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UDC 616:619+598.2(574) (045) **Research article**

Spread of highly pathogenic avian influenza in Kazakhstan: investigating the role of bird migration and threats to poultry farming

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Abstract

Background and Aim. Highly pathogenic avian influenza (HPAI) remains a serious threat to industrial poultry farming and human health. The virus is highly variable and can be transmitted through the migratory flows of wild birds, which contribute to its widespread distribution. This study aimed to analyze the epidemiology of HPAI in Kazakhstan and assess the role of migratory birds therein.

Materials and Methods. The study assessed data on outbreaks of HPAI in Kazakhstan for the period 2005 to 2024. Information on migratory bird species in Kazakhstan territories and their migration routes was obtained by the "Institute of Zoology". The research applied classical methods of epidemiological analysis, statistical modeling of epizootics, and data visualization using ArcGIS Pro software.

Results. Over the past 20 years (2005 to 2024), outbreaks of HPAI have been periodically recorded in Kazakhstan, with cases of infection in both domestic and wild birds. The pathogens mainly comprised viruses of the H5N1, H5N8, and other H5 strains. Wild migratory birds played the main role in the emergence and spread of HPAI. The territory of Kazakhstan contained the convergence point of two of their most important migration routes: the Central Asian-Indian and West Asian-African routes. A total of 489 bird species has been registered in Kazakhstan, most of which are seasonal migrants flying through the country; accordingly, they have a significant impact on the epizootic process of HPAI.

Conclusion. Analysis of epizootiological data showed that the dates and locations of HPAI outbreaks directly correlated with the stages and routes of the seasonal migration of migratory birds. Predictive modeling of virus spread showed that the northern and western regions of the country, where most of the country's poultry farms are located, were at the highest risk.

Keywords: Bird migration; epidemiological monitoring; forecasting; highly pathogenic avian influenza; Kazakhstan.

Introduction

Highly pathogenic avian influenza (HPAI) is a highly contagious viral infection that can affect all types of birds. The most susceptible domestic species are turkeys and chickens. Wild birds can serve as carriers of the infection; however, due to their natural resistance, they do not get sick, as a rule, and cover significant distances during migration [1].

HPAI, caused by the type A influenza virus (*Orthomyxoviridae*), poses a serious threat to industrial poultry farming and human health. The virus's high variability and ability to recombine and overcome the interspecies barrier create a constant risk of new epizootics and pandemics [2].

Bird migration has a significant impact on the epizootic process of avian influenza. In Kazakhstan, 489 species of birds have been registered, of which 396 nest in the republic's territory and the rest are seasonal migrants flying through the country during spring and autumn migrations [3].

Since migratory birds are the main reservoir of HPAI, outbreaks of influenza in poultry farms usually occur during their seasonal migrations in spring and autumn. Since 2020, outbreaks of HPAI A (H5N1) have been registered in Kazakhstan and Central Asian countries, confirming the active circulation of the virus in the region. In September 2020, mass cases of infection among poultry occurred in the North Kazakhstan, Akmola, and Pavlodar regions, causing significant mortality and the introduction of quarantine measures. In June 2021, the virus was detected in wild waterfowl in the North Kazakhstan region, indicating its circulation among natural reservoirs of infection [4, 5].

However, the high concentration of birds in a limited area makes poultry farms vulnerable to the introduction of the virus. The main routes of penetration into industrial farms include contact with infected wild birds; viral transfer through contaminated feed, water, and equipment; and mechanical transmission through transport and personnel's shoes and clothing [6]. HPAI outbreaks lead to huge economic losses due to the forced slaughter of infected birds, the introduction of quarantine measures, disinfection, and the temporary cessation of production. For example, in countries affected by HPAI epidemics, losses to the poultry industry are estimated to amount to millions of dollars, including the costs of disease control, compensation to farmers, and the decrease in export potential [7].

In addition, the infection of poultry with HPAI viruses creates a risk of transmission to humans [8]. Historically, HPAI outbreaks have had serious epidemiological consequences; for example, the 1997 H5N1 outbreak in Hong Kong and the 2013 H7N9 outbreak in China resulted in severe infections in humans. Therefore, monitoring bird migration flows, studying the epizootiology of the virus, and developing effective prevention methods are paramount to reduce the risks of infection introduction into poultry farms [9, 10].

