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Article

Environmental Suitability to Highly Pathogenic Avian Influenza in Kazakhstan Using Data on Eurasian Outbreaks 2020 - 2024

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Abstract: Highly pathogenic avian influenza (HPAI) is a highly contagious disease of domestic, synanthropic, and wild birds that has demonstrated a sharp rise globally since 2020. The study here is intended to assess the quality of reporting HPAI outbreaks in Kazakhstan using outbreaks' location in neighboring countries (2020–2024) as training data to build an ecological niche model of suitability to the disease in the country. Afghanistan, China, Hong Kong, Iran, Iraq, Pakistan and Russia were chosen as training countries for fitting a Maximum entropy (Maxent) model, which was then tested using the locations of HPAI outbreaks in Kazakhstan. The results suggest good performance of the model in explaining Kazakhstani outbreaks (test AUC = 0.88 vs AUC=0.93 for training data). HPAI outbreaks reported in Kazakhstan fall mainly in areas treated as highly suitable by the model. The number of outbreaks per each analyzed country is also well explained by a summary area of suitable places per country as predictor ($p < 0.001$, $R^2 = 0.75$), with Kazakhstan demonstrating no significant deviation from the found dependency. Results suggest that, although sensitivity of the surveillance system in the country is uncertain, it may be able to accomplish the objective of identifying regions affected by the virus incursions.

Keywords: highly pathogenic avian influenza; outbreaks; epidemiology; Maxent; Kazakhstan; suitability; underreporting

1. Introduction

Highly pathogenic avian influenza (HPAI) is a highly contagious disease of domestic, synanthropic and wild birds, occurring as an epizootic or enzootic disease, characterized by damage to the respiratory organs and gastrointestinal tract, general depression, and decreased productivity. HPAI is caused by various antigenic variants of the influenza virus subtype A [1]. The World Organisation for Animal Health (WOAH, former OIE) classifies HPAI as a particularly dangerous transboundary zoonotic infection [2]. Acute epizootic outbreaks caused by subtypes H5 and H7 of the virus are the most dangerous and, as a rule, are accompanied by catastrophic consequences with losses of 75 to 100% of the livestock [3]. Bird flu is also a serious public health problem. According to the World Health Organization (WHO), between 2003 and 2020, 861 cases of H5N1 influenza with 455 fatal outcomes have been registered among the population of 17 countries [4,5].

According to WHO, in 2020, HPAI was registered in 20 countries of the world (countries of Europe, Africa, Asia, including Russia, China, Kazakhstan, etc.) [2,6–9]. At the time when this

manuscript was written in January 2025, HPAI routinely recurs and is registered in many countries of Europe, Africa, Asia. For example, in November 2024 alone, about 16 cases of infection of domestic and wild birds were notified to the WOA information system WAHIS, including countries such as Germany, the Netherlands, Hungary, the Philippines, etc. In total, 90 HPAI outbreaks were registered in the world in 2024 [10]. HPAI is a transboundary animal disease by nature. For example, in 2020, when an epidemic of was reported in Kazakhstan, outbreaks (January-May) were also recorded in China, Russia, Iraq, Vietnam [10–14]. Ongoing outbreaks are still present in Afghanistan, China, India, Korea, the Philippines and Vietnam among poultry (subtypes H5, H5N1, H5N2, H5N5, H5N6 and H7N9) [4,10,12,15,16].

The epidemiological situation of HPAI is difficult for Kazakhstan. The first HPAI outbreaks in Kazakhstan were registered in 2005 [17,18]. Subsequently, intensive vaccination of poultry was implemented. However, despite all the measures taken, in 2020 outbreaks of avian influenza caused enormous damage to the poultry industry of Kazakhstan. In September 2020, the Ministry of Agriculture of the Republic of Kazakhstan reported a HPAI outbreak in the North Kazakhstan region and its spread to other regions. In total, 11 outbreaks of infection were registered that year in the Akmola, Almaty, Kostanay, Pavlodar and North Kazakhstan regions [19]. In 2021, five more outbreaks of infection were notified in the Akmola, Aktobe, Pavlodar and North Kazakhstan regions [6,10,20]. In the outbreaks, quarantine was declared and temporary restrictions were introduced on the export of live poultry and poultry products, which had a significant impact on the rise in prices for eggs and poultry meat [21].

