Letters in Animal Biology

Journal homepage: www.liabjournal.com

Highly pathogenic Avian Influenza (H5N1) in Latin America: Epidemiology, control strategies, and One Health implications

Ximena Grijalva-Trejo, Carlos Vásquez*

Facultad de Ciencias Agropecuarias, Universidad Técnica de Ambato. Province of Tungurahua, Ecuador

Article info

Received: 27 September 2025
Received in revised form: 03 January 2026
Accepted: 06 January 2026
Published online: 11 January 2026

Keywords

Animal diseases
Poultry
One Health
Surveillance
Biosecurity
Vaccination strategies

* *Corresponding author:*
Carlos Vásquez
Email: *ca.vasquez@uta.edu.ec*

Reviewed by:

Consent to publish the names of reviewers could not be obtained

Abstract

Avian influenza (AI) remains a major and persistent threat to animal and public health due to its high pathogenicity, zoonotic potential, and capacity for transboundary dissemination. The introduction of highly pathogenic avian influenza (HPAI) H5N1 clade 2.3.4.4b into the Americas in 2022 marked a critical shift in the regional epidemiological landscape, with Latin America emerging as one of the most vulnerable region. This review synthesises current knowledge on the aetiology, molecular determinants of pathogenicity, transmission dynamics, and the regional epidemiological situation of avian influenza from 2019 to 2025. Multiple Latin American countries, including Peru, Chile, Argentina, Ecuador, Mexico, Colombia, Brazil and Bolivia, have reported outbreaks in wild birds, domestic poultry, and mammals, alongside sporadic human cases. Key regional drivers include migratory bird flyways, informal live-bird trade, and uneven diagnostic and surveillance capacities, all of which facilitate viral persistence and spread. Management strategies are critically analysed, encompassing epidemiological surveillance, contingency planning and notification to the World Organisation for Animal Health (WOAH), farm-level biosecurity, movement restrictions, stamping-out and carcass disposal, vaccination approaches, and training of producers and veterinarians. Experiences from Mexico, Egypt, and China illustrate both the potential and the challenges of vaccination, reinforcing the need for risk-based application, DIVA-compatible diagnostics, and rigorous value-chain surveillance. Despite progress, structural weaknesses in veterinary infrastructure, cross-border coordination, and genomic surveillance persist. Strengthening One Health framework, harmonising regional policies, and sustained investment in laboratory and field capacities are essential to mitigate the continuing threat of HPAI and to safeguard food security, trade, biodiversity, and public health in Latin America.

1. Introduction

Avian influenza has emerged as one of the most significant animal health threats of past few decades, particularly highly pathogenic strains of the H5 and H7 subtypes, which are capable of wiping out entire flocks in a matter of days, resulting in both economic devastation and disruption of rural livelihoods (Paredes Cabezas et al. 2023; Rodriguez et al. 2025). Over the past two decades, avian influenza has demonstrated its recurrent and unpredictable nature, with outbreaks reported across nearly every continent due to its high pathogenicity in poultry and remarkably rapid genetic evolution, influenced by migratory bird movements, international trade, and environmental changes (Nagoba et al. 2025). In addition to its impact on animal health and production, avian influenza is recognised as a public health concern due to its zoonotic potential. Since the first human case of H5N1 in Hong Kong in 1997, sporadic cases of human infection continue to emerge with higher fatality rate, underscoring the virus's dangerous capacity to cross species barriers (Musa et al. 2024). These characteristics have placed avian influenza at the centre of global health discussions, particularly under the "One Health" framework, which recognizes the interconnectedness of animal health, human health, and environmental conditions (Rehman et al. 2023).

In recent years, the Americas have experienced successive waves of avian influenza, and the introduction of the H5N1 clade 2.3.4.4b in 2022 marked a turning point for the region (Bruno et al. 2025; Xie et al. 2025). This lineage spread quickly across the continent, affecting both wild and domestic birds, and several mammalian species, challenging countries with different preparedness and response capacities (Cui et al. 2022; Kovács et al. 2025a). In Peru and Chile, early detections in wild seabirds were followed by rapid spillover into poultry and marine mammals, with genomic evidence indicating shared viral ancestry and underscoring the transboundary nature of outbreaks and the need for coordinated regional surveillance (Sevilla et al. 2024). Similarly, Argentina experienced a severe outbreak in 2023 that originated in wild birds and spread to commercial poultry, resulting in temporary loss of avian influenza–free status and trade disruptions; however, the prompt implementation of stamping-out policies and intensified surveillance enabled containment within months, albeit with substantial economic costs (Vagnozzi 2024).

By contrast, Brazil's long-standing national poultry health framework, characterized by strict biosecurity and vertically integrated production, limited incursions into commercial farms despite viral detection in wild birds in 2023, nevertheless, ongoing risks associated with migratory pathways persist (Rauber 2023). Conversely, Ecuador, illustrates the vulnerability of less integrated systems, where outbreaks during 2022-2023 resulted in extensive culling and movement restrictions, in the absence of adequate compensation mechanisms, disproportionate financial losses among small and medium producers due to limited compensation mechanisms (Paredes Cabezas et al. 2023). Collectively, these experiences illustrate the uneven impact of avian influenza across Latin America. Countries with stronger surveillance and biosecurity infrastructures, such as Brazil, have so far contained outbreaks, while others with more fragmented systems have suffered deeper shocks. Given the unpredictable spread virus through migratory birds and cross-border trade means no country can face the threat alone. The challenge ahead lies in building resilient, coordinated responses that go beyond national borders based on the principles of One Health. Hence, collaboration, transparency, and shared investment in prevention will be essential to safeguard the poultry industry and public health in the region.

2. Methodology

This review was conducted to synthesise evidence published between 2019 and 2025 on the epidemiology, transmission dynamics, and management strategies of highly pathogenic avian influenza (HPAI), with a specific focus on Latin America. The electronic databases PubMed, Scopus, and Web of Science were systematically searched from July to October 2025. The search strategy combined controlled vocabulary and free-text terms related to avian influenza and regional scope, including: "avian influenza", "H5N1", "highly pathogenic avian influenza", "HPAI", "clade 2.3.4.4b", "Latin America", "Americas", "poultry", "wild birds", "mammalian spillover", "vaccination", "biosecurity", and "surveillance". Boolean operators were applied to refine retrieval, and the reference lists of key articles were screened to identify additional relevant publications.

Peer-reviewed articles were included if they addressed avian influenza epidemiology, transmission, pathogenicity, surveillance, control measures, or vaccination strategies relevant to Latin America, or if they provided mechanistic insights applicable to the region. Both observational and modelling studies were considered. The review primarily included publications in English, Spanish, and Portuguese. Studies focusing exclusively on unrelated influenza subtypes, experimental laboratory research lacking epidemiological relevance, or geographic regions without conceptual relevance to the Americas were excluded, unless cited for comparative or mechanistic purposes. Given the operational and policy-oriented nature of avian influenza control, grey literature was systematically included. Official reports, epidemiological updates, and technical guidance from PAHO, FAO, WHO, WOAH, and national animal health authorities were incorporated to capture up-to-date outbreak data, surveillance findings, and regulatory frameworks not yet reflected in the peer-reviewed literature.