Thus, this study aimed to analyze the epidemiology of HPAI in Kazakhstan and assess the role of migratory birds therein.

Materials and Methods

The study used data on avian influenza outbreaks in Kazakhstan for the period 2005–2024, registered in the World Animal Health Information System (WAHIS) of the World Organization for Animal Health, official data from the country's state veterinary service, and our own field studies conducted in 2023 and 2024.

The main research methods included the following:

- collection of epizootiological data on HPAI outbreaks;
- analysis of bird migration routes;
- use of GIS technologies for mapping risk zones; and
- statistical modeling of epizootics using ArcGIS Pro software.

Data on the species of birds migrating through the territory of Kazakhstan and their migration routes were obtained by the "Institute of Zoology." In this institution, through ringing and subsequent monitoring, a large dataset on the timing of seasonal migration, migration routes, and nesting sites was collected. Based on the obtained materials, databases were created, indicating the geographic coordinates of all the parameters of interest, which were subsequently used with the ArcGIS Pro program for data visualization and analysis.

Results and Discussion

Over the past 20 years (from 2005 to 2024), outbreaks of HPAI have been periodically recorded in Kazakhstan. Moreover, outbreaks were recorded both among poultry kept in organized poultry farms and private households and among representatives of wild fauna. Statistics showed the occurrence of HPAI outbreaks in the country approximately every 3 to 4 years. Outbreaks were mainly caused by the H5N1, H5N8, and other H5 influenza subtypes. Given the well-developed poultry sector and the frequency of outbreaks, HPAI is gradually acquiring the status of an endemic infection in Kazakhstan. Data on registered cases of HPAI in Kazakhstan from 2005 to 2024 are presented in Table 1.

Table 1 – Data on outbreaks of highly pathogenic avian influenza in Kazakhstan (2005-2024)

№	Types of birds	Region of outbreak	Genotype/Serotype/ Subtype
1	Black-headed gull (*Chroicocephalus ridibundus*)	Pavlodar	H5 (N not typed)
2	Greylag goose (*Anser anser*)	North Kazakhstan	H5 (N not typed)
3	Greylag goose (*Anser anser*)	North Kazakhstan	H5 (N not typed)
4	Mallard (*Anas platyrhynchos*)	North Kazakhstan	H5 (N not typed)
5	Black raven (*Corvus corone*)	North Kazakhstan	H5 (N not typed)
6	Whistling teal (*Anas crecca*)	North Kazakhstan	H5 (N not typed)
7	Teal (*Anas crecca*)	North Kazakhstan	H5N8
8	Lesser white-fronted goose (*Anser erythropus*)	North Kazakhstan	H5N1
9	Greater white-fronted goose (*Anser albifrons*)	North Kazakhstan	H5N1
10	Mallard (*Anas platyrhynchos*)	Aqmola	H5N1
11	Greylag goose (*Anser anser*)	Qostanay	H5N8
12	Greylag goose (*Anser anser*)	Almaty	H5N1
13	Poultry (*Gallus gallus*)	North Kazakhstan	H5N1
14	Poultry (*Gallus gallus*)	Aqtobe	H5N1
15	Domestic goose (*Anser anser domesticus*)	Atyrau	H5N1
16	Dalmatian pelican (*Pelecanus crispus*)	Mangghystau	H5N1

As shown in Table 1, during the analyzed period, a total of 16 outbreaks of infection were registered in the WAHIS system for the territory of Kazakhstan.

The sample included outbreaks among farm and wild birds, as well as among other representatives of wild fauna. In most outbreaks, the causative agent of the disease belonged to the H5 subtype; however, in several cases, the neuraminidase (N) of the HPAI virus was not typed. Unfortunately, this factor limits the possibilities for epidemiological analysis and accurate identification of the routes of spread of the virus. In some cases, subtypes H5N1 and H5N8 were identified, which confirms the circulation of classical forms of the virus, posing a threat to both birds and humans.

Subsequently, based on epidemiological data, we produced a cartographic visualization of HPAI outbreaks registered in the country for the period 2020 to 2024 (Figure 1).