Several routes of seasonal bird migration pass through the territory of Kazakhstan. At the same time, the Central Asian-Indian and East Asian bird migration routes intersect with the Black Sea-Mediterranean and East African-West Asian pathways in the west of the Republic [22]. In Kazakshtan, 130 species of birds have been registered during the nesting, molting, seasonal migrations and wintering periods. Every year, the number of nesting bird species reaches 10 million, 2-3 million birds arrive for molting, and about 50 million migratory birds stop on Kazakhstani water bodies during the spring and autumn migrations [23]. At the same time, a number of studies by Kazakh scientists confirm the transcontinental route of introduction of the HPAI virus, where wild migratory birds play the role of a reservoir. Thus, whole-genome sequencing of avian influenza virus in Kazakhstan during disease outbreaks in 2020 showed that the isolated strains are associated with isolates from Southern Russia, the Russian Caucasus, the Ural region, Southwestern Siberia and Eastern Europe [6]. In Northern Kazakhstan, the influenza virus strain A/chicken/North Kazakhstan/184/2020 (H5N8) was isolated, phylogenetic analysis of which showed significant genetic similarity of the isolate in all eight genes with highly pathogenic H5 influenza viruses isolated from poultry in the Middle East and West Africa [20]. Also, during the influenza outbreaks in 2021 in the North Kazakhstan and Akmola regions among poultry caused by the avian influenza A/H5N8 virus, it was established that the Kazakhstani isolates of HPAI H5N8 belong to the 2.3.4.4b clade with a high level of homology (98.42–98.70%) to the strains from China [21]. In addition, during the epidemiological surveillance of avian influenza viruses in wild birds in 2018–2019, the simultaneous circulation of genome segments of Asian, European, and Australian genetic lineages of the H3N8 AIV virus was established in wild birds in Kazakhstan, which confirms the important role of Kazakhstan and Central Asia as a center for the transmission of avian influenza viruses, linking the migration routes from East Asia to Europe and vice versa [24].

At the same time, despite the long history of studying the ecology of avian influenza viruses in Kazakhstan, many key aspects of the HPAI epidemiology remain insufficiently studied. In particular, anthropogenic and natural-climatic factors influencing the epidemiology of the disease have not been determined, the mechanisms of transboundary spread of infection are not fully understood, and there is no ranking of the territory with an assessment of the risk of occurrence and spread. The purpose of this work was to model the suitability of the territory of Kazakhstan for the occurrence of HPAI outbreaks using an ecological niche model based on information from a number of neighboring countries with similar climatic conditions, as well as to assess the impact of a number of climatic,

landscape and socio-economic factors on the epidemiological process of the disease. Results will help evaluate the effectiveness of the surveillance system for HPAI in Kazakhstan, contributing to the implementation of measures intended to prevent and mitigate the impact of the disease in the country.

2. Materials and Methods

2.1. Study Area

The study area comprised Kazakhstan and neighboring countries in Eurasia considered to be similar to Kazakhstan in terms of their climatic and geographic conditions and in which HPAI outbreaks were reported in 2020 – 2024. Those countries included Afghanistan, China and Hong Kong, Iran, Iraq, Pakistan and Russia (Figure 1). Inclusion of those countries was necessary because of the limited number of outbreaks reported in Kazakhstan. The addition of data from countries considered to be similar to Kazakhstan is expected to support the identification of associations between outbreaks and predictors, contributing to the ultimate objective of identifying areas in which the disease may have been under-reported in Kazakhstan.

2.2. HPAI Data

Spatially referenced data on Highly pathogenic avian influenza (HPAI) outbreaks were collected from FAO EMPRES-i database (<https://empres-i.apps.fao.org/>). The attributes of the data include geographical coordinates, virus serotype, location name, dates of disease observation and reporting, and the source of information. Only outbreaks attributed to WOA (former OIE) were used for the analysis. The total number of HPAI outbreaks during the study period were 17 in Kazakhstan (hereinafter “test data”) and 444 in the rest of the study area (hereinafter “training data”) (Table 1). Outbreaks in domestic and wild birds were treated together as indicators of HPAI virus presence [25].

