

The largest highly pathogenic avian influenza epidemic in Japan

An excerpt from the Report on the epidemiological investigation of the highly pathogenic avian influenza outbreaks during the 2022-2023 season

In the 2022-2023 season (hereinafter referred to as “this season”), Japan experienced the largest highly pathogenic avian influenza (HPAI) epidemic in its history. Between the first outbreak in the poultry farm on October 28, 2022, and the last outbreak on April 7 of the following year, a total of 84 outbreaks in 26 prefectures were confirmed in poultry premises, and approximately 17.71 million birds were culled. A total of 242 cases of HPAI virus infection were also confirmed in wild birds.

Outbreaks in domestic poultry

The first two outbreaks of this season occurred in October 28, 2022, at a layer farm in Okayama Prefecture and a broiler farm in Hokkaido, which was the earliest date in comparison to previous years. Subsequently, until April 7 of the following year, a total of 84 cases (83 cases of H5N1 and 1 case of H5N2) were confirmed at poultry premises for layers, broilers, breeders, domes-

tic ducks, quails, ostrich, emus, and guinea fowls, and approximately 17.71 million domestic birds were subjected to culling. Although two consecutive seasons of outbreaks were previously confirmed in 2016-2017 and 2017-2018, this is the first time that three consecutive seasons have occurred, counting from the 2020-2021 season.

The outbreak began in the Chugoku and Hokkaido regions, followed by the Shikoku, Kanto, Kinki, Kyushu, Hokuriku, Tohoku, and Tokai regions, and finally, 26 prefectures from Hokkaido to Okinawa were affected (Fig.S1-1). This was the largest outbreak ever recorded in terms of the number of affected prefectures, outbreaks, and culling of birds. In 11 prefectures (Hokkaido, Gunma, Chiba, Niigata, Aichi, Shiga, Okayama, Hiroshima, Kagawa, Fukuoka, and Kagoshima), multiple outbreaks were observed within the 3km radius, and the possibility of disease spread among neighboring farms cannot be denied. There were also cases on farms that had experienced outbreaks in the past.

When affected farms were classified by use, the layer farms accounted for the largest number of cases (61).

Ten of them kept more than 500,000 birds, and the number of birds culled on these large layer farms accounted for 54% of the total number of birds culled. When compared by using the existing farm database, the layer farms tended to be more affected by HPAI than broiler farms. In addition, a comparison of the stocking size of affected farms and nearby non-outbreak farms for layer farms and broiler farms, respectively, showed that the stocking size of affected farms tended to be larger than that of non-affected farms in layer farms. Consistent with the outbreaks in the past, many of the affected farms were in the vicinity of ponds, rivers, waterways, rice paddies, etc., to which migratory birds may migrate. Some of the farms were located close to the coast. In addition, many affected farms were located near wooded areas suitable for wildlife, including wild birds. Wild birds such as crows and their traces were observed on the affected premises and surrounding woods at the time of on-site epidemiological investigation conducted following the outbreak. There have been cases where the HPAI virus has been detected in dead crows found near farms or on farm property,

and crows are thought to be a possible source of infection.

Many outbreaks were also observed in domesticated birds other than chickens, such as guinea fowl, accounting for 13% of all outbreaks. In addition, 10 cases of outbreaks in birds other than poultry kept at the exhibition facilities were confirmed in 6 prefectures.

Table S1-1 Number of cases in poultry by use

Use	Number of cases
layers(incl.growers)	61
broilers	11
breeding flock for broilers	1
ducks	7
quails	1
emus	2
guinea fowl	1
total	84

Fig. S1-1 Location of the confirmed HPAI cases in poultry and wild birds during the 2022-2023 season

