Comparative Immunology, Microbiology and Infectious Diseases 123 (2025) 102387

Contents lists available at ScienceDirect

Comparative Immunology, Microbiology and Infectious Diseases

journal homepage: www.elsevier.com/locate/cimid

Full length article

Multivariable analysis of highly pathogenic H5N1 and H5Nx avian influenza in wild birds and poultry in Asian subregions

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ARTICLE INFO

Keywords:
Avian influenza
H5 HPAI
Wild birds
Poultry

ABSTRACT

The spread of highly pathogenic avian influenza (HPAI) virus in wild birds, poultry, and other livestock worldwide has caused great concerns, especially in Asia, where the migration routes of many wild birds intersect with poultry farms. This often leads to interactions between wild and domestic birds during seasonal migration. These interactions influence the emergence and re-emergence of subclades and serotypes of avian influenza in Asia countries that are endemic to the disease. Using outbreak data from the Food and Agriculture Organization (FAO), we examine the geographical distribution of confirmed HPAI H5 cases in wild birds and poultry across Asia between January 2004 and August 2024. H5N1 is the most prevalent serotype among all HPAI H5 serotypes reported, followed by H5N8. The temporal analysis reveals three waves of outbreaks across Asian regions: an initial peak in 2004–2005, a second wave around 2009–2011, and a third, more recent wave, from 2017 to 2023. Multivariable Poisson regression models were used to assess the geographical, seasonal and yearly patterns of confirmed HPAI H5 cases among different categories of birds. The results indicate that these factors significantly influence the prevalence of HPAI H5, with a higher risk of H5N1 in Southeast Asia and H5N8 in East Asia, particularly during the winter and in poultry, as compared to wild birds. Our findings highlight the need for targeted surveillance, risk-based management, and coordinated interventions to mitigate the spread of HPAI H5 in high-risk areas. This study provides valuable insights that could be used to improve biosecurity measures and inform policies for the effective control and prevention of HPAI outbreaks in Asia.

1. Introduction

High Pathogenic Avian Influenza (HPAI), like the H5N1 and H5Nx viruses, is a major global issue causing serious illness in both birds and humans. The H5N1 virus has killed a large number of birds worldwide, affecting over 400 bird species, including wild ducks, penguins, and cranes [1]. It has been reported to produce high mortality rate and poses a big risk especially to poultry and wild birds that migrate [2]. For example, the recent outbreak of HPAI in Greece in 2022 impacted 60% of the pelican breeding population [3].

The ecology of avian influenza virus is inherently tied to the biology of its natural hosts and their environments. For instance, the Whooper Swan (*Cygnus cygnus*) and Hooded Crane (*Grus monacha*), which are often associated with freshwater wetlands, contrast with species like the Large-Billed Crow (*Corvus macrorhynchos*), which are more adaptable and frequently inhabit agricultural and urban areas. These ecological differences influence their roles in the maintenance and spread of avian influenza virus across ecosystems [4–6].

While H5N1 and H5Nx viruses mainly infect birds, they can also affect mammals such as humans, pigs, and cats. Asia is a major area for H5N1 and H5Nx outbreaks due to the high number of large poultry farms and migratory birds, which can carry the virus [7–10]. Moreover, changes in temperature and the environment can alter bird migration, affecting how the virus spreads. For example, in warmer climates, the virus may survive longer especially in water sources [11].

Analyzing risk factors such as poultry density, migratory bird patterns, and environmental factors like climate and habitat type is essential to understand the drivers of the spread of H5. It has been suggested that host plays a major role in the severity of infection and the likelihood of cross-species transmission [12]. Other identified key factors that contribute to the emergence of HPAI H5N1 outbreaks in Asia include highly dense poultry farming, frequent movement of migratory birds, and environmental conditions [13]. Some highly dense areas like Southeast and East Asia work indeed as a catalyst that support virus spreading, especially in live bird markets and backyard farms [14]. Migratory birds along routes such as the East Asia-Australasia Flyway

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https://doi.org/10.1016/j.cimid.2025.102387
Received 7 June 2025; Received in revised form 11 July 2025; Accepted 16 July 2025

Table 1
Proportions of serotypes across animal categories.

Animal category	Serotype	Count	Proportion (%)
Wild birds ($n = 1510$)			
	H5N1	843	55.83
	H5N2	7	0.46
	H5N5	35	2.32
	H5N6	246	16.29
	H5N8	326	21.59
	H5Nx	53	3.51
Poultry ($n = 19819$)			
	H5N1	16 062	81.04
	H5N2	1112	5.61
	H5N3	28	0.14
	H5N5	100	0.50
	H5N6	1191	6.01
	H5N8	1277	6.44
	H5Nx	49	0.25

Table 2
Top five species in each animal category in the dataset.

Animal category	Species	Count	Proportion (%)
Wild birds ($n = 1510$)			
	Large-Billed Crow	204	13.5
	Unspecified Bird	195	12.9
	Whooper Swan	119	7.88
	Crow	57	3.77
	Hooded Crane	56	3.71
Poultry ($n = 19819$)			
	Chicken	9565	48.3
	Unspecified Bird	6797	34.3
	Duck	2451	12.4
	Goose	457	2.31
	Common Quail	245	1.24

frequently carry H5N1 over long distances, introducing the virus to new areas. Additionally, they interact with domestic poultry around shared water sources, enhancing the risk of transmission [15,16]. The warm and humid climate of Asia allows the virus to survive longer in the environment, and seasonal monsoon flooding can heighten transmission by increasing contacts between wild birds and poultry [2].