2.3. Study Design

First, the environmental suitability to HPAI was evaluated for the whole study area using only training data. Subsequently, the model was tested on Kazakhstan data to evaluate whether the fitted model was able to adequately predict the observed HPAI outbreaks in Kazakhstan, and whether there are areas of over- or underprediction. Finally, the numbers of HPAI outbreaks by country were compared to the summary environmental suitability in the corresponding country, calculated as the sum of cells with suitability >50%.

An ecological niche model based on the principle of Maximum Entropy (Maxent) was used to evaluate an environmental suitability to HPAI [25]. We chose a set of potential explanatory variables including a number of climatic, landscape and socioeconomic factors (Table 2), which demonstrated significance in explaining the observed distribution of HPAI cases in similar studies [25,27–29]. The set of environmental variables included: population density, land cover, human footprint index, chicken population density, maximum green vegetation fraction, altitude, mean yearly air temperature, yearly precipitation, minimum temperature of coldest month, precipitation seasonality, precipitation of driest quarter and precipitation of warmest quarter. All raster layers were clipped by the extent of the study area and transformed to the same resolution of 10×10 km², defined by the layer with the coarsest resolution (namely FAO global chicken density). Model performance was assessed by the mean AUC value that indicates an ability of the model to correctly predict any random presence location. AUC values exceeding 0.8 are normally considered a “high indicator”, values 0.7<AUC<0.8 are considered “good indicator”, while AUC around 0.5 indicate no predictive power of the model [30].

Further, test data (namely HPAI outbreaks in Kazakhstan) were used in the same model to assess the model performance. The AUC value was obtained and compared with the AUC of trained model.

Test data were overlaid with the predicted suitability surface and conclusions were made about the adequateness of the prediction.

To test the importance of the variables, a Jackknife test was used. For each individual variable, it runs model without this variable, and with only this variable, comparing a test gain with the full model.

To assess potential over- or underreporting of HPAI outbreaks by country, we calculated a summary suitability as a number of raster cells per country, where the predicted suitability exceeds 50%. We then plotted this summary suitability against the reported number of HPAI outbreaks and applied a Negative Binomial linear regression model to assess a goodness of the summary suitability as a predictor of the number of outbreaks per country.

2.4. Software

Spatial data mapping and processing was performed by means of ArcGIS for Desktop v 10.8.2 (Esri, Redlands, CA, USA). Maxent model was fitted in Maxent software [31]. Negative Binomial model was built in statistically oriented programming software R with MASS package [32].

Table 1. The number of HPAI outbreaks within the study area, 2020 - 2024.

Number of HPAI outbreaks	In domestic birds	In wild birds
Afghanistan	1	0
China	1	13
Hong Kong	0	12
Iran	57	5
Iraq	8	0
Kazakhstan	14	3
Pakistan	5	0
Russia	241	101



Figure 1. Study area and HPAI outbreaks, 2020 – 2024.

Table 2. The list of environmental variables used in ecological niche modeling of HPAI in Eurasian countries.

Variable name	Variable meaning	Measurement unit
alt	Altitude above the sea level	meters
landcov	Type of land cover	categories
mgvf	Maximum green vegetation fraction	%
pop_dens	Population density	Persons/km ²
hum_ftprnt	Human footprint index (a measure of human influence on the terrestrial systems of the Earth)	index
chicken_dens	Chicken density	Head/km ²
bio_1	Annual Mean Air Temperature	°C*10
bio_6	Minimum Air Temperature of Coldest Month	°C*10
bio_12	Annual Precipitation	Millimeters
bio_15	Precipitation Seasonality	%
bio_17	Precipitation of Driest Quarter	Millimeters
bio_18	Precipitation of Warmest Quarter	Millimeters

3. Results

The Maxent model created with the training data provided a predictive suitability map (Figure 2) and demonstrated good performance with a mean AUC of 0.93. Most contributing variables were chicken population density, human footprint index, and mean yearly air temperature (Figure 3)

A resulting predicted suitability is presented in the map (Figure 2) overlaid with training data.



