



OFFLU call for avian influenza and wild bird situation update

5 December 2022

On 5th December 2022, OFFLU held an online discussion with experts of all regions representing many countries to share information on avian influenza situation in poultry and wild birds since 1st October 2022.

The goal of this meeting was to get an improved understanding of the current situation and share initial findings and experiences on the most recent wave of outbreaks in poultry and wild birds in different countries.

Participants:

Ian Brown (UK); Alice Fusaro (Italy); Timm Harder (Germany); Eric Niqueux, Beatrice Grasland (France); David Swayne, David Suarez, David Stallknecht, Jonathan Sleeman, Andy Ramey, Julianna Lenocho (USA); Yohannes Berhane (Canada); Dilmara Reischak (Brazil); Abdelsatar Arafa (Egypt); Celia Abolnik, Lia Rotherham (South Africa); Samantha Letsholo (Botswana); Clement Meseko (Nigeria); Hualan Chen, Yanbing Li, Jiming Chen (China); Viktor Irza (Russia); Yoshi Sakoda (Japan); Chakradhar Tosh (India); Youn-Jeong Lee and other experts (Rep. Korea), Andrew Breed, Les Sims (Australia); Ron Fouchier (Netherlands); Sasan Fereidouni, Pastor Alfonso (Cuba), Nestor Alfonso, Experts from Colombia; Lidewij Wiersma, Amelia Coggon, Akiko Kamata (FAO); Aspen Hammond and WHO GIP colleagues; Keith Hamilton, Gounalan Pavade (WOAH).

Japan:

This season to date there is already more outbreaks noticed compared to last winter in poultry. There are many outbreaks in chickens and a small number in ducks. The number of outbreaks detected in wild birds is unprecedented. Noted a change in wild bird species compared to last year – last year it was crows and this year cranes were affected (in addition to water birds both years). Incursions are caused by the same viruses which Europe and North America were experiencing in 2021-2022 which gives evidence for re-incursion due to migrating birds. The viruses currently causing disease are slightly different to what is found in European countries.

India:

There is active and passive surveillance in poultry and wild birds. Active surveillance is detecting predominantly H9N2 in chickens, ducks and wild birds and passive surveillance is detecting H5N1 virus in domestic ducks, chickens and wild birds. In the southern part of India there were outbreaks in ducks with clinical signs being seen including corneal opacity and

torticollis. The cleavage site of these viruses was confirmed as being highly pathogenic in chickens. Increased mortality was noted in backyard chickens, and H5N1 virus was confirmed. Gross pathology included congestion, oedema and haemorrhages in lungs. A wild dead bird (Pond heron) was confirmed with H5N1 virus infection.

Rep. of Korea:

There is a nationwide active surveillance program, particularly since the first detection of HPAI in wild birds this season. Broiler chickens are tested before movement to slaughter houses, broiler ducks are tested multiple times before movement to slaughter houses and other poultry farms are tested on a biweekly basis. So far there have been cases of HPAI reported in layers broilers, breeders, broilers and ducks. Most were reported due to the increase in dead birds and some were detected in periodic active surveillance including ad hoc active surveillance. HPAI H5N1 have been reported in wild birds including faecal samples, dead birds and captured wild birds. IVPI testing on the virus isolated from the index case confirmed HPAI, and transmissibility was also confirmed in chickens. These viruses have been identified as clade 2.3.4.4b viruses closely related to H5N1 viruses in Europe from 2021 and 2022. Several distinct genotypes identified including novel reassortants carrying internal genes of LPAIV have been detected.

China:

Since October China has not detected any H5N1 in wild birds or poultry. The last wild bird detection was in July 2022. Active avian influenza surveillance in wild birds is currently limited due to COVID-19 as no travel is allowed to carry out surveillance. Active surveillance is carried out in live bird markets and on farms. Viruses which have been detected most recently were similar to the vaccine seed strain. Vaccination is mandatory in all birds.

Australia:

No new HPAI outbreaks in Australia recently. Passive surveillance is carried out in wild birds and in poultry farms, there is also an active surveillance program in wild birds. More information can be found [here](#). A recent interesting publication on low pathogenic viruses summarising their transmission dynamics can be found [here](#).

Russia:

The most recent outbreaks were in the far east of Russia and Sakhalin Island on a broiler farm. This year the distribution of outbreaks is interesting and unusual compared to previous years. Russia has seen a mass mortality of crows at the same time as Japan reported mass mortality of crows.