Figure 1 – Visualization of outbreaks of highly pathogenic avian influenza in Kazakhstan in 2020-2024

Most outbreaks of HPAI were registered in the country's northern regions, especially North Kazakhstan. Outbreaks were also noted in the western (Atyrau, Mangistau) and southeastern (Almaty) regions. It is worth mentioning that when HPAI was registered in the country, the pathogen was not only found in domestic and wild birds but also isolated from some wild animals. At the same time, in most cases, the source of infection remained unknown, even though it is known from the disease epidemiology that wild migratory birds are the main reservoirs and carriers.

Birds become infected with HPAI through direct contact with the source of infection, as well as through environmental objects (most often water) contaminated with the saliva, nasal secretions, and feces of infection carriers. As the experience of Asian countries shows, the contamination of water bodies with the pathogen is caused not only by the presence of infected birds but also by feeding farmed fish with bird droppings.

The Republic of Kazakhstan, with its vast territory and diverse landscapes, is not only a nesting place for birds but also a region where two of their most important migration routes converge: the Central Asian-Indian and the West Asian-African routes. Millions of birds flying along these routes use the territory of Kazakhstan for molting and stopovers. Migration is influenced by wetlands, which are especially abundant in the northern part of the country.

There are 489 species of birds registered in Kazakhstan, of which 396 nest in its territory, with the rest being seasonal migrants flying through the country during spring and autumn migrations. At the same time, bird migration has a significant impact on the epizootic process of avian influenza.

The main carriers of avian influenza of epidemiological significance for Kazakhstan are as follows: swans (*Cygnus* spp.): mute swan (*Cygnus olor*), whooper swan (*Cygnus cygnus*), Bewick's swan (*Cygnus columbianus*); geese (*Anser* spp.): greylag goose (*Anser anser*), white-fronted goose (*Anser albifrons*), lesser white-fronted goose (*Anser erythropus*); ducks (*Anas spp.*): mallard (*Anas platyrhynchos*), teal (*Anas crecca*), northern pintail (*Anas acuta*); order Charadriiformes: migratory waterbirds, gulls (*Larus* spp.): herring gull (*Larus argentatus*), black-headed gull (C*hroicocephalus ridibundus*); waders (*Scolopacidae, Charadriidae*): black-tailed godwit (*Limosa limosa*), Eurasian curlew (*Numenius arquata*); order Pelecaniformes, pelicans (*Pelecanus spp*.): Dalmatian pelican (*Pelecanus crispus*), great white pelican (*Pelecanus onocrotalus*); cormorants (*Phalacrocorax* spp.): great cormorant (*Phalacrocorax carbo*).

Currently, most scientists hold a point of view that can be called "synthetic": the flight of birds covers a wide front, but within it are areas with increased concentrations: migration routes (flyway) that form migration corridors when merged. The main corridors of migratory birds through the territory of the Republic of Kazakhstan are as follows (Figure 2):

- routes from African and South European wintering grounds in the Mangistau, Atyrau, and West Kazakhstan regions;
- routes from Pakistani and Indian wintering grounds in the South Kazakhstan, Kyzylorda, Kostanay, and North Kazakhstan regions; and
- routes from South Asian wintering grounds in the Almaty, East Kazakhstan, and Pavlodar regions.