Gilbert et al. [17] compared various risk factors for H5N1 virus in Southeast Asia and mapped the key environmental variables by developing a model for Thailand poultry and testing it in the Vietnam population to validate. A research conducted for ducks in spreading H5N1 virus, suggested that this virus becomes nonpathogenic after extended shredding but increases the potential to spread in a quasi-species including humans [18]. Sangrat et al. [19] analyzed the risks of H5N1 virus in Thailand and found that the central and lower northern regions are the most vulnerable, especially near water bodies and rice fields. Migratory birds and free-grazing ducks often come into contact with contaminated water, increasing the chance of virus spreading. A detailed study for HPAI H5N1 viral and bird migration networks in Asia has been conducted in Tian et al. [14]. Based on the HPAI H5N1 cases occurred in South Asia between January 2006 and June 2019, Chowdhury et al. [20] reported multiple clades of the H5N1 virus in wild birds and poultry and a few human cases.

Under these facts, it is vital to discuss and analyze the characteristics of this deadly virus to protect birds, humans, and other mammals. Previous studies have mainly focused on the H5N1 serotype. In this study paper we present a comprehensive analysis by combining data on all HPAI H5 serotypes in wild birds and poultry. Under a risk assessment approach, this study provides key insights for effective disease management and prevention. Identifying high-risk areas and seasonal patterns can help farmers, biosecurity experts and policy makers implement optimal control strategies against the virus.

2. Methods

2.1. Data and preprocessing

This study uses avian influenza outbreak data from the Food and Agriculture Organization (FAO), compiled via mandatory country reporting, national veterinary authority submissions, and cross-validation with the World Organization for Animal Health (WOAH) databases. The dataset covers Asia subregions, relying on compulsory notifications under international agreements to ensure data completeness and accuracy. Routine cross-checks with regional surveillance programs minimize reporting bias and enhance data reliability [21–23].

Outbreak data for HPAI H5 in Asia subregions between January 2004 and August 2024 were obtained from FAO Global Animal Disease Information System (EMPRES-i) database [24]. The dataset has various variables including HPAI H5 serotypes, country, subregions, administration levels of outbreak, number of cases, dates of reported cases, animal species, longitude and latitude of the outbreak. For the purpose of this study, we classified the animal species into two category: wild birds and poultry. To capture the time series and seasonal effects on the outbreak of HPAI H5, we set up new variables, year and season, from the reported dates.

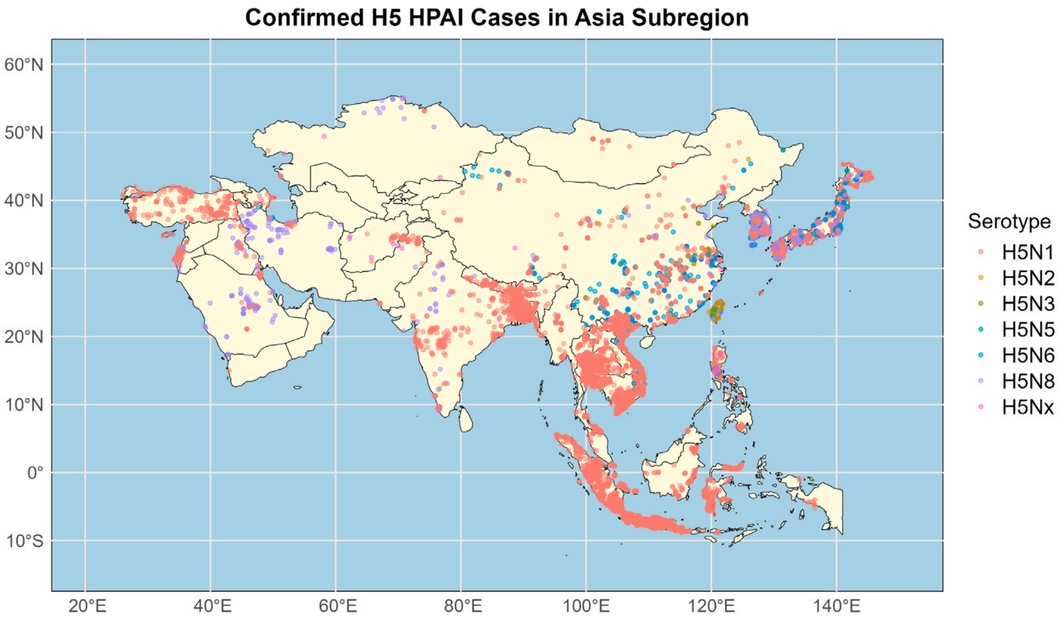
2.2. Statistical analysis

Statistical analysis was carried out on FAO confirmed cases of HPAI H5 serotypes in Asia between January 2004 and August 2024. The distributions of number of confirmed cases for HPAI H5 serotypes and seasonal trends based on subregions were examined. Also, the number of cases associated with poultry and wild birds was considered. Serotypes were compared against independent variables including subregion, year, season, and animal type. The χ^2- test was used to determine the association between the HPAI H5 confirmed cases and predictor variables. Multivariable Poisson regression analysis, a class of generalized linear model, was fitted to the number of confirmed cases of HPAI H5 serotypes, aggregated across subregion and time, treated as the dependent variable. In all cases, $p-\text{values} < 0.001$ were considered statistically significant based on the likelihood ratio test (LRT). The goodness-of-fit of the models were evaluated using the Pseudo-R^2. All analysis was conducted in R version 4.4.0 [25]. We used the `naturalearth` package [26] to visualize the spatial distribution of HPAI H5 serotypes confirmed cases in Asia subregions.

