of captive bush dogs in a wildlife collection. The infection was retrospectively detected following failure to detect other pathogens. Next generation sequencing was initially used to determine infection with HPAIV H5N1 and following this detection a full set of tissues and samples were assessed and the extent of infection was defined. In total, ten out a group of 15 bush dogs succumbed to infection with a range of clinical signs culminating in termination on welfare grounds or death of the animals. The most likely infection route is through ingestion of contaminated meat, either provided or following wild bird ingress into the enclosure. Genetic evaluation of the virus found that an AIV09 like virus was the infecting agent. No adaptive mutations were detected over those previously detected in mammalian positives and zoonotic risk remains low from this virus.

This highlights the need for surveillance of mammalian species for H5 AIVs, in combination with in-depth genomic analysis to better understand the ability of these viruses to cross species barriers, and the potential risk they may pose to public health.

Appendix 4 - Stakeholder engagement and biosecurity guidance

During this and previous reporting seasons of the HPAI H5N1 outbreak, the three administrations in Great Britain worked closely with APHA's NEEG veterinary field epidemiologists, virologists, operational staff and private veterinarians to engage with all affected sectors of the poultry industry (the stakeholders).

In this context, external stakeholders are individuals or groups outside government who can affect or be affected by the disease control policies for HPAI.

In addition to routine policy/operational liaison with the main stakeholders within the commercial sector (the Avian Core Group), there was also strong engagement with a broad range of other kept bird sectors to provide regular updates on the disease situation within the UK, Europe and worldwide and facilitate discussions of issues arising.

These included the:

1. The Avian Influenza Outbreak and Biosecurity Communications Stakeholder Group – includes some of the Core Group and the wider interested parties for example, hobbyists, the Poultry Club (pedigree birds and the show sector), birds of prey, racing pigeons and waterfowl groups.
2. The Avian Influenza Outbreak Gamebird Industry Focus Group.
3. The Avian Influenza Outbreak Birds of Prey Industry Focus Group.
4. The British Veterinary Poultry Association.

Using a variety of inclusive and accessible communication methods, including social media channels, they provided regular updates on the disease situation and shared information about commonly observed biosecurity deficiencies found on IPs. They also provided practical advice about measures that could be taken to reduce the likelihood of incursion of the virus onto poultry (and other captive bird) holdings.

The Department for Environment, Food & Rural Affairs (Defra) hosted a number of webinars ("Stop the Spread") of presentations by policy colleagues, veterinary field epidemiologists and operational staff, for relevant stakeholder groups.

Examples of these can be seen at:

['Stop the spread' webinars - GOV.UK \(www.gov.uk\)](http://www.gov.uk)

Additional webinars were hosted by Scottish and Welsh Governments:

1. Scottish Government: "Defend your flock: best practice biosecurity workshop"
2. Welsh Government: "Addressing Highly Pathogenic Avian Influenza in Wales"

Throughout each reporting season the APHA NEEG Field Epidemiology team and APHA Operational colleagues held online meetings with a number of large integrated commercial poultry companies with IPs in order to present the findings of epidemiological investigations into their individual outbreaks and provided advice on potential biosecurity improvements.

Following requests from industry the APHA NEEG Field Epidemiology team collated a photo library of observed examples of both good and suboptimal biosecurity from a variety of poultry premises (IPs and other premises visited for for example, licencing and biosecurity assessments of premises). Working closely with other poultry industry bodies this guidance was shared with poultry producers:

[Biosecurity photobook highlights good practice - The British Poultry Council](#)

The three administrations have published biosecurity checklists for avian influenza:

[Avian influenza prevention zone \(AIPZ\): biosecurity checklist for bird keepers - GOV.UK \(www.gov.uk\)](#)

[Biosecurity and preventing disease in poultry and kept birds | GOV.WALES Protecting+poultry+health+and+preventing+disease.pdf \(www.gov.scot\)](#)

APHA also worked with a private veterinary surgeon specialising in poultry to produce and publish short, practically informative videos aimed at the smallholder and hobbyist sector:

<https://youtu.be/y6wGh8tTnw0?si=zbcTRiCCohH3UQRJ>