

Systematic Literature Review: Distribution and Diversity of Avian Influenza Subtypes in Migratory Wild Birds in Asia and Australia

Rosanty*, Putri Pandarangga, Novalino H. G. Kallau

Universitas Nusa Cendana, Indonesia

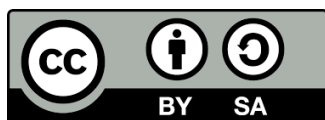
Email: rosanty0408@gmail.com

Keywords:

Avian Influenza Virus; AIV;
Migratory Wild Birds;
Shorebirds; Waterfowl; East
Asian-Australasian Flyway

Abstract

Avian influenza A viruses (AIVs) have been detected in migratory wild birds, raising concerns regarding their geographic distribution, subtype diversity, and surveillance along the East Asian–Australasian Flyway. This systematic literature review synthesized findings from studies investigating AIVs in migratory wild birds across Asia and Australia. Relevant literature was identified through searches of PubMed, Scopus, ScienceDirect, and Google Scholar, resulting in 29 eligible articles selected according to predefined inclusion criteria. The synthesis examined reported geographic locations, avian host groups, viral subtypes, diagnostic methods, and prevalence estimates. The included studies documented AIV detections in China, South Korea, Japan, Bangladesh, Siberian Russia, and Australia, predominantly among species belonging to the orders Anseriformes and Charadriiformes. Multiple hemagglutinin (HA) and neuraminidase (NA) subtype combinations were identified, including viruses belonging to the H5, H6, H4, H3, and H7 hemagglutinin subtype groups. Common diagnostic approaches included reverse transcription polymerase chain reaction (RT-PCR), quantitative reverse transcription PCR (RT-qPCR), virus isolation, genomic sequencing, and phylogenetic analysis. Reported detection positivity rates and prevalence estimates varied considerably, with many studies reporting values below 10%. However, differences in sampling strategies, sample denominators, and laboratory methods limited direct comparisons across studies. The observed geographic patterns reflected the distribution of published surveillance activities rather than the complete geographic distribution of AIVs, while viral detection alone did not establish cross-regional transmission by individual migratory birds. The findings highlighted the importance of standardized surveillance protocols and integrated One Health monitoring to improve understanding of AIV distribution and subtype diversity. Furthermore, inconsistencies in reported sample denominators and subtype counts underscored the need for careful verification and harmonization of extracted data to strengthen the reliability of future surveillance syntheses.



This is an open access article under the [CC BY-SA](https://creativecommons.org/licenses/by-sa/4.0/) license.

Copyright © 2026 by Author. Published
by
Riviera Publishing

INTRODUCTION

Avian influenza is an infectious disease caused by influenza A viruses (IAVs) belonging to the family Orthomyxoviridae. It has attracted considerable global attention because of its implications for animal health, the poultry industry, and public health (Ayuti et al., 2024). Avian influenza A viruses (AIVs) infect a wide range of avian hosts, including domestic poultry and various species of wild birds (Suarez, 2010). Wild birds, particularly migratory

waterbirds, are recognized as natural reservoirs of numerous influenza A virus subtypes (Blagodatski et al., 2021). Most low-pathogenicity avian influenza (LPAI) viruses circulate naturally in wild bird populations without causing apparent clinical signs (Swayne, 2020). However, in recent decades, highly pathogenic avian influenza (HPAI) viruses, particularly those belonging to the H5 subtype, have increasingly been detected in wild bird populations and have been associated with viral dissemination across geographic regions, including along migratory pathways (Wille & Barr, 2022).

Migratory birds can travel across national and continental boundaries, potentially facilitating the geographic dissemination of AIVs (Prosser et al., 2011). Through seasonal movements, these birds may contribute to the introduction, maintenance, and dispersal of various AIV subtypes, including LPAI and HPAI viruses, into new geographic areas, including regions where infections have not previously been documented (Caliendo et al., 2022). The involvement of migratory birds in HPAI epidemiology is particularly concerning because certain HPAI viruses can cause severe disease and high mortality in domestic poultry, resulting in substantial economic losses and potential public health consequences (Swayne, 2020; Wille & Barr, 2022). High mortality rates, potentially reaching 90% under specific outbreak conditions, have been reported, although these estimates depend on the viral subtype, host species, and epidemiological circumstances (Wahyuni et al., 2022). Furthermore, certain AIV subtypes possess zoonotic potential and can infect humans and other mammals (Mostafa et al., 2018). Consequently, AIV surveillance and control remain important components of global animal and public health strategies. Nevertheless, detecting viral genetic material in migratory bird species does not independently establish specific cross-border transmission events, and mortality estimates must be interpreted within their respective host and outbreak contexts.

Asia and Australia are connected by one of the world's major migratory bird routes, the East Asian–Australasian Flyway (EAAF), which supports seasonal movements of numerous migratory waterbird species (Amano et al., 2010). This flyway extends from Arctic breeding grounds through East and Southeast Asia to Australia and New Zealand and supports the movements of more than 50 million migratory waterbirds representing hundreds of populations (Murray et al., 2014). The extensive mobility of wild birds along this route creates opportunities for the geographic dissemination of infectious agents, including AIVs (Verhagen et al., 2015). Surveillance studies conducted in China, Japan, South Korea, India, Bangladesh, Nepal, and Australia have documented various AIV subtypes in migratory wild bird populations, suggesting potential relationships between migratory movements and the geographic distribution of these viruses across Asia and Australia (Takekawa et al., 2010; Wille et al., 2022).

Published studies have demonstrated considerable variation in the geographic distribution and subtype diversity of AIVs detected in migratory wild birds across countries and host species (Dupas et al., 2026). Multiple hemagglutinin subtypes, including H5, H7, and H9, as well as various hemagglutinin–neuraminidase combinations, have been reported in wild bird populations, with differences in observed detection rates and prevalence estimates across geographic regions (Tan et al., 2025). These variations may reflect ecological conditions, migratory patterns, host species composition, environmental characteristics, and differences in surveillance intensity and diagnostic methods (Couty et al., 2026; Verhagen et al., 2015).

However, evidence concerning the geographic distribution and subtype diversity of AIVs in migratory wild birds across Asia and Australia remains dispersed across scientific publications, limiting the development of an integrated understanding of reported viral occurrence and diversity within these regions (Dupas et al., 2026).

Findings from surveillance studies also require careful interpretation regarding geographic distribution and host movements. Viral detection in a sampled bird or geographic location provides evidence of viral occurrence under specific sampling conditions and diagnostic procedures. However, such detection does not independently demonstrate migration-mediated transmission without supporting epidemiological, movement-tracking, or genomic evidence. Similarly, prevalence estimates and detection positivity rates reported across studies may not be directly comparable because of differences in host species, sample sizes, specimen types, sampling strategies, and diagnostic targets. These methodological inconsistencies highlight an important evidence-synthesis gap extending beyond the descriptive identification of countries and viral subtypes.

Despite the growing number of AIV surveillance studies, relatively few reviews have systematically integrated evidence on the geographic distribution and subtype diversity of AIVs in migratory wild birds across Asia and Australia. Synthesizing these findings is important for understanding reported epidemiological patterns, identifying frequently detected viral subtypes, and supporting the development of targeted surveillance and disease prevention strategies. An integrated evidence base may also inform animal health policies and strengthen the application of the One Health approach to zoonotic disease surveillance and control. Accordingly, this study employed a systematic literature review to identify and synthesize published evidence concerning the geographic distribution and subtype diversity of AIVs detected in migratory wild birds across Asia and Australia. The review specifically examined reported surveillance locations, avian host groups, diagnostic approaches, and viral subtype combinations rather than attempting to provide an exhaustive account of infections throughout the flyway. Its findings were intended to support future research and surveillance planning by identifying documented patterns and limitations in the available evidence.