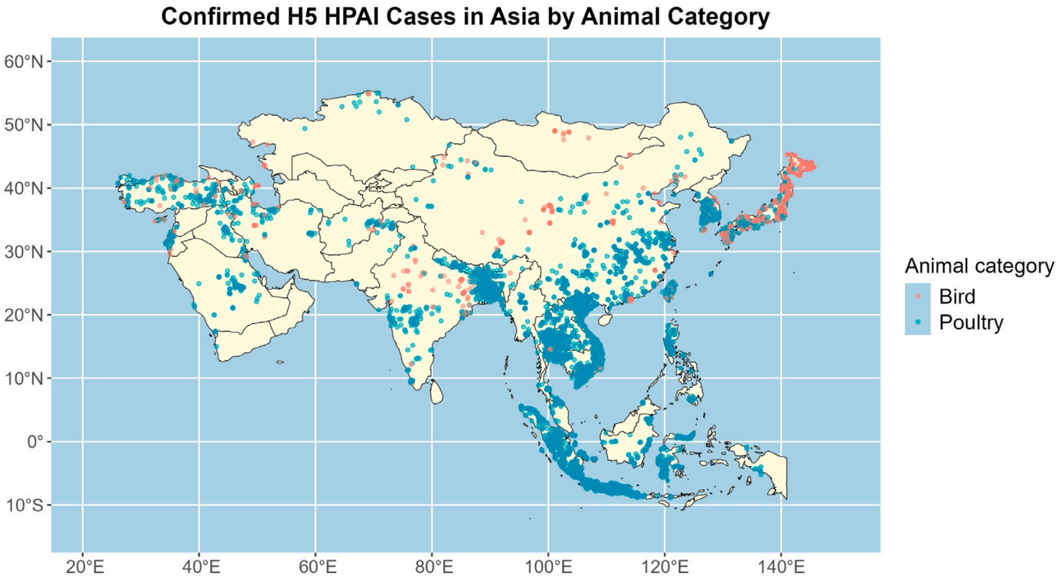
3. Results

3.1. Exploratory data analysis

Between January 2004 and August 2024, 1510 and 19819 confirmed cases of HPAI H5 were reported for wild birds and poultry, respectively, in Asian subregions (Table 1). Table 2 shows the top 5 species in each category that appear in the dataset. Specifically, nearly half of the poultry are chicken and around another one-third ‘unspecified birds’. The species of wild birds are more diverse, with Large-Billed Crow being the most common. The geographical distributions of the confirmed cases according to serotypes and animal category across the subregions are shown in Fig. 1. The H5N1 is the most prominent among the serotypes followed by H5N8. As seen in Tables 1, 843 (55.83%) of confirmed cases in wild birds belonged to H5N1 and 16062 (81.04%) of the same serotype reported in the poultry across the five Asian subregions. The number of cases of H5 HPAI serotypes in each subregion is shown in Fig. 2(a). The count of H5N1 in all subregions is more than the counts of other serotypes, apart from the Central Asia region where the count of H5N8 (56.52%) is more than H5N1 (26.09%). The highest number of HPAI H5 cases was observed in the South-Eastern Asia with 13582 (96.73%) H5N1 of the total 14041 reported cases. We further observed that the number of cases of H5N1,



(a) Distribution of H5 HPAI serotypes in Asia subregions.

