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Original Article

Retrospective Investigation Of Highly Pathogenic Avian Influenza Outbreaks In Iran During 2015-2021

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Abstract

Highly pathogenic avian influenza (HPAI) is responsible for severe outbreaks in domestic and wild poultry. Furthermore, the disease has zoonotic potential posing great risk to human's health worldwide. In current study the spatial and temporal distribution of HPAI outbreaks in Iran during 2015 to 2021 were evaluated using the information obtained from the OIE World Animal Health Information Database (WAHIS). During the period of study, 90 outbreaks were reported from 17 (54%) provinces. The highest number of outbreaks were reported from South Khorasan province (28%) followed by Mazandaran (14%). The outbreaks occurred throughout the year with no significant difference between two semesters ($p>0.05$). The majority of outbreaks occurred in domestic poultry (85%). The identified subtypes were H5N8 (90%) followed by H5N1 (3%) and H5N6 (1%). Co-occurrence of H5N8 and H5N1 subtypes observed in 5% of outbreaks. The incidence of subtypes with zoonotic potential (H5N1, H5N6) pose a continued risk to public health. One health approach and inter-sectoral cooperation is recommended for early detection and reporting of HPAI outbreaks with more focus on high-risk areas.

Keywords: Highly pathogenic avian influenza, Iran, Outbreak, Retrospective

Introduction

Avian influenza is known as a highly contagious and zoonotic disease of domestic and wild avian species. The etiologic agent type A influenza virus belongs to Orthomyxoviridae genus Influenzavirus (1). There are 16 known serologically distinct subtypes based on the surface hemagglutinins and 9 based on neuraminidases (2). Avian influenza viruses are divided into the highly pathogenic avian influenza (HPAI) and the low pathogenic avian influenza virus (LPAI). HPAI viruses cause acute systemic disease with high morbidity and mortality (3). Aquatic wild birds are considered as a natural host for the virus with mild and self-limiting illness (4). In favorable environmental conditions, the virus remains infective for more than 6 months contributing to the sustained endemic transmission of the virus in the natural host populations (5).

AI virus is transmitted from wild birds to domestic poultry with remarkable socioeconomic consequences. High morbidity and a case fatality rate is observed in chickens following infection with HPAI viruses (6). Furthermore, accidental transmission of AI virus from infected birds to humans occurs sporadically. Since 1959 more than 1500 human cases of avian influenza have been reported and the majority of cases caused following infection with HPAI virus H5N1 (4). In Iran, the first case of H5N1 was reported from wild birds in 2006 (7). The virus is transmitted to humans following contact with sick or asymptomatic infected poultry (8).

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The high majority of the population in Iran depends on agriculture as a way of livelihood. During the past decades, industrial and backyard poultry breeding has increased remarkably which potentially increase the possible public health threat of avian influenza.

Moreover, there are several live bird markets in different parts of Iran which further substantiate the likelihood of avian influenza transmission to humans (9). Globally more than 15,000 outbreaks were reported to the World Organization for Animal Health (OIE) in domestic birds from 2005 to 2018 (10).

Deep understanding the spatial and temporal distribution of HPAI is essential to develop a preventive plan and controlling future outbreaks. In this study, we described the spatial and temporal distribution of HPAI outbreaks in Iran from January 2015 to April 2021. The findings of this study will contribute to determine times, high risk areas and hosts most associated with infection in Iran.

Methods

Sources of Data

We obtained data for all reported HPAI outbreaks in poultry between January 2015 to April 2021 from the World Animal Health (OIE) Information Database (WAHIS) (11). The data included date of outbreak onset (year), semester (January-June, July-December), place of outbreak, identified serotype or subtype, animal category (domestic, wild), affected species, number of cases and number of recorded deaths for each outbreak.

Data Analysis

The data were transferred to a spreadsheet program (Excel 2016, Microsoft). Descriptive statistical analysis was conducted to examine the frequencies and annual patterns of HPAI outbreaks. The data were checked for normality using the Shapiro-Wilk Test. We obtained a p-value of < 0.05 showing non-normality of the distribution. The differences in number of outbreaks between semesters were investigated using the non-parametric Mann–Whitney U test for independent samples. The spatial distribution of HPAI virus subtypes was determined. Data analysis was performed using Microsoft Excel 2016 and STATA version 14.00 (Stata Corp, Texas, USA). A p-value of < 0.05 was considered as the significance level. ArcGIS 10.1 was used to create the maps.

Results

A total of 90 HPAI outbreaks were reported during study period, with an average of 7 outbreaks per semester. The number of outbreaks in each year is shown in Figure1. The highest number of outbreaks were occurred in first semester of 2021 (42%) followed by 2017 (17%).