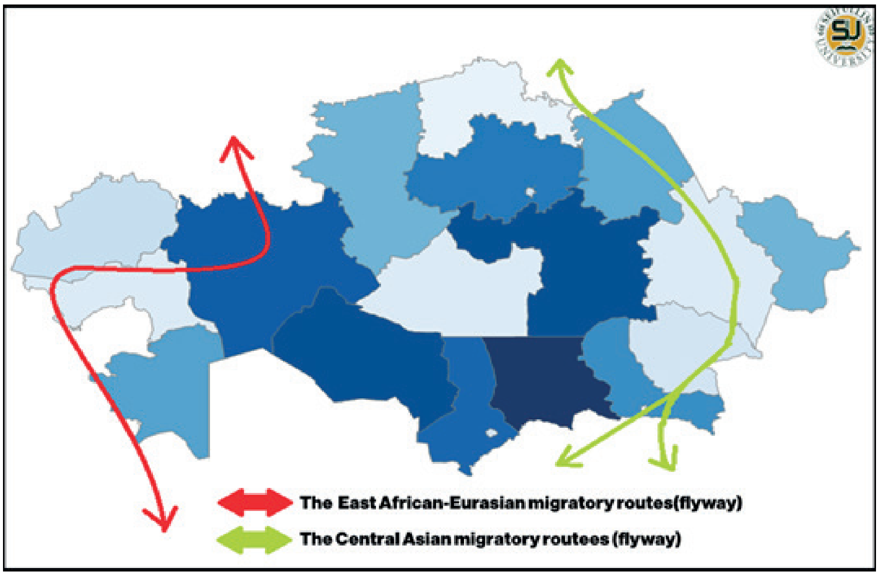

Figure 2 – Main migration routes of birds

The available epidemiological data on the locations and dates of the primary outbreaks of HPAI in Kazakhstan demonstrated a direct correlation with the stages and routes of seasonal migration of migratory birds through the country. At the same time, predictive modeling of the emergence and spread of the virus showed that the northern and western regions were at the highest risk. Importantly, most of the country's poultry farms are located in areas with a high risk of HPAI outbreaks. Currently, 65 poultry farms are operating in the country for meat and egg production, most of which are located in the northern, northwestern, and western regions of the country (Figure 3).

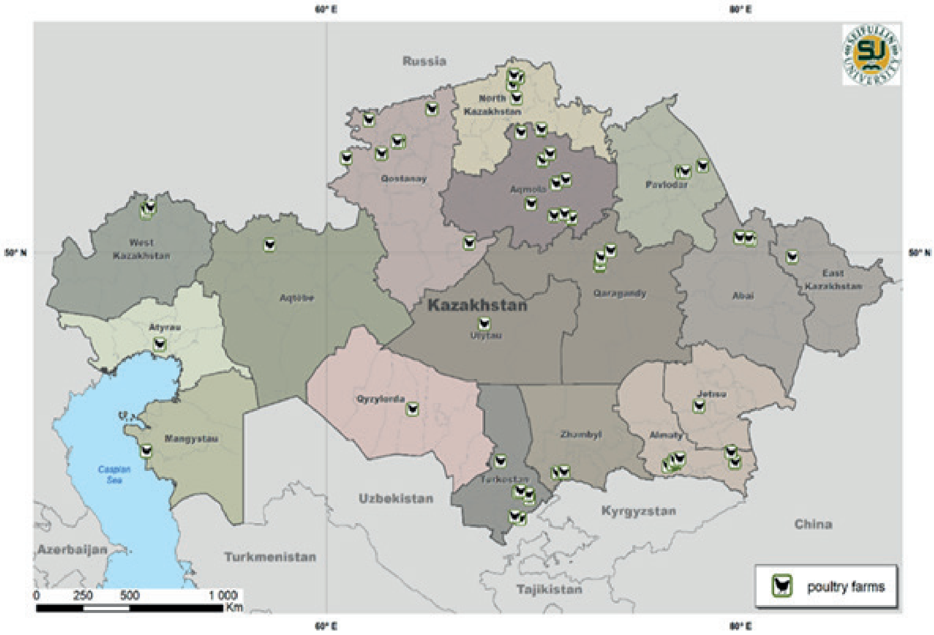

Figure 3 – Visualization of the location of industrial poultry farms in Kazakhstan

In Kazakhstan, industrial poultry farms contain more than 80% of the total poultry population. That is, outbreaks of HPAI at such enterprises always lead to an exacerbation of the epizootic situation and huge economic losses. Therefore, the obtained data show the importance of continuous epidemiological surveillance of HPAI in Kazakhstan. Enhanced biological safety measures, monitoring of migratory birds, and the development of diagnostic centers for the early detection of infection are necessary.

HPAI poses a threat to many countries due to the impact of the disease on wild bird popula-tions, direct and indirect losses to the poultry industry, and potential impact on public health [11, 12]. Seasonal migrations of wild birds play an important role in the intercontinental spread of the disease, and transmission occurs at the interface between wild and domestic birds, despite efforts by governments in both developed and developing countries, including biosecurity and other preventive measures [13, 14].