3. Aetiological agent of avian influenza

Avian influenza (AI) is caused by influenza A viruses (family Orthomyxoviridae), which possess a segmented, negative-sense RNA genome that enables frequent genetic reassortment and rapid evolution. Among viral proteins, haemagglutinin (HA) and neuraminidase (NA) are central to pathogenicity, host adaptation, and antigenic diversity, and therefore constitute key targets for vaccine design and molecular surveillance (Luo et al. 2023). From a veterinary and public health perspective, subtypes H5 and H7 are of particular relevance, as only these have been shown to evolve from low pathogenic avian influenza viruses (LPAIVs) into highly pathogenic avian influenza viruses (HPAIVs) under natural conditions (Charostad et al. 2023). This transition is primarily driven by the acquisition of a polybasic cleavage site in the HA protein, which allows systemic viral replication in poultry and is routinely monitored as a molecular marker of virulence in genomic surveillance programs (Luczo and Spackman 2025).

Since its emergence in southern China in the mid-1990s, H5N1 has diversified into multiple genetic clades and reassortant forms (H5Nx), achieving an unprecedented global distribution. This evolutionary plasticity has facilitated repeated spillover events into mammalian hosts, including terrestrial and marine species, raising concerns regarding viral adaptation beyond avian reservoirs and reinforcing the importance of whole-genome sequencing for risk assessment (Krammer et al. 2025; Luczo and Spackman 2025). While other subtypes, such as H7N9, have demonstrated zoonotic potential, their primary relevance in this context lies in highlighting how reassortment and HA mutations can enhance mammalian infectivity rather than in their epidemiology per se (Luczo and Spackman 2025; Shi et al. 2023). Finally, enzootic LPAIVs such as H9N2, despite causing limited clinical disease in poultry, play a critical role as internal gene donors, contributing to the emergence of novel reassortant strains with altered pathogenicity or host range. Consequently, sustained genomic surveillance across both high- and low-pathogenic lineages remains essential to inform vaccine strain selection, detect markers of mammalian adaptation, and anticipate shifts in epidemic potential (Yang et al. 2025).

3.1. Pathogenicity

The distinction between high and low pathogenicity lies in the molecular structure of the HA cleavage site. LPAIVs contain a monobasic motif cleaved only by trypsin-like proteases in the respiratory and intestinal tracts, restricting viral replication to localised tissues. Conversely, HPAIVs bear polybasic motifs, cleaved by ubiquitous proprotein convertases such as furin, enabling systemic infection and high mortality in gallinaceous birds (Luczo and Spackman 2025). While domestic chickens and turkeys are highly susceptible to HPAIVs, many wild species, particularly mallards remain fairly asymptomatic, facilitating long-distance dissemination of HAPIVs along the migratory routes and hence complicate the detection and control efforts (Krammer et al. 2025).

3.2. Transmission dynamics and natural reservoirs

Wild aquatic birds, particularly members of the orders *Anseriformes* (ducks, geese, swans) and *Charadriiformes* (gulls, shorebirds), serve as the primordial reservoirs of influenza A viruses (Luczo and Spackman 2025). Transmission occurs predominantly via the faecal-oral route in aquatic habitats, facilitating long-distance spread through migration (Shi et al. 2023). Spillover into domestic poultry creates opportunities for viral amplification and adaptation, resulting in emergence of highly pathogenic phenotypes such as H5N1 clad 2.2.4.4b, with expanded host range, including mammals such as minks, foxes, and marine mammals (Krammer et al. 2025). Charostad et al. (2023) highlighted that HPAI H5N1 remains an imminent threat, with World Health Organisation reporting 878 confirmed human infections and 458 deaths, reflecting a persistently high case fatality rate (52.16%) across 23 countries up to mid-2023. These findings emphasise the virus's expanding ecological niche, affecting not only poultry but also wild birds and marine mammals, raising concerns over zoonotic risk and potential adaptation for efficient human-to-human transmission. However, field investigations in Europe further illustrate the role of biosecurity and rapid response in limiting viral persistence. Iancu et al. (2025) documented persistence of H5N1 following a 2024 outbreak in backyard flocks in Romania, confirming viral detection in chickens and geese but showed no evidence of prolonged circulation beyond the outbreak period, underscoring the importance of biosecurity and rapid depopulation measures to prevent environmental persistence. In a related analysis, these authors reviewed the evolution of HPAI strains in Europe (2005–2023), noting the dominance of H5N1 clade 2.3.4.4b and its reassortment capacity with other subtypes, facilitating geographical spread and persistence.

4. Epidemiological overview of Latin America

Since 2019, Latin America has witnessed the introduction and dissemination of highly pathogenic avian influenza (HPAI) A (H5N1) clade 2.3.4.4b, with outbreaks reported in both wild and domestic birds, as well as sporadic human cases in countries such as Ecuador, Chile, Peru, Argentina, Mexico and, more recently (2024-2025), Brazil (Azat et al. 2024; Cruz et al. 2023; Marandino et al. 2025; PAHO 2025a). The outbreaks have not been confined to commercial poultry but have also affected wild avifauna, including both migratory and resident species, alongside backyard flocks (Azat et al. 2024; Cruz et al. 2023). In addition, detections in mammals, such as pinnipeds and marine felids, have been documented, underlining the interspecies transmission risks and the potential for further ecological disruption (Plaza et al. 2024; Ulloa et al. 2023). Such cross-species spillovers are of particular concern given the ongoing evolution of the virus and its demonstrated capacity to infect a wide range of hosts.

Between 2022 and 2025, the Pan American Health Organization (PAHO), the World Health Organization (WHO), and the Food and Agriculture Organization of the United Nations (FAO) issued multiple alerts and situation updates emphasising the rising number of detections, the need for reinforced surveillance, and the importance of coordinated intersectoral responses framed within a One Health approach (Marandino et al. 2025; PAHO 2025a). The coordinated involvement of animal health, human health, and environmental sectors is regarded as critical to mitigating the risk of further spread and zoonotic transmission. Several regional risk factors contribute to the emergence and dissemination of HPAI in Latin America. These include the expansion of intensive poultry production and large-scale commercial flocks, which act as amplification points during outbreaks; the persistence of backyard poultry systems that increase opportunities for contact with wild birds; the extensive migratory flyways of aquatic birds linking the Americas to other continents; and the informal trade and movement of live birds, which facilitate viral dissemination (Azat et al. 2024; PAHO 2025a). Furthermore, constraints in surveillance, diagnostic, and response capacities across several countries exacerbate the vulnerability of the region, delaying timely detection and effective containment (Marandino et al. 2025).

4.1. Recent cases and outbreaks (2022-2025)

Group 1: Coastal wildlife-driven epidemics (Peru, Chile, Argentina)

In several South American countries, H5N1 clade 2.3.4.4b epidemics were primarily driven by coastal wildlife transmission. In Peru, Chile, and Argentina, early detection in migratory and resident seabirds along the Pacific and South Atlantic coasts was followed by widespread spillover into marine mammals, particularly pinnipeds, and subsequent exposure of backyard and commercial poultry. Genomic analyses from Peru and Argentina confirmed clade 2.3.4.4b circulation with evidence of sustained environmental persistence, reinforcing concerns regarding biodiversity impacts and long-term ecological reservoirs (Cruz et al. 2023; Leguia et al. 2023; Rimondi et al. 2024; Uhart et al. 2024). In Chile, spatio-temporal modelling linked outbreak occurrence to ecological and anthropogenic drivers, generating risk maps that informed targeted surveillance across wildlife, poultry, and human interfaces (Azat et al. 2024; Castillo et al. 2023). Collectively, these coastal epidemics underscore the central role of wildlife-driven transmission and the necessity of integrated genomic and ecological surveillance frameworks.