The median number of outbreaks was not different between two semesters ($p=0.611$). During this period, 1762231 and 1376 cases were recorded in domestic poultry and wild birds respectively. Totally, 65833 deaths were recorded and 2778487 domestic poultry killed and disposed. The majority of outbreaks occurred in domestic poultry (n=77, 85%).The wild species affected were Whooper Swan, Little Grebe, Hooded Crow, Gadwall, Greylag goose, White Stork and Common Coot. The spatial distribution of outbreaks is shown in Figure 2. The outbreaks were reported from 17 out of 31 provinces.

The highest number of outbreaks occurred in Sarbisheh county in South Khorasan province (28%) followed by Mazandaran (14%). The data on virus subtypes showed that the majority of outbreaks were occurred by subtype H5N8 (90%) followed by H5N1 (3%) and H5N6 (1%). In five outbreaks both H5N8 and H5N1 subtypes were reported. The distribution of subtypes is shown in Figure2.

Discussion

Despite intensive preventive and control measures, HPAI still occurs in many countries of the world. To better understanding the epidemiology of HPAI outbreaks in Iran, we described the geographical and temporal occurrence of HPAI using retrospective data between 2015 and 2021. HPAI is listed as a notifiable disease by the OIE. Following the identification of birds with clinical signs

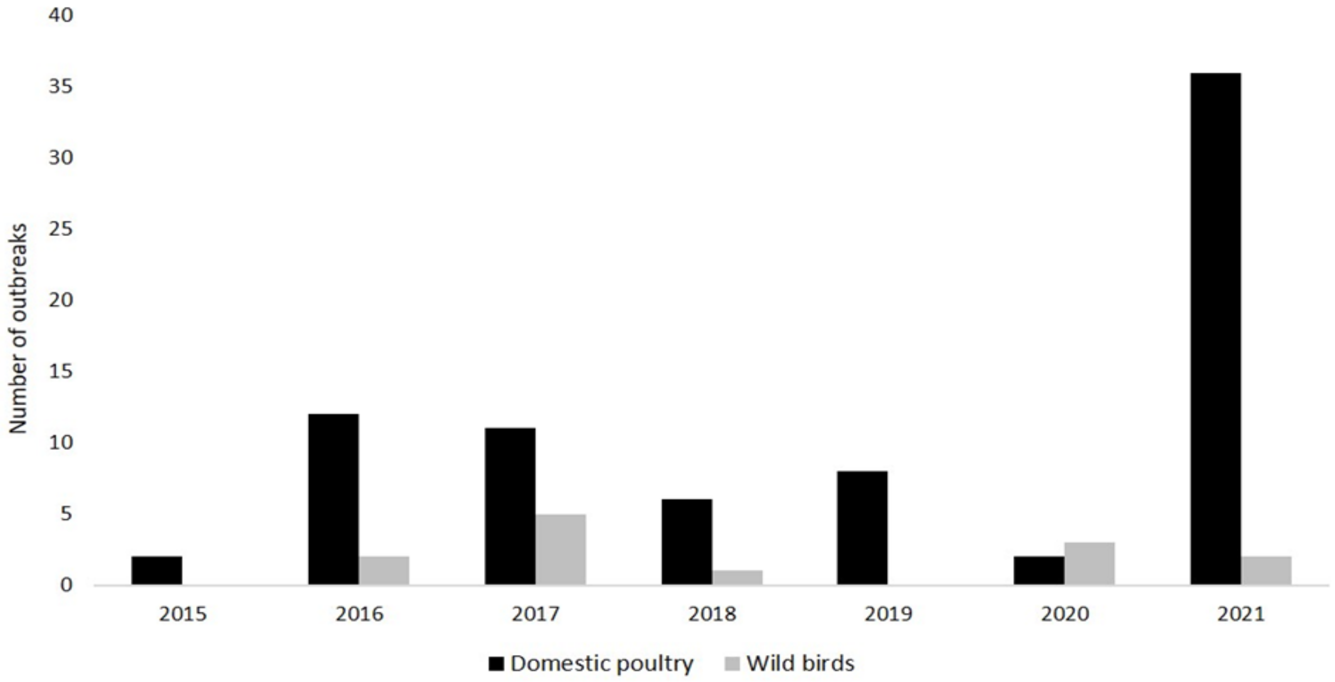
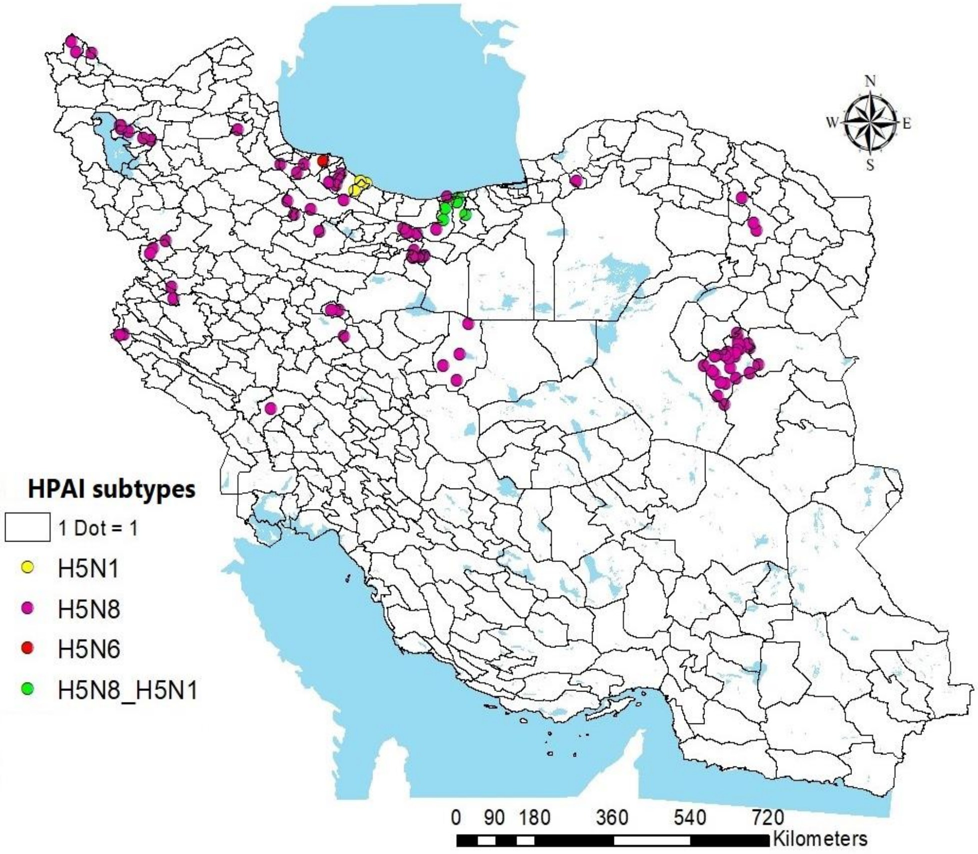