Figure 2. Predicted environmental suitability to HPAI obtained by Maxent modeling on training data.

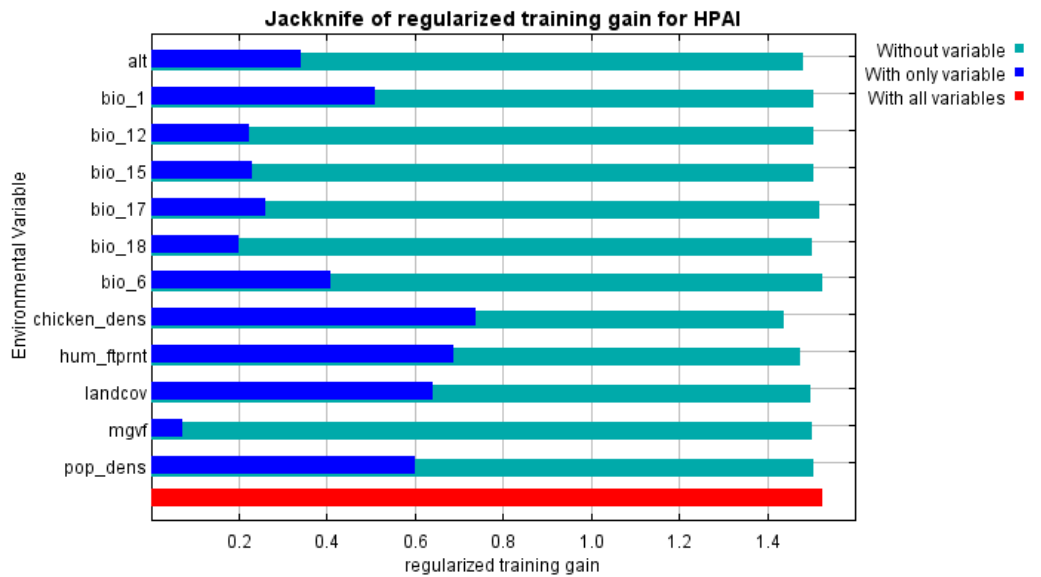


Figure 3. Results of Maxent Jackknife test to assess relative contribution of variables on training data.

Nor surprisingly, being applied to outbreaks in Kazakhstan (test data), the model demonstrated a slightly lower AUC of 0.883 compared to the value reported for all the assessed countries. Relative contribution of variables showed an increased significance of bio_1 (mean yearly air temperature) and altitude, while keeping significance of previously revealed predictors.

A map of predicted suitability for Kazakhstan overlaid with test data is presented in Figure 4. The map suggests that most of HPAI outbreaks in Kazakhstan were recorded in areas predicted by Maxent as “suitable”, which confirms the adequateness of the model and underlines a possibility of the further improvement of the model by adjusting the set of environmental variables. Relative importance of variables per the results of Jackknife test is presented in Figure 5. In addition to previously identified significant factors, mean annual temperature and maximum green vegetation fraction were found to influence the observed distribution of HPAI outbreaks in Kazakhstan.

The summary suitability against the reported number of outbreaks by country is presented in Table 3 and plotted in Figure 6. The regression model reveals a high significance of the summary suitability as a predictor of the number of outbreaks with $p < 0.001$ and $R^2 = 0.75$.