Group 2: Backyard-driven poultry exposure (Ecuador, Bolivia, Colombia)

In contrast, Ecuador, Bolivia, and Colombia exemplify transmission dynamics dominated by backyard and peri-domestic poultry systems. In Ecuador, the first human H5 infection reported in Latin America in January 2023 was epidemiologically linked to backyard poultry exposure, yet rapid One Health coordination prevented secondary human cases and no sustained avian circulation was detected following strengthened biosecurity and pre-vaccination screening (Puga-Torres et al. 2025; WHO 2023). Bolivia reported recurrent focal outbreaks in backyard and small commercial flocks, with illegal live-bird movements identified as a key dissemination pathway; nevertheless, culling and movement controls enabled containment despite resource constraints (PAHO 2023, 2025a). Similarly, Colombia has experienced repeated poultry outbreaks across multiple departments since 2022, prompting investments in laboratory capacity, intersectoral preparedness exercises, and surveillance strengthening in regions characterized by dense poultry production and major migratory flyways (PAHO 2025b). Together, these cases highlight backyard poultry as a critical interface for viral amplification and zoonotic risk, emphasizing the need for sustained community engagement and joint human-animal surveillance.

Group 3: Commercial sentinel events (Mexico, Brazil)

Finally, Mexico and Brazil illustrate the role of commercial poultry systems as sentinel points for regional risk. In Mexico, the first laboratory-confirmed human H5N1 case reported in April 2025 triggered intensified surveillance across commercial and backyard poultry, enhanced risk communication, and active case finding, highlighting vulnerabilities at the human-animal interface in rural settings (PAHO 2025b; WHO 2024). In Brazil, detection of HPAI in a commercial breeder farm in May 2025 marked a critical inflection point for the global poultry market, prompting immediate stamping-out, trade restrictions, and implementation of zoning and compartmentalisation measures aligned with WOAH standards (Martins-Filho and Quintans-Júnior 2025; Ministério da Agricultura e Pecuária 2025). These events demonstrate how incursions into highly biosecure commercial systems function as early warning signals with disproportionate economic and trade consequences, reinforcing the importance of rapid detection, transparency, and farm-level biosecurity.

4.2. Regional epidemiological patterns

Across Latin America, three consistent epidemiological patterns of avian influenza are present:

(i) migratory and costal wildlife corridors sustain viral introductions and mammalian spillover;

(ii) backyard poultry systems remain critical points of exposure; and

(iii) trade impacts follow swiftly once commercial flocks are involved.

PAHO's 2025 updates quantify continuing outbreaks and recommend enhanced, integrated surveillance under One Health.

4.3. Regional risk factors

While several empirical studies informing risk-factor analyses originate from Europe, South Asia, and Southeast Asia, they are cited here to illustrate mechanistic drivers of avian influenza amplification and exposure, rather than to imply direct equivalence across regions. Poultry production systems, governance structures, and compensation schemes differ substantially between these settings and Latin America; nevertheless, the underlying biological and behavioural processes, such as density-dependent transmission, biosecurity breaches, and wildlife–backyard–market interfaces, remain broadly comparable. Where available, regional evidence from Latin America is prioritised to validate and contextualise these mechanisms, particularly with respect to backyard exposure, wildlife-mediated spread, and surveillance gaps, which have been consistently documented across the Americas in PAHO reports and country-level investigations. Regional risk factors for the emergence and spread of avian influenza in Latin America arise from the interaction of poultry production systems, ecological pathways, and structural surveillance gaps. Intensive poultry production may amplify viral transmission once introduced into flocks, while backyard systems remain critical exposure points due to frequent contact between domestic and wild birds and limited biosecurity (Das Gupta et al. 2022; Islam et al. 2024) (Table 1).

Migratory flyways play a pivotal role in the intercontinental and intra-continental spread of HPAI A (H5Nx) clade 2.3.4.4b (Yang et al. 2024). After its explosive expansion across Eurasia, clade 2.3.4.4b was detected in North America in late 2021, with phylogeographic analyses indicating multiple introductions via major migratory flyway corridors, notably the Atlantic route (via Iceland to eastern Canada) and the Pacific route (via Alaska). These two entry pathways structured subsequent viral dissemination across the Americas, with rapid southward spread along coastal and continental flyways, particularly affecting waterfowl and seabird populations (Erdelyan et al. 2024; Kandeil et al. 2023). The temporal progression depicted in Fig. 1 highlights a well-defined north-south gradient, with initial establishment in North America followed by sequential detection in Peru and Chile along the Pacific corridor in late 2022, and subsequent eastward dissemination to Atlantic-bordering countries such as Argentina, Uruguay, and Brazil. This spatiotemporal pattern is consistent with southbound migratory pulses and with continuous phylogeographic reconstructions of North American genotypes, providing supporting evidence for synchrony between avian movement ecology and viral spread, and reinforcing the role of flyway connectivity in shaping transcontinental transmission dynamics (Signore et al. 2025).

Subsequent arrival of clade 2.3.4.4b into South America showed a characteristic pattern, with entry along the Pacific coast of Peru and Chile in late 2022, followed by eastward propagation to Atlantic-bordering countries such as Argentina, Uruguay, Brazil. The progression is consistent with seabird and shorebird connectivity along Pacific and South Atlantic corridors (Marandino et al. 2025). Reports of H5N1 detections on sub-Antarctic islands and the Antarctic Peninsula further support a coastal, flyway-linked dissemination that aligned with seabird ranging behaviour and mixed-colony networks (Neira et al. 2025). In addition to wildlife-mediated spread, informal trade and movement of live birds further exacerbate risk, as live-bird markets and uncontrolled poultry commerce create opportunities for species mixing and local to regional transmission. The risk is further compounded by

Table 1. Evidence supporting amplification of HPAI in intensive poultry systems and exposure risks in backyard flocks[*]

Study/ source	Setting	Key findings	Implications
PAHO (2025a)	Region of the Americas (Peru, Ecuador)	Majority of outbreaks in backyard flocks (Peru 61 in 2024; Ecuador Pastaza 2024); limited commercial impact	Confirms in Latin America that backyard systems are main points of exposure and spread
Gilbert et al. (2017)	Global review	Rapid intensification of poultry production increases risk of AIV persistence and reassortment; especially in Asia.	Provides global framework linking intensive poultry landscapes to viral emergence
Guinat et al. (2025)	Transmission modelling, Europe	Farm infectious period ≈ 9 days; duck farm density and short inter-premises distances were major drivers of HPAI spread	Intensive farm clusters amplify epidemics once virus introduced
Islam et al. (2024)	Commercial chicken farms, Bangladesh	AIV-positive farms had lapses in visitor/vehicle control, poor cleaning & disinfection, and lack of wild-bird proofing	Core biosecurity steps critical to stop amplification in intensive flocks
Das Gupta et al. (2022)	Backyard farms, Bangladesh	Proximity to water bodies, contact with wild birds, and low biosecurity scores significantly increased AI risk	Backyard flocks serve as bridges between wild reservoirs and domestic poultry
Chakma et al. (2021)	Live bird markets, Dhaka	High risk of H5 contamination in slaughter/processing areas and stalls with backyard-origin birds	Backyard birds entering markets act as contamination sources
Høg et al. (2021)	Commodity chains, Southeast Asia	Identified behaviours (e.g., mixing species, lack of segregation in live-bird trade) that maintain AIV transmission	Backyard & smallholder systems feed into live-bird chains sustaining virus circulation

[*] *Studies from outside Latin America are included to illustrate general transmission mechanisms, while regional data from the Americas confirm the relevance of these pathways under local production and surveillance contexts*

Fig. 1. *Migratory flyways and dissemination of HPAI A(H5N1) clade 2.3.4.4b in the Americas (2021-2025)*

uneven surveillance and diagnostic capacities, where delays in molecular detection and reporting allow silent expansion of the virus, an issue repeatedly flagged in PAHO epidemiological updates (PAHO 2025a). Collectively, these factors call for strengthened and integrated surveillance and biosecurity under a One Health framework to preempt and contain future outbreaks.