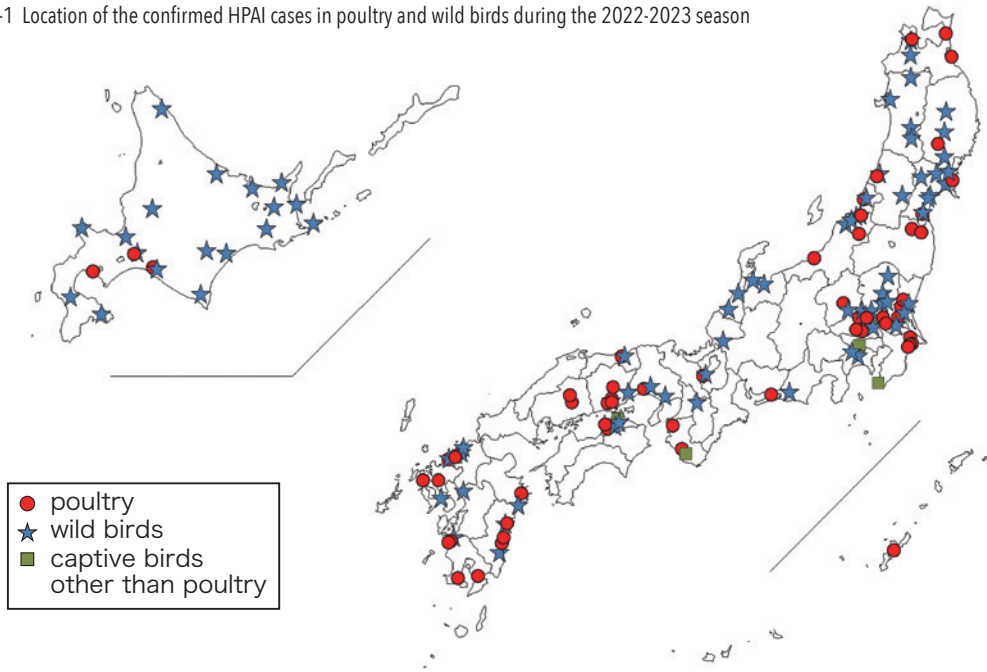
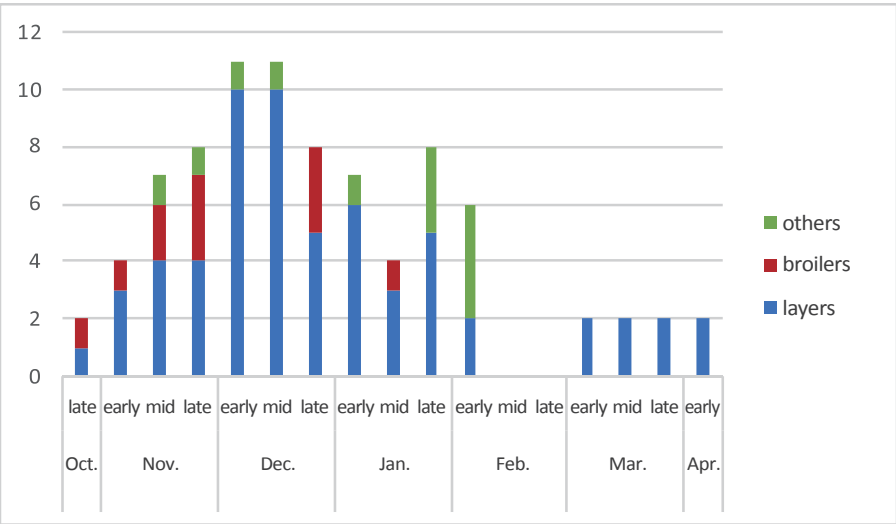