The novelty of this review lies in its integrated synthesis of geographic surveillance reports, avian host groups, AIV subtype combinations, laboratory detection methods, and reported prevalence estimates within the migratory context of Asia and Australia. Its practical significance arises from the risk of misinterpreting geographic gaps in published surveillance as evidence of viral absence or directly comparing findings obtained through heterogeneous sampling and diagnostic procedures. Therefore, the primary objective was to systematically map and critically synthesize the findings of eligible studies while identifying methodological limitations affecting cross-study comparisons and One Health surveillance decisions. The review did not attempt to reconstruct individual viral transmission routes or estimate the overall prevalence of AIV infections across the entire region.

METHOD

This study employed a systematic literature review (SLR) to identify, evaluate, and synthesize relevant research findings using structured and transparent procedures (Snyder, 2019). The review followed the Preferred Reporting Items for Systematic Reviews and Meta-

Analyses (PRISMA) 2020 guidelines, encompassing identification, screening, eligibility assessment, and inclusion of studies in the final synthesis (Page et al., 2021).

Literature searches were conducted across four scientific databases and search platforms: PubMed, Scopus, ScienceDirect, and Google Scholar. Search terms related to the disease included "avian influenza," "avian influenza virus," "AIV," "bird flu," and "highly pathogenic avian influenza." Population-related terms included "wild birds," "migratory birds," "wild migratory birds," "waterfowl," and "shorebirds." Additional terms addressing geographic distribution and surveillance included "distribution," "geographical distribution," "occurrence," "surveillance," "detection," and "epidemiology." These terms were combined with geographic keywords referring to Asia and Australia to identify relevant publications. Although the review covered both regions, eligible studies from Asia were identified primarily in China, South Korea, Japan, Bangladesh, and Siberian Russia. Several of these locations were associated with major migratory bird routes, including the East Asian–Australasian Flyway (EAAF). The absence of eligible publications from other Asian countries, including Indonesia, Malaysia, Thailand, and Vietnam, did not indicate the absence of avian influenza A viruses (AIVs) in those countries. Rather, it reflected the results of the literature search and study selection process. Consequently, the geographic distribution presented in this review represented published surveillance evidence rather than the complete distribution of AIVs across Asia and Australia.

The inclusion criteria comprised original research articles published in English-language scientific journals between 2016 and 2026, available in full text, and reporting AIV detection or surveillance in migratory wild birds in Asia or Australia. Eligible studies were required to provide information on at least one relevant outcome, including geographic distribution, viral subtypes, diagnostic methods, prevalence estimates, or avian host species. Review articles, systematic reviews, meta-analyses, conference proceedings, editorials, and book chapters were excluded. Studies involving only domestic poultry, conducted outside the specified geographic regions, lacking relevant data or accessible full text, containing insufficient methodological information, or identified as duplicates were also excluded. Data were extracted from eligible articles, including authorship, publication year, study location, sample size, avian host species, AIV subtypes, diagnostic methods, and reported prevalence or detection positivity rates. The extracted findings were synthesized narratively and categorized according to geographic distribution, migratory bird species, AIV subtype diversity, diagnostic approaches, and reported infection prevalence. Following the selection process, 29 articles met the eligibility criteria and were included in the final synthesis.

The narrative synthesis was based on the 29 eligible publications identified through the review process. Reported prevalence estimates, detection positivity rates, and viral subtype classifications were interpreted in relation to the host populations, sampling strategies, and diagnostic methods used in individual studies rather than combined into pooled prevalence estimates or used to reconstruct viral transmission pathways. However, complete database-specific search strategies, reviewer-level screening decisions, study quality assessments, and standardized sample denominators were not fully documented. These limitations restricted the reproducibility of the review and the comparability of findings across studies. Furthermore, the absence of eligible publications from certain countries was interpreted as a limitation of the

available evidence rather than an indication that AIVs were absent from those geographic locations.

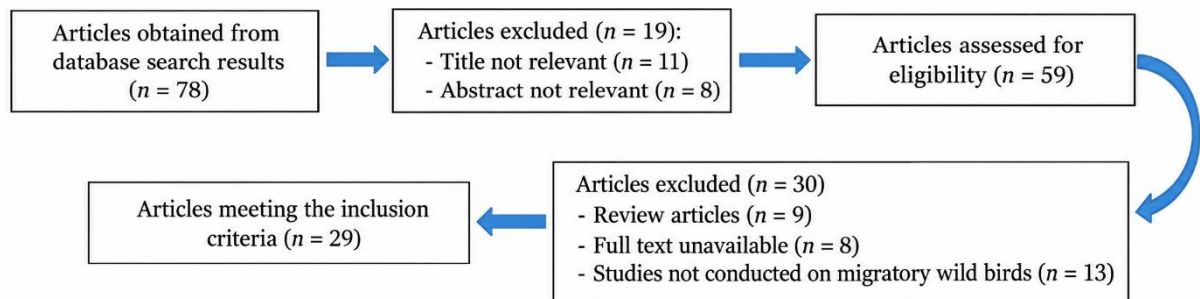


Figure 1. PRISMA Flowchart

Source: Not specified in the original manuscript

RESULTS AND DISCUSSION

Results

Based on the literature selection process using the PRISMA guidelines, 29 scientific articles were obtained that met the inclusion criteria and were analyzed in this study. The characteristics of each extracted study included the location of the study, the number of samples, the identified AIV subtype, the species of migratory wild birds, diagnostic methods, and the prevalence of infection. All articles reported the presence of AIV in migratory wild birds in several Asian countries, namely China, South Korea, Japan, Bangladesh, and Russia (Siberia), as well as Australia. The results of the synthesis of these studies provide an overview of the distribution of AIV in migratory wild birds in the Asian and Australian regions, as presented in Table 1.

Table 1. Research characteristics regarding distribution Avian Influenza Virus (AIV) in migratory wild birds in Asia and Australia

Source	Location	Sample (positive)	Virus Subtypes	Types of Birds	Method	Prevalence
Wille <i>et al.</i> (2022)	Australia	397 positive	H3N8, H6N2, H11N9, H4N6, H5N3, H1N1, and H9N2	Shorebirds (Order Charadriiformes), including <i>Arenaria interpres</i> , <i>Calidris acuminata</i> , and <i>Limosa lapponica</i> . The group Anseriformes and Charadriiformes,	RT-PCR, Next Generation Sequencing (NGS), Phylogenetic analysis, Genomic analysis	Low (no numerical data)
Tang <i>et al.</i> (2020)	Shanghai, China	5112 (452)	H5N6, H4N2, and H6N2.	includes <i>Anas crecca</i> , <i>Anas poecilorhyncha</i> , <i>Anas platyrhynchos</i> , <i>Anas penelope</i> ,	qRT-PCR and sequencing	8,8%

Source	Location	Sample (positive)	Virus Subtypes	Types of Birds	Method	Prevalence
				<i>Anas clypeata</i> , <i>Calidris tenuirostris</i> , <i>Calidris canutus</i> , <i>Calidris alpina</i> , <i>Calidris acuminata</i> , <i>Limosa lapponica</i> , and <i>Arenaria interpres</i> .		
Onuma <i>et al.</i> (2017)	Japan	19,407 (352)	H3, H4, H6, H10, H11, H12	Mallard/Eastern Spot-billed duck group and Northern pintail	RT-LAMP, embryonated chicken eggs, DNA barcoding (COI gene sequencing), Virus subtype analysis	1,8%
Hoye <i>et al.</i> (2021)	King Island, Tasmania (2009–2012), Victoria & South Australia (additional survey)	1.060	H3N5, H6N8, H10N8	Migratory shorebird <i>Arenaria interpres</i> (ruddy turnstone)	RT-PCR, virus isolation, sequencing, phylogenetic analysis, and serology HI assay	6,3%
Khatun <i>et al.</i> (2024)	Bangladesh	850 (22)	H4N2 and H4N6	Waterfowl and Migratory Shorebirds	RT-qPCR, virus isolation, sequencing, phylogenetic analysis	11,96%
Zhao <i>et al.</i> (2022)	Eastern China	19 virus isolates	H7N7	Whooper swan	Virus isolation, genomic analysis, receptor-binding analysis, phylogenetic analysis	NR
Kim <i>et al.</i> (2019)	Korea	1.145 (50)	H1N1, H1N3, H2N1, H2N7, H3N2, H3N8, H4N1, H4N6, H5N2, H6N2, H6N8,	Wild migratory birds	rRT-PCR, virus isolation (VI), cRT-PCR, Next Generation Sequencing (NGS)	0,45%