Across the Americas, official risk assessments repeatedly stress that early detection and timely reporting are critical for controlling avian influenza; however, the capacity to meet these standards are variable between countries and sectors, creating windows for onward transmission. The 2024-2025 PAHO alerts and epidemiological updates explicitly urge Member States to strengthen laboratory diagnosis, epidemiological investigation, notification, and rapid response, signalling persistent operational gaps that can delay case confirmation and control actions, such as the predominance of 2024 outbreaks in backyard flocks in Peru (Adlhoch et al. 2023). On similar lines, global and regional guidance from FAO/WHO/WOAH calls for increased surveillance and timely reporting to enable early case finding across domestic birds, wild birds, and mammals, reflecting continued heterogeneity in field and laboratory capacities (WHO 2024). Comparative work on influenza surveillance in Latin America and the Caribbean documents uneven detection capacity and reporting infrastructure on the human-health side, an important One-Health signal that diagnostic and notification systems remain asymmetric across the region (Hoyos-Cerón et al. 2025). Genomic studies during the 2022-2023 South American wave, particularly in Peru, emphasised the need for continuous genomic surveillance to avoid mass animal deaths following rapid coastal spread, implying that diagnostic lags and under-ascertainment facilitated expansion before robust confirmation and reporting were in place (Sevilla et al. 2024). Collectively, these evidences indicate that heterogeneous early-warning capacity, from field detection and sampling to molecular confirmation and notification, can prolong detection-to-response intervals, allowing further viral amplification in both backyard and commercial settings.

5. Management and control strategies

5.1. Active and passive epidemiological surveillance

Sustained epidemiological surveillance remains the cornerstone of early warning, outbreak detection, and demonstration of freedom from infection. Active surveillance through targeted sampling at risk interfaces such as wetlands, live-bird markets, high-density production zones need to be combined with passive surveillance based on prompt reporting of morbidity/mortality events by concerned personnel (Duan et al. 2023; Vredenberg et al. 2025). Current standards emphasise multi-stream surveillance across poultry and wild birds, with RT-qPCR confirmation and wild-bird monitoring for early warning. PAHO's 2025 updates show how regionally coordinated, risk-based monitoring improves situational awareness and comparability across Member States (PAHO 2025b).

5.2. Contingency planning and notification

National contingency plans should codify incident command, sampling logistics, laboratory surge capacity, and international notification procedures to WOAH to preserve transparency and enable zoning for trade (Simancas-Racines et al. 2023). Timely notification under the WOAH Terrestrial Code, Chapter 10.4, provides the legal/technical basis for zoning and the conditions to regain free status after control measures, such as three months post-stamping-out with surveillance. The involved countries are increasingly pre-negotiating recognition of zoning arrangements to minimise unnecessary trade disruption during outbreaks while following the necessary control measures warranted (Canadian Food Inspection Agency 2025).

5.3. Farm-level biosecurity

On-farm biosecurity is the most cost-effective barrier against the introduction and onward spread of HPAI, which includes exclusion of wild birds, controlled access for people, vehicles, and equipment, routine cleaning and disinfection, separation of age groups, and avoiding birds of unknown health status (Conan et al. 2012; Islam et al. 2024). FAO guidance further details market and farm biosecurity such as water management, fomite control, structured cleaning cycles, and stall segregation, to reduce viral amplification at production and retail nodes (FAO 2008).

5.4. Movement restrictions

Immediate movement restrictions within protection and surveillance zones reduces farm-to-farm spread while epidemiological investigations and tracing are completed (Simancas-Racines et al. 2023). WOAH Terrestrial Code provisions on zoning, compartmentalisation, and containment zones guide proportionate restrictions and the conditions for safe movements of birds and products, such as testing, time–temperature treatments, and compartment certification (Knobler et al. 2005). Countries that pre-negotiate mutual recognition of zoning reduce collateral trade impacts while maintaining sanitary protection (Canadian Food Inspection Agency 2025).

5.5. Depopulation (stamping-out) and carcass disposal

Where permitted and operationally feasible, stamping-out of infected and at-risk flocks is still a primary option for rapid control of outbreak, provided humane methods and biosecure logistics are ensured (Knobler et al. 2005). Safe and timely carcass disposal by on-site burial or composting, incineration, rendering, or permitted landfill with leachate control are essential to prevent environmental contamination and re-seeding (Miller et al. 2020).

5.6.Vaccination

Vaccination is increasingly recognised as a complementary control measure to biosecurity, movement control, and stamping-out in the management of highly pathogenic avian influenza (HPAI), particularly in settings where repeated incursions challenge exclusive reliance on culling strategies (Capua and Marangon 2003; Nielsen et al. 2023). WOAH affirms that vaccination, when implemented in accordance with the Terrestrial Manual and accompanied by surveillance demonstrating absence of field infection, is compatible with the maintenance of HPAI-free status and international trade (Sajjadi et al. 2025). Comparative experiences from Mexico, China, and Egypt illustrate that the epidemiological impact of vaccination is highly contingent on programme design, implementation capacity, and post-vaccination surveillance rather than on vaccine use per se. In Mexico, vaccination has been deployed episodically during H5N1 waves, primarily within commercial poultry sectors, as a risk-management tool to mitigate outbreak impact. Field evaluations indicate that while vaccination can raise population immunity, heterogeneity in serological responses and coverage across production systems necessitates close integration with surveillance to detect residual or silent circulation (Maya Badillo et al. 2025).

In contrast, China represents a long-standing model of nationwide H5 vaccination, where sustained high coverage and periodic vaccine updates have been associated with substantial reductions in poultry mortality and marked declines in zoonotic spillover, particularly following the implementation of bivalent H5/H7 vaccination. However, this success has been accompanied by strong selective pressure on viral populations, with antigenic drift and genetic divergence repeatedly eroding vaccine protection, thereby necessitating continuous genomic surveillance and frequent strain updating (Li et al. 2025). The decades long nationwide H5 vaccination have reduced poultry mortality and human spillover in China, but antigenic drift and divergence can erode protection, requiring periodic vaccine updates and strong post-vaccination surveillance. Egypt provides a contrasting example in which long-running vaccination programmes have coexisted with persistent enzootic circulation. Evaluations indicate that uneven coverage, strain mismatch, variable vaccine quality, and fragmented implementation across production systems have limited the ability of vaccination to interrupt transmission, allowing ongoing viral evolution and recurrent public health risk (Fahim et al. 2025).

Across these contexts, there is broad consensus that vaccination should be risk-based, targeting high-exposure species, production systems, and seasons, and should be inseparably linked to Differentiating Infected from Vaccinated Animals (DIVA) strategies and rigorous value-chain surveillance. Operational frameworks developed by the European Food Safety Authority (EFSA) specify surveillance designs for both emergency and preventive vaccination, including sampling intensities stratified by poultry type and flock size, and emphasise post-vaccination surveillance as a prerequisite for safe movement of birds and products (Nielsen et al. 2023). These principles are now embedded within EU regulatory frameworks governing vaccination, surveillance, and trade (European Commission 2025). The WOAH Terrestrial Manual further details DIVA-compatible diagnostic approaches, including NP/Matrix-based ELISAs, neuraminidase-differentiation assays, and NS1-based serology, that enable reliable discrimination between vaccinated and naturally infected birds, thereby preserving surveillance sensitivity and the credibility of certification under vaccinated settings (Liu et al. 2010; Sajjadi et al. 2025). Complementing this, FAO operational guidance stresses the importance of risk-based surveillance across the entire poultry value chain, from farms to live-bird markets and movement networks, particularly where vaccination is implemented at scale (FAO 2025b). Finally, effective vaccination strategies depend on operational readiness, including training of producers and veterinary personnel in early disease recognition, biosecurity-compliant sampling, reporting pathways, and risk communication. Harmonised guidance from PAHO, FAO, and WOAH highlights that vaccination must be embedded within broader preparedness and response systems to avoid delayed detection and unintended viral persistence (Kovács et al. 2025b; WHO 2024).

