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Spatiotemporal dynamics and ecological risk factors of high pathogenic avian influenza A(H5N1) in Canadian wildlife: A One Health surveillance analysis

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ABSTRACT

High pathogenic avian influenza A(H5N1) has expanded geographically and ecologically, affecting wild birds, mammalian wildlife, domestic animals, and humans. Wildlife surveillance provides critical early warning for One Health preparedness, yet national-scale analyses integrating host ecology, spatial patterns, seasonality, viral lineage, and risk factors remain limited. This study analysed Canadian wildlife HPAI A(H5N1) surveillance records from 2022 to 2026 to characterise spatiotemporal dynamics and identify factors associated with detection counts. A retrospective analysis of 2,657 detections across 13 provinces and territories was conducted using descriptive epidemiology, spatial clustering methods, and Negative Binomial mixed models. Detections were predominantly avian (93.3%), with waterfowl and raptors as the major host groups, while mammals accounted for a smaller but epidemiologically important proportion (6.7%). Detection burden was highest in 2022, with increased activity in autumn and spring. Ontario, Alberta, and British Columbia were identified as major hotspots, with evidence of local clustering in parts of the Prairie region. Reassortant Eurasian–North American lineages dominated detections (80.8%) and were strongly associated with higher detection counts. Modelling results identified year, season, and lineage as key predictors. These findings support risk-based One Health surveillance prioritising high-burden regions, migration-associated periods, key avian host groups, reassortant viral lineages, and continued monitoring of mammalian wildlife.

1. Introduction

High pathogenic avian influenza A(H5N1) has become an expanding One Health challenge because its transmission dynamics involve wild birds, domestic poultry, mammalian wildlife, humans, and shared environments. The One Health approach recognises the interdependence of human, animal, and ecosystem health and emphasises cross-sector collaboration for prevention, detection, preparedness, and response [31, 13]. In avian influenza, this framework is especially relevant because viral maintenance and spillover occur across ecological interfaces linking migratory birds, domestic animals, contaminated environments, and occupationally exposed human populations [14, 19].

Wild birds are central to avian influenza ecology. Waterbirds are recognised as important reservoirs, while viral persistence and transmission are shaped by host species, migration, environmental conditions, and contact with domestic birds [8, 26, 29]. Long-distance dispersal of avian influenza viruses has also been linked to migratory bird networks and intercontinental movement pathways [17, 28]. The recent HPAI H5 clade 2.3.4.4b panzootic has altered the geographic range and host breadth of HPAI outbreaks, causing extensive mortality in wild birds, outbreaks in poultry, and increasing spillovers into mammals [9, 19].

The arrival of HPAI A(H5N1) clade 2.3.4.4b in North America was closely linked to wild-bird movement. In December 2021, H5N1 HPAI viruses were detected in poultry and a free-living gull in St. John's, Newfoundland and Labrador, with phylogenetic evidence consistent with transatlantic movement from northwestern Europe [4]. Genomic analyses in the United States subsequently identified multiple wild-bird introductions and extensive reassortment with North American avian influenza viruses [32]. In Canada, national surveillance during the first year after incursion documented HPAIV detections across all provinces and territories, diverse taxonomic groups, and both Eurasian-origin and reassortant viral lineages [15].

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The Canadian outbreak also had major conservation implications, especially for seabirds in eastern Canada. Large-scale mortality assessments estimated more than 40,000 HPAI-attributable wild-bird deaths in eastern Canada during spring and summer 2022, with seabirds and sea ducks accounting for most estimated mortalities [2]. Live-bird surveillance in Atlantic Canada further showed evidence of active infection and elevated H5 antibody seroprevalence in seabird populations after the incursion, highlighting the value of combining carcass-based surveillance with live-bird and serological monitoring [25]. Seabird impacts have also been documented internationally, including severe demographic consequences in Northern Gannets during the current H5N1 panzootic [18]. International comparisons also show that avian influenza ecology is context-dependent; for example, long-term surveillance in New Zealand found low-pathogenic H5 and H7 viruses mainly in resident mallards, with limited evidence of influenza viruses in major migratory bird populations visiting New Zealand [27].

Risk-based HPAI surveillance increasingly relies on integrating wildlife, environmental, poultry, and movement data. Adaptive and predictive modelling studies have shown that waterfowl abundance, avian influenza prevalence, poultry density, environmental conditions, and climate-related variables can help identify spatiotemporal outbreak risk [23, 22, 33]. Environmental drivers such as temperature, hydrology, habitat, and land use may also influence viral persistence, host movement, and outbreak risk [11, 21]. These findings support the use of integrated spatiotemporal and ecological modelling to guide surveillance priorities.

Despite growing evidence on HPAI A(H5N1), there remains a need for national-scale analyses that integrate Canadian wildlife surveillance data across multiple years, provinces, host categories, seasons, migration periods, and viral lineages. This study analysed Canadian wildlife HPAI A(H5N1) surveillance records from 2022 to early 2026. The objectives were to: (i) describe temporal and seasonal patterns of wildlife detections; (ii) identify province-level spatial hotspots and local clustering; (iii) characterise host-category and viral lineage patterns; and (iv) model ecological and temporal risk factors associated with detection counts using Negative Binomial generalised linear mixed models. The study was framed as a One Health surveillance analysis with implications for preventive monitoring, preparedness, and targeted risk communication.

2. Materials and Methods

2.1. Study Design and Data Source

This retrospective observational study analysed Canadian wildlife HPAI A(H5N1) surveillance records to describe temporal, spatial, host-associated, and virological patterns and to identify predictors of detection counts within a One Health surveillance framework.