Source	Location	Sample (positive)	Virus Subtypes	Types of Birds	Method	Prevalence
Over <i>et al.</i> (2018)	Central China	1.647 (11)	H9N2, H10N5, H11N3, H11N9 H7N7, H5N3, H5N6, H6N1, H6N2, H6N8	Wild migratory birds	Virus isolation in embryonic SPF chicken eggs (10 days), confirmed by RT-PCR	0,65%
Hassan <i>et al.</i> (2017)	Bangladesh	3.585	H5N1, H5, H7	Migratory and resident wild birds (<i>Anseriformes</i> , <i>Charadriiformes</i>)	RT-PCR and c-ELISA	19%
Zhang <i>et al.</i> (2025)	Nansi Lake, China	1.417 (30)	H5N1, H5N2, H5N6, H7N9, H9N2	Migratory wild birds (<i>Wild goose</i> , <i>Swan</i> , <i>Egret</i>)	qRT-PCR, virus isolation, sequencing, phylogenetic analysis, HI assay, MN assay	2,1%
Xu <i>et al.</i> (2023)	Shanghai, China	4.451 (622)	H4N2	Common teal, Eurasian wigeon, Falcated duck	qRT-PCR, sequencing, phylogenetic analysis	13,97%
Zhang <i>et al.</i> (2020)	Poyang Lake, Jiangxi, China	488 (14)	H5N6	Mallard, <i>Streptopelia decaocto</i> , <i>Luscinia cyane</i> , Quail	Swab sampling, virus isolation, RT-PCR, sequencing	2,87%
A <i>et al.</i> (2023)	Shaanxi, Northwest China	14 (3)	H5N8	Wild migratory waterbirds (<i>Podiceps nigricollis</i> , <i>Podiceps cristatus</i>)	Oxford Nanopore sequencing, phylogenetic analysis, histopathology	21,4%
Shen <i>et al.</i> (2024)	Shandong, Eastern China	35.749 (24)	H11N2, H11N3, H11N9	Swans, Wild ducks, Gulls, Egrets, Eurasian coots, shorebirds	RT-PCR, virus isolation, sequencing, phylogenetic analysis	0,067%

Source	Location	Sample (positive)	Virus Subtypes	Types of Birds	Method	Prevalence
Yao <i>et al.</i> (2022)	Central China	10.910 (89)	H1N1, H1N2, H5N6, H5N7, H5N8, H6N1, H6N2, H6N5, H6N6, H9N2, H10N2, H10N7	Wild migratory birds/waterfowl	RT-PCR, sequencing, phylogenetic analysis	0,82%
Zhang <i>et al.</i> (2023)	China	126 (1)	H3N8	Wild migratory waterbirds (Chinese pond heron)	RT-PCR, sequencing, phylogenetic analysis	0,79%
Zhang <i>et al.</i> (2024)	Qinghai Lake, China	4.937 (13)	H5N1 clade 2.3.4.4b	Wild migratory waterbirds (<i>Anser indicus</i>)	Surveillance, virus isolation, NGS, phylogenetic analysis	1,1%
Tang <i>et al.</i> (2019)	Shanghai, China	2.394 (160)	H8N4	Common teal	RT-PCR, sequencing, phylogenetic analysis	6,68%
Chai <i>et al.</i> (2022)	Liaoning, China	4.455 (27)	H3N8, H4N6, H4N7, H7N4, H7N7, H10N7, H13N6	Wild migratory shorebirds (<i>Numenius madagascariensis</i> , <i>Numenius minutus</i>)	Virus isolation, RT-PCR, sequencing, phylogenetic analysis	0,61%
The <i>et al.</i> (2023)	Northern China	2 (2)	H5N1 clade 2.3.4.4b.2	Whooper swan (<i>Cygnus cygnus</i>), Black swan (<i>Cygnus atratus</i>)	qRT-PCR, virus isolation, Sanger sequencing, phylogenetic analysis	100%
Kim <i>et al.</i> (2021)	South Korea	16.317 (445)	H1–H12, N1–N9	Wild migratory waterfowl (Predominantly mallard ducks)	RT-PCR, virus isolation, sequencing, pathogenicity assessment	2,72%
Hassan <i>et al.</i> (2020)	Bangladesh	41	H1, H2, H3, H4, H5, H6, H9, H12, H13, H16	Ferruginous duck, Tufted duck, Ruddy shelduck, Northern pintail, Little grebe,	c-ELISA, HI test	H5: 65.9%; H9: 56%

Source	Location	Sample (positive)	Virus Subtypes	Types of Birds	Method	Prevalence
Stuttgart <i>et al.</i> (2023)	China	15.899 (162)	H3N8 (main), H1N1, H4N6, H5N1, H5N8, H6N1, H7N4, H9N2, H10N4, H10N8, H13N6, H16N3	<i>Lesser whistling duck, Gadwall</i> <i>Wild migratory waterbirds (Wild ducks and gulls)</i>	PCR, virus isolation, sequencing, phylogenetic analysis	1,02%
Li <i>et al.</i> (2021)	Yellow River Reservoir Area, China	25 (13)	H5N8 clade 2.3.4.4b	<i>Whooper swan (Cygnus cygnus)</i>	qRT-PCR, NGS, phylogenetic analysis	52%
Wille <i>et al.</i> (2019)	Australia	1.531 (23)	H5Nx, H5N1, H5N6, H5N8 clade 2.3.4.4	<i>Red-necked stint (Calidris ruficollis)</i>	Elisa, HI Test	1,5%
Spain <i>et al.</i> (2023)	South Korea	6.758 (75)	H1N1, H6N1, H5N3, H6N2, H7N7	<i>Anser spp</i>	Virus isolation, RT-PCR, sequencing, phylogenetic analysis	1,11%
Sharshov <i>et al.</i> (2023)	Siberia, Russia	606 (37)	Not specified	<i>Wild ducks, migrating birds, siberia flyways</i>	RT-PCR, sequencing	6,1%
Tian <i>et al.</i> (2023)	China	7.934 (17)	H5N1 clade 2.3.4.4b	<i>Wild migratory birds (Whooper swan, Mandarin duck)</i>	Virus isolation, HI test, RT-PCR, sequencing	0,21%
The <i>et al.</i> (2023)	Yunnan, China	820 (15)	H5N8, H9N2	<i>Common crane (Grus grus)</i>	RT-PCR, NGS, phylogenetic analysis	1,83%

The results of the study showed that AIV was detected in various species of migratory wild birds, with the majority coming from the waterfowl and shorebirds belonging to the orders Anseriformes and Charadriiformes. Some of the reported species include *Anas crecca*, *Anas*

acuta, *Anas platyrhynchos*, *Cygnus cygnus*, *Arenaria interpres*, *Calidris ruficollis*, and several other species of migratory wild birds. A total of 24 combinations of AIV subtypes were successfully identified, namely H1N1, H1N3, H2N1, H2N7, H3N8, H4N2, H4N6, H5N1, H5N6, H6N8, H6N1, H6N2, H6N8, H7N7, H8N4, H9N2, H10N4, H10N7, H10N8, H11N2, H11N3, H11N9, H13N6, and H16N3. Among these subtypes, the H5, H6, H4, H3, and H7 subtypes were the most frequently reported subtypes in the studies analyzed.

The diagnostic methods used in the study consist of molecular and serological methods. The most widely used molecular methods include reverse transcription polymerase chain reaction (RT-PCR), quantitative reverse transcription polymerase chain reaction (qRT-PCR), viral isolation, sequencing, and phylogenetic analysis, while serological methods include enzyme-linked immunosorbent assay (ELISA), competitive ELISA (c-ELISA), hemagglutination inhibition (HI) assay, and microneutralization (MN) assay. In addition to identifying the presence of viruses, these methods are also used to determine the AIV subtypes and genetic characteristics of circulating viruses in migratory wild bird populations.