6. Challenges and opportunities

Highly Pathogenic Avian Influenza (HPAI) continues to spread across the Americas, with outbreaks reported between 2022-2025 in both commercial and backyard poultry systems, wild birds, and even marine mammals. The persistence of clade 2.3.4.4b and the socio-economic impact of recent events underscore the urgent need to address structural weaknesses and enhance regional cooperation.

6.1. Structural challenges in animal health systems

Many countries in Latin America face structural weaknesses in animal health that limit preparedness and response to HPAI, such as ageing or insufficient laboratory and field infrastructure, shortage in workforce, uneven funding for veterinary services, and fragmented legal or regulatory frameworks. As a result, these deficits constrain timely outbreak detection, rapid mobilisation of resources, and the implementation of coordinated control measures such as rapid stamping-out, movement controls, and compensatory schemes for producers (PAHO 2025b).

6.2. Limited cross-border cooperation

Given the transboundary nature of HPAI, effective control measures require real-time data sharing, harmonised response protocols, and joint contingency planning between neighbouring countries. However, persistent gaps in formal cross-border cooperation and information exchange have hindered joint investigations and synchronized interventions in the Americas. PAHO consultations stress that weak cross-sectoral and international linkages have slowed HPAI responses, underscoring the need for stronger legal and operational frameworks for rapid cross-border action (PAHO 2025a).

6.3. Need to harmonise regional policies

Heterogeneous national policies on notification, zoning, vaccination strategies, trade restrictions, and surveillance complicate regional management of HPAI and can create perverse incentives for under-reporting or delayed control measures. To address this, harmonisation of technical standards, regulatory approaches and risk-based trade arrangements across the region would reduce these frictions, facilitate mutual recognition of disease status, and help align national control strategies with international standards (WOAH/FAO), while protecting both animal health and livelihoods (FAO 2025a).

6.4. Strengthening molecular diagnostics and genomic surveillance

Rapid, decentralised molecular diagnostics and genomic sequencing are indispensable for early detection, source tracing, and monitoring viral evolution. Yet, capacity and expertise remain uneven across the region. Strengthening distributed laboratory networks, harmonising protocols, and fostering South-South capacity building would improve detection timeliness and enable genomic epidemiology to inform targeted interventions (Márquez et al. 2025).

7. Key priorities for Latin America

Based on the epidemiological patterns observed during the 2022-2025 HPAI waves, three main areas stand out as crucial for improving the region's ability to prepare for and respond to future outbreaks. First, there is a clear need to strengthen early warning systems through the integration of multiple surveillance streams, specifically those targeting wild birds, poultry, and mammalian infections. In this context, many recent outbreaks have shown that viral detection in wildlife preceded incursions into poultry populations, yet early signals were occasionally missed because atypical infections in mammals were not reported or assessed in a timely manner. Therefore, improved coordination across surveillance systems and more rapid data sharing would help reduce detection-to-response intervals, thereby mitigating onward transmission and outbreak amplification.

Second, in practice, heterogeneity in regulatory frameworks may disincentivize timely outbreak notification, particularly among small-scale and backyard poultry producers who face potential economic losses. Consequently, harmonization of standards and the adoption of proportionate, risk-based trade measures would support more equitable and effective responses, while simultaneously facilitating early reporting without imposing disproportionate economic penalties.

Third, sustained investment in molecular diagnostics and genomic sequencing capacity is essential. In this regard, the virus has undergone rapid evolutionary change, particularly within the clade 2.3.4.4b lineage circulating across the Americas, thereby underscoring the importance of real-time genetic characterization. Accordingly, strengthening in-country sequencing capacity, standardizing analytical pipelines, and enabling timely cross-border data sharing would substantially enhance the early detection of genetic shifts with epidemiological or phenotypic significance, while also informing vaccine strain selection and supporting coordinated regional responses to emerging threats. In summary, effective control of HPAI in Latin America requires a coordinated regional strategy that integrates enhanced surveillance, greater policy alignment, and the strategic use of genomic data, all implemented within a One Health framework.

8. Conclusions

Avian influenza has become entrenched as a recurrent and unpredictable challenge in Latin America, with the continued spread of H5N1 clade 2.3.4.4b exposing profound vulnerabilities across diverse production systems. Regional experience demonstrates that countries with robust biosecurity, vertically integrated industries, and effective contingency planning, such as Brazil, are better positioned to contain outbreaks, whereas fragmented backyard systems face disproportionate losses. Structural challenges, including uneven laboratory capacity, delayed reporting, and limited cross-border coordination, continue to hinder timely responses. Nonetheless, recent advances in genomic surveillance, policy harmonisation, and vaccination strategies provide new opportunities to strengthen preparedness. A regional strategy grounded in One Health principles, integrating active and passive surveillance, risk-based vaccination with DIVA approaches, and transparent notification to WOAH, will be crucial. Building long-term resilience requires sustained investment in veterinary services, enhanced biosecurity practices at all levels of production, and continuous training for producers and veterinarians. Ultimately, Latin America's ability to mitigate the socioeconomic and public health impacts of avian influenza will depend on coordinated action that bridges national boundaries, aligns with international standards, and addresses the interconnected realities of animal, human, and environmental health.

Declarations

Funding: Not applicable

Conflict of interest: All authors declare no conflicts of interest

Acknowledgements: The authors gratefully acknowledge the Facultad de Ciencias Agropecuarias from Universidad Técnica de Ambato for its support in the realisation of this research

Ethics approval: Not applicable

References

Adlhoch C, Fusaro A, Gonzales JL, Kuiken T, Mirinavičiūtė G, Niqueux É, Ståhl K, Staubach C, Terregino C, Willgert K, Baldinelli F, Chuzhakina K, Delacourt R, Georganas A, Georgiev M, Kohnle L. (2023). Avian influenza overview September–December 2023. EFSA Journal 21: 8539. https://doi.org/10.2903/j.efsa.2023.8539

Azat C, Alvarado-Rybak M, Aguilera JF, Benavides JA. (2024). Spatio-temporal dynamics and drivers of highly pathogenic avian influenza H5N1 in Chile. Frontiers in Veterinary Science 11: 1387040. https://doi.org/10.3389/fvets.2024.1387040

Bruno A, Mora D de, Olmedo M, Garcés J, Marzal A, Garcia-Bereguiain MA. (2025). Highly pathogenic avian influenza A (H5N1) virus outbreaks in South America in 2022–2024: a comprehensive review of an ongoing panzootic. Virology 610: 110602. https://doi.org/10.1016/j.virol.2025.110602

Canadian Food Inspection Agency. (2025). Regulatory Cooperation Council - Foreign Animal Disease Zoning Recognition. https://inspection.canada.ca/en/about-cfia/partnerships/rcc/foreign-animal-disease-zoning-recognition?utm_source=chatgpt.com. Accessed September 26, 2025

Capua I, Marangon S. (2003). The use of vaccination as an option for the control of avian influenza. Avian Pathology 32(4): 335–343. https://doi.org/10.1080/0307945031000121077