Wildlife HPAI surveillance data were obtained from the public High Pathogenicity Avian Influenza wildlife dashboard hosted through the Canadian Food Inspection Agency (CFIA)/ArcGIS platform and linked by the Canadian Wildlife Health Cooperative (CWHC) [6, 7, 10]. The dashboard provides laboratory-confirmed HPAI detections in Canadian wildlife and can be queried by species or species group, province, collection date, and animal status at sampling. The original dashboard URL used for data extraction was:

<https://cfia-ncr.maps.arcgis.com/apps/dashboards/89c779e98cdf492c899df23e1c38fdbbc>.

Records comprised laboratory-confirmed HPAI A(H5N1) detections reported in Canadian wildlife between 2022 and 2026. Variables extracted included province, collection date, result authorisation date, animal class, bird group, common name, scientific name, infection status, viral strain, viral lineage, and geographic coordinates when available. Records before 2022 were excluded because they represented epidemiologically distinct events preceding the current H5N1 epidemic wave.

Each record represented a wildlife detection event. Individual records were used for descriptive summaries, whereas aggregated detection counts were used for spatiotemporal analyses, retrospective surveillance evaluation, and risk-factor modelling.

2.2. Data Cleaning and Preparation

Raw data were imported into R, column names were standardised, dates were converted to date format, and categorical variables were harmonised. Missing categorical values were recoded as “Unknown” where appropriate. Exact duplicate rows were removed, followed by removal of likely epidemiological duplicates using province, common name, scientific name, collection date, status, strain, and lineage. Records before 2022 were excluded because detection counts were too small for stable annual comparisons.

2.3. Derived Variables

Temporal variables included year, month, ISO week, season, and migration period. Seasons were defined as winter, December–February; spring, March–May; summer, June–August; and autumn, September–November. Spring and fall migration periods were defined as March–May and September–November, respectively.

Province was the primary spatial unit. Province-level detection counts were joined to Canadian province and territory boundaries for mapping and spatial autocorrelation analysis. Host variables included animal class, common name, scientific name, bird group, host type, and bird category. Avian records were classified as birds and mammalian records as mammals. Mortality-associated detections included records coded as “Dead” or “Euthanized”.

2.4. Descriptive and Spatiotemporal Analysis

Descriptive analyses summarised detections across temporal, spatial, host, and virological variables. Temporal patterns were visualised using annual, monthly, and weekly epidemic curves.

Province-level hotspot classification was performed using quartiles of total detection counts. Provinces and territories were classified into low, moderate, high, and very high detection categories. Spatial patterns were mapped using Canadian province and territory boundary data.

Spatial autocorrelation was assessed using Global Moran’s I and Local Indicators of Spatial Association (LISA) to evaluate overall and local clustering of province-level detection counts [20, 1]. Spatial weights were constructed using k-nearest-neighbour relationships based on province and territory geometry. Local Moran’s I results were classified as high-high, low-low, high-low, low-high, or not significant.

2.5. Risk-Factor Modelling

Risk-factor modelling was conducted using generalised linear mixed models to identify predictors associated with HPAI detection counts. Because detection counts were overdispersed and clustered by province and host species, Negative Binomial generalised linear mixed models were used as the main modelling approach [3]. The selection of temporal, spatial, host, and virological predictors was informed by previous HPAI risk-factor studies showing that outbreak occurrence and detection intensity vary by season, geography, host category, poultry and wild-bird ecology, and environmental conditions [12, 23, 22].

The primary outcome was detection count per province–time–host–lineage stratum. Detection records were aggregated by province, year, season, migration period, host category, species, host type, and lineage. Rare species with fewer than five detections were collapsed into an “Other Rare Species” category. Rare lineages with fewer than ten detections were collapsed into an “Other/Rare Lineage” category.

The main season-based Negative Binomial model was specified as:

$$Y_i \sim \text{NegBin}(\mu_i, \theta), \quad (1)$$

$$\log(\mu_i) = \beta_0 + \beta_1 \text{Year}_i + \beta_2 \text{Season}_i + \beta_3 \text{BirdCategory}_i + \beta_4 \text{Lineage}_i + \beta_5 \text{HostType}_i + u_{\text{province}[i]} + u_{\text{species}[i]}. \quad (2)$$

A migration-period sensitivity model was fitted by replacing season with migration period. Season and migration period were not included in the same main model because migration period was derived from month and strongly overlapped with seasonal classification. A Poisson GLMM was fitted as a baseline comparison model. A zero-inflated Negative Binomial model was also fitted to assess whether excess zeros were better accounted for using a zero-inflation component. Model fit was compared using Akaike Information Criterion. Residual diagnostics were conducted using simulation-based residuals in DHARMa, including tests for overdispersion and zero inflation [16]. Fixed-effect estimates were exponentiated and reported as incidence rate ratios (IRRs) with 95% confidence intervals.

2.6. Retrospective Evaluation of a Risk-Based HPAI Surveillance Framework

A targeted surveillance framework was developed using the principal epidemiological findings identified in this study. Priority surveillance targets were defined as provinces with the highest detection burdens, host categories most frequently associated with detections, and seasons with elevated HPAI activity.

A composite surveillance score was constructed by assigning one point to each priority criterion met by an individual record. Records with a surveillance score of two or greater were classified as high-priority surveillance targets. The framework was retrospectively evaluated using historical surveillance data from 2022–2026 by calculating annual and overall detection coverage, defined as the proportion of HPAI detections that would have been captured under the proposed surveillance strategy.

