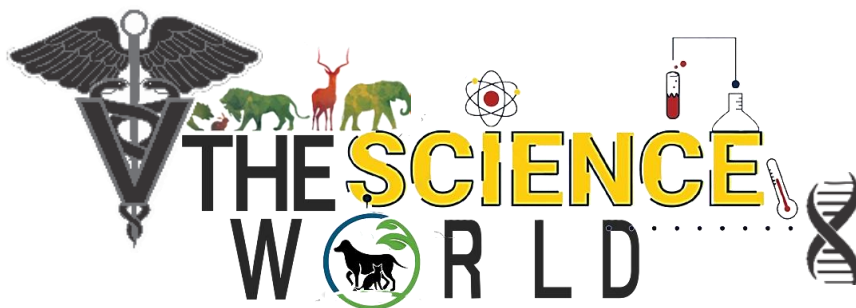




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Bird Flu Beyond Birds: The Changing Face of H5N1

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Abstract

Highly pathogenic avian influenza (HPAI) A(H5N1), traditionally recognized as a devastating disease of poultry and wild birds, has increasingly demonstrated its ability to cross species barriers and infect a wide range of mammals. The detection of H5N1 in terrestrial and aquatic mammals, companion animals such as cats and more recently dairy cattle has expanded the epidemiological significance of this virus beyond the avian population. These developments highlight the complex interactions among wildlife, livestock, companion animals, humans and the environment. For veterinarians, the changing host range of H5N1 presents new challenges in clinical recognition, differential diagnosis, biosecurity, surveillance and zoonotic risk assessment. Molecular diagnostics and genomic surveillance have become increasingly important for early detection and understanding viral evolution and transmission. In this context, a coordinated One Health approach integrating veterinary, medical and environmental surveillance is essential. This article highlights the changing epidemiology of H5N1, its emergence beyond birds, implications for companion animals and livestock, zoonotic concerns and the crucial role of veterinarians in prevention, early detection and outbreak preparedness.

Key words: Avian influenza, Biosecurity, One Health, Species spillover, Zoonotic disease

1. Introduction

For decades, avian influenza—commonly known as “bird flu”—has been regarded primarily as a disease of poultry and wild birds. However, the epidemiology of highly pathogenic avian influenza (HPAI) has changed considerably in recent years. The emergence and global spread of H5N1 viruses, particularly those belonging to the A(H5) lineage, have demonstrated an increasingly complex interaction between birds, mammals, livestock, wildlife



and humans. From poultry farms and migratory birds to cats, marine mammals and dairy cattle, the virus has repeatedly demonstrated its ability to cross species barriers.

The current H5N1 situation is remarkable not only because of its geographic spread, but also because of its expanding host range. Since the emergence of the H5 clade 2.3.4.4b viruses in 2020, extensive outbreaks have occurred among wild birds and poultry across multiple continents, with spillover infections increasingly documented in mammals (Larsen *et al.*, 2025). By 2026, H5 viruses have been detected in birds and/or mammals on all continents except Oceania, while infections have been reported in diverse mammalian species, including aquatic mammals and dairy cattle.

According to the Food and Agriculture Organization (FAO), HPAI viruses with zoonotic potential continue to circulate globally. Between 23 July and 26 August 2026, 574 HPAI outbreaks or events in animals were officially reported from 22 countries or territories, including 195 caused by H5N1. The same update notes continued infection of multiple mammalian species, including dairy cattle (Wogick and Goyal, 2026).

The implications extend beyond animal health. Humans can occasionally acquire H5N1 following close or prolonged exposure to infected animals or contaminated environments. According to the joint FAO/WHO/WOAH assessment published in May 2026, the current global public-health risk posed by circulating HPAI A(H5) viruses remains low, although the risk for people with occupational or frequent animal exposure can be higher depending on local epidemiological conditions and protective measures.

For veterinarians, this changing epidemiological landscape is particularly important. A veterinarian may be the first professional to encounter an unusual mortality event in poultry, neurological disease in a companion animal following exposure to birds, unexplained illness in livestock, or disease among wildlife. Recognizing these events and linking them with relevant exposure histories can contribute to early detection and appropriate response. Thus, H5N1 is no longer simply a poultry-health issue. It represents a complex One Health challenge, in which the health of wildlife, livestock, companion animals, humans and the environment is interconnected.