The prevalence of AIV reported in the analyzed studies showed quite wide variation, ranging from 0.067% to 52%. The lowest prevalence was reported by Shen et al. (2024) in China, while the highest prevalence was reported by Li et al. (2021) in the population Whooper Swan (*Cygnus cygnus*) in China. Despite this, most studies report an AIV prevalence of less than 10%, which suggests that AIV remains detected in migratory wild bird populations in various regions of Asia and Australia. Reported percentages should not be pooled or directly ranked without separating assay type, virus detection versus serological evidence, sample denominator, and sampling population.

A map of the distribution of Avian Influenza cases in migratory wild birds in Asia and Australia can be seen in Figure 2.

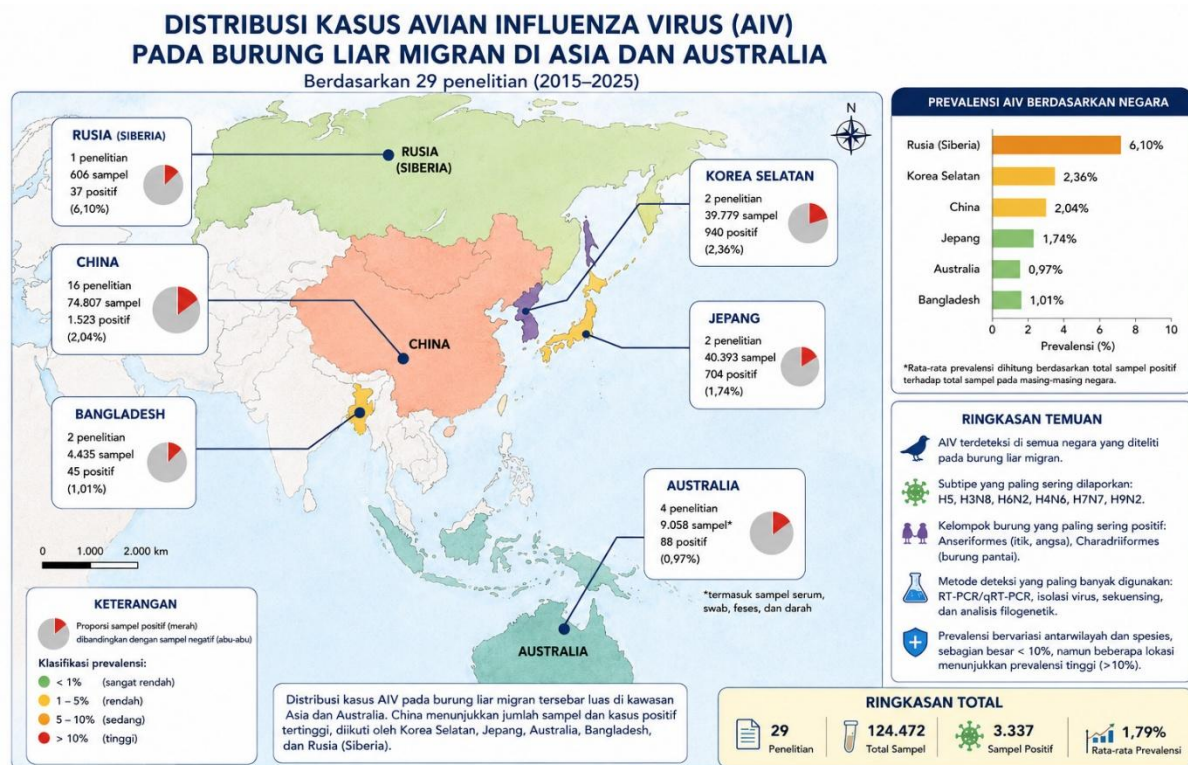


Figure 2. Distribution map of Avian Influenza cases in migratory wild birds in Asia and Australia

Source: Not specified in the original manuscript

Discussion

This discussion describes the distribution of AIV in the Asia and Australia regions, the diversity of subtypes and prevalence found, the diagnostic methods used in detecting AIV, and the urgency of surveillance in migratory wild birds in Asia and Australia. Based on the results of this SLR, it is reported that AIV is spread in various populations of migratory wild birds in Asia and Australia. Most of the research results obtained come from countries on the East Asian–Australasian Flyway (EAAF) migration path such as China, South Korea, Japan, Bangladesh, Russia (Siberia), and Australia. Despite the imbalance in the geographical distribution of the study and the unavailability of data from several other Asian countries, the results of this study still show that AIV circulates in migratory wild bird populations by utilizing its migration routes. The absence of research from other Asian countries such as Indonesia, Vietnam, Thailand, Malaysia, and other Asian countries, does not rule out the possibility that AIV is not present in these regions. This condition is due to the limitations of research that generally only detects AIV in commercial poultry farms, differences in surveillance intensity, variations in disease reporting systems, and non-compliance with inclusion criteria in this SLR. The results obtained better illustrate the distribution of available research than the actual and comprehensive distribution of AIV detection in migratory wild birds throughout Asia. This condition shows the importance of increasing early detection/surveillance in all other Asian regions to obtain a more comprehensive picture of the distribution of AIV in migratory wild birds, considering that wild birds act as natural reservoirs and have the ability to migrate long distances across countries and continents.

In addition to the geographical distribution of AIV in Asia and Australia, the results of this study also show that the presence of AIV in migratory wild birds is closely related to the characteristics of host species that play a role in maintaining and spreading the virus in nature. The bird groups that are widely reported in this study come from the group of waterbirds (waterfowl) and shorebirds (shorebirds) in order Anseriformes and Charadriiformes. This is in line with Hill et al. (2022) that most of the diversity of Influenza A viruses found in wild birds comes from birds of the order Anseriformes and Charadriiformes. According to Vittecoq et al. (2017), the ecological characteristics of these two groups of birds are highly dependent on aquatic habitats because they are not only a place of food source and resting place during migration, but also a gathering place for migratory wild birds in large populations from various countries of origin thus increasing the chances of contact between individual birds and between other types of animals that can potentially be infected with AIV. In addition, AIV transmission can be through contaminated water, feces, saliva, nasal secretions, or direct contact with sick or dead individuals. In contrast, groups of migratory birds of prey (Raptors) are relatively rarely reported in this study because they generally do not act as the main reservoir of the virus. Infection in raptors is more common incidental because they consumed the carcasses of birds that had been infected with AIV, so it showed more spillover infection compared as a natural reservoir of the virus (Ringenberg et al., 2024). Therefore, the waterfowl and shorebirds has become a major focus in AIV surveillance of migratory wild birds.

The high diversity of host species involved in the spread of AIV has contributed to the discovery of various AIV subtypes in migratory wild bird populations. The diversity of AIV subtypes found in this study is related to the variation of two viral surface glycoproteins, namely hemagglutinin (HA) and neuraminidase (NA). The HA protein plays a role in the process of binding to the receptors of the host cell and facilitates the entry of the virus into the cell, while the NA protein plays a role in the release of new viral particles from the infected cell so as to support the spread of the virus to other cells (Du et al., 2019). To date, 18 HA subtypes and 11 NA subtypes have been identified, but most of the subtypes circulating in wild birds are known to come from the H1–H16 and N1–N9 groups (Xu et al., 2023). The results of the AIV subtype study in Asia and Australia that were successfully identified included H1N1, H1N3, H2N1, H2N7, H3N8, H4N2, H4N6, H5N1, H5N6, H5N8, H6N1, H6N2, H6N8, H7N7, H8N4, H9N2, H10N4, H10N7, H10N8, H11N2, H11N3, H11N9, H13N6, and H16N3. The high genetic diversity of AIV is generally related to the ability of viruses to undergo mutations and genetic reassortment, i.e. the exchange of segments of genetic material between influenza viruses that infect the same host so that they can produce new genetic combinations that contribute to the emergence of new subtypes (Postnikova et al., 2021). This process can increase the epidemiological complexity of AIV in migratory wild bird populations. The count of unique AIV subtype combinations should be rechecked against all included studies because repeated subtype labels can inflate the reported number.