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2.7. Software

Analyses were performed in R using `tidyverse` for data processing and visualisation, `sf` and `spdep` for spatial analysis, `glmmTMB` for mixed-effects count models, and `DHARMA` for residual diagnostics.

2.8. Ethical Considerations

This study used secondary surveillance data and did not involve direct contact with animals or humans. No personally identifiable human information was analysed. The analysis was conducted at aggregated spatial, temporal, and host-group levels to support wildlife disease surveillance, One Health risk interpretation, and preventive public-health preparedness.

3. Results

3.1. Dataset Overview

After cleaning, deduplication, and exclusion of 2021 records, the final analytical dataset contained 2,657 HPAI A(H5N1) wildlife detections from 13 Canadian provinces and territories between 7 January 2022 and 25 March 2026. The dataset included 112 wildlife species grouped into eight host categories. Most detections were avian ($n = 2,478$; 93.3%), while mammals accounted for 179 detections (6.7%). Mortality-associated records accounted for 1,980 detections (74.5%).

3.2. Temporal and Seasonal Distribution of HPAI Detections

Annual detection counts varied substantially across the study period. The highest number of detections occurred in 2022, with 1,199 records, representing 45.1% of the final analytical dataset. Detection counts were lower in 2023 and 2024, with 423 and 363 detections, respectively, before increasing again in 2025 to 605 detections. A smaller number of detections was recorded in 2026, reflecting partial-year surveillance through March 2026.

The monthly epidemic curve showed pronounced temporal heterogeneity, with a large spring peak in 2022 and recurring detection activity in later years (Figure 1). Weekly epidemic curves supported the presence of distinct epidemic waves, although monthly aggregation provided a clearer summary of the main temporal pattern. Additional annual, weekly, and threshold-based epidemic-wave plots are provided in Supplementary Figures S1–S3.

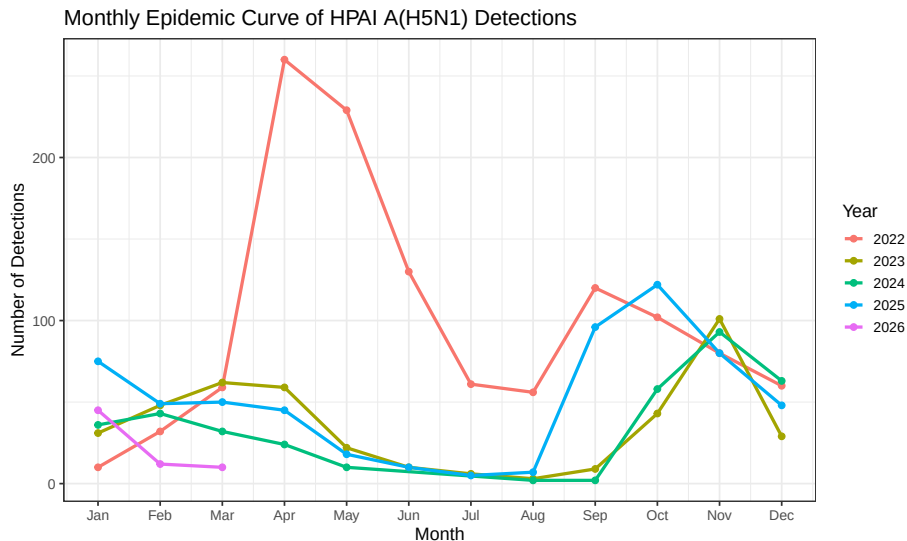


Figure 1: Monthly epidemic curve of HPAI A(H5N1) detections in Canadian wildlife, 2022–2026. Detection counts varied substantially by year and month, with a pronounced spring peak in 2022 and recurring detection activity in later years. The 2026 data represent partial-year surveillance through March 2026.

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Table 1

Summary characteristics of the 2022 HPAI epidemic wave in Canadian wildlife. For brevity, only the five provinces and five host categories with the highest numbers of detections are shown.

Category	Subcategory	Detections (n)	Percentage (%)
Province	Quebec	209	17.4
	British Columbia	177	14.8
	Ontario	172	14.3
	Saskatchewan	149	12.4
	Alberta	144	12.0
Host category	Waterfowl	435	36.3
	Raptors	320	26.7
	Corvids	137	11.4
	Seabirds	112	9.3
	Gulls/Terns	107	8.9
Viral lineage	Reassortment Eu&Na	917	76.5
	Fully Eurasian	269	22.4

Note: Percentages were calculated relative to the 1,199 HPAI detections reported in Canadian wildlife during 2022.

Seasonal analysis showed that detections were unevenly distributed across seasons. Autumn had the highest number of detections, with 906 records, followed closely by spring with 880 detections. Winter accounted for 581 detections, while summer had the lowest detection count, with 290 records. These represented 34.1%, 33.1%, 21.9%, and 10.9% of detections, respectively.

Migration-period classification showed a similar distribution. Fall migration accounted for 906 detections, spring migration accounted for 880 detections, and non-migration periods accounted for 871 detections. These represented 34.1%, 33.1%, and 32.8% of detections, respectively. Although fall and spring migration periods were important contributors to detection activity, the substantial number of detections during non-migration periods indicates that HPAI A(H5N1) surveillance should not be restricted to migration seasons alone.

Detailed seasonal and migration-period summaries are provided in Supplementary Table S2. Province-level migration-period variation is shown in Supplementary Figure S9.

