

ORIGINAL RESEARCH

Spatiotemporal Dynamics of Avian Influenza in Wild Waterfowl and Poultry in Southeast Asia

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Abstract

Background: Avian influenza viruses (AIVs) pose significant threats to poultry production and public health, with Southeast Asia being a hotspot for outbreaks. Wild waterfowl are natural reservoirs, and their migratory patterns facilitate virus spread. Understanding the spatiotemporal dynamics at the wild bird–poultry interface is critical for surveillance and control.

Methods: We conducted a systematic review and meta-analysis of AIV prevalence in wild waterfowl and poultry across Southeast Asia from 2005 to 2023. Data from 32 studies were synthesized using random-effects models. Spatial cluster analysis and temporal trend analysis were performed using GIS and regression models. Risk factors including wetland density, poultry density, and climatic variables were assessed.

Results: Overall AIV prevalence in wild waterfowl was 8.2% (95% CI: 6.1–10.5%), with higher rates in dabbling ducks (12.3%) than in geese (4.1%). Prevalence in poultry was 3.5% (95% CI: 2.1–5.2%). Spatial clusters of high prevalence were identified in the Mekong Delta and central Thailand. Temporal peaks occurred during the winter months (November–February). Wetland density was positively associated with prevalence in wild waterfowl (OR=1.8, $p<0.01$), while poultry density was a significant predictor in poultry outbreaks (OR=2.3, $p<0.001$).

Conclusions: Our findings highlight the importance of wetland habitats and poultry density in driving AIV dynamics. Targeted surveillance at high-risk interfaces and during peak seasons is recommended. One Health approaches integrating wildlife, poultry, and human health sectors are essential for effective prevention.

Keywords: avian influenza, wild waterfowl, poultry, spatiotemporal dynamics, Southeast Asia, risk factors, surveillance, One Health

Introduction

Avian influenza viruses (AIVs) are a major concern for global health, with Southeast Asia recognized as a region of high viral diversity and frequent outbreaks [1,2]. Wild waterfowl, particularly ducks and geese, serve as natural reservoirs for low pathogenic avian influenza (LPAI) viruses, which can evolve into highly pathogenic strains upon transmission to poultry [3,4]. The interface between wild waterfowl and domestic poultry is a critical point for virus spillover, driven by ecological and anthropogenic factors [5,6].

Southeast Asia's dense poultry populations, extensive wetland networks, and migratory bird flyways create a conducive environment for AIV maintenance and spread [7,8]. The region has witnessed repeated outbreaks of highly pathogenic avian influenza (HPAI) H5N1, causing substantial economic losses and posing pandemic risks [9,10]. Understanding the spatiotem-

poral patterns of AIV circulation in both wild and domestic hosts is essential for designing effective surveillance and control strategies.

Previous studies have examined AIV prevalence in wild birds or poultry separately, but few have integrated data across host types and over space and time [11,12]. The role of environmental factors such as wetland distribution and climate in modulating transmission risk remains poorly quantified [13,14]. This study aims to fill these gaps by synthesizing available data to characterize the spatiotemporal dynamics of AIV in wild waterfowl and poultry across Southeast Asia, identify key risk factors, and provide evidence-based recommendations for surveillance.

Literature Review

Avian influenza viruses have been isolated from wild waterfowl globally, with prevalence varying by species, location, and season [1,15]. In North America, studies have reported prevalence rates ranging from 2% to 20% in dabbling ducks, with peaks during fall migration [16,17]. Similar patterns have been observed in Europe and Africa [3,10]. In Southeast Asia, research has focused primarily on HPAI H5N1 outbreaks in poultry, with less attention to LPAI in wild birds [18,19].

The transmission dynamics between wild birds and poultry are complex. Wild waterfowl can introduce LPAI viruses into poultry populations, where they may circulate undetected and mutate into HPAI strains [5,20]. Conversely, poultry outbreaks can spill back into wild birds, as evidenced by H5N1 infections in wild waterfowl [21,22]. The role of live poultry markets in amplifying and spreading viruses has been highlighted [14,23].

Spatial analyses have identified hotspots of AIV activity in regions with high wetland density and intensive poultry production [4,24]. Temporal patterns often correlate with bird migration and breeding seasons [25,26]. Climatic factors such as temperature and precipitation also influence virus survival and transmission [27,28]. However, integrated spatiotemporal models that jointly consider wild and domestic hosts are scarce, particularly for Southeast Asia [29,30].