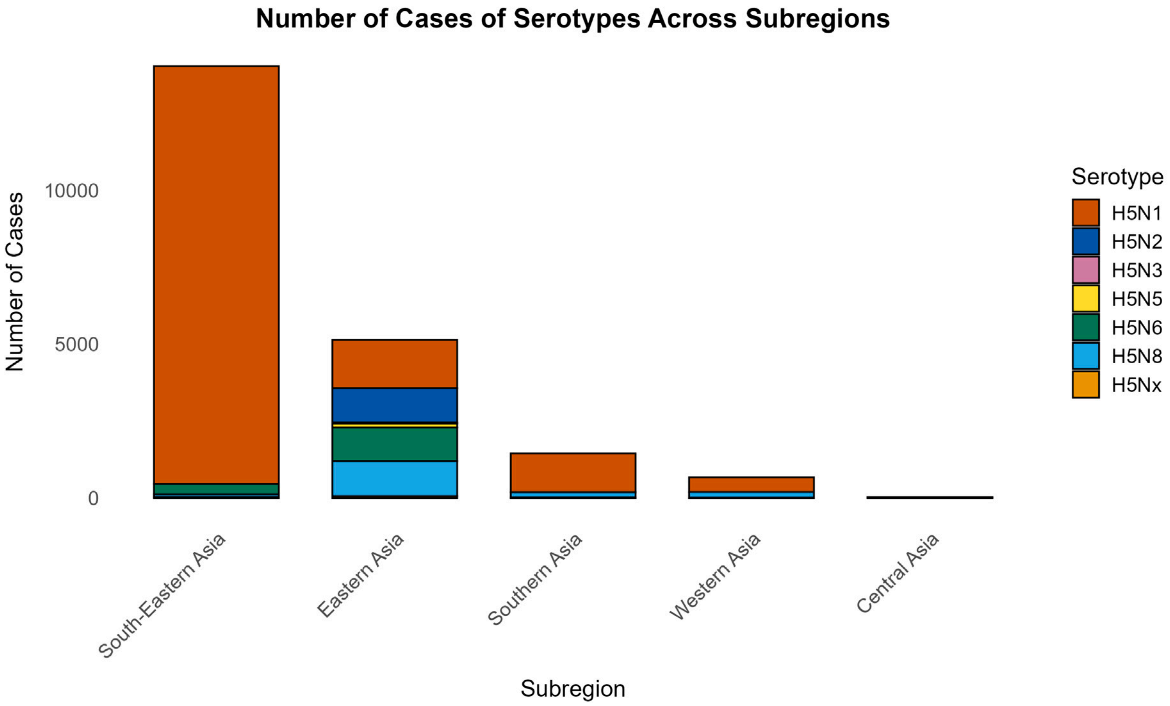


(b) Distribution of HPAI H5 in Asia subregions by animal category.

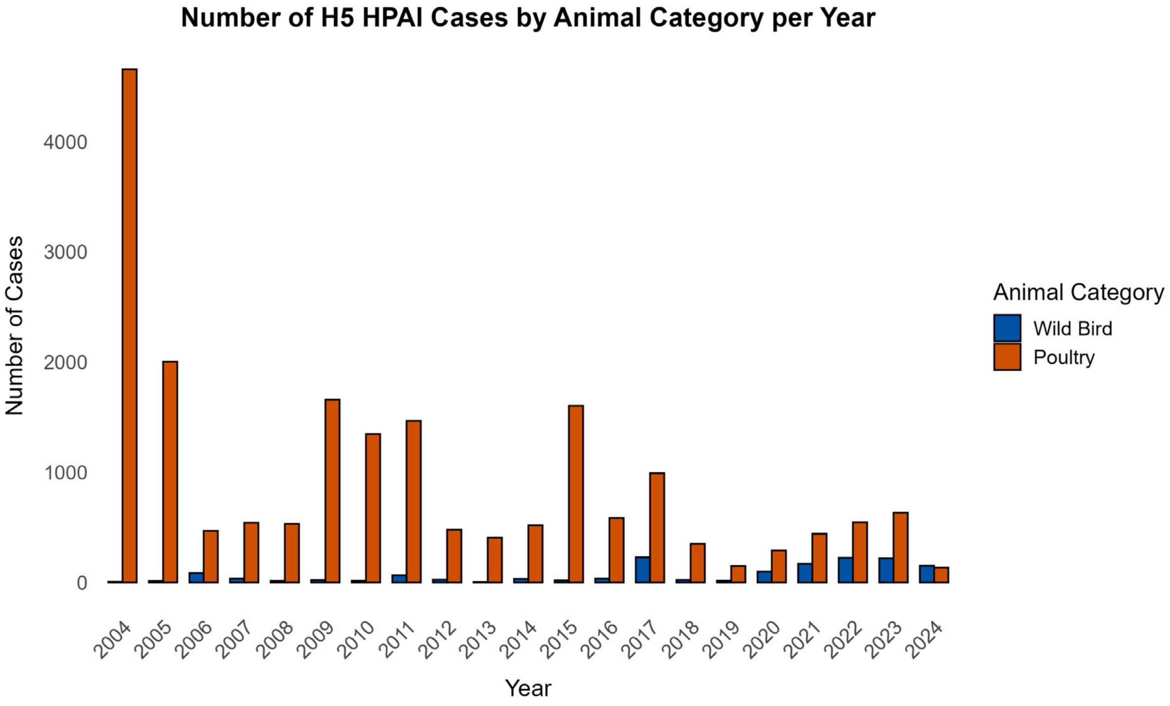
Fig. 1. Geographical distributions of H5 HPAI confirmed cases in Asia subregions between January 2004 – August 2024.

H5N2, H5N6 and H5N8 serotypes are of the same scale in the Eastern Asia subregion (Fig. 2(a)). Fig. 2(b) depicts the epidemic curve of all HPAI H5 serotypes in wild birds and poultry by year. The peak in number of cases observed in poultry between 2004 and 2005 was due to an outbreak in Asia in that period. The epidemic curve shows another outbreak between 2009 and 2015. There is propagated epidemic of HPAI H5 in the poultry category. The number of cases in wild birds started to increase from year 2017 which later reduced between 2018 and 2019 with gradual increase in the number of cases in wild birds from year 2020. As seen in Fig. 3, overall, winter is the peak period with H5N1 having the highest number of reported cases followed by H5N8 serotype.

In this study, our analysis primarily focused on two serotypes: H5N1 and H5N8, while the extended analysis combined all H5 serotypes. We present the association between serotypes and potential risk factors including subregions, year, animal category, and season. The χ^2- test



(a) Number of HPAI H5 serotypes by subregions.



(b) Yearly distribution of HPAI H5 confirmed cases in wild birds and poultry.

Fig. 2. Bar plots of HPAI H5 confirmed cases in Asia subregions between January 2004 – August 2024.

Table 3
H5N1 model fit summary.