Given the importance of the role of migratory wild birds as a natural reservoir of AIV and the potential for the spread of this virus, a surveillance system supported by accurate diagnostic methods and high sensitivity is needed. (This will be discussed later on about diagnostic methods). Based on the results of this study, most of the studies used molecular methods, such as RT-PCR, qRT-PCR, virus isolation, Sequencing, and phylogenetic analysis, while serological methods, such as ELISA, Competitive ELISA (c-ELISA), Hemagglutination inhibition (HI) assay, and Microneutralization (MN) assay. The dominance of the use of molecular methods in the analyzed studies shows that the method is still the main standard in AIV surveillance. The RT-PCR and qRT-PCR methods were chosen because they have high sensitivity, specificity, and accuracy in detecting viral genetic material compared to conventional diagnostic methods (Tseng et al., 2014). Once the presence of the virus is confirmed, the identification of the subtype is carried out through amplification of the HA and NA genes, then continued with Sequencing to determine the subtype of the virus and obtain information about its genetic characteristics. This approach has proven to be effective in supporting AIV surveillance in wild birds, both migratory and endemic birds by monitoring the genetic changes of the virus, knowing kinship relationships, and understanding the distribution patterns of AIV in the migratory pathways of wild birds (Azeem & Yoon, 2025). In contrast to molecular methods that detect viral genetic material so that it describes the presence of active infection, serological methods are used to detect antibodies to AIV as an indicator of previous exposure to the virus and are able to identify infections that are subclinical or asymptomatic. Therefore, serological methods not only provide information about the immune status of a population, but are also able to identify infections that are subclinical or asymptomatic, describe changes in disease patterns in animal populations, provide information for vaccination strategies, risk communication and resource allocation during response to

outbreaks (Badra et al., 2025). Thus, molecular methods and serological methods have complementary roles in AIV surveillance.

The use of these diagnostic methods also affects the detection ability of AIV in migratory wild bird populations. This is reflected in the variation in the prevalence of AIV reported in the studies analyzed, which show differences in the level of viral circulation in different locations, bird species, and sampling periods. Based on the results of this study, the prevalence of AIV in migratory wild birds in the Asian and Australian regions ranges from 0.067% to 52%, with the lowest prevalence reported by Shen et al. (2024) in Shandong, China and the highest prevalence is reported by Li et al. (2021) in the population Whooper Swan (*Cygnus cygnus*) in China. Despite this, most of the studies analyzed reported a prevalence of AIV below 10%, indicating that the virus generally circulates at a relatively low rate in migratory wild bird populations. The variation in prevalence suggests that AIV circulation is influenced by various interrelated factors, both biological, ecological, and methodological factors. From a biological aspect, each bird species has different levels of immunity, migration patterns, and ability to defend viruses that affect the chances of infection and spread of the virus (Bui et al., 2017). Water birds (waterfowl) and shorebirds (shorebirds) is known to be the main reservoir of AIV so it has an important role and maintains the circulation of the virus in nature, even though the bird does not show clinical (subclinical) symptoms. From an ecological aspect, the variation in the prevalence of AIV is influenced by habitat characteristics, migration seasons, and population dynamics of migratory wild birds. Migratory wild birds use wetland habitats as stopovers, foraging and resting locations during migration, increasing the frequency of contact between individuals and between species and increasing the chances of transmission of AIV through direct contact and environmental media, especially feces-contaminated water (Vittecoq et al., 2017). In addition, the prevalence of AIV also fluctuates following the migration season. In the migration and stopover periods, the mixing of bird populations from different migration routes increases the chances of introduction and exchange of viruses between populations, while outside the migration season the prevalence tends to be lower because the bird population is more dispersed (Lewis et al., 2013). In addition to biological and ecological factors, prevalence variations are also influenced by methodological aspects, such as the type of sample used, sample size, surveillance strategies, and diagnostic methods applied to each study. Molecular methods, such as RT-PCR and qRT-PCR, are more effective at detecting active infections through the identification of viral genetic material, while serological methods identify antibodies as indicators of previous exposure. These differences in working principles can result in different prevalence estimates so that the interpretation of results needs to consider the diagnostic approach used. According to Verhagen et al. (2021), variations in AIV surveillance results in wild birds are influenced by surveillance design, sampling coverage, target species, and spatial and temporal distribution of sampling.

Overall, the results of this study show that AIV is still circulating in migratory wild bird populations in Asia and Australia with a high subtype diversity and variation in prevalence between regions and between species. These findings indicate that migratory wild birds act as a natural reservoir as well as a medium for the spread of AIV through cross-border migration routes without causing clinical symptoms, thus strengthening surveillance in wild bird populations, especially in wetland areas and stopover sites (Stopover Sites) is critical to support

early detection, monitoring of viral circulation dynamics, and identification of the emergence of new subtypes. In addition, limited data from several countries in Asia indicate the need to expand surveillance coverage through cross-border cooperation, standardization of diagnostic methods, and exchange of epidemiological data in order to obtain a more comprehensive picture of AIV distribution. These efforts are in line with the approach One Health, which emphasizes multi-sector collaboration between animal health, human health, and environmental health in preventing the spread of AIV, reducing risk spillover to domestic and human poultry, and strengthen preparedness for potential future outbreaks (Pardini et al., 2026). The implementation of this approach can be carried out through the integration of surveillance systems and early warning systems (Early Warning System) as part of the implementation of One Health (Kelly et al., 2020). The integration includes the use of wild bird monitoring data to support the application of biosecurity on poultry farms and risk assessment at the domestic wild-bird interface (Verhagen et al., 2021). In addition, the One Health approach also emphasizes the importance of monitoring community groups at high risk of exposure and strengthening cross-sector coordination through the exchange of epidemiological data and response to disease events (Bordier et al., 2020).

CONCLUSION

This study highlighted the important role of migratory wild birds as natural reservoirs and potential contributors to the geographic dissemination of avian influenza A viruses (AIVs) along migratory routes connecting Asia and Australia. The diversity of detected viral subtypes reflected the genetic and ecological complexity of AIV circulation in wild bird populations, while variations in reported prevalence suggested potential influences of host species, environmental conditions, migration patterns, and surveillance methods. However, the findings documented viral detection in the locations covered by the included studies and did not establish direct evidence of cross-regional transmission by individual migratory birds. Accordingly, integrated surveillance incorporating standardized diagnostic methods and cross-sectoral collaboration within the One Health framework was recommended to improve early detection, strengthen epidemiological risk assessment, and support AIV prevention and control in wildlife, domestic poultry, and human populations. Further research should expand geographic coverage, particularly in underrepresented Asian countries, and employ harmonized laboratory protocols, clearly defined sampling denominators, and integrated ecological, migratory movement, and viral genomic sequence data. These improvements would strengthen the comparability of surveillance findings and provide a more comprehensive understanding of AIV distribution, subtype diversity, and potential transmission pathways across the Asia–Australia region.

FUNDING

The author states that no financial support has been received for the implementation of this research and/or the publication of this article.

CONFLICT OF INTEREST

The author states that this research was conducted without any commercial or financial relationship that can be interpreted as a potential conflict of interest.

AUTHOR CONTRIBUTION

Rosanty contributes to the preparation of research concepts, literature search, study selection, data extraction, data synthesis, interpretation of findings, and preparation of initial draft manuscripts. Putri Pandarangga contributes to research supervision, methodological direction, development of background narratives and basis of thought that explains the urgency of systematic literature review (SLR), providing critical input in the discussion section, validation of the review process, and revision of manuscripts related to scientific substance. Novalino H. G. Kallau contributes to research supervision, scientific interpretation of findings, critical review of manuscripts, manuscript examination, correction of typing errors, and improvement of grammatical accuracy and language usage. All authors have reviewed and approved the final version of the manuscript and are willing to take responsibility for their respective contributions and the integrity of the research as a whole.