Castillo A, Fasce R, Parra B, Andrade W, Covarrubias P, Hueche A, Campano C, Tambley C, Rojas M, Araya M, Hernández F, Bustos P, Fernández J. (2023). The first case of human infection with H5N1 avian Influenza A virus in Chile. Journal of Travel Medicine 30(5): taad083. https://doi.org/10.1093/jtm/taad083

Chakma S, Osmani MG, Akwar H, Hasan Z, Nasrin T, Karim MR, Samad MA, Giasuddin M, Sly P, Islam Z, Debnath NC, Brum E, Magalhães RS. (2021). Risk areas for influenza A(H5) environmental contamination in live bird markets, Dhaka, Bangladesh. Emerging Infectious Diseases 27(9): 2399–2408. https://doi.org/10.3201/eid2709.204447

Charostad J, Rezaei Zadeh Rukerd M, Mahmoudvand S, Bashash D, Hashemi SMA, Nakhaie M, Zandi K. (2023). A comprehensive review of highly pathogenic avian influenza (HPAI) H5N1: An imminent threat at doorstep. Travel Medicine and Infectious Disease 55: 102638. https://doi.org/10.1016/j.tmaid.2023.102638

Conan A, Goutard FL, Sorn S, Vong S. (2012). Biosecurity measures for backyard poultry in developing countries: A systematic review. BMC Veterinary Research 8: 240. https://doi.org/10.1186/1746-6148-8-240

Cruz CD, Icochea ME, Espejo V, Troncos G, Castro-Sanguinetti GR, Schilling MA, Tinoco Y. (2023). Highly pathogenic avian influenza A (h5n1) from wild birds, poultry, and mammals, Peru. Emerging Infectious Diseases 29(12): 2572–2576. https://doi.org/10.3201/eid2912.230505

Cui P, Shi J, Wang C, Zhang Y, Xing X, Kong H, Yan C, Zeng X, Liu L, Tian G, Li C, Deng G, Chen H. (2022). Global dissemination of H5N1 influenza viruses bearing the clade 2.3.4.4b HA gene and biologic analysis of the ones detected in China. Emerging Microbes and Infections 11: 1693–1704. https://doi.org/10.1080/22221751.2022.2088407

Das Gupta, S, Barua B, Fournié G, Hoque MA, Henning J. (2022). Village and farm-level risk factors for avian influenza infection on backyard chicken farms in Bangladesh. Scientific Reports 12: 13009. https://doi.org/10.1038/s41598-022-16489-5

Duan C, Li C, Ren R, Bai W, Zhou L. (2023). An overview of avian influenza surveillance strategies and modes. Science in One Health 2: 100043. https://doi.org/10.1016/j.soh.2023.100043

Erdelyan CNG, Kandeil A, Signore AV, Jones MEB., Vogel P, Andreev K, Bøe CA, Gjerset B, Alkie TN, Yason C, Hisanaga T, Sullivan D, Lung O, Bourque L, Ayilara I, Pama L, Jeevan T, Franks J, Jones JC, Seiler JP, Miller L, Mubareka S, Webby RJ, Berhane Y. (2024). Multiple transatlantic incursions of highly pathogenic avian influenza clade 2.3.4.4b A(H5N5) virus into North America and spillover to mammals. Cell Reports 43: 114479. https://doi.org/10.1016/j.celrep.2024.114479

European Commission. (2025). Avian influenza. https://food.ec.europa.eu/animals/animal-diseases/diseases-and-control-measures/avian-influenza_en Accessed September 26, 2025.

Fahim M, Alim W, Abukamar S, El-Shesheny R, Roshdy WH, Hassan H, Mohsen A, Afifi S, Fattah MA, Hammad R, Kandeel A. (2025). Study of the effectiveness of a supported intervention package in reducing the risk of avian influenza human exposure through the reduction of infections in poultry: Egypt, 2006–2021. Virology Journal 22: 170. https://doi.org/10.1186/s12985-025-02810-x

FAO (Food and Agriculture Organization of the United Nations). (2008). Biosecurity for Highly Pathogenic Avian Influenza: Issues and options. https://www.thepoultrysite.com/articles/biosecurity-for-highly-pathogenic-avian-influenza-issues-and-options?utm_source=chatgpt.com. Accessed September 26, 2025.

FAO (Food and Agriculture Organization of the United Nations). (2025a). FAO presents recommendations in response to the reappearance of highly pathogenic avian influenza in Latin America and the Caribbean. https://www.fao.org/americas/news/news-detail/recomendaciones-influenza-aviar/en. Accessed October 1, 2025.

FAO (Food and Agriculture Organization of the United Nations). (2025b). Strengthening vaccination and surveillance strategies in the fight against avian influenza. Animal Health. https://www.fao.org/animal-health/news-events/news/detail/strengthening-vaccination-and-surveillance-strategies-in-the-fight-against-avian-influenza/en. Accessed October 1, 2025.

Gilbert M, Xiao X, Robinson TP. (2017). Intensifying poultry production systems and the emergence of avian influenza in China: A "One Health/Ecohealth" epitome. Archives of Public Health 75: 48. https://doi.org/10.1186/s13690-017-0218-4

Guinat C, Valenzuela Agüí C, Briand FX, Chakraborty D, Fourtune L, Lambert S, Jimenez Pellicer A, Rautureau S, Gerbier G, du Plessis L, Stadler T, Grasland B, Paul MC, Vergne, T. (2025). Poultry farm density and proximity drive highly pathogenic avian influenza spread. Communications Biology 8: 1306. https://doi.org/10.1038/s42003-025-08687-4

Høg E, Fournié G, Hoque MA, Mahmud R, Pfeiffer DU, Barnett T. (2021). Avian influenza risk environment: live bird commodity chains in Chattogram, Bangladesh. Frontiers in Veterinary Science 8: 694753. https://doi.org/10.3389/fvets.2021.694753

Hoyos-Cerón T, Albarrán-Tamayo F, Bañuelos-Hernández B, Londoño-Avendaño MA. (2025). Disparities in influenza control and surveillance in Latin America and the Caribbean. Viruses 17: 225. https://doi.org/10.3390/v17020225

Iancu I, Bărbuceanu F, Tîrziu E, Pascu C, Luminit C, Degi J, Badea C, Gligor A, Bucur I, Popa SA, Gurau M, Herman V. (2025). Determination of H5N1 Avian Influenza Virus Persistence Following a 2024 Backyard Poultry Outbreak in Romania. Veterinary Sciences 12: 922. https://doi.org/10.3390/vetsci12100922

Islam A, Rahman MZ, Hassan MM, Epstein JH, Klaassen M. (2024). Farm biosecurity practices affecting avian influenza virus circulation in commercial chicken farms in Bangladesh. One Health 18: 100681. https://doi.org/10.1016/j.onehlt.2024.100681

Kandeil A, Patton C, Jones JC, Jeevan T, Harrington WN, Trifkovic S, Seiler JP, Fabrizio T, Woodard K, Turner JC, Crumpton JC, Miller L, Rubrum A, DeBeauchamp J, Russell CJ, Govorkova EA, Vogel P, Kim-Torchetti M, Berhane Y, Stallknecht D, Poulson, Kercher L, Webby RJ. (2023). Rapid evolution of A(H5N1) influenza viruses after intercontinental spread to North America. Nature Communications 14: 3082. https://doi.org/10.1038/s41467-023-38415-7

Knobler SL, Mack A, Mahmoud A, Lemon SM. (2005). The threat of pandemic influenza: Are we ready. National Academies Press, Washington DC.