	Exp(coeff.)	2.5%	97.5%	z	p	p(LRT)
(Intercept)	0.017	0.007	0.037	−9.978	< 0.0001	
Subregion (Reference - Central Asia)						
Eastern Asia	262.833	117.901	585.925	13.621	< 0.0001	< 0.001
South-Eastern Asia	2263.667	1016.797	5039.537	18.918		
Southern Asia	209.667	94.016	467.583	13.063		
Western Asia	80.333	35.912	179.702	10.678		
Season (Reference - Fall)						
Spring	1.041	0.993	1.091	1.669	0.095	< 0.001
Summer	0.593	0.562	0.627	−18.590	0.000	
Winter	2.307	2.216	2.402	40.648	0.000	
Animal Category (Reference - Wild Bird)						
Poultry	19.053	17.779	20.420	83.412	< 0.0001	< 0.001
Year (Reference - 2004)						
2005	0.432	0.410	0.455	−31.477	< 0.0001	< 0.001
2006	0.119	0.109	0.129	−47.416		
2007	0.124	0.114	0.135	−47.354		
2008	0.117	0.107	0.128	−47.428		
2009	0.361	0.341	0.381	−35.867		
2010	0.292	0.275	0.310	−39.986		
2011	0.328	0.310	0.348	−37.828		
2012	0.107	0.097	0.117	−47.457		
2013	0.088	0.080	0.097	−47.213		
2014	0.091	0.082	0.100	−47.274		
2015	0.063	0.056	0.071	−45.971		
2016	0.069	0.062	0.078	−46.423		
2017	0.050	0.044	0.057	−44.643		
2018	0.020	0.016	0.024	−37.386		
2019	0.009	0.006	0.012	−30.182		
2020	0.007	0.005	0.010	−28.593		
2021	0.029	0.024	0.034	−40.578		
2022	0.148	0.137	0.160	−46.850		
2023	0.130	0.120	0.142	−47.263		
2024	0.051	0.044	0.058	−40.077		
MODEL FIT:						
$\chi^2(28) = 70564.384,\ p < 0.0001$						
Pseudo-R^2 (McFadden) = 0.762						
AIC = 22120.852, BIC = 22257.773						

($p \leq 0.001$) shows that all the predictors were associated with H5 HPAI cases. The results of the Poisson regression model show that all the investigated outbreak risk factors are significantly relevant to the prevalence of all H5 HPAI serotypes considered in this study.

3.2. H5N1

Table 3 shows the summary and the estimated coefficients for the H5N1 Poisson regression model. The pseudo-R^2 indicates a satisfactory fit. Statistically significant effects were found for all factors ($p < 0.001$). All subregions had a higher number of H5N1 cases compared to Central Asia, with the highest prevalence appeared in South-Eastern Asia. The number of cases were the highest in winter and the lowest in summer. Those in fall and spring were similar. Compared to wild birds, there were 19 times more reported cases for poultry (95% CI: 17.8–20.4). Year-to-year fluctuation was evident, with generally more cases reported in earlier years (before 2012). Fig. 4 shows the estimated coefficients for each risk factor influencing HPAI H5N1 cases.

3.3. H5N8

The results for H5N8 are similar to those for H5N1 (see Table 4), in the sense that all factors had a significant effect on the number of cases. However, it is observed that there were no H5N8 cases prior to 2014. Most of the H5N8 cases happened in Eastern Asia, followed by Western Asia. Winter, followed by spring, were the two seasons with the highest number of H5N8 cases. The number of reported H5N8 cases for poultry were almost 4 times that for wild birds (95% CI: 3.47–4.42). In 2015 and 2021, there were substantially higher number of reported cases.

3.4. All H5 subtypes

Combining all H5 serotypes, Table 5 shows the fitted model. As suggested by the pseudo-R^2, the model provides a satisfactory fit. As in the other two models, all factors had a significant effect on the number of cases. South-Eastern Asia had the most number of cases, followed by Eastern Asia. The majority of cases were reported in winter, followed by spring. Poultry had 13 times more cases compared to wild birds, and most cases were reported in earlier years.

4. Discussion and conclusion

The re-emergence and outbreak of H5N1 clade 2.3.4.4b HPAI in the United States (US) of America in March 2024 in dairy herds has been linked to migratory birds [27,28]. Since the occurrence of H5N1 clade 2.3.4.4b HPAI in 2020, there have been numerous outbreak globally, mostly in Asia and Europe, with subsequent spillback to birds and other mammals including humans, the risk of HPAI as next pandemic keeps to grow [29,30]. Asia continent, one of the hub for various HPAI subtypes, has witnessed various outbreaks associated to migratory birds and contaminated environments. The avian populations in Asia are endemic to HPAI [31–33]. This study addresses a critical gap by analyzing the prevalence of HPAI across the five subregions of Asia, providing key