Fig. S1-2 Number of HPAI cases in poultry by month



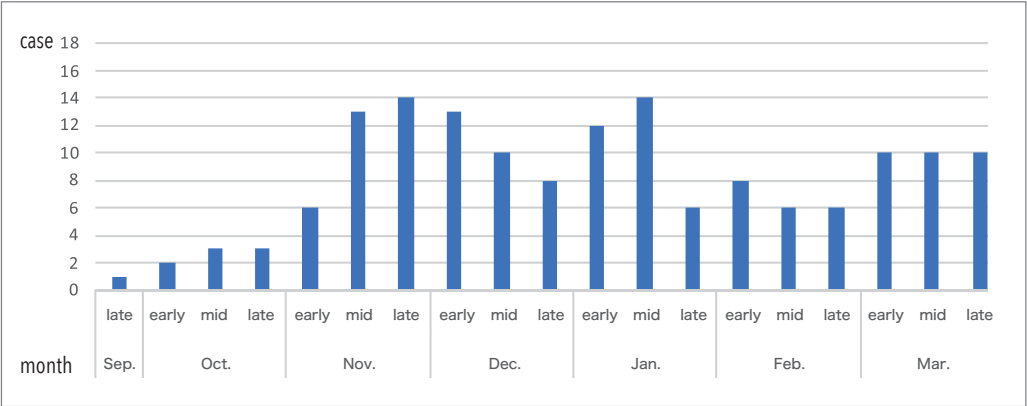
HPAI cases in wild birds

The first confirmed case of HPAIV infection in wild birds this season was a falcon recovered in Kanagawa Prefecture on September 25, 2022. Infections in wild birds were confirmed in 28 prefectures from Hokkaido to Kagoshima, including 19 prefectures where outbreaks in domestic poultry were also confirmed. Out of 242 wild bird cases, 79 cases were confirmed in Kagoshima prefecture. This is due to the large-scale infection of cranes in Izumi City and the regular surveillance of crane roosts for the virus, which makes it easy to detect infection.

Regarding bird species, a total of 242 cases were confirmed in 26 species, including 39 cases in 8 species of ducks (swans, geese, and ducks), 79 cases in 8

species of waterfowl other than ducks, 28 cases in 7 species of raptors, and 72 cases in 3 species of crows. This is the largest outbreak to date, both in terms of the variety of bird species and a number of cases. The fact that the first wild bird case detected in September was a falcon, a resident bird, and that several raptors were confirmed to be infected in other prefectures in October suggests that the infection had spread to some extent among wild birds that are preyed by raptors in the early stages of the fall migration season. In addition, as in the previous season, many cases were detected in crows, drawing more attention to crows as a potential source of infection to poultry. As for wild animals other than wild birds, an HPAIV-positive case of a dead fox in Hokkaido was reported.

Fig. S1-3 Number of HPAI-positive cases in wild birds



Response to HPAI outbreak in poultry

In the event of an outbreak of HPAI on poultry farms, response measures such as stamping-out of birds and proper disposal of carcasses were implemented based on the “Guidelines for the Prevention of Specific Domestic Animal Infectious Diseases Related to Highly Pathogenic Avian Influenza and Low Pathogenic Avian Influenza” (published by the Minister of Agriculture, Forestry and Fisheries on July 1, 2020). Prefectural governments, the MAFF, other relevant ministries and agencies, the National Livestock Breeding Center, relevant institutions and organizations, municipalities, the Self-Defense Forces and other relevant parties cooperated in implementing of these measures. To conduct containment measures on affected farms, prefectural governments, municipalities, Japan agricultural cooperatives and other agriculture-related organizations, construction organizations, carbon dioxide gas suppliers, pest control organizations, DIY stores, and other material suppliers actively cooperated. In addition, per-

sonnel and stockpiles were shared from other prefectures. As a result, on-farm containment measures were implemented promptly and smoothly.

Despite the largest epidemics on record, these efforts resulted in an average of 7.1 days to complete on-farm containment measures, compared to 11.0 days in the 2020-2021 season. Containment measures were completed more quickly than in past seasons, particularly for farms with more than 500,000 birds, with 19.6 days this season compared to 28.0 days in the 2020-2021 season. In addition, the National Institute of Animal Health (NIAH) of the National Agriculture and Food Research Organization (NARO) was on duty 24 hours to provide prompt confirmation in order to take response measures as soon as possible. No new outbreaks were confirmed after the outbreak at a layer farm in Hokkaido on April 7, and all containment measures were completed on April 14. All movement restrictions were lifted on May 6. Accordingly, Japan’s free status for HPAI has been recovered with a start date of May 13, 2023.



Photo courtesy of Kagoshima Prefecture

Characteristics of the HPAIV isolated in this season

Based on the genomic analysis of the HA gene segment of all HPAIVs isolated from the poultry cases in this season, HPAIVs were classified into three groups (20E, 21E, and 21RC) that are closely related to the European strains of the 2020 season, the European strains of the 2021 season, and the West Siberian and Chinese strains of the 2021 season. Furthermore, the results of the whole genome analysis of the eight gene segments revealed that a total of 17 genotypes including two types of 20E, four types of 21E, and 11 types of 21RC were introduced when classified into genotypes based on their combinations (Fig.S1-4).