3.3. Characteristics of the 2022 Epidemic Wave

The largest outbreak wave occurred in 2022, during which 1,199 HPAI detections were reported across Canadian wildlife populations (Table 1). Spatially, detections were concentrated in Quebec (17.4%), British Columbia (14.8%), Ontario (14.3%), Saskatchewan (12.4%), and Alberta (12.0%), which together accounted for 70.9% of all detections recorded during the year. Smaller proportions were reported from Manitoba (7.7%), Newfoundland and Labrador (5.8%), Nova Scotia (5.4%), New Brunswick (5.1%), and Prince Edward Island (4.3%), while the northern territories collectively contributed less than 1% of detections.

Host-category analyses revealed that waterfowl constituted the largest proportion of detections in 2022 (36.3%), followed by raptors (26.7%), corvids (11.4%), seabirds (9.3%), and gulls/terns (8.9%). Together, waterfowl and raptors accounted for 63.0% of all detections, highlighting the important role of both migratory reservoir species and predatory birds in the epidemiology of the outbreak. Mammalian detections represented 5.7% of records, indicating limited but notable cross-species spillover.

Viral lineage composition was dominated by reassortant Eurasian–North American H5N1 viruses, which accounted for 76.5% of detections in 2022. Fully Eurasian lineages represented 22.4% of detections, while only 1.1% of records lacked lineage information. The predominance of reassortant viruses during the outbreak year suggests that these lineages were primarily associated with the widespread dissemination of HPAI across multiple host groups and geographic regions.

Overall, these findings indicate that the 2022 epidemic wave was characterized by broad geographic spread across several provinces, dominance of waterfowl and raptor hosts, and widespread circulation of reassortant Eurasian–North American H5N1 viruses. These patterns provide additional context for understanding the temporal peak observed in 2022 and help identify the geographic, ecological, and virological factors most strongly associated with the largest outbreak wave during the study period.

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Compared with subsequent years, 2022 showed a greater concentration of detections among waterfowl and raptor hosts and a higher proportion of reassortant Eurasian–North American lineages, supporting their contribution to the major epidemic wave.

3.4. Spatial Hotspots and Geographic Clustering

Province-level mapping showed marked geographic heterogeneity in HPAI A(H5N1) wildlife detections across Canada (Figure 2). Ontario recorded the highest number of detections ($n = 618$), followed by Alberta ($n = 429$) and British Columbia ($n = 391$). These three provinces were classified as very high detection hotspots. Quebec ($n = 298$), Saskatchewan ($n = 249$), and Nova Scotia ($n = 195$) were classified as high detection provinces. Manitoba, Prince Edward Island, and Newfoundland and Labrador were classified as moderate detection provinces, while New Brunswick, Yukon, Northwest Territories, and Nunavut were classified as low detection areas.

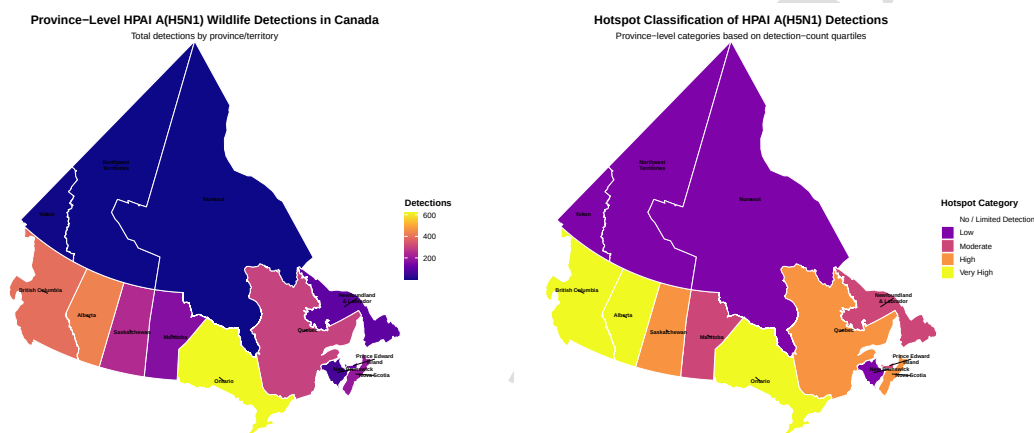


Figure 2: Spatial distribution and hotspot classification of HPAI A(H5N1) detections in Canadian wildlife. Left: province- and territory-level detection counts aggregated across the study period. Right: hotspot categories based on quartiles of total detection counts. The maps show marked geographic heterogeneity, with detections concentrated in a subset of provinces.

Global Moran's I did not provide evidence of statistically significant overall spatial autocorrelation in province-level detection counts (Moran's $I = -0.0176$, expected $I = -0.0833$, $p = 0.3266$). Local Moran's I identified one significant high-high cluster in Saskatchewan (Local Moran's $I = 0.2697$, $z = 2.5109$, $p = 0.0120$) and a significant low-high spatial outlier in Manitoba (Local Moran's $I = -0.2495$, $z = -2.6800$, $p = 0.0074$). All other provinces and territories were not statistically significant in the Local Moran's I analysis. Additional province-year, province-month, province-season, and region-season heatmaps are provided in Supplementary Figures S5–S8. The Local Moran's I cluster map is provided in Supplementary Figure S15, and significant Local Moran's I results are summarised in Supplementary Table S5.

3.5. Geographic Variation in Host Categories

Substantial geographic variation was observed in the distribution of HPAI detections among host categories across Canadian provinces (Figure 3). Waterfowl accounted for the highest numbers of detections in most provinces, particularly in Quebec, British Columbia, Ontario, Saskatchewan, and Alberta. Raptors were also consistently represented across multiple provinces and constituted an important secondary host category.