Kazakhstan, located in the center of Central Asia, is under constant threat of avian influenza, as evidenced by outbreaks in recent years in the northern, eastern, and southern regions [15, 16].

Considering the epizootic situation of this disease in Kazakhstan in previous years, as well as the global situation this year, the probability of an epizootic outbreak remains high. The main threat of spread stems from wild migratory birds, especially ducks, geese, and swans [17, 18].

Given the geographical location of the republic, Kazakhstan's reservoirs are the most important reserves in Asia, housing aquatic and near-water bird species. In the republic, 489 species of birds have been registered during the nesting, molting, seasonal migration, and wintering periods. Every year, the number of nesting bird species reaches 10 million, 2–3 million birds fly in for molting, and about 50 million migratory birds stop at the reservoirs during spring and autumn migrations [19].

Several seasonal bird migration routes pass through the territory of Kazakhstan. The Central Asian-Indian and West Asian bird migration routes intersect with the Black Sea-Mediterranean and East African-West Asian channels in the west of the republic [20].

The present study of the epizootic situation in Kazakhstan identified migratory corridors, nesting sites, and water bodies as vulnerable points for the monitoring and control of HPAI. Outbreaks of the disease are statistically associated with a high density of water resources, which necessitates in-tensive surveillance in these regions. Waterfowl are extremely important carriers of the avian influen-za virus, as they can transmit it over long distances. Interaction between different bird species in their usual resting and breeding areas can facilitate the transmission of the avian influenza virus between species [21].

The patterns identified in Kazakhstan are consistent with data obtained in other regions along the main Eurasian migratory flyways. For example, studies in China, Mongolia, Russia, and Kazakhstan have also demonstrated a close association between H5N1 outbreaks and the presence of wetlands that serve as resting and feeding sites for migratory waterfowl, and have proposed various hypotheses to explain the movement of H5N1 from China to Mongolia, Russia, and Kazakhstan [22]. These findings support the view that aquatic ecosystems serve as critically important reservoirs for the persistence and spread of avian influenza viruses. Researchers reported two significant patterns of H5N1 spread from Asia. A comprehensive analysis of bird migration routes and wild bird behavior suggested that the introduction of H5N1 into Mongolia occurred as a result of wild bird movements from China several months before the outbreaks. These events were repeatedly linked to the seasonal migrations of swans, geese, and ducks, with H5N1 and H5N8 subtypes predominating [23]. This is consistent with data from Kazakhstan, where the northern and western regions with dense wetlands and a high level of poultry farming are the most vulnerable. This indicates that the role of wild birds as long-distance carriers is not unique to Kazakhstan but is part of the global epidemiological picture. Nevertheless, the central geographical position of Kazakhstan and the convergence of numerous fly-ways appear to intensify these risks, creating overlapping migratory corridors that increase opportuni-ties for virus exchange. This highlights Kazakhstan as a particularly important "epidemiological bridge" between Asia, Europe, and Africa. Taken together, these comparisons show that although the specific outbreak patterns observed in Kazakhstan are determined by local landscapes and the distri-bution of domestic poultry, they are also consistent with broader global mechanisms of highly patho-genic avian influenza spread. Thus, the conclusions drawn from this study contribute not only to na-tional veterinary surveillance but also to the general understanding of avian influenza epidemiology across continents. A comprehensive understanding of the spread of HPAI requires an integrated ap-proach that includes monitoring bird migration routes, strengthening biosecurity measures at poultry farms, and informing the public about potential threats and ways to prevent them. Cooperation among international and regional organizations in sharing information and developing prevention strategies is also important. Effective risk management of HPAI requires the integration of data from multiple sources and sectors to develop a holistic strategy to protect bird health and prevent human epidemics.

Conclusion

Analysis of epizootological data shows that the dates and locations of HPAI outbreaks directly correlate with the stages and routes of seasonal migration of migratory birds. Predictive modeling of the spread of the virus showed that the northern and western regions of the country, where most of the country's poultry farms are located, are at the highest risk.

Authors' Contributions

SA, YM, AM and SR: developed the concept and design of the study. SR conducted a comprehensive literature search, analyzed the collected data, and drafted the manuscript. SA and YM, AM: Performed final revision and proofreading of the manuscript. All authors have read, reviewed, and approved the final manuscript.

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