2. What is H5N1?

Influenza A viruses are RNA viruses belonging to the family *Orthomyxoviridae* and is classified into four types: A, B, C, and D. Their classification is based largely on two surface proteins—haemagglutinin (H) and neuraminidase (N), with 18 known subtypes of H and 11 of N. However, the five subtypes of most significant epidemiological relevance are H1N1, H2N2, H3N2, H5N1, and H7N9. Influenza A has been responsible for most of the pandemics



documented in human history, including the Spanish flu (H1N1) in 1918, the Asian flu (H2N2) in 1957, the Hong Kong flu (H3N2) in 1968, and swine flu (H1N1), the result of a mutation of the original virus, in 2009. The first outbreaks of avian influenza caused by the H5N1 subtype were recorded in poultry in Scotland, United Kingdom (UK), in 1959 and geese in Guangdong Province, China, in 1996 (Sanchez-Rojas *et al.*, 2025).

Avian influenza A viruses, particularly the H5N1 subtype, pose a persistent threat, with pandemic potential due to their genetic recombination capacity, interspecies adaptability, and high lethality. H5N1 refers to an influenza A virus subtype carrying the H5 haemagglutinin and N1 neuraminidase proteins. Certain H5 viruses are classified as highly pathogenic avian influenza (HPAI) viruses because they can produce severe disease and high mortality in susceptible poultry. However, pathogenicity is host-dependent and infection does not necessarily produce the same clinical outcome in every species. Wild birds, particularly migratory waterfowl and other aquatic birds, can play an important role in the ecology and spread of avian influenza viruses (Simancas-Racines *et al.*, 2025).

One of the remarkable characteristics of influenza A viruses is their capacity for genetic change. Their segmented genome allows genetic reassortment when different influenza viruses infect the same host cell, while mutations can accumulate during viral replication. These processes contribute to the emergence of viruses with altered biological characteristics, including changes in host range and transmission patterns.

The H5N1 viruses currently circulating globally are not a single genetically uniform virus. They comprise evolving viral lineages and reassortants that have changed over time. The contemporary H5 lineage, particularly clade 2.3.4.4b viruses, has become widely distributed among wild birds and poultry and has subsequently been detected in numerous mammalian species. The current global situation has involved repeated transmission between wild birds, domestic poultry and increasingly, mammals.

3. From Birds to Mammals: Crossing the Species Barrier

One of the most striking features of the recent H5N1 situation is its expanding host range. Although highly pathogenic avian influenza viruses are primarily associated with birds, contemporary H5 viruses have been detected in an increasingly diverse range of mammals (Larsen *et al.*, 2025). Mammalian infections can occur through several routes. Direct contact with infected birds or their secretions and excretions is an important pathway, while contaminated feed, water, equipment and environments may provide additional opportunities for exposure. Predatory and scavenging mammals may also become infected after consuming infected birds or other contaminated animal material. Consequently, species that live at the



interface of wildlife, livestock and human activities may have greater opportunities for viral exposure.

The detection of H5N1 in mammals, however, should not be interpreted as evidence that the virus has become uniformly adapted to mammals. Spillover infection and sustained transmission are different epidemiological events. In many mammalian species, infections appear to follow exposure to infected birds or contaminated environments. Nevertheless, repeated spillover events provide opportunities for the virus to replicate in new hosts and acquire genetic changes, making continued surveillance important.

The mammalian host range now includes several epidemiologically important groups:

- **Terrestrial wildlife:** foxes, skunks and other carnivorous or scavenging mammals can become infected, often following exposure to infected birds.
- **Marine mammals:** seals, sea lions and other marine mammals have experienced H5 virus infections, particularly in areas with substantial virus circulation among wild birds.
- **Companion animals:** cats have emerged as an important veterinary concern because infection can follow hunting, consumption of infected birds or exposure to contaminated animal products and environments.
- **Livestock:** the detection of H5N1 in dairy cattle represented a major shift in the epidemiological landscape and demonstrated that the virus could establish transmission within a mammalian production system.

The consequences of infection can also vary considerably between species. Some infected mammals may show respiratory disease, whereas others can develop neurological signs, systemic illness or death. In cats, for example, neurological manifestations have been reported in association with H5N1 infection. In dairy cattle, reduced milk production and abnormal milk have been among the notable clinical findings reported during outbreaks.

The expanding host range also highlights the importance of the wildlife–livestock–companion animal interface. An infected wild bird may contaminate an environment, a domestic animal may subsequently encounter that environment, and people may then be exposed while handling the animal. Such interconnected pathways demonstrate why infectious disease surveillance cannot be restricted to a single species.