Regional differences in host-category composition were evident. Seabirds and gulls/terns contributed relatively higher numbers of detections in Atlantic provinces, including Nova Scotia and Newfoundland and Labrador, whereas waterfowl and raptors predominated throughout central and western Canada. Corvids were detected across most provinces but generally occurred at lower frequencies than waterfowl and raptors. Mammalian detections remained comparatively uncommon and were distributed across a limited number of provinces.

These findings demonstrate that distinct host groups contributed differently to regional HPAI detection patterns and provide additional ecological context for the spatial hotspots identified in previous analyses. Incorporating geographic

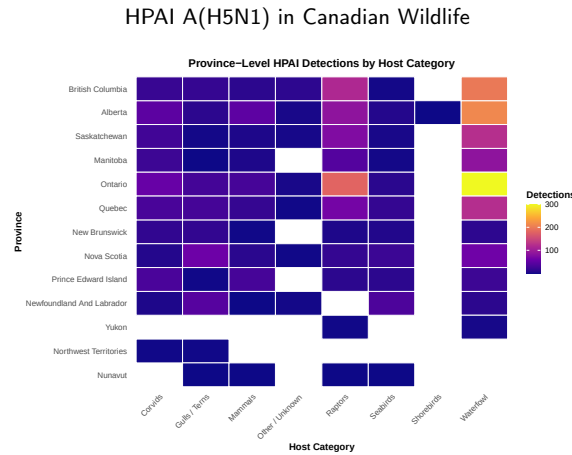


Figure 3: Province-level distribution of HPAI A(H5N1) detections by host category in Canadian wildlife from 2022–2026. Detection counts were aggregated by province and host category. Warmer colours indicate higher numbers of detections, illustrating regional differences in the contribution of host categories to reported HPAI cases.

variation in host composition may improve targeted wildlife surveillance strategies and enhance understanding of HPAI transmission dynamics across Canada.

3.6. Host Ecology and Viral Lineage Patterns

Host-category analysis showed that HPAI detections were concentrated among a limited number of ecological host groups (Figure 4). Waterfowl represented the largest host category, with 1,170 detections, accounting for 44.0% of the final dataset. Raptors were the second most frequent host category, with 617 detections, representing 23.2% of detections. Corvids accounted for 287 detections, followed by gulls/terns with 229 detections, mammals with 179 detections, and seabirds with 138 detections.

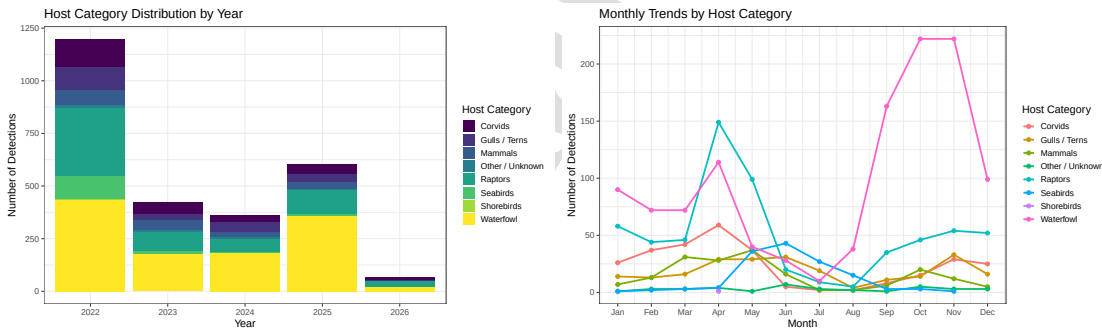


Figure 4: Host-category patterns of HPAI A(H5N1) detections in Canadian wildlife. Left: annual detection counts by host category from 2022 to 2026. Right: monthly detection trends by host category aggregated across the study period. Waterfowl and raptors contributed substantially to detection patterns, while corvids, gulls/terns, seabirds, and mammals contributed smaller but epidemiologically relevant components.

Lineage distribution was dominated by reassortment Eurasian and North American viruses. Reassortment Eu&Na lineage accounted for 2,148 detections, representing 80.8% of all records. Fully Eurasian lineage accounted for 494 detections, representing 18.6%, while lineage was unknown for 15 detections, representing 0.6% of the dataset. The full host-category and lineage distributions are provided in Supplementary Tables S3 and S4. Species-level yearly and monthly detection trends are provided in Supplementary Figures S11 and S12, and province-level host-category variation is shown in Supplementary Figure S10.

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3.7. Geographic Distribution of Viral Lineages

Geographic differences in viral lineage distribution were observed across Canadian provinces (Figure 5). Reassortant Eurasian–North American H5N1 viruses dominated detections in nearly all provinces and accounted for the majority of cases nationally. Fully Eurasian lineages were detected across several provinces but occurred at substantially lower frequencies than reassortant viruses, while records with unknown lineage assignments were uncommon.

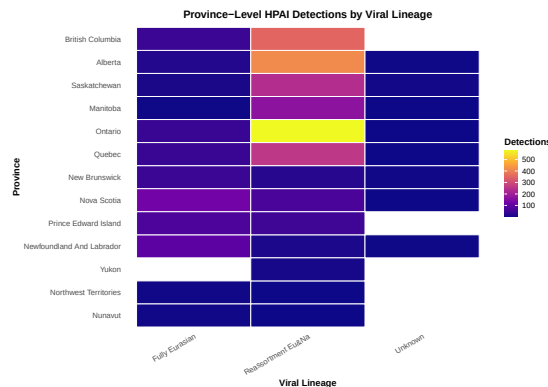


Figure 5: Province-level distribution of HPAI A(H5N1) detections by viral lineage in Canadian wildlife from 2022–2026. Detection counts were aggregated by province and viral lineage, illustrating the widespread predominance of reassortant Eurasian–North American H5N1 viruses across Canada.