Canada:

Canada is experiencing the second wave of outbreaks. The reassortant patterns of the virus differ depending on the flyway (segregated east to west). In the 2nd wave, we are seen newer reassortment patterns involving North American low pathogenic lineage segments compared to what we saw during the first wave. The majority of the Canadian outbreaks are caused by Newfoundland like GsGd lineage H5N1 viruses and its different reassortment variants. However, during the 2nd wave, we have at least 5 outbreaks in BC involving GsGd lineage H5N1 viruses that came to North America via the Pacific coast. We still see evidence of presence wholly Eurasian H5N1 viruses in the Atlantic coast and handful of cases in the

Mississippi flyway. Most of the outbreaks in domestic poultry are caused by different reassortant viruses. HPAI outbreaks in most of the domestic poultry premises were detected through passive surveillance (more than 90%), although some were through active high risk contact surveillance and others through active surveillance. We had few cases of outbreaks involving broilers with subclinical infection where presence of the virus was detected as a result of dead bird sampling. Wild bird species and domestic poultry are equally affected. Duck farms are overrepresented in these events especially in Quebec and Ontario. Summary of wild life cases can be found at the link below. List of wild mammals infected with the virus involved red foxes, striped skunks, black bears, seals and a dolphin.

<https://cfia-ncr.maps.arcgis.com/apps/dashboards/89c779e98cdf492c899df23e1c38fdbbc>

USA:

There have been 3 introductions into the US from Europe (2) and Asia (1). Active surveillance is carried out in wild birds in the United States. Over 3500 wild bird detections, more detailed information can be found [here](#). There are continued large mortality in wild geese dabbling ducks including teal as well as mammalian spill overs. Very little onward spread between farms is seen and most evidence is of wild bird introduction through contaminated environment into poultry farms or backyard birds. There is long term surveillance on blue winged teal which have shown this year to have higher incidence of HPAI than what is usually seen with LPAI viruses. In the southeast there are many black vultures (self-perpetuating probably due to contact) and also turkey vultures infected with HPAI. There are outbreaks in snow geese. Population effects are being seen in wild bird populations with significant ecological impacts of these. Challenge studies show that ducks are very susceptible and transmit easily the virus. Chickens have high mortality however there is no contact transmission. Turkeys appear to transmit the virus easier than chickens but not as well as turkeys.

Brazil:

RESUDIA is a network containing 9 countries which are doing active and passive surveillance in the region. This includes Argentina, Bolivia, Brazil, Colombia, Chile, Ecuador, Paraguay, Perú and Uruguay. LFDA-SP on behalf of RESUDIA has requested the support of FAO to provide reagents to countries in the region.

Colombia:

There have been 19 outbreaks so far. Two outbreaks have been detected in backyard flocks which had contact with wild ducks. Official national lab detected by RT PCR and sanger sequencing. Samples were sent to LFDA-SP for confirmation. LFDA-SP is supporting by sending reagents (RT-PCR and AGID).

Perú:

Detections in Pelicans, and backyard poultry.

Ecuador:

Unusual mortality was seen in laying hens and confirmation of H5 was achieved by RT-PCR. LFDA-SP is providing technical support to the country and sending kits and receiving samples for confirmation.

Venezuela:

A state of alert in the coastal states after detecting presence of H5 in pelicans. No more information is available.

Nigeria:

The current outbreak started in December in 2021, this has continued in many administrative regions of Nigeria throughout 2022. Many different domestic species have been affected including chickens, ducks, waterfowl and guineafowl. A few cases have also been confirmed in wild waterfowl, geese and other birds. While H5N1 dominates there are also cases of H5N8 and H9N2. There were suspected reassortants of these viruses to H5N2. It looks like there is persistence of what was introduced last year. The last confirmed case was on the 2nd December 2022.

Egypt:

Active and passive surveillance is carried out in poultry from farms, backyard poultry and live bird markets. In the last 2 months there have been few cases reported (4 H5N8 and 9 H9N2). In 2022, there have been H5N8 positive cases in commercial farms, household birds, slaughterhouses and the majority have been in live bird markets. There has been one H5N1 case during 2022. The H5 peak of infection last year was in January to April. The viruses sequenced are clade 2.3.4.4b however there are a few different clusters arising in Egypt.

Since October 2022 there have been no detections in wild birds or mammals due to limited surveillance activity in wild birds. Vaccination is used in Egypt and vaccines are evaluated against 2021/2022 circulating strains. H5N1 viruses from 2021/22 were characterised from wild migratory birds and were sequenced. Symptoms from 6 cases ranged from neurological signs to dead. Phylogenetic analysis of the HA and NA genes show a monophyletic group of Egyptian viruses of clade 2.3.4.4b. They make two groups clustering with viruses from 2021 in Africa and some others more similar to American poultry viruses. Other genes show there have been reassortment of these viruses with low pathogenic viruses.