4. When Cows Entered the Bird Flu Story

One of the most unexpected developments in the H5N1 story occurred in March 2024, when the virus was detected in dairy cattle in the United States (Sanchez-Rojas *et al.*, 2025). This marked an important shift because cattle had not traditionally been considered a significant host for highly pathogenic avian influenza. Affected dairy cows commonly showed a sudden drop in milk production and abnormal, thickened or colostrum-like milk, along with reduced feed intake, fever and lethargy. Investigations also provided evidence of transmission between cattle and between dairy farms, with animal movement and routine farm operations contributing to spread.

The emergence of H5N1 in dairy cattle therefore expanded the veterinary significance of the virus beyond birds. It also highlighted the importance of farm biosecurity, movement control, milk-based surveillance and protection of people working closely with infected animals. For veterinarians, the lesson is clear: when an avian virus appears in an unexpected mammalian host, surveillance must be ready to follow it.

5. Cats: An Unexpected Concern in the H5N1 Story

Cats have emerged as an important companion-animal concern in the H5N1 story. Infection has been reported following exposure to infected birds, contaminated environments and infected animal products, including raw meat or milk. Cats may develop severe disease, particularly respiratory and neurological signs (Salvaggiulo *et al.*, 2026).

Veterinarians should be alert when cats present with fever, lethargy, anorexia, respiratory distress, ataxia, tremors, seizures or sudden behavioural changes, especially when there is a history of hunting birds or exposure to sick or dead animals. Importantly, infection in cats does not mean that cats are a major reservoir of H5N1. In many situations, infection is linked to exposure to an infected source. Nevertheless, cats can serve as an important sentinel at the wildlife–human interface, making recognition, appropriate precautions and timely reporting essential.

6. From Animals to Humans: The Zoonotic Threat

The expanding host range of H5N1 has increased concern about its zoonotic potential. Human infections have most often been associated with close or prolonged contact with infected animals or contaminated environments, particularly among poultry workers, dairy workers, veterinarians and other animal handlers. Human illness can range from conjunctivitis and mild respiratory signs to severe respiratory or systemic disease (Peacock *et al.*, 2025). However, animal-to-human spillover should not be confused with sustained human-to-human transmission; the latter remains a different epidemiological concern.



For veterinarians, every suspected animal infection carries an additional question: could this case pose a risk to the people handling the animal? Recognizing exposure, using appropriate personal protective equipment (PPE), following sampling precautions and promptly reporting suspected cases are therefore essential components of zoonotic disease prevention.

7. H5N1 Through a One Health Lens

H5N1 is no longer a disease concern limited to poultry. Its movement among wild birds, poultry, livestock, wildlife, companion animals, humans and the environment demonstrate how closely these systems are connected. The environment can act as an important interface. Contaminated water, soil, equipment, footwear, feed and animal housing may facilitate indirect exposure, particularly where infected birds and domestic animals share the same surroundings. This makes One Health surveillance essential. Despite growing recognition of HPAI's transboundary nature, significant gaps remain in policy coordination at both the regional and inter regional levels. Clear alignment and collaboration are needed to ensure consistent and effective responses. For example, weaknesses in cooperative mechanisms across ASEAN and the EU—highlighted during the 2004 outbreak—underscore the importance of coordination and strong regional organizational involvement (Chou *et al.*, 2025). Veterinarians are central to this approach—not only as clinicians, but also as early-warning professionals who can recognize unusual disease, assess exposure risks, initiate appropriate precautions and support surveillance and reporting.

8. Diagnosis and Surveillance

Clinical signs and exposure history may raise suspicion, but laboratory confirmation is essential. Real-time RT-PCR is commonly used to detect influenza A viral RNA, while genomic sequencing can help track viral evolution and transmission. Virus isolation and identification remain the most reliable and widely accepted methods for confirming the presence of avian influenza virus. Virus isolation and identification remain the most reliable and widely accepted methods for confirming the presence of avian influenza virus

9. Treatment or Culling: What Happens to Infected Animals?

Unlike many bacterial infections, H5N1 has no established specific treatment protocol for animals. In poultry outbreaks, culling of infected and epidemiologically linked birds is commonly used to rapidly control transmission. For infected mammals, management depends on the species, clinical condition, transmission risk and applicable veterinary regulations. Isolation, supportive care where appropriate, biosecurity and surveillance are important, while removal or culling may be considered by veterinary authorities in specific situations. Thus, the



response to H5N1 is