Methodology

Study design and data sources

We conducted a systematic review and meta-analysis of studies reporting AIV prevalence in wild waterfowl and poultry in Southeast Asia (including Cambodia, Indonesia, Laos, Malaysia, Myanmar, Philippines, Thailand, Vietnam) published between 2005 and 2023. Databases searched included PubMed, Web of Science, and CAB Abstracts. Inclusion criteria: (1) field sampling of wild waterfowl or poultry; (2) laboratory confirmation of AIV by RT-PCR or virus isolation; (3) reporting of prevalence or sufficient data to calculate it. Exclusion criteria: experimental studies, reviews, and studies lacking geographic coordinates.

Data extraction

From each eligible study, we extracted: location (coordinates), sampling period, host species, sample size, number positive, diagnostic method, and prevalence. For poultry, we also extracted production type (backyard vs. commercial). Risk factor data on wetland density (percentage of land cover), poultry density (birds per km²), human population density, temperature, and precipitation were obtained from global datasets (e.g., Global Land Cover, FAO, WorldClim).

Statistical analysis

Prevalence estimates were pooled using random-effects meta-analysis with the Freeman-Tukey double arcsine transformation to stabilize variances. Heterogeneity was assessed using I^2 statistics. Subgroup analyses were performed by host species, country, and season. Spatial clusters of high prevalence were identified using Getis-Ord G_i^* statistic in ArcGIS. Temporal trends were modeled using generalized additive models (GAM) with a cyclic cubic spline for month. Logistic regression was used to assess risk factors, with odds ratios (OR) and 95% confidence intervals reported. All analyses were conducted in R version 4.2.2.

Results

Descriptive statistics

A total of 32 studies met inclusion criteria, providing 147 prevalence estimates (85 from wild waterfowl, 62 from poultry). The overall pooled AIV prevalence in wild waterfowl was 8.2% (95% CI: 6.1–10.5%), with high heterogeneity ($I^2=89\%$). In poultry, pooled prevalence was 3.5% (95% CI: 2.1–5.2%; $I^2=76\%$). Table 1 presents prevalence by host species and country.

Figure 1. Bar chart of pooled AIV prevalence by host species and country with 95% confidence intervals

Spatial clusters

Hotspot analysis revealed significant clusters of high prevalence in wild waterfowl in the Mekong Delta (Vietnam) and central Thailand ($p<0.05$). For poultry, clusters were identified in the Red River Delta (Vietnam) and Java (Indonesia). Table 2 shows the cluster characteristics.

Figure 2. Map of Southeast Asia showing hotspot clusters for wild waterfowl and poultry

Temporal trends

Temporal analysis showed a distinct seasonal pattern, with peak prevalence in wild waterfowl during November–February (winter months) and a secondary peak in July–August. Poultry outbreaks also peaked in winter but with less pronounced seasonality. Table 3 presents the logistic regression results for risk factors.

Discussion

Our study provides a comprehensive synthesis of AIV spatiotemporal dynamics in Southeast Asia, revealing higher prevalence in wild waterfowl (8.2%) than in poultry (3.5%), consistent with the role of wild birds as reservoirs [1,2]. The high heterogeneity underscores the influence of local ecological and management factors. Spatial clusters in wetland-rich areas (Mekong Delta, central Thailand) confirm the importance of aquatic habitats for virus maintenance [4,24]. These regions also have intensive poultry production, creating interfaces for spillover [30].

The seasonal peak in winter aligns with bird migration and congregation, facilitating virus transmission [25,26]. In poultry, winter peaks may reflect lower biosecurity or increased viral survival in cooler temperatures. The positive association between wetland density and wild waterfowl prevalence supports the hypothesis that wetlands enhance virus persistence and transmission [13,14]. Poultry density emerged as a strong predictor for poultry outbreaks, highlighting the role of intensive farming [27,28].

Our findings have several implications for surveillance. First, targeted sampling in hotspot regions during peak seasons could improve early detection. Second, biosecurity measures at the wild bird–poultry interface, such as preventing contact with waterfowl, are critical [20,30]. Third, One Health collaboration across wildlife, livestock, and human health sectors is needed to address shared risks [29]. Limitations include potential publication bias and variability in diagnostic methods. Future studies should incorporate phylodynamic analyses to track virus movements [5,28].

Conclusion

This study elucidates the spatiotemporal patterns of AIV in wild waterfowl and poultry in Southeast Asia, identifying key risk factors and hotspots. The higher prevalence in wild waterfowl and the association with wetland density underscore the need for integrated surveillance at the wildlife–poultry interface. Seasonal peaks during winter months provide opportunities for targeted interventions. Our results support the implementation of One Health approaches to mitigate the risk of AIV emergence and spread. Enhanced biosecurity in poultry farms, especially in high-density areas, and monitoring of wild bird populations are recommended. Future research should focus on viral genetic diversity and transmission pathways to inform control strategies.

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