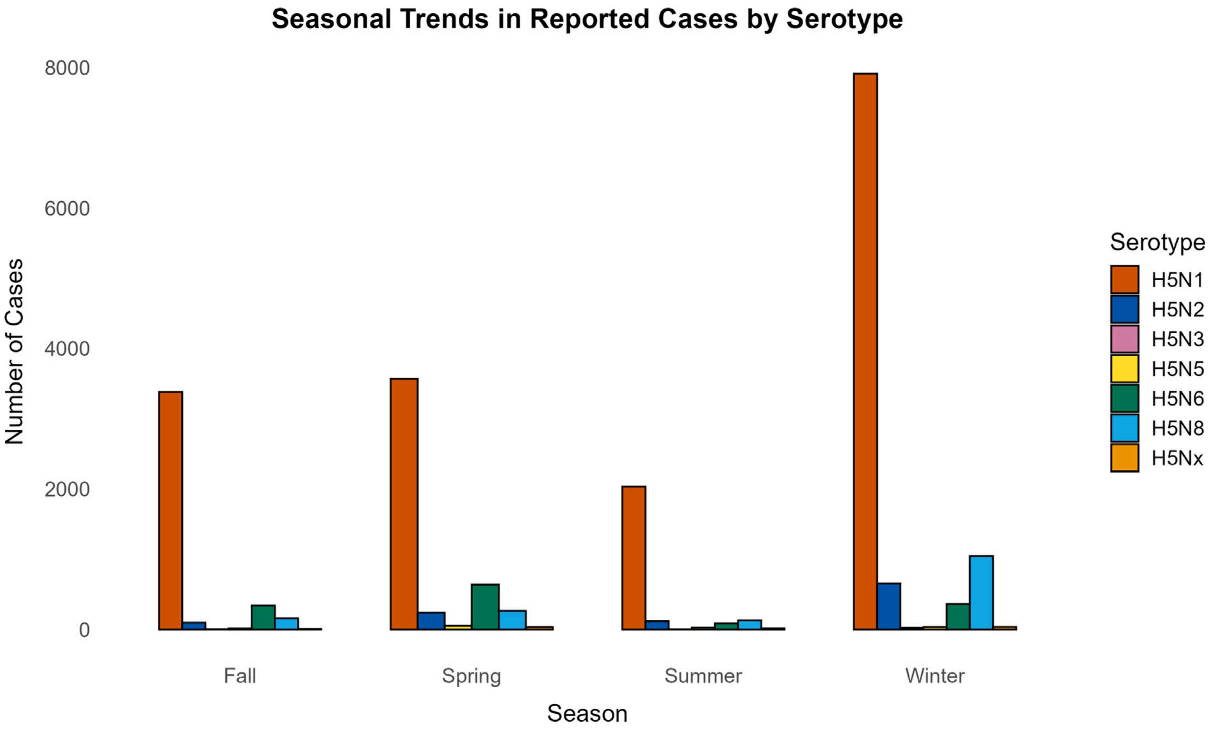


Fig. 3. Seasonal trend in reported cases by serotype.

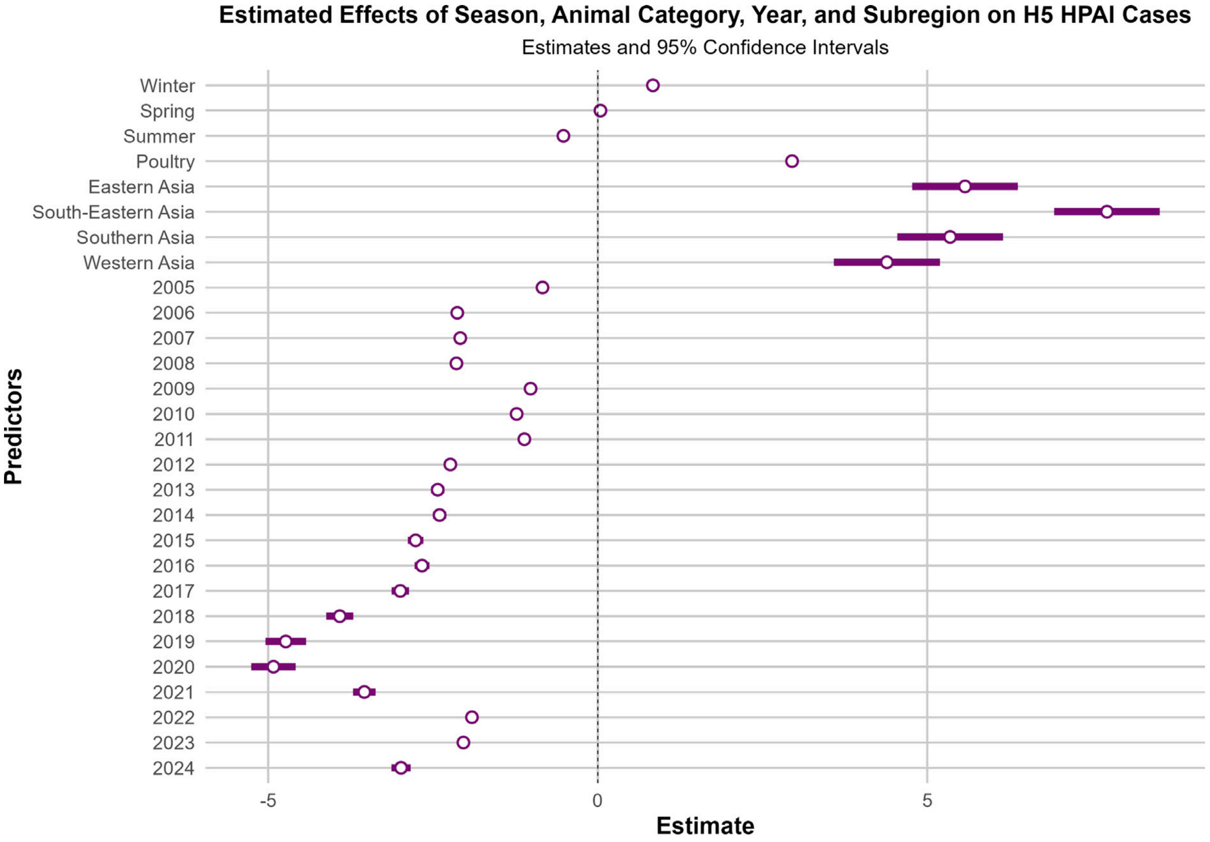


Fig. 4. Estimated coefficients for different risk factors influencing H5N1 HPAI cases from 2004 to 2024.