The highest numbers of lineage-associated detections were observed in British Columbia, Alberta, Saskatchewan, Ontario, and Quebec, consistent with the major outbreak regions identified in previous analyses. The widespread occurrence of reassortant viruses across geographically distinct provinces suggests that these lineages played a central role in the dissemination of HPAI throughout Canada during the study period.

Overall, these findings indicate that the large-scale outbreaks observed since 2022 were associated with broad geographic spread of reassortant Eurasian–North American H5N1 viruses across multiple provinces and host communities.

3.8. Risk-Factor Modelling Dataset

The zero-filled analytical modelling dataset contained 149,760 province–time–host–lineage strata. Across these strata, there were 2,657 total detections. The mean detection count was 0.018 and the variance was 0.133, giving a variance-to-mean ratio of 7.47. This indicated substantial overdispersion and supported the use of a Negative Binomial modelling framework rather than a simple Poisson model.

The modelling dataset was high zero-heavy, with 148,693 zero-count strata, representing 99.29% of rows, and 1,067 positive-count strata, representing 0.71% of rows. The final modelling dataset included 13 provinces/territories, 58 species groups, eight bird categories, and three lineage groups. A summary of the zero-filled modelling dataset is provided in Supplementary Table S6.

3.9. Risk Factors Associated with HPAI Detection Counts

Model comparison supported the Negative Binomial season model as the primary risk-factor model. This model had the lowest AIC (13,195.84), followed closely by the zero-inflated Negative Binomial season model (AIC = 13,197.84). The Negative Binomial migration model had a higher AIC (13,257.25), and the Poisson model had the poorest fit (AIC = 20,609.60). Full model comparison results are provided in Supplementary Table S7.

Simulation-based residual diagnostics supported the adequacy of the Negative Binomial season model. The model showed no evidence of problematic overdispersion (dispersion test $p = 0.330$) and no evidence of residual zero inflation (zero-inflation test $p = 0.860$). The zero-inflated model did not improve fit relative to the simpler Negative Binomial model. Simulation-based diagnostic test results are summarised in Supplementary Table S8, and residual diagnostic plots are provided in Supplementary Figures S16 and S17.

In the final Negative Binomial season model, detection counts were significantly lower in all years after 2022. Compared with 2022, the IRR was 0.24 for 2023, 0.20 for 2024, 0.28 for 2025, and 0.03 for 2026. Compared with

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Table 2

Key fixed-effect estimates from the main Negative Binomial generalised linear mixed model for HPAI A(H5N1) detection counts in Canadian wildlife.

Predictor	IRR	95% CI	p-value
Year 2023 vs 2022	0.24	0.19–0.30	< 0.001
Year 2024 vs 2022	0.20	0.16–0.25	< 0.001
Year 2025 vs 2022	0.28	0.23–0.35	< 0.001
Year 2026 vs 2022	0.03	0.02–0.04	< 0.001
Autumn vs Winter	1.51	1.22–1.88	< 0.001
Spring vs Winter	1.39	1.12–1.73	0.003
Summer vs Winter	0.61	0.48–0.79	< 0.001
Shorebirds vs Waterfowl	0.04	0.01–0.35	0.003
Fully Eurasian lineage	40.39	23.30–70.00	< 0.001
Reassortment Eu&Na lineage	129.80	75.37–223.52	< 0.001

winter, autumn had a significantly higher expected detection count (IRR = 1.51, 95% CI: 1.22–1.88), and spring also had a higher expected detection count (IRR = 1.39, 95% CI: 1.12–1.73). Summer had a significantly lower expected detection count than winter (IRR = 0.61, 95% CI: 0.48–0.79).

Lineage was strongly associated with detection counts. Fully Eurasian lineage had a substantially higher expected detection count (IRR = 40.39, 95% CI: 23.30–70.00), while Reassortment Eu&Na lineage had the highest expected detection count (IRR = 129.80, 95% CI: 75.37–223.52). Adjusted model predictions are shown in Figure 6.

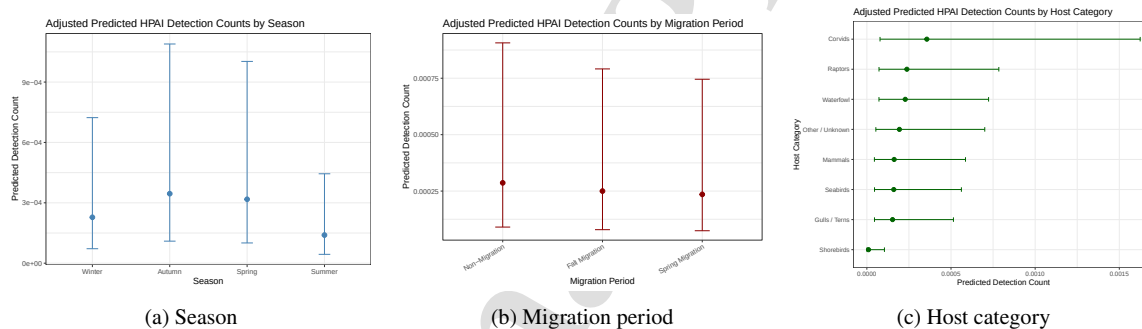


Figure 6: Adjusted predicted HPAI A(H5N1) detection counts from the Negative Binomial generalised linear mixed model. Panels show adjusted predictions by season, migration period, and host category. Predictions account for fixed effects and province- and species-level random intercepts.

