

Highly pathogenic avian influenza outbreaks for four consecutive seasons

An excerpt from the Report on the epidemiological investigation of the highly pathogenic avian influenza outbreaks during the 2023-2024 Season

The 2023-2024 season (hereinafter referred to as “the season”) marked the four consecutive seasons of outbreaks of highly pathogenic avian influenza (HPAI). The number of outbreaks in wild birds was the second highest, following the last season, while outbreaks in domestic poultry were limited to 11 cases in 10 prefectures.

Outbreaks in domestic poultry

This season, the first outbreak was confirmed on November 25, 2023, at a layer farm in Saga Prefecture. A total of 11 cases (10 cases of H5N1 and 1 case of H5N6) were confirmed at the premises for layers, broilers, breeders, and multiple poultry species, including domestic ducks and geese in 10 prefectures until the last case was confirmed on April 29, 2024, and a total of approximately 860,000 birds were destroyed. Although both the number of outbreaks and the number of birds destroyed were lower than the previous season’s record of 84 outbreaks in 26 prefectures, which was the largest epidemic on record, this was the first

time that HPAI outbreaks occurred in Japan for four consecutive seasons since the 2020-2021 season. Following the first outbreak reported in Kyushu region (Saga Prefecture), outbreaks have been observed nationwide in Kanto region (Ibaraki, Saitama, Gunma, and Chiba Prefectures), Kyushu region (Kagoshima Prefecture), Tokai region (Gifu Prefecture), Chugoku region (Hiroshima and Yamaguchi Prefectures), and Shikoku region (Kagawa Prefecture) (Chart S 1-1). Only two cases occurred within the same prefecture. In those cases, the farms were located 70 km or more apart, suggesting that there was no farm-to-farm transmission in neighboring farms.

Out of these 11 cases, layers farms accounted for the largest number of cases (8), followed by broilers (1), breeders (1), and multiple poultry species (1). The largest farm size was about 360,000 birds in the fifth case, which occurred in Gunma Prefecture, while the other cases involved farms with less than 100,000 birds. In the previous season, four of the 61 outbreaks among layer farms occurred on large-scale farms with more than 1 million birds, but there were no outbreaks on such large-scale farms this season. As in the past, many

of the affected farms had ponds, rivers, waterways, or rice paddies around which ducks and other waterfowl could gather. Additionally, many farms had woods where crows and other wild birds and wild animals could be based. In some cases, HPAI viruses (HPAIV) have been detected in dead crows found in the vicinity of the affected farm or on the farm property, and it is considered that crows may have been the source of infection.

In all cases, the national and prefectural governments, relevant agencies, organizations, municipalities, and the Self-Defense Forces cooperated to implement prompt control measures. All measures were completed on May 4, 2024, and all movement restrictions were lifted on May 26. Subsequently, Japan submitted a self-declaration of disease-free status for HPAI to WOA on June 2, 2024.

HPAI cases in wild birds

The first report of HPAIV infection in wild birds was in a large-billed crow recovered in Bibai City in Hokkaido on October 4, 2023, followed by a case in Eastern buzzard collected in Kushiro, Hokkaido on October 18.

156 HPAI cases in wild birds were confirmed in 64 cities in 28 prefectures until the last case confirmed in a large-billed crow in Sapporo city, Hokkaido on April 30, 2024. These cases were confirmed with not only the samples collected from carcasses of wild birds, but also includes 5 cases with fecal matter from ducks and other birds, and environmental water samples, and one case with a blow fly sample. H5N1 was identified in 123 cases, H5N5 in 31 cases, and H5N6 in one case. Additionally, both H5N1 and H5N5 HPAIV were simultaneously detected in one case. The first case was found in early October, and the number of cases began to increase gradually, peaking in mid-November to mid-December. The next peak was observed from mid-February to mid-March (Chart S1-2). These peaks coincide with the arrival of migratory birds in Japan during the fall migration and the spring migration from wintering grounds to breeding grounds. In terms of bird species, there were 38 cases of 8 species of waterfowls, 14 cases of 5 species of waterbirds other than waterfowls, 20 cases of 7 species of birds of raptors, and 74 cases of 3 species of crows.