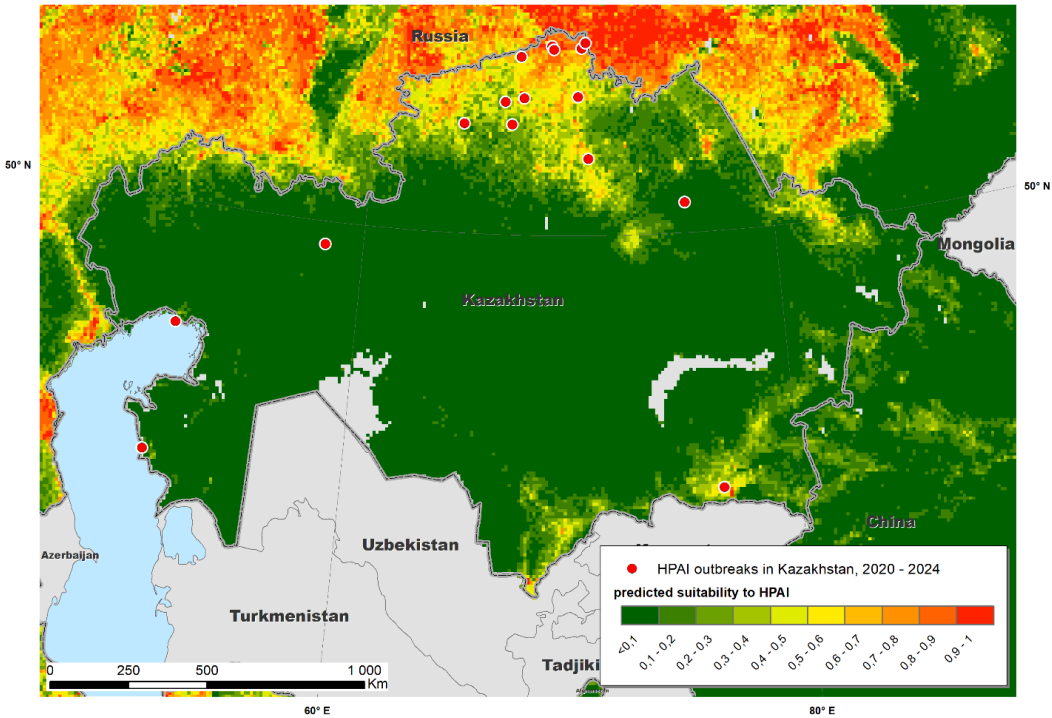


Figure 4. Predicted environmental suitability to HPAI overlaid with test data (Kazakhstan).

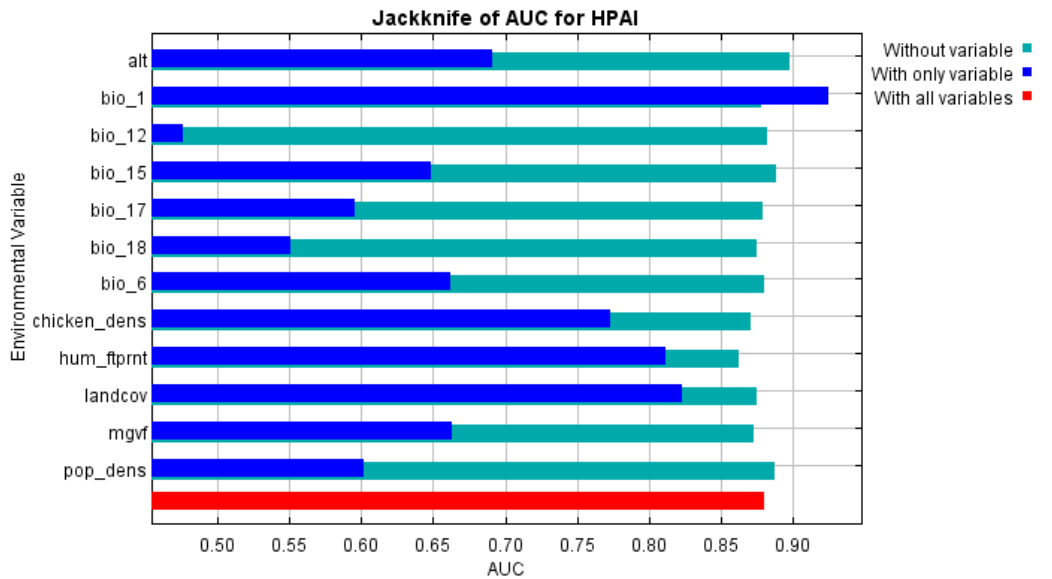


Figure 5. Results of Maxent Jackknife test to assess relative contribution of variables on test data.