Collectively, the mixed-effects modelling results provide statistical support for the descriptive epidemiological patterns identified throughout this study. The elevated detection burden observed during the 2022 epidemic wave corresponded with significant temporal, ecological, and virological effects identified by the models. In particular, seasonal migration periods, host-category composition, and viral lineage emerged as important predictors of HPAI detection intensity. These findings suggest that the observed spatiotemporal patterns were not solely attributable to geographic variation in surveillance effort but instead reflect interactions among host ecology, migratory processes, and viral evolutionary dynamics. Integrating descriptive epidemiology with risk-factor modelling therefore provides a more comprehensive understanding of the mechanisms underlying HPAI spread across Canadian wildlife populations.

3.10. A Risk-Based Surveillance Framework for HPAI Detection

A targeted HPAI surveillance framework was developed using the principal epidemiological findings of this study. Priority surveillance targets included five provinces (Quebec, British Columbia, Ontario, Saskatchewan, and Alberta), two major host categories (waterfowl and raptors), and the spring and autumn seasons, which were consistently associated with elevated HPAI activity.

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Table 3

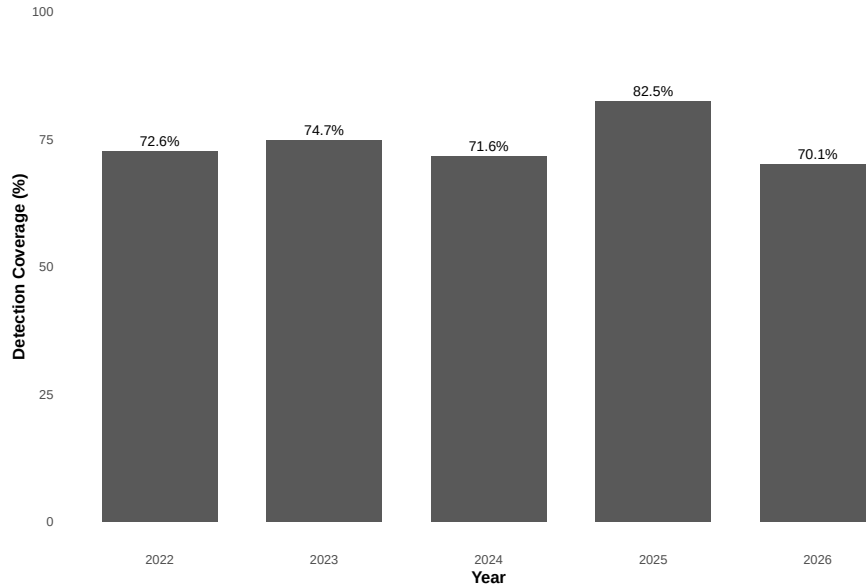
Retrospective performance of the proposed targeted HPAI surveillance framework.

Year	Total detections	Captured detections	Detection coverage (%)
2022	1199	870	72.6
2023	423	316	74.7
2024	363	260	71.6
2025	605	499	82.5
2026	67	47	70.1
Overall	2657	1992	75.0

Note: The framework prioritised five provinces (Quebec, British Columbia, Ontario, Saskatchewan, and Alberta), two host categories (waterfowl and raptors), and the spring and autumn seasons.

A composite surveillance score was constructed using these components to identify high-priority surveillance targets. Retrospective evaluation demonstrated that the proposed framework would have captured 1,992 of 2,657 HPAI detections reported between 2022 and 2026, corresponding to an overall detection coverage of 75.0%. This reflects detection coverage rather than outbreak prediction accuracy or surveillance sensitivity and should therefore be interpreted as an estimate of the proportion of historical detections captured by the framework.

Performance remained relatively stable across years, with estimated detection coverage ranging from 70.1% to 82.5% (Table 3). Detection coverage was highest in 2025 (82.5%) and lowest in 2026 (70.1%), although all years exceeded 70% coverage.

Retrospective Performance of the Proposed Surveillance Framework**Figure 7:** Annual detection coverage achieved by the proposed targeted HPAI surveillance framework during retrospective evaluation from 2022–2026.

These findings suggest that a targeted surveillance strategy focused on high-risk provinces, priority host groups, and peak transmission seasons could substantially improve surveillance efficiency while reducing the geographic and ecological scope of monitoring activities. Although retrospective in nature, this framework demonstrates the potential utility of epidemiologically informed surveillance approaches for enhancing HPAI preparedness and early detection efforts across Canada.

4. Discussion

This study provides a national One Health analysis of high pathogenic avian influenza A(H5N1) detections in Canadian wildlife from 2022 to early 2026. The findings show that detection patterns were consistently structured by temporal dynamics, geographic variation, host ecology, and viral lineage, highlighting the complex ecological and epidemiological drivers of HPAI transmission.

The temporal distribution of detections was strongly influenced by the initial emergence and subsequent progression of clade 2.3.4.4b HPAI A(H5N1) in North America. The highest detection burden occurred in 2022, corresponding to the early phase following the late-2021 introduction into eastern Canada. Although detection counts declined in 2023 and 2024, the resurgence observed in 2025 suggests continued viral circulation in wildlife populations, supporting the need for sustained long-term surveillance.

Seasonality was a key determinant of detection intensity. Detection counts were significantly higher in autumn and spring compared with winter, while summer exhibited reduced detection activity. These patterns are consistent with known avian influenza dynamics influenced by migration, seasonal aggregation, environmental persistence, and changing host-contact structures. However, the substantial number of detections observed during non-migration periods indicates that transmission is not restricted to migratory events alone. Consequently, surveillance efforts should be maintained year-round, with targeted intensification during high-risk seasonal windows.