Chart S1-1 Location of the confirmed HPAI cases in poultry and wild birds during the 2023-2024 season

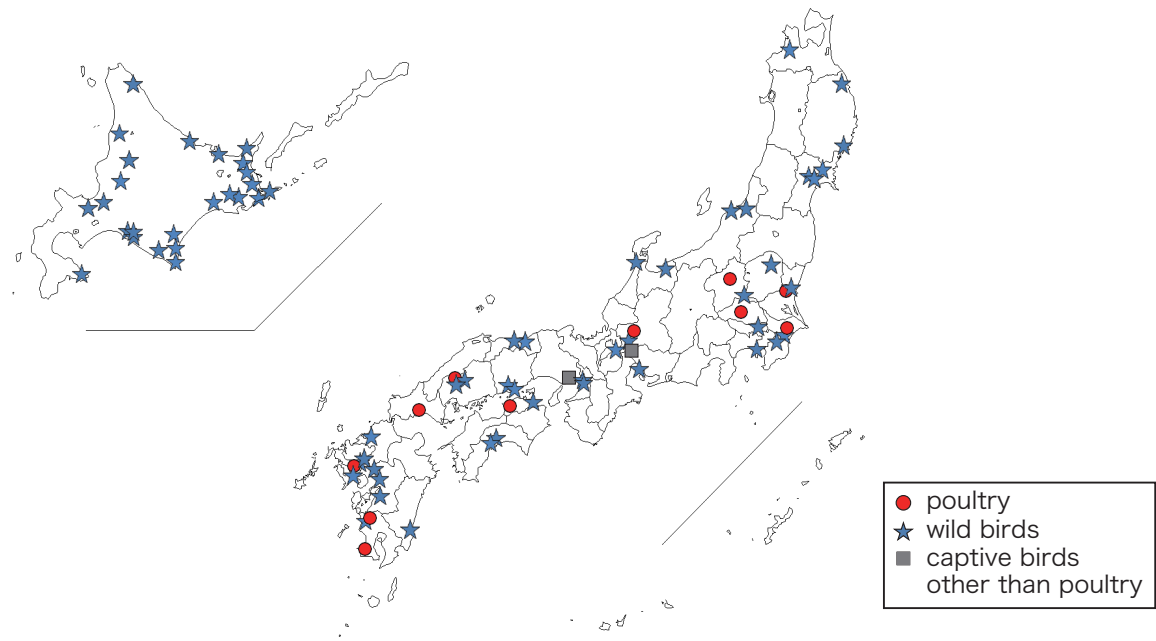
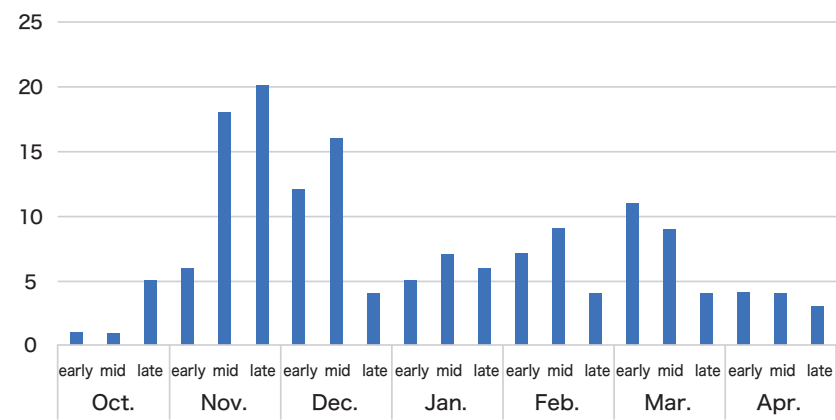