Table 3. Summary suitability by country and reported number of HPAI outbreaks.

Country	Summary suitability	Number of HPAI outbreaks reported
Afghanistan	36	1
China	277	14
Hong Kong	1	12
Iran	2665	62
Iraq	638	8
Kazakhstan	1060	17
Pakistan	75	5

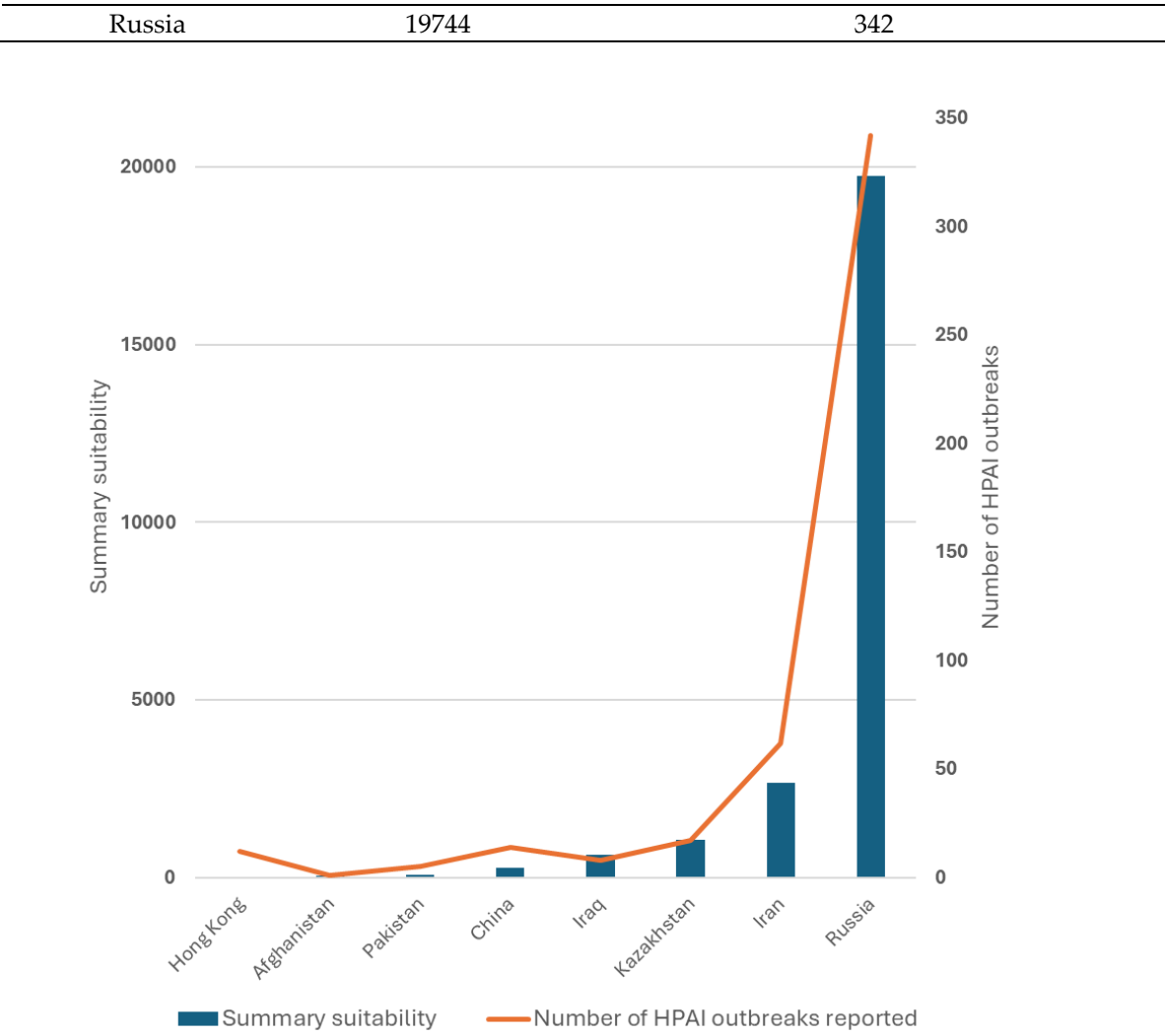


Figure 6. Predicted summary suitability compared to the number of reported HPAI outbreaks.