Kovács L, Farkas M, Dobra PF, Lennon G, Könyves LP, Rusvai M. (2025a). Avian Influenza clade 2.3.4.4b: Global impact and summary analysis of vaccine trials. Vaccines 13: 453. https://doi.org/10.3390/vaccines13050453

Kovács, L., Klaucke, C. R., Farkas, M., Bakony, M., Jurkovich, V., & Könyves, L. (2025b). The correlation between on-farm biosecurity and animal welfare indices in large-scale turkey production. Poultry Science 104: 104598. https://doi.org/10.1016/j.psj.2024.104598

Krammer F, Hermann E, Rasmussen AL, Krammer F, Hermann E, Rasmussen AL. (2025). Highly pathogenic avian influenza H5N1: history, current situation, and outlook. Journal of Virology 99(4): e02209-24. https://doi.org/10.1128/jvi.02209-24

Leguia M, Garcia-Glaessner A, Muñoz-Saavedra B, Juarez D, Barrera P, Calvo-Mac C, Jara J, Silva W, Ploog K, Amaro L, Colchao-Claux P, Johnson CK, Uhart MM, Nelson MI. Lescano J. (2023). Highly pathogenic avian influenza A (H5N1) in marine mammals and seabirds in Peru. Nature Communications 14: 5489. https://doi.org/10.1038/s41467-023-41182-0

Li B, Raghwani J, Hill SC, François S, Lefrancq N, Liang Y, Wang Z, Dong L, Lemey P, Pybus OG, Tian H. (2025). Association of poultry vaccination with interspecies transmission and molecular evolution of H5 subtype avian influenza virus. Science Advances 11(4): eado9140. https://doi.org/10.1126/sciadv.ado9140

Liu Y, Mundt E, Mundt A, Sylte M, Suarez DL, Swayne DE, García M. (2010). Development and evaluation of an avian influenza, neuraminidase subtype 1, indirect enzyme-linked immunosorbent assay for poultry using the differentiation of infected from vaccinated animals control strategy. Avian Diseases 54: 613–621. https://doi.org/10.1637/8844-040409-Reg.1

Luczo JM, Spackman E. (2025). Molecular evolution of the H5 and H7 highly pathogenic avian influenza virus haemagglutinin cleavage site motif. Reviews in Medical Virology 35: e70012. https://doi.org/10.1002/rmv.70012

Luo J, Zhang Z, Zhao S, Gao R. (2023). A comparison of etiology, pathogenesis, vaccinal and antiviral drug development between influenza and COVID-19. International Journal of Molecular Sciences 24: 6369. https://doi.org/10.3390/ijms24076369

Marandino A, Tomás G, Panzera Y, Williman J, Dezordi FZ, Wallau GL, Rodríguez S, Pérez R, Bassetti L, Negro R, Uriarte V, Leizagoyen C, Pérez R. (2025). Converging Transmission Routes of the Highly Pathogenic Avian Influenza H5N1 Clade 2.3.4.4b Virus in Uruguay: Phylogeographic Insights into Its Spread Across South America. Pathogens 14: 793. https://doi.org/10.3390/pathogens14080793

Márquez S, Vasquez-Aleman G, Juarez JG, Cerpas C, Cardenas P, Bennett S, Balmaseda A, Harris E, Coloma J. (2025). Enhancing capacities in genomic surveillance capabilities for SARS-CoV-2 and dengue virus: A South-South collaborative partnership. PLOS Global Public Health 5: e0004365. https://doi.org/10.1371/journal.pgph.0004365

Martins-Filho PR, Quintans-Júnior LJ. (2025). Brazil's first H5N1 outbreak in commercial poultry: a sentinel event for cross-border preparedness. Journal of Travel Medicine 32(5): taaf050. https://doi.org/10.1093/jtm/taaf050

Maya Badillo BA, Hernández García DL, Moreno García RA, Orta Pineda G, Alcázar Ramiro CJ, Castillo Castillo J, Solís Hernández M, Navarro López R, García López A. (2025). H5N1 highly pathogenic avian influenza vaccination:

Seroresponse of mexican poultry in the 2022–2024. Vaccine: X 26: 100709. https://doi.org/10.1016/j.jvacx.2025.100709

Miller LP, Miknis RA, Flory GA. (2020). Carcass management guidelines: Effective disposal of animal carcasses and contaminated materials on small to medium-sized farms. In: Carcass management guidelines. Food and Agriculture Organization of the United Nations. https://doi.org/10.4060/cb2464en. Accessed September 26, 2025

Ministério da Agricultura e Pecuária. (2025). Ministry of Agriculture and Livestock confirms first case of avian influenza in a commercial poultry farm in Brazil. https://www.gov.br/agricultura/en/news/ministry-of-agriculture-and-livestock-confirms-first-case-of-avian-influenza-in-a-commercial-poultry-farm-in-brazil?utm_source=chatgpt.com. Accessed September 26, 2025

Musa E, Nia ZM, Bragazzi NL, Leung D, Lee N, Kong JD. (2024). Avian Influenza: Lessons from past outbreaks and an inventory of data sources, mathematical and AI models, and early warning systems for forecasting and hotspot detection to tackle ongoing outbreaks. Healthcare 12: 1959. https://doi.org/10.3390/healthcare12191959

Nagoba BS, Dhotre SV, Sonar MN, Gavkare AM, Mumbre SS, Dhotre PS. (2025). Recent advances in avian influenza virus: Molecular pathogenesis, emerging strains, and next-generation therapeutics. World Journal of Virology 14(3): 109161. https://doi.org/10.5501/wjv.v14.i3.109161

Neira V, Ariyama N, Castillo-Torres PN, Brito B, Muñoz G, Díaz Morales KB, Almonacid LI, Bennett-Laso B, Berazay B, Barták M, Medina R, González-Aravena M, Pardo-Roa C. (2025). Genetic Characterization of Highly Pathogenic Avian Influenza A(H5N1) Clade 2.3.4.4b, Antarctica, 2024. Emerging Infectious Diseases 31(8): 1618–1620. https://doi.org/10.3201/eid3108.250186

Nielsen SS, Alvarez J, Bicout DJ, Calistri P, Canali E, Drewe JA, Garin-Bastuji B, Gonzales Rojas JL, Gortázar C, Herskin M, Michel V, Miranda Chueca MÁ, Padalino B, Roberts HC, Spoolder H, Stahl K, Velarde A, Winckler C, Bastino E, Bortolami A, Guinat C, Harder T, Stegeman A, Terregino C, Asensio IA, Mur L, Broglia A, Baldinelli F, Viltrop A. (2023). Vaccination of poultry against highly pathogenic avian influenza - Part 1: Available vaccines and vaccination strategies. EFSA Journal 21: 8271. https://doi.org/10.2903/j.efsa.2023.8271

PAHO (Pan American Health Organization). (2023). Epidemiological Update caused by influenza A (H5N1): Outbreaks of avian influenza caused by influenza A(H5N1) in the Region of the Americas. www.paho.org. Accessed July 14, 2025

PAHO (Pan American Health Organization). (2025a). Epidemiological update: Avian Influenza A (H5N1) in the Americas region. https://www.paho.org/en/documents/epidemiological-update-avian-influenza-ah5n1-americas-region-15-october-2025. Accessed July 14, 2025.

PAHO (Pan American Health Organization). (2025b). Colombia strengthens its preparedness against Avian Influenza with the EVIR Workshop. https://www.paho.org/en/news/3-4-2025-colombia-strengthens-its-preparedness-against-avian-influenza-evir-workshop?utm_source=chatgpt.com. Accessed July 14, 2025.