Viruses in groups 20E, 21RC, and 21E were shown to be closely related to viruses isolated from wild birds in Japan this season. The 21RC and 21E groups were also shown to be closely related to viruses isolated from wild birds and poultry outside Japan this season. Some of the viruses were found to have the same origin of all eight gene segments as the viruses from last season's outbreak in domestic birds (Fig. S1-5). It is unlikely, however, that last season's viruses were maintained among poultry and wild birds but instead were transported to breeding sites of migratory birds located outside of Japan during the summer and reintroduced

into Japan with the arrival of migratory birds this season. The reason for this assumption is that the virus is difficult to survive in the environment, and it was not detected during the summer months (May to mid-September 2022) when migratory birds, which play an important role in the circulation and maintenance of the virus, were not present. It is considered that these three groups of viruses were introduced into Japan almost simultaneously and have been maintained and spread throughout the country for some period of time.

In terms of virulence, this season marked the most diverse genotypes of viruses ever seen in the country. Although all of them had a 100% fatality rate when successfully infected by inoculation tests on chickens, there were differences in the time to death and potential to spread infection.

Given the current situation of outbreaks in various parts of the world and the emergence of diverse viruses, the risk of an outbreak of HPAI in Japan is still considered high. For more information, please see the Report on the epidemiological investigation or the highly pathogenic avian influenza outbreaks in the 2022-2023 Season.

<https://www.maff.go.jp/j/syouan/douei/tori/attach/pdf/220929-301.pdf>

Fig.S1-4 Genetic diversity of H5N1 and H5N2 HPAI virus based on phylogenetic analysis targeting 8 segments

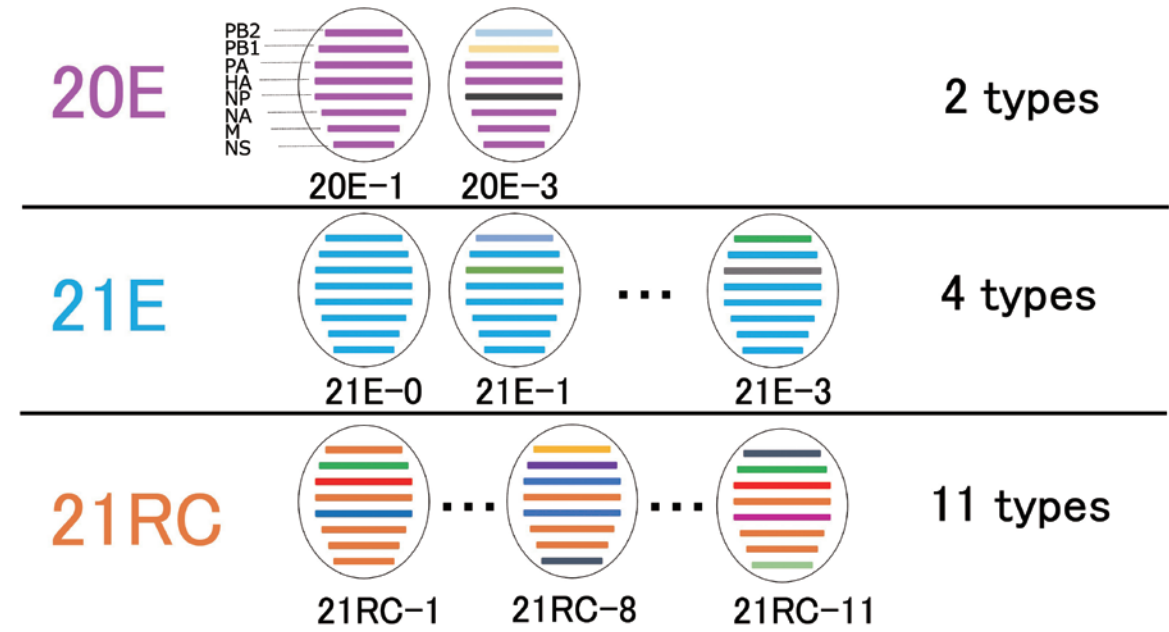


Fig. S1-5 Transition of genotypes of HPAI virus recovered during 2021, 2021-2022 and 2022\2023 seasons based on combination of segments