4. Discussion

The study here contributed to elucidate the most general patterns on environmental suitability for HPAI outbreaks in Kazakhstan. Human-related factors (such as human footprint index and chicken density) were more strongly associated with reported HPAI outbreaks than climate and landscape factors, such as annual mean air temperature, annual precipitation and altitude. The land cover demonstrated relatively low relation with HPAI outbreaks, with croplands, cropland/natural vegetation mosaic, urban/built-up and water areas been the most frequent categories for HPAI. For the most influential variable, namely, chicken density, a positive relation was found with suitability to HPAI, which indicates a naturally expected relation between presence of a highly dense susceptible population and disease. A similar dependency was found for the human footprint index. A stronger human impact indicates higher exposure to HPAI (presumably due to most intensive between-farm contact as well as increased probability of the disease detection). A similar pattern in terms of human footprint index was found by [27].

A comparison between the summary suitability (expressed as a sum of raster cells with suitability of >50%) by country, and the corresponding number of reported HPAI outbreaks 2020 – 2024 suggested that Kazakhstan generally follows the pattern for the rest of analyzed countries. Consequently, with the revealed associations, three highly suitable areas for HPAI were identified. Two of those three areas, located in the northern part of the country, along the Russian border, and in south-western regions, close to Kyrgyzstan and China, were likely associated with high poultry

and human density, thus, suggesting a high risk for cases in domestic susceptible populations. The remaining area of elevated suitability was identified in the western region, close to the Caspian Sea.

The Caspian Sea is located on the migration routes of wild birds, and it is part of the Central Asian Flyway. This route covers vast areas from Siberia to South Asia, including the western regions of Kazakhstan. Migratory birds such as ducks, geese, swans, birds of prey and rare species such as pink flamingos actively follow the wetlands and coastal areas of the Caspian Sea for stopovers, nesting and wintering. Due to the diversity of ecosystems in the Caspian Basin, this region provides important resources for maintaining the biological diversity of migratory species. Of particular importance are the unique ecosystems of the Ural (Zhayyk) River delta and the northern coast of the Caspian Sea, where vast wetlands are formed. These areas serve not only as transit points for millions of migratory birds, but also as concentration sites for rare, endangered species. Most importantly, the western regions of Kazakhstan (Atyrau, Mangistau and West Kazakhstan) are characterized by the active development of the poultry industry. Proximity of poultry farms to migration routes increases the likelihood of contact between domestic and wild birds, which increases the risk for transmission of infectious diseases, such as HPAI.

Interestingly, HPAI outbreaks reported in Kazakhstan were located in high risk predicted areas, suggesting that cases that may have not been identified by the current surveillance system are likely to have occurred on the same areas in which outbreaks were reported. This observation suggests that, even in the presence of under-reporting, affected regions were properly identified, facilitating the design and implementation of actions intended to contain disease spread.

An important limitation of this study is that the association of predictive variables could only be assessed with the presence of reported outbreaks, rather than true presence of the disease. For that reason, it is possible that the associations reported here could indicate the likelihood of identifying the disease, rather than the probability of disease occurrence. The inclusion of data from other countries in the region represented an attempt to mitigate the impact of such limitation, at least in part, by adding information from countries in which different surveillance strategies were implemented. Nevertheless, it is uncertain how effective this strategy may have been in adjusting for potential reporting bias. In summary, the results here contributed to identify three areas of high risk for HPAI cases in Kazakhstan, associated with the presence of wild and domestic birds. Development and implementation of a system intended to early detect the risk for incursions in those areas could help to anticipate the introduction of the disease into the country, selectively triggering active sampling and control activities, ultimately, contributing to prevent further dissemination of the disease in the country.

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Data Availability Statement: The data used in the present research (specifically, HPAI outbreaks location data and environmental layers) are publicly available, and their sources are listed.

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