Fig 1. Yearly distribution of HPAI outbreaks in Iran, January 2015 to April 2021

Fig 2. Spatial distribution of HPAI outbreaks in Iran, January 2015 to April 2021



suspicious of HPAI infection, the case must be reported to the local veterinary authorities or veterinarians by farmer.

Our finding showed that during nearly seven-year period the disease was regularly reported. The disease causes remarkable economic losses due to high mortality rate, as well as stamping out policy imposed by the government in affected and surrounding farms.

Similar study in South Korea showed the occurrence of 393 H5N8 outbreaks in less than two years which is considerably higher compared to Iran (12). Since the exact time of outbreak onset was not available in our data, we were not able to investigate monthly and seasonal trends. However, previous reports suggest the higher occurrence of the disease in beginning of cold and wet seasons in Iran (13). Previous study in South Asia have shown the higher incidence of the disease in cold months from November to March (14). It was proved in our findings as no significant difference was found between semesters. During late autumn, numerous different species of water birds migrate from Siberia and northern Russia to wetlands located in southern part of Caspian Sea where they remain for several months before migrating further north. Close contact of wild birds with backyard chickens increases the risk of transmission of avian influenza virus. Molecular investigations in wintering water birds of Iran have also showed the higher prevalence of avian influenza virus in February and November. However, the study found no evidence for presence of HPAI H5N1 subtype (13).

In our study, the H5N8 subtype was responsible for majority of outbreaks. The subtype is highly prevalent and since 2016, it has been reported in 47 countries (9). In Iran, H5N8 subtype was first identified in a commercial layer farm in Tehran Province in 2006 (7). Although no human cases have been reported, the subtype was found responsible for high scale outbreak in poultry farms (9, 15).

Previous study showed that during 2010 to 2016 the majority of avian influenza outbreaks were caused by H5N1 worldwide (16). However, there are few reported of H5N1 in poultry in Iran. H5N1 cause large outbreaks in domestic poultry along with sporadic poultry-to-human transmission and illness (17). Wild birds are natural host of the virus and carry the virus while staying asymptomatic (18).

Regular circulation of H5N1 in poultry and seasonal influenza viruses in humans facilitate genetic reassortment and emergence of novel virus strains with the potential threat for public health (15).

Conclusion

The result of the current study shows that HPAI is regularly observed in high-risk areas in Iran. The disease was prevalent in provinces hosting migratory birds. Active surveillance, proper biosecurity measures and movement control is recommended. The incidence of specific subtypes with potential transmission to humans is an alarm and require effective implementation of plans with improved inter-sectoral collaboration and one health approach to prevent outbreaks..

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Conflict of Interest

No conflict of interest is declared.

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Ethics

We hereby declare all ethical standards have been respected in preparation of the submitted article.

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