Table 4
H5N8 Model fit summary.

	Exp(coeff.)	2.5%	97.5%	z	p	LRT
(Intercept)	0.012	0.007	0.023	−14.043	< 0.0001	< 0.001
Subregion (Reference - Central Asia)						
Eastern Asia	87.385	50.587	150.949	16.029	< 0.0001	< 0.001
South-Eastern Asia	7.154	4.004	12.780	6.646		
Southern Asia	13.231	7.530	23.248	8.980		
Western Asia	14.538	8.289	25.501	9.337		
Season (Reference - Fall)						
Spring	1.652	1.359	2.009	5.028	0.000	< 0.001
Summer	0.807	0.641	1.017	−1.814	0.070	
Winter	6.497	5.504	7.669	22.104	0.000	
Animal Category (Reference - Wild Bird)						
Poultry	3.917	3.469	4.424	22.004	0.000	< 0.0001
Year (Reference - 2014)						
2015	7.013	5.506	8.933	15.781	0.000	< 0.0001
2016	0.880	0.632	1.225	−0.757	0.449	
2017	2.453	1.876	3.209	6.551	0.000	
2018	1.413	1.052	1.900	2.293	0.022	
2019	0.200	0.115	0.348	−5.690	0.000	
2020	2.533	1.939	3.310	6.816	0.000	
2021	4.800	3.743	6.156	12.358	0.000	
2022	0.373	0.242	0.576	−4.449	0.000	
2023	0.707	0.497	1.005	−1.935	0.053	
MODEL FIT:						
$\chi^2(17) = 5295.545,\ p < 0.0001$						
Pseudo-R^2 (McFadden) = 0.615						
AIC = 3349.693, BIC = 3421.539						

insights into the risk factors driving its spread and persistence in the continent.

Using the data on reported cases of HPAI H5 between January 2004 and August 2024 from FAO, the present study provides a detailed analysis of the spatial and temporal distribution of HPAI H5 serotypes across Asia subregions. The results indicate significant role of H5N1 in driving avian influenza outbreaks in poultry and wild birds, with substantial contribution from H5N8 and H5N6 serotypes. The higher case counts in poultry compared to wild birds shows the poultry populations are more susceptible to HPAI which may be due to high bird density, farm practices, and exposure in live bird markets.

Our findings highlight important patterns in the distribution of outbreaks across both poultry and wild bird populations. Species such as Large-Billed Crows, Whooper Swans, and Hooded Cranes were prominent in the dataset, reflecting the involvement of both local bridge hosts and long-lived migratory waterbirds in disease dynamics.

We found that South-Eastern Asia emerged as the most affected subregion, particularly during the winter season, when the virus is more stable and persists in the environment. These results are consistent with the study of global spread of H5N1 influenza virus [34], suggesting that HPAI virus survives longer in cooler temperatures, making it more stable and facilitate transmission, particularly through contaminated environment shared by poultry and wild birds.

Poisson regression models are commonly used to model count data, such as the number of confirmed HPAI H5 cases in this paper. Recent examples of using Poisson regression models in the context of risk analysis of avian influenza include [35] and [36]. In assessing the significance of coefficients in generalized linear models, the use of LRT is common [37]. Our multivariable Poisson regression analyses showed that subregion, season, year, and animal category are all statistically significant predictors of HPAI H5 serotype occurrence in Asia. No overdispersion was found in any of the models.

Although H5N1 is the primary serotype of concern and most widely studied, the contribution of other serotypes such as H5N6 and H5N8 to HPAI outbreak is non-negligible, particularly in terms of intercontinental spread of clade 2.3.4.4 viruses, reassortment events, and outbreaks in wild birds and poultry. These reflects their growing significance in both avian and zoonotic contexts [28]. Our result reveals emerging patterns of H5N6 and H5N8 occurrences across every season (Fig. 3), suggesting a shift in the evolutionary landscape of HPAI viruses. As such, one of the future works is to further our analysis on HPAI H5 serotypes within Eastern Asia where multiple serotypes co-circulate (Fig. 2(a)).

One of the key findings of the study is the identification of poultry as a primary risk factor for HPAI H5 spread in Southeast Asia. This aligns with previous research in Southeast Asia that highlighted the role of free-grazing ducks in rice fields as a significant contributor to viral transmission [38]. The current study expands on this knowledge by demonstrating that the poultry population is the main factor to put areas at risk of HPAI H5N1 spread across a broader geographical range.

The integration of different subregions data along with the Central Asia in this study offers valuable insights into the interplay between local persistence and long-distance dispersal of the virus [39]. This is particularly relevant given the recent outbreaks in various parts of Asia, including the detection of HPAI H5N1 in wild birds in China's Qinghai province [40]. The role of wild birds is also significant in viral transmission. The bird markets, common in Asian countries due to cultural preferences for freshly slaughtered meat, provide ideal conditions for virus amplification and may serve as important reservoirs for HPAI circulation.