Chart S1-2 Number of HPAI cases in wild birds



Characteristics of the HPAIV isolated in this season

Of the 11 outbreaks in poultry this season, H5N6 HPAIV was isolated only in the ninth case, and H5N1 HPAIV was isolated in the rest of 10 cases. Based on the genomic analysis of the HA gene segment of the HPAIVs, all HPAIVs isolated from poultry cases in this season belonged to Clade 2.3.4.4b. The HA genes were classified into two groups: The H5N1 subtype was classified as a group closely related to the 2021-2022 European isolates (G2d), and the H5N6 subtype was classified as a group closely related to the 2021 West Siberian and Central and Southern Chinese isolates (G2c). On the other hand, HA genes of the H5N5 subtype detected only in wild birds were classified into two groups: a group closely related to the 2020-2021 European isolates(G2a) and G2d.

Further classification based on a combination of eight gene segments of HPAIV isolated from poultry cases resulted in two groups of HPAIV, which were clas-

sified as G2d-0 and G2c-12, respectively. G2a-2 and G2d-4 were detected in HPAIV isolated from wild birds and environmental samples in addition to the two genotypes detected in poultry. In summary, a total of four types of reassortment viruses, G2a-2, G2d-0, G2d-4, and G2c-12, have intruded into Japan this season (Chart S1-3).

The G2d-0 virus, which was detected in most cases in poultry this season, was also detected in poultry in the 2021-2022 and 2022-2023 seasons. However, since it is unlikely that the virus was maintained in wild birds and poultry during the summer with high temperatures, it is plausible to consider that the virus prevalent this season was reintroduced into Japan by migratory birds.

Since the G2c-12 virus possessed gene segments derived from avian influenza viruses circulating among wild waterfowl, it is thought that the G2c virus was brought to breeding and stopover sites in Siberia during the northward migration of migratory birds and

spread among migratory birds at these sites, caused reassortment with viruses circulating among waterfowl (Chart S1-4, Chart S1-5).

The viruses obtained from crows that died on or near the farm premises at the three outbreak farms, from environmental samples including flies, and from the carcass of a black rat found in the poultry shed on the affected premises showed a high degree of genetic similarity to the H5N1 HPAIV isolated from the poultry on the respective case farms. While this suggests that these animals may have been a source of virus introduction to the farms, it is also possible that wild birds and small animals on or near the outbreak farms may have become infected with HPAIV as a result of spill-over from the affected farms. All chickens inoculated intranasally with high doses of two different viruses (H5N1 and H5N6) isolated from poultry cases in this season died within a few days. In fact, the number of dead chickens in the HPAI outbreaks actually increased over time. These findings suggested that increased

mortality in poultry is a good indicator for early detection and early reporting of HPAI outbreaks.

For more information, please see the Report on epidemiological investigation of the highly pathogenic avian influenza outbreaks in the 2023-2024 Season.

https://www.maff.go.jp/j/syoutan/douei/tori/attach/pdf/r5_hpai_kokunai-153.pdf

Chart S1-3 Genetic diversity of HPAIV of H5N1, H5N5 and H5N6 HPAI virus based on phylogenetic analysis targeting 8 segments