Spatial analyses revealed marked geographic heterogeneity in detection burden. Ontario, Alberta, and British Columbia were consistently identified as high-burden regions, while additional provinces showed moderate to high detection levels. These patterns likely reflect a combination of ecological factors, host density, surveillance intensity, and reporting capacity. Importantly, detection hotspots should be interpreted as areas of high observed detection burden rather than definitive estimates of underlying infection prevalence, as surveillance-based data are inherently influenced by reporting processes and sampling effort.

Host ecology played a central role in structuring detection patterns. Waterfowl represented the dominant host group, consistent with their established role as natural reservoirs and dispersal agents of avian influenza viruses. Raptors, corvids, gulls/terns, seabirds, and mammals also contributed meaningfully to detections, reflecting multiple ecological transmission pathways, including environmental exposure, predation, and scavenging.

The involvement of seabirds and mammalian wildlife also highlights broader conservation and One Health considerations. Recent studies have documented large-scale mortality events among seabirds associated with clade 2.3.4.4b H5N1 outbreaks, particularly within breeding colonies and migratory populations, raising concerns about the impacts of repeated outbreaks on vulnerable species and ecosystem functioning [5, 30, 24]. Although the present study was not designed to evaluate population-level consequences, the observed involvement of these wildlife groups underscores the importance of integrated wildlife surveillance for early detection and conservation planning.

Viral lineage was one of the strongest predictors of detection intensity. Reassortant Eurasian–North American viral lineages dominated the dataset and were associated with substantially higher detection counts compared with other lineage groups. These findings are consistent with genomic evidence indicating multiple introductions and extensive reassortment events following the emergence of clade 2.3.4.4b in North America. However, the large magnitude of lineage-associated incidence rate ratios should be interpreted relative to the reference lineage category and may partly reflect sparse counts in less frequent lineage groups.

Beyond identifying temporal and spatial hotspots, the additional comparative analyses revealed that the 2022 epidemic wave was characterized by widespread circulation of reassortant Eurasian–North American H5N1 viruses, substantial contributions from waterfowl and raptor hosts, and broad geographic dissemination across multiple provinces.

The modelling results support the use of a Negative Binomial generalised linear mixed modelling framework for analysing wildlife surveillance data. The dataset exhibited substantial overdispersion and a high proportion of zero-count strata, making standard Poisson approaches unsuitable. Year, season, and lineage emerged as the main drivers of detection intensity, reinforcing the importance of integrating temporal, ecological, and virological factors in risk assessment models.

This study has several limitations. The analysis was based on surveillance detections rather than true infection prevalence and is therefore subject to biases associated with reporting effort, carcass detection probability, wildlife density, laboratory submission practices, and regional surveillance capacity. Mortality-associated detections may over-represent severe infections, while mild or subclinical infections are likely underrepresented. Additionally, province-level aggregation may mask finer-scale ecological variability, and key environmental covariates such as habitat,

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climate, and poultry interface dynamics were not included. Host-category classification also introduced partial overlap with host-type variables, limiting estimation of certain model parameters. The proposed surveillance framework was evaluated using the same surveillance dataset from which priority targets were derived and therefore should be externally validated using independent datasets or future surveillance periods before broader implementation

Despite these limitations, the findings provide important insights for surveillance and risk management. A risk-based One Health surveillance approach should prioritise high-burden regions, migration-associated periods, waterbird and scavenger-associated host groups, reassortant viral lineages, and continued monitoring of mammalian wildlife. These results provide a practical framework for designing targeted surveillance strategies in regions experiencing ongoing HPAI expansion. Future research should aim to integrate wildlife surveillance with environmental, genomic, poultry, and public health data to strengthen early warning systems and improve preparedness for HPAI A(H5N1) and other emerging zoonotic threats.

5. Conclusion

Canadian wildlife HPAI A(H5N1) detections from 2022 to early 2026 showed clear temporal, spatial, host-associated, and virological structure. Detections were concentrated in high-burden provinces, were dominated by avian hosts, particularly waterfowl and raptors, and were higher during autumn and spring. Reassortant Eurasian–North American viral lineages were the dominant lineage group and were strongly associated with detection intensity. These findings support risk-based One Health surveillance that prioritises high-burden regions, migration-associated periods, waterbird and scavenger-associated host groups, reassortant viral lineages, and mammalian wildlife monitoring. Future surveillance should integrate wildlife, domestic animal, environmental, genomic, and public health data to improve early warning and preparedness for HPAI A(H5N1) and other emerging zoonotic threats.

Declaration of Competing Interest

The authors declare no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data Availability

The analysis used secondary wildlife surveillance data obtained from public HPAI wildlife surveillance dashboards hosted through the Canadian Food Inspection Agency/ArcGIS platform and linked by the Canadian Wildlife Health Cooperative. Derived analytical datasets and code may be made available upon reasonable request, subject to data-use permissions and institutional requirements.

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CRedit authorship contribution statement

Hammed Olawale Fatoyinbo: Conceptualization, methodology, data curation, investigation, formal analysis, supervision, resources, visualization, writing—original draft, writing—review and editing. **Hoyeon Jeong:** Data curation, methodology, investigation, resources, visualization, writing—review and editing.

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Manuscript Title

Spatiotemporal dynamics and ecological risk factors of highly pathogenic avian influenza A(H5N1) in Canadian wildlife: A One Health surveillance analysis

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