Overall, this study makes a significant contribution to our understanding of HPAI H5N1 dynamics in Asia by providing an analysis of risk factors across multiple subregions. First, we underscore the need for targeted surveillance and control measures, particularly in areas with high poultry populations. Second, the research also emphasizes the importance of a One Health approach, considering the complex interactions between domestic poultry, wild birds, and human populations in the spread and persistence of HPAI H5N1. As the virus continues to pose a threat to poultry, wild birds, and humans, with ongoing outbreaks and the potential for reassortment, this study provides crucial insights to inform more effective prevention and control strategies across Asia and beyond.

Table 5
All H5 HPAI serotypes model fit.

	Exp(coeff.)	2.5%	97.5%	z	p	LRT
(Intercept)	0.068	0.045	0.103	−12.755	0.000	
Subregion (Reference - Central Asia)						
Eastern Asia	223.696	148.525	336.911	25.893	< 0.0001	< 0.001
South-Eastern Asia	610.478	405.568	918.918	30.741	< 0.0001	
Southern Asia	62.913	41.675	94.974	19.710		
Western Asia	29.261	19.312	44.336	15.924		
Season (Reference - Fall)						
Spring	1.178	1.130	1.229	7.662	< 0.0001	< 0.001
Summer	0.594	0.565	0.625	−20.243		
Winter	2.470	2.381	2.562	48.384		
Animal Category (Reference - Wild Bird)						
Poultry	13.125	12.456	13.830	96.443	< 0.0001	< 0.001
Year (Reference - 2004)						
2005	0.432	0.410	0.455	−31.478	< 0.0001	< 0.001
2006	0.119	0.109	0.130	−47.412		
2007	0.124	0.114	0.135	−47.355		
2008	0.117	0.107	0.128	−47.428		
2009	0.361	0.341	0.381	−35.868		
2010	0.292	0.275	0.310	−39.961		
2011	0.329	0.310	0.348	−37.802		
2012	0.108	0.099	0.118	−47.459		
2013	0.089	0.080	0.098	−47.224		
2014	0.118	0.108	0.129	−47.418		
2015	0.348	0.329	0.368	−36.624		
2016	0.133	0.122	0.145	−47.208		
2017	0.262	0.246	0.279	−41.698		
2018	0.080	0.072	0.089	−46.966		
2019	0.035	0.030	0.041	−42.188		
2020	0.084	0.076	0.093	−47.088		
2021	0.131	0.121	0.143	−47.244		
2022	0.165	0.153	0.178	−46.305		
2023	0.183	0.170	0.197	−45.619		
2024	0.076	0.067	0.086	−42.304		
MODEL FIT:						
$\chi^2(28) = 67378.717,\ p < 0.0001$						
Pseudo-R^2 (McFadden) = 0.665						
AIC = 33941.093, BIC = 34078.015						

Vaccination remains a cornerstone of avian influenza control in Asia, with heterogeneity in coverage, vaccine efficacy, and strain matching contributing to regional outbreak variability. Simultaneously, natural immunity in wild bird populations, notably long-lived migratory species such as Hooded Cranes and Whooper Swans, modulates susceptibility and viral persistence. Adopting a One Health approach and integrating comprehensive vaccination data with wild bird immunological profiles will improve the accuracy of epidemiological models and support optimized surveillance and intervention strategies [22,41].

5. Limitations

This study has a number of limitations associated to our focus on Asia subregion, which however do not demerit or undermine the significance of the findings. First, vaccination data for commercial poultry were not available in the dataset, preventing adjustment for potential differences in vaccination coverage, schedules, and effectiveness across countries and production systems. This may have introduced bias in the estimated associations between risk factors and outbreak incidence. Second, natural immunity in wild birds, particularly long-lived migratory species such as Hooded Cranes and Whooper Swans commonly observed in East Asia, was not accounted for due to lack of data on prior exposure histories. Third, while strain sequence data were included, no accompanying metadata on sequencing platforms or protocols were provided, limiting assessment of methodological consistency across regions. Finally, although a variety of wild bird species were represented, including Large-Billed Crows, Whooper Swans, and unspecified birds, there was insufficient ecological annotation (e.g., migratory behavior, habitat use) to stratify these species into functional groups (e.g., aquatic birds, scavengers, bridge species). This constrained our ability to fully examine their respective roles in sustaining and propagating outbreak waves across different subregions. Future studies incorporating vaccination records, immunity data, and species-level ecological information could provide more granular insights and enhance predictive modeling efforts for avian disease control in Asia.

CRediT authorship contribution statement

Hammed Olawale Fatoyinbo: Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Parul Tiwari:** Writing – review & editing, Writing – original draft, Validation, Software, Methodology, Investigation, Formal analysis, Data curation. **Ryan H.L. Ip:** Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Methodology, Investigation, Formal analysis, Data curation. **Victor Miranda:** Writing – review & editing, Writing – original draft, Validation, Methodology.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Declaration of competing interest

All authors declare that they have no conflicts of interest.

Acknowledgments

The authors would like to thank the reviewers for their valuable comments and constructive suggestions, which have greatly improved the quality of this manuscript. We also acknowledge the Food and Agriculture Organization (FAO) for making the dataset publicly available.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at HPAI Asian-Subregions GitHub repository.

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