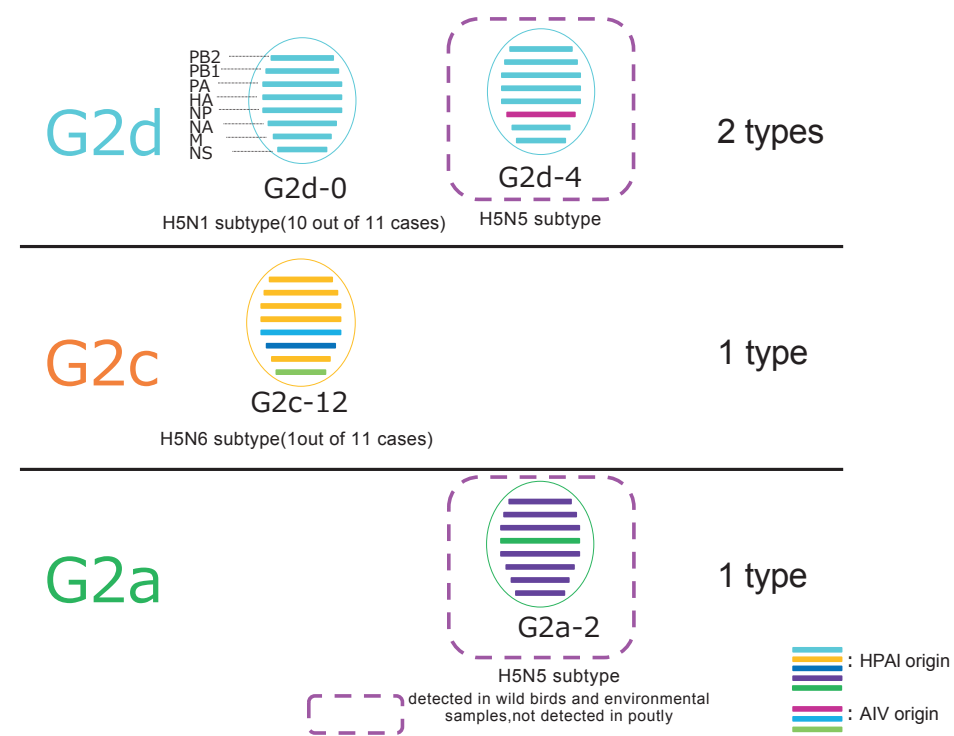
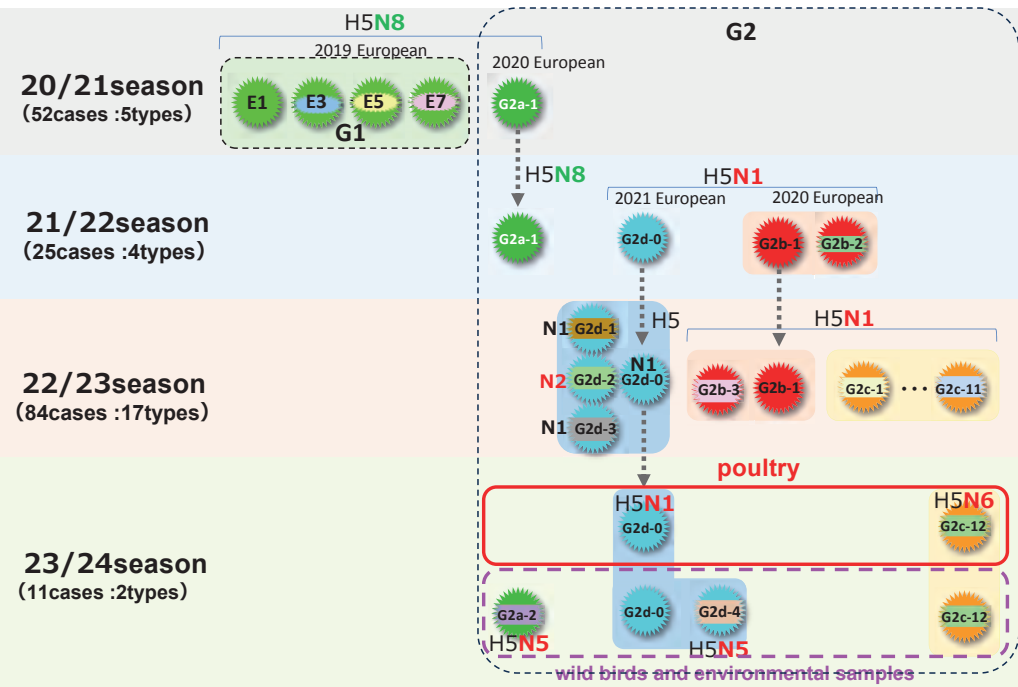


Chart S1-5 Transition of genotypes of HPAIV recovered in 2020-2021, 2021-2022, 2022-2023, 2023-2024 seasons



Source: Report on epidemiological investigation of the highly pathogenic avian influenza outbreaks in the 2021-2022, 2022-2023, 2023-2024 season