GENERATIVE ARTIFICIAL INTELLIGENCE USAGE STATEMENT

The authors state that generative artificial intelligence (AI) was used in the preparation of this manuscript. Some of these manuscripts were compiled using Chat GPT and Perplexity AI. The authors used Chat GPT to improve grammar, summarize tables of research results from previous research summaries, and create Figure 1, while Perplexity AI was used to search for reputable and up-to-date journals related to manuscript content. The use is carried out in compliance with applicable ethical guidelines regarding the use and disclosure of generative AI in scientific research. Each author has made substantial intellectual contributions to this work. The entire content of the manuscript has been carefully reviewed to ensure its accuracy, and the author is solely responsible for the integrity and final content of the manuscript.

REFERENCES

- Amano, T., Székely, T., Koyama, K., Amano, H., & Sutherland, W. J. (2010). A framework for monitoring the status of populations: An example from wader populations in the East Asian-Australasian Flyway. *Biological Conservation*, 143(9), 2238–2247. <https://doi.org/10.1016/j.biocon.2010.06.010>.
- Ayuti, S. R., Khairullah, A. R., Lamid, M., Al-Arif, M. A., Warsito, S. H., Silaen, O. S. M., Moses, I. B., Hermawan, I. P., Yanestria, S. M., Delima, M., Ferasyi, T. R., & Aryaloka, S. (2024). Avian influenza in birds: Insights from a comprehensive review. *Veterinary World*, 17(11), 2544–2555. <https://doi.org/10.14202/vetworld.2024.2544-2555>.
- Azeem, S., & Yoon, K.-J. (2025). Diagnostic assays for avian Influenza virus surveillance and monitoring in poultry. *Viruses*, 17(228), 1–25.
- Badra, R., Zhang, W., Tam, J. S. L., Webby, R., Werf, S. van Der, Nikisins, S., Cullinane, A., Gharaibeh, S., Njouom, R., Peiris, M., Kayali, G., & Heraud, J. (2025). Role and contribution of serological surveillance in animals and exposed humans to the study of zoonotic Influenza disease epidemiology: A scoping review. *Pathogens*, 14(739), 1–21.
- Blagodatski, A., Trutneva, K., Glazova, O., Mityaeva, O., Shevkova, L., Kegeles, E., Onyanov, N., Fede, K., Maznina, A., Khavina, E., Yeo, S. J., Park, H., & Volchkov, P. (2021). Avian

- Influenza in wild birds and poultry: Dissemination pathways, monitoring methods, and virus ecology. *Pathogens*, 10(5), 1–23. <https://doi.org/10.3390/pathogens10050630>.
- Bordier, M., Uea-Anuwong, T., Binot, A., Hendrikx, P., & Goutard, F. L. (2020). Characteristics of One Health surveillance systems: A systematic literature review. *In Preventive Veterinary Medicine (Vol. 181). Elsevier B. V.* <https://doi.org/10.1016/j.prevetmed.2018.10.005>.
- Bui, C., Rahman, B., Heywood, A. E., & MacIntyre, C. R. (2017). A meta-Analysis of the prevalence of Influenza A H5N1 and H7N9 infection in birds. *Transboundary and Emerging Diseases*, 64(3), 967–977. <https://doi.org/10.1111/tbed.12466>.
- Caliendo, V., Lewis, N. S., Pohlmann, A., Baillie, S. R., Banyard, A. C., Beer, M., Brown, I. H., Fouchier, R. A. M., Hansen, R. D. E., Lameris, T. K., Lang, A. S., Laurendeau, S., Lung, O., Robertson, G., van der Jeugd, H., Alkie, T. N., Thorup, K., van Toor, M. L., Waldenström, J., ... Berhane, Y. (2022). Transatlantic spread of highly pathogenic avian Influenza H5N1 by wild birds from Europe to North America in 2021. *Scientific Reports*, 12(1), 1–18. <https://doi.org/10.1038/s41598-022-13447-z>.
- Chai, H., Li, X., Li, M., Lv, X., Yu, W., Li, Y., Sun, J., Li, Y., Sun, H., Tian, J., Xu, Y., Bai, X., Peng, P., Xie, L., Qin, S., An, Q., Zhang, F., Zhang, H., Du, J., ... Maa, J. (2022). Emergence, evolution, and pathogenicity of Influenza A (H7N4) virus in shorebirds in China. *Journal of Virology*, 96(3), 1–13.
- Couty, M., Guinat, C., Fornasiero, D., Briand, F. X., Henry, P. Y., Grasland, B., Palumbo, L., & Le Loc'h, G. (2026). The role of wild birds in the global highly pathogenic avian Influenza H5 panzootic, 2020–2023. *NPJ Biodiversity*, 5(1). <https://doi.org/10.1038/s44185-025-00114-5>.
- Du, R., Cui, Q., & Rong, L. (2019). Competitive cooperation of hemagglutinin and neuraminidase during Influenza A virus entry. *Viruses*, 11(458), 1–13. <https://doi.org/10.3390/v11050458>.
- Dupas, M. C., Falcucci, A., Pittiglio, C., Roche, X., Cinardi, G., Delgado, A., Seck, I., Dhingra, M., & Gilbert, M. (2026). Patterns of avian Influenza virus detection from active surveillance in wild birds: A systematic review and meta-analysis. *One Health*, 22(January). <https://doi.org/10.1016/j.onehlt.2026.101338>.
- España, E., Shim, S. M., Song, E. J., Nam, J. H., Jeong, S.-H., Padasas, B. T., Kim, S.-H., & Kim, J.-K. (2023). Surveillance of avian Influenza viruses from 2014 to 2018 in South Korea. *Scientific Reports*, 13(8410), 1–10. <https://doi.org/10.1038/s41598-023-35365-4>.
- Hassan, M. M., Hoque, A., Debnath, N. C., Yamage, M., & Klaassen, M. (2017). Are poultry or wild birds the main reservoirs for avian Influenza in Bangladesh? *ecoHealth*, 14(3), 490–500. <https://doi.org/10.1007/s10393-017-1257-6>.
- Hassan, M. M., Zowalaty, M. E. El, Islam, A., Khan, S. A., Rahman, K., Järhult, J. D., & Hoque, A. (2020). Prevalence and diversity of avian Influenza virus hemagglutinin sero-Subtypes in poultry and wild birds in Bangladesh. *Vet. Sci*, 7(73). <https://doi.org/10.3390/vetsci702007>.
- He, Z., Jin, T., Wu, W., Zhao, Z., Lu, Z., Song, S., Liu, K., & Shao, Z. (2023). Emerging highly pathogenic avian Influenza (H5N8) virus in *Podiceps nigricollis* in northwest China in 2021. *Transboundary and Emerging Diseases*. <https://doi.org/https://doi.org/10.1155/2023/7896376>.
- Hill, N. J., Bishop, M. A., Trovão, N. S., Ineson, K. M., Schaefer, A. L., Puryear, W. B., Zhou, K., Foss, A. D., Clark, D. E., MacKenzie, K. G., Jonathon D. Gass, J., Borkenhagen, L. K., Hall, J. S., & Runstadler, J. A. (2022). Ecological divergence of wild birds drives avian Influenza spillover and global spread. *PLoS Pathog*, 18(5), 1–25. <https://doi.org/10.1371/journal.ppat.1010062>.
- Hoye, B. J., Donato, C. M., Lisovski, S., Deng, Y., Warner, S., Hurt, A. C., & Klaassen, M.

- (2021). Reassortment and persistence of Influenza A viruses from diverse geographic origins within Australian wild birds : Evidence from a small, isolated population of ruddy turnstones. *J. Virol*, 95. <https://doi.org/https://doi.org/10.1128/JVI.02193-20>.
- Kelly, T. R., Machalaba, C., Karesh, W. B., Crook, P. Z., Gilardi, K., Nziza, J., Uhart, M. M., Robles, E. A., Saylor, K., Joly, D. O., Monagin, C., Mangombo, P. M., Kingebeni, P. M., Kazwala, R., Wolking, D., Smith, W., & Mazet, J. A. K. (2020). Implementing One Health approaches to confront emerging and re-emerging zoonotic disease threats: Lessons from PREDICT. *One Health Outlook*, 2(1), 1–7. <https://doi.org/10.1186/s42522-019-0007-9>.
- Khatun, M. N., Tasnim, S., Hossain, R., Rahman, Z., Hossain, T., Chowdhury, E. H., & Parvin, R. (2024). Molecular epidemiology of avian Influenza viruses and avian coronaviruses in environmental samples from migratory bird inhabitants in Bangladesh. *Front. Vet. Sci*, 11(1446577). <https://doi.org/10.3389/fvets.2024.1446577>.
- Kim, E., Kim, Y., Mi, S., Yu, K., & Casel, M. A. B. (2021). Pathogenic assessment of avian Influenza viruses in migratory birds. *Emerging Microbes & Infections*, 10. <https://doi.org/10.1080/22221751.2021.1899769>.
- Kim, G., Kim, T., Son, J., Lai, V. D., Park, J., Wang, S., Jheong, W., & Mo, I. (2019). The difference of detection rate of avian Influenza virus in the wild bird surveillance using various methods. *J Vet Sci*, 20(5), 1–12. <https://doi.org/https://doi.org/10.4142/jvs.2019.20.e56>.
- Lewis, N. S., Javakhishvili, Z., Russell, C. A., Machabishvili, A., Lexmond, P., Verhagen, J. H., Vuong, O., Onashvili, T., Donduashvili, M., Smith, D. J., & Fouchier, R. A. M. (2013). Avian influenza virus surveillance in wild birds in Georgia: 2009–2011. *PLoS ONE*, 8(3), 2009–2011. <https://doi.org/10.1371/journal.pone.0058534>.
- Li, J., Zhang, C., Cao, J., Yang, Y., Dong, H., Cui, Y., Yao, X., Zhou, H., Lu, L., Lycett, S., Wang, X., Song, H., Liuc, W., Gao, G. F., Shi, W., & Bi, Y. (2021). Re-emergence of H5N8 highly pathogenic avian Influenza virus in wild birds, China. *Emerging Microbes & Infections*, 10. <https://doi.org/10.1080/22221751.2021.1968317>.
- Liu, H., Xiong, C., Chen, J., Guang, C., Zhang, J., Li, Y., Xiong, Y., Wang, R., Cao, Y., Chen, Q., Liu, D., Wang, H., & Chen, J. (2018). Two genetically diverse H7N7 avian Influenza viruses isolated from migratory birds in central China. *Emerging Microbes & Infections*, 7(62). <https://doi.org/10.1038/s41426-018-0064-7>.
- Mostafa, A., Abdelwhab, E. M., Mettenleiter, T. C., & Pleschka, S. (2018). Zoonotic potential of Influenza A viruses: A comprehensive overview. *Viruses*, 10(9), 1–38. <https://doi.org/10.3390/v10090497>.
- Murray, N. J., Clemens, R. S., Phinn, S. R., Possingham, H. P., Fuller, R. A. (2014). Tracking the rapid loss of tidal wetlands in the yellow sea. *Frontiers in Ecology and the Environment*, 12(5), 267–272. <https://doi.org/10.1890/130260>.
- Onuma, M., Kakogawa, M., Yanagisawa, M., Haga, A., Okano, T., Yasuko, N., Okano, T., Goka, K., & Asakawa, M. (2017). Characterizing the temporal patterns of avian Influenza virus introduction into Japan by migratory birds. *J. Vet. Med. Sci*, 79(5), 943–951. <https://doi.org/10.1292/jvms.16-0604>.
- Page, M. J., McKenzie, J. E., Bossuyt, P. M., Boutron, I., Hoffmann, C., Mulrow, C. D., Shamseer, L., Tetzlaff, J. M., Akl, E. A., Brennan, S. E., Chou, R., Glanville, J., Grimshaw, J. M., Hróbjartsson, A., Lalu, M. M., Li, T., Loder, E. W., Mayo-wilson, E., McDonald, S., ... Moher, D. (2021). The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. *BMJ*, 372. <https://doi.org/10.1136/bmj.n71>.
- Pardini, A., Garnhartner, R. L., Vogel, M., & Bachmann, M. F. (2026). Avian Influenza and One Health: Bridging animal and human Health through integrated surveillance and vaccination. *Front. Cell. Infect. Microbiol.*, 16(1659738), 1–16. <https://doi.org/10.3389/fcimb.2026.1659738>.

- Postnikova, Y., Treshchalina, A., Boravleva, E., Gambaryan, A., Ishmukhametov, A., Matrosovich, M., Fouchier, R. A. M., Sadykova, G., Prilipov, A., & Lomakina, N. (2021). Diversity and reassortment rate of Influenza A viruses in wild ducks and gulls. *Viruses*, 13(1010), 1–14. <https://doi.org/10.3390/v13061010>.
- Prosser, D. J., Cui, P., Takekawa, J. Y., Tang, M., Hou, Y., Collins, B. M., Yan, B., Hill, N. J., Li, T., Li, Y., Lei, F., Guo, S., Xing, Z., He, Y., Zhou, Y., Douglas, D. C., Perry, W. M., Newman, S. H. (2011). Wild bird migration across the qinghai-Tibetan plateau: A transmission route for highly pathogenic H5N1. *PLoS ONE*. Vol 6, Issue 3. <https://doi.org/10.1371/journal.pone.0017622>.
- Ringenberg, J. M., Weir, K., Humberg, L., Voglewede, C., Oswald, M., Root, J. J., Dilione, K., Casey, E., Milleson, M., Linder, T., & Lenocho, J. (2024). Prevalence of avian Influenza virus in atypical wild birds host groups during an outbreak of highly pathogenic strain EA/AM H5N1. *Transboundary and Emerging Diseases*, 1–10. <https://doi.org/10.1155/2024/4009552>.
- Sharshov, K., Dubovitskiy, N., Derko, A., Loginova, A., Kolotygin, I., Zhironov, D., Sobolev, I., Kurskaya, O., Alekseev, A., Druzyaka, A., Ktitorov, P., Kulikova, O., He, G., Wang, Z., Bi, Y., & Shestopalov, A. (2023). Does avian coronavirus co-Circulate with avian paramyxovirus and avian Influenza virus in wild ducks in Siberia? *viruses*, 17(1121). <https://doi.org/10.3390/v15051121>.
- Shen, J., Zhang, H., Sun, X., Zhang, Y., Wang, M., Guan, M., Liu, L., Li, W., Xu, H., Xie, Y., Ren, A., Cao, F., Liu, W., Deng, G., Guo, J., & Li, X. (2024). Evolution and biological characteristics of H11 avian Influenza viruses isolated from migratory birds and pigeons. *Emerging Microbes & Infections*, 13(2398641). <https://doi.org/https://doi.org/10.1080/22221751.2024.2398641>.
- Snyder, H. (2019). Literature review as a research methodology: An overview and guidelines. *Journal of Business Research*, 104(July), 333–339. <https://doi.org/10.1016/j.jbusres.2019.07.039>.
- Suarez, D. L. (2010). Avian influenza: our current understanding. *Animal Health Research Reviews*, 11(1), 19–33. <https://doi.org/10.1017/S1466252310000095>.
- Swayne, D. E. (2020). Diseases of poultry (14th ed.). *Wiley-Blackwell*.
- Takekawa, J. Y., Newman, S. H., Xiao, X., Prosser, D. J., Spragens, K. A., Palm, E. C., Yan, B., Li, T., Lei, F., Zhao, D., Douglas, D. C., Muzaffar, S. B., & Ji, W. (2010). Migration of waterfowl in the East Asian Flyway and spatial relationship to HPAI H5N1 outbreaks. *Avian Diseases*, 54(1 Suppl), 466–476. <https://doi.org/10.1637/8914-043009-Reg.1>.
- Tan, W. X., Qin, S. Y., Yang, X., Li, X. M., Li, J. H., Cao, H., Jiang, J., Zhao, Q., Sun, H. T. (2025). Global prevalence and distribution of H9 subtype of avian influenza viruses in wild birds: Literature review with meta-analysis. *Vector-borne and Zoonotic Diseases*, 25(5), 346–358. <https://doi.org/10.1089/vbz.2024.0111>.
- Tang, L., Tang, W., Li, X., Hu, C., Wu, D., Wang, T., & He, G. (2020). Avian Influenza virus prevalence and subtype diversity in wild birds in Shanghai, China, 2016–2018. *Viruses*, 12(1031), 2016–2018.
- Tang, W., Li, X., Hu, C. H., Zhu, C., Li, Z., Wu, D., Wang, T., & He, G. (2019). Isolation of H8N4 avian Influenza virus from wild birds in Shanghai, China. *Acta Virologica*, 63, 121–125. https://doi.org/10.4149/av_2019_116.
- Tian, J., Bai, X., Li, M., Zeng, X., Xu, J., Li, P., Wang, M., Song, X., Zhao, Z., Tian, G., Liu, L., Guan, Y., Li, Y., & Chen, H. (2023). Highly pathogenic avian Influenza virus (H5N1) clade 2.3.4.4b introduced by wild birds, China, 2021. *Emerging Infectious Diseases*, 29(7), 1367–1375.
- Tseng, C., Tsai, H., & Chang, C. (2014). A complete molecular diagnostic procedure for applications in surveillance and subtyping of avian Influenza virus. *BioMed Research*

- International*, 2014, 13–15. <https://doi.org/10.1155/2014/653056>.
- Verhagen, J. H., Fouchier, R. A. M., & Lewis, N. (2021). Highly pathogenic avian influenza viruses in the wild – domestic bird interface in Europe: Future directions for research and surveillance. *Viruses*, 13(212). <https://doi.org/10.3390/v13020212>.
- Verhagen, J. H., Herfst, S., Fouchier, R. A. M. (2015). How a virus travels the world. *Science*, 347(6222). <https://doi.org/10.1126/science.1259924>.
- Vittecoq, M., Gauduin, H., Oudart, T., Bertrand, O., Roche, B., Guillemain, M., & Boutron, O. (2017). Modeling the spread of avian Influenza viruses in aquatic reservoirs: A novel hydrodynamic approach applied to the Rhône Delta (Southern France). *Science of the Total Environment*, 595, 787–800. <https://doi.org/10.1016/j.scitotenv.2017.03.165>.
- Wahyuni, S., Wicaksono, A., Suprayogi, A. (2022). Incidence and risk of avian Influenza transmission in laying hen farms in Pinrang regency. *Indonesian Journal of Agricultural Sciences*. 27(3), 397–405. <https://doi.org/10.18343/jipi.27.3.397>.
- Wang, Y., Wang, M., Zhang, H., Zhao, C., Zhang, Y., Shen, J., Sun, X., Xu, H., Xie, Y., Gao, X., Cui, P., Chu, D., Li, Y., Liu, W., Peng, P., Deng, G., Guo, J., & Li, X. (2023). Prevalence, evolution, replication and transmission of H3N8 avian Influenza viruses isolated from migratory birds in eastern China from 2017 to 2021. *Emerging Microbes & Infections*, 12(2184178), 1–18. <https://doi.org/10.1080/22221751.2023.2184178>.
- Wille, M., & Barr, I. G. (2022). Resurgence of avian influenza virus. *Science*, 376(6592), 459–460. <https://doi.org/10.1126/science.abo1232>.
- Wille, M., Grillo, V., Pedrosa, S. B. de G., Burgess, G. W., Crawley, A., Dickason, C., Hansbro, P. M., Hoque, A., Horwood, P. F., Kirkland, P. D., Kung, N. Y., Lynch, S. E., Martin, S., McArthur, M., Riley, K. O., Read, A. J., Warner, S., Hoyer, B. J., Lisovski, S., ... Wong, F. Y. K. (2022). Australia as a global sink for the genetic diversity of avian Influenza A virus. *PLoS Pathog*, 18(5), 1–26. <https://doi.org/10.1371/journal.ppat.1010150>.
- Wille, M., Lisovski, S., Risely, A., Ferenczi, M., Roshier, D., Wong, F. Y. K., Breed, A. C., Klaassen, M., & Hurt, A. C. (2019). Serologic evidence of exposure to highly pathogenic avian Influenza H5 viruses in migratory shorebirds, Australia. *Emerging Infectious Diseases*, 25(10).
- Xu, Y., Tang, L., Gu, X., Bo, S., Ming, L., Ma, M., Zhao, C., Sun, K., Liu, Y., & He, G. (2023). Characterization of avian Influenza A (H4N2) viruses isolated from wild birds in Shanghai during 2019 to 2021. *Poultry Science*, 102(10), 102948. <https://doi.org/10.1016/j.psj.2023.102948>.
- Yang, J., Zhang, C., Yuan, Y., Sun, J., Lu, L., Sun, H., Sun, H., Chu, D., Qin, S., Chen, J., Zhang, C., Hao, X., Shi, W., Liu, W., Gao, G. F., Digard, P., Lycett, S., & Bi, Y. (2023). Novel avian Influenza virus (H5N1) clade 2.3.4.4b reassortants in migratory birds, China. *Emerging Infectious Diseases*, 29(6), 6–11. <https://doi.org/10.3201/eid2906.221723>.
- Yang, Q., Xue, X., Zhang, Z., Wu, M. J., Ji, J., Wang, W., Yin, H., Li, S., Dai, H., Duan, B., Liu, Q., & Song, J. (2023). Clade 2.3.4.4b H5N8 subtype avian Influenza viruses were identified from the common crane wintering in Yunnan province, China. *Viruses*, 15(38). <https://doi.org/10.3390/v15010038>.
- Yao, Z., Zheng, H., Xiong, J., Ma, L., Gui, R., Zhu, G., Li, Y., Yang, G., Chen, G., Zhang, J., & Chen, Q. (2022). Genetic and pathogenic characterization of avian Influenza virus in migratory birds between 2015 and 2019 in central. *Microbiology Spectrum*, 10(4), 1–15. <https://doi.org/10.1128/spectrum.01652-221>.
- Zhang, H., Han, S., Wang, B., Xing, Y., Yuan, G., Wang, Y., Zhao, Z., Li, G., Li, Q., Pan, J., Li, W., & He, H. (2023). Genetic characterization and pathogenesis of avian Influenza virus H3N8 isolated from Chinese pond heron in China in 2021. *Viruses*, 15(383). <https://doi.org/10.3390/v15020383>.

- Zhang, S., Liang, Y., Wang, D., Shang, C., Wei, W., Zhao, X., Li, L., Jiang, W., Guo, B., Jiao, B., Ma, J., Qiu, Y., Cui, Y., Wang, G., Chen, J., Xu, Q., Lv, C., Hong, F., Wang, G., & Fang, L.-Q. (2025). Avian Influenza surveillance among migratory birds, poultry, and humans around Nansi Lake, China, 2021 – 2024. *Viruses*, 17(1117), 1–16. <https://doi.org/10.3390/v17081117>.
- Zhang, T., Fan, K., Zhang, X., Xu, Y., Xu, J., Xu, B., & Li, R. (2020). Diversity of avian Influenza A (H5N6) viruses in wild birds in southern China. *Journal of General Virology*, 101, 902–909. <https://doi.org/10.1099/jgv.0.001449>.
- Zhang, X., Wu, J., Wang, Y., Hao, M., Liu, H., Fan, S., Li, J., Sun, J., He, Y., Zhang, Y., & Chen, J. (2024). Highly pathogenic avian Influenza A virus in wild migratory birds, Qinghai Lake, China, 2022. *Emerging Infectious Diseases*, 30(10), 2135–2139.
- Zhao, C., Guo, J., Zeng, X., Shi, J., Deng, G., Zhang, Y., Wang, Y., Ma, Q., Gao, X., Cui, P., Liu, L., Li, X., & Chen, H. (2022). Novel H7N7 avian Influenza viruses detected in migratory wild birds in eastern China between 2018 and 2020. *Microbes and Infection* 24, 24(105013). <https://doi.org/10.1016/j.micinf.2022.105013>.