Paredes Cabezas M del R, Carrasco Ruano YT, Jácome Benítez SM. (2023). Impacto económico de la gripe aviar en el sector avícola. Visionario Digital 7(4): 224–235. https://doi.org/10.33262/visionariodigital.v7i4.2910

Plaza PI, Gamarra-Toledo V, Rodríguez Euguí J, Rosciano N, Lambertucci SA. (2024). Pacific and Atlantic sea lion mortality caused by highly pathogenic Avian Influenza A(H5N1) in South America. Travel Medicine and Infectious Disease 59: 102712. https://doi.org/10.1016/j.tmaid.2024.102712

Puga-Torres B, Navarrete H, de la Torre D. (2025). Molecular surveillance confirms absence of avian influenza virus type A in Ecuadorian poultry: A retrospective reverse transcription quantitative polymerase chain reaction study from April 2023 to June 2024. Veterinary World 18(8): 2287–2294. https://doi.org/10.14202/vetworld.2025.2287-2294

Rauber RH. (2023). Avian influenza and the Brazilian poultry production: Current situation and prevention strategies. German Journal of Veterinary Research 3(4): 13–19. https://doi.org/10.51585/gjvr.2023.4.0064

Rehman S, Effendi MH, Witaningruma AM, Nnabuikeb UE, Bilal M, Abbas A, Abbas RZ, Hussain K. (2023). Avian influenza (H5N1) virus, epidemiology and its effects on backyard poultry in Indonesia: a review. F1000Research 11: 1321. https://doi.org/10.12688/f1000research.125878.2

Rimondi A, Vanstreels RET, Olivera V, Donini A, Lauriente MM, Uhart MM. (2024). Highly pathogenic Avian Influenza A(H5N1) Viruses from multispecies outbreak, Argentina, August 2023. Emerging Infectious Diseases 30(4): 812–814. https://doi.org/10.3201/eid3004.231725

Rodriguez Z, O'Connor A, Bradford BJ, Picasso-Risso C. (2025). Characterization and health, productivity, and economic effects of highly pathogenic avian influenza H5N1 outbreak in dairy cattle. Journal of Dairy Science 108(6): 6349–6358. https://doi.org/10.3168/jds.2025-26377

Sajjadi NC, Abolnik C, Baldinelli F, Brown I, Cameron A, de Wit S, Dhingra M, Espeisse O, Guerrin JL, Harder T, Ho J, Chua TH, Hussein K, Lyons N, Monne I, Okamuro Y, Pacheco DT, Pavade G, Poncon N, Prajitno TY, Stegeman A. (2025). Vaccination and surveillance for high pathogenicity avian influenza in poultry-current situation and perspectives. Biologicals 91: 101840. https://doi.org/10.1016/j.biologicals.2025.101840

Sevilla N, Lizarraga W, Jimenez-Vasquez V, Hurtado V, Molina IS, Huarca L, Lope-Pari P, Vargas I, Arotinco G, Padilla-Rojas C. (2024). Highly pathogenic avian influenza A (H5N1) virus outbreak in Peru in 2022–2023. Infectious Medicine 3: 100108. https://doi.org/10.1016/j.imj.2024.100108

Shi J, Zeng X, Cui P, Yan C, Chen H. (2023). Alarming situation of emerging H5 and H7 avian influenza and effective control strategies. Emerging Microbes and Infections 12: e2155072. https://doi.org/10.1080/22221751.2022.2155072

Signore AV, Giacinti J, Jones MEB, Erdelyan CNG, McLaughlin A, Alkie TN, Cox S, Lair S, Jardine CM, Stevens B, Bravo-Araya M, Pople N, … Berhane Y. (2025). Spatiotemporal reconstruction of the North American A(H5N1) outbreak reveals successive lineage replacements by descendant reassortants. Science Advances 11: eadu4909. https://doi.org/10.1126/sciadv.adu4909

Simancas-Racines A, Cadena-Ullauri S, Guevara-Ramírez P, Zambrano AK, Simancas-Racines D. (2023). Avian Influenza: Strategies to manage an outbreak. Pathogens 12: 610. https://doi.org/10.3390/pathogens12040610

Uhart MM, Vanstreels RET, Nelson MI, Olivera V, Campagna J, Zavattieri V, Lemey P, Campagna C, Falabella V, Rimondi A. (2024). Epidemiological data of an influenza A/H5N1 outbreak in elephant seals in Argentina indicates mammal-to-mammal transmission. Nature Communications 15: 9516. https://doi.org/10.1038/s41467-024-53766-5

Ulloa M, Fernández A, Ariyama N, Colom-Rivero A, Rivera C, Nuñez P, Sanhueza P, Johow M, Araya H, Torres JC, Gomez P, Muñoz G, Agüero B, Alegría R, Medina R, Neira V, Sierra E. (2023). Mass mortality event in South American sea lions (*Otaria flavescens*) correlated to highly pathogenic avian influenza (HPAI) H5N1 outbreak in Chile. Veterinary Quarterly 43(1): 1–10. https://doi.org/10.1080/01652176.2023.2265173

Vagnozzi AE. (2024). Review of the Highly Pathogenic Avian Influenza in Argentina in 2023: Chronicle of its emergence and control in poultry. Pathogens 13: 810. https://doi.org/10.3390/pathogens13090810

Vredenberg I, van Schaik G, Velkers FC, Fabri T, Spierenburg MAH, Germeraad EA, van der Poel WHM, Stegeman A. (2025). Assessing the use of different surveillance components to detect highly pathogenic avian influenza outbreaks in poultry in the Netherlands in low- and high-risk years. Transboundary and Emerging Diseases 2025: 7441785. https://doi.org/10.1155/tbed/7441785

WHO (World Health Organization). (2023). Human infection caused by avian influenza A(H5)-Ecuador. Disease Outbreak News. https://www.who.int/emergencies/disease-outbreak-news/item/2023-DON434. Accessed September 26, 2026.

WHO (World Health Organization). (2024). Updated joint FAO/WHO/WOAH public health assessment of recent influenza A (H5) virus events in animals and people. https://www.who.int/publications/m/item/updated-joint-fao-who-woah-assessment-of-recent-influenza-a(h5n1)-virus-events-in-animals-and-people_dec2024. Accessed September 27, 2026.

Xie Z, Yang J, Jiao W, Li X, Iqbal M, Liao M, Dai M, Xie Z, Yang J, Jiao W, Li X, Iqbal M, Liao M, Dai M. (2025). Clade 2.3.4.4b highly pathogenic avian influenza H5N1 viruses: knowns, unknowns, and challenges. Journal of Virology 99(6): e00424-25. https://doi.org/10.1128/jvi.00424-25

Yang Q, Wang B, Lemey P, Dong L, Mu T, Wiebe RA, Guo F, Trovão NS, Park SW, Lewis N, Tsui JLH, Bajaj S, Cheng Y, Yang L, Haba Y, Li B, Zhang G, Pybus OG, Tian H, Grenfell B. (2024). Synchrony of bird migration with global dispersal of Avian Influenza reveals exposed bird orders. Nature Communications 15: 1126. https://doi.org/10.1038/s41467-024-45462-1

Yang Y, Yang Z, Zhang X, Niu B, Huang Q, Li Y, Yin H, Zhang X, Liao M, Jia W. (2025). Rapid detection of Pan-Avian Influenza Virus and H5, H7, H9 subtypes of Avian Influenza Virus using CRISPR/Cas13a and lateral flow assay. Poultry Science 104: 104745. https://doi.org/10.1016/j.psj.2024.104745

Citation

Grijalva-Trejo X, Vásquez C. (2025). Highly pathogenic Avian Influenza (H5N1) in Latin America: Epidemiology, control strategies, and One Health implications. Letters in Animal Biology 06(1): 09 – 18. *https://doi.org/10.62310/liab.v6i1.268*