South Africa:

The peak of the epidemic was in 2021 however there has been persistence of cases into 2022 which is unusual. The last cases in coastal seabirds were in August however it's expected to pick up in December. In October there were spill over cases into poultry and the most recent is outbreaks in ostriches. There isn't much active surveillance in wild birds however this will recommence the beginning of February. Active surveillance is still carried out in poultry. There are currently no die offs reported in wild birds. An H5N2 HPAI reassortant which was reported 2 weeks ago in backyard poultry however there is the possibility that this is a mixed infection as there is H6N2 LPAI present in the country, but this is pending deep sequencing data for confirmation. 90-100 genomes published hopefully in the new year. There are many point introductions in H5N1 viruses and little evidence of lateral spread but there is no reassortment with wild bird viruses, one mixed infection with H9N2 (K3 lineage).

Botswana:

The first outbreak of AI in the country was last year between June and September 2021 which was similar to other H5N1s found in the region of clade 2.3.4.4b including chickens and the African fish eagle. Active surveillance is carried out in wildlife and domestic poultry, but no outbreaks reported since September 2021.

Europe overview:

H5N1 (2.3.4.4b) Outbreaks in wild birds and poultry this season have been reported in 23 countries in Europe. The EURL has sequenced and deposited whole genome sequence data onto GISAID from 11 European countries so far. There are 10 different genotypes with the majority belonging to 3 different genotypes which have been persistent in Europe this summer. Many of these genotypes have emerged from local reassortment events based on genetic information available. There has been spill over events into mammals. Genetic analysis of viruses from an H5N1 outbreak on a Mink farm belong to a genotype which has been detected in Europe for the first time in spring. This genotype is a consequence of the high virus circulation in seabirds over the summer months and reassortment with gull adapted H13 subtype. This has been identified in multiple countries mainly in wild birds but has also responsible for a case in another mammalian species. There has also been detection of a genotype possessing a reassortant PB2 gene segment which had not previously been identified in Europe which was responsible for outbreaks in layers.

France:

This season there have been high mortality in Gulls (caused by the same genotype as described above) and Gannets (unique genotype) along the northern coast of France between May and September. Since August there have been many detections in wild birds. For poultry, there is an increase in the last week of poultry farms affected particularly in the west of France. There are also many backyard farms affected which points to introductions from wild birds. There have been 3 genotypes which have been detected but one majority genotype. Vaccine challenge studies using RNA and subunit vaccines are underway in ducks to evaluate the protection and shedding and challenge to evaluate transmission will be carried out in January 2023.

Germany:

Situation is the same as described in the rest of Europe. There are H5N1 2.3.4.4b transmission studies underway in pigs. Viruses were inoculated intranasally or alimentally. Over 2 weeks no clinical signs were observed. There was scattered and discrete virus shedding at day 2 for the intranasally infected group and day 4 for the alimentally infected group. There were no gross pathological changes and low virus loads in very few tissues including lung. Only one pig which had been inoculated by ingestion of a virus-infected embryonated chicken egg had seroconverted. There was no virus excretion or seroconversion in contact pigs. It seems that pigs are largely resistant to H5N1 infection.

UK:

Skewed epidemic which has occurred early on this season. Poultry cases in backyard flocks all around the coast and inland. As others reported this virus is primary introduction from wild birds and not due to lateral spread. About 30% flocks are backyard. Most of the commercial poultry sector is affected and there have been increases in game birds including wild and captive pheasants. Raptors have been highly susceptible and many more layer hens than what we have seen in the past. There have been variable clinical signs in broilers as reported by others but also cases with severe disease signs and rapid spread amongst a large number of birds. In wild birds there were peaks of this virus in summer in ecologically important populations of seabirds with global relevance. The virus has been transmitting in colonies with closely nesting seabirds allowing for easy spread of virus. The toll on these populations is one

of concern as they have low reproductive rates and environmental persistence in sites. This group of H5N1 viruses seem to have a propensity to spread to a wider range of hosts. This could be due to much greater environmental contamination which leads to more exposure risk for a greater range of species. There have also been spill over into mammals of scavengers of sick or dead birds which tend to suffer neurological disease. Genetically there aren't any consistent changes which indicate an elevated risk of a particular type of viruses. Genotypically there are one or two genotypes which dominate however numerous different genotypes.

General comments:

OFFLU could strive to support network members and improve the connected response to avian influenza outbreaks including advocating for surveillance in wild birds in certain regions and advances in bioinformatic analysis, capacity building including proficiency testing support and reagent support for Next Generation Sequencing. Challenges were discussed including the difficulties in the control of the virus due to the high viral load in wild birds, the lack of international genetic nomenclature for the virus and the need to look at risk management.

Action points:

- Aim to schedule follow up call for situation update in 3 months' time (Secretariat)
- Discuss on AI risk management based on epidemiology of circulating strains (Epidemiology technical activity group)
- Discuss genotype nomenclature like HA based system (AI technical activity)
- There is a lack of background surveillance in wild birds for non H5 viruses and that is really hampering understanding virus evolution. Advocate for surveillance in wild birds in all regions, Advance bioinformatic analysis, capacity building including sequencing, PT support and NGS reagent support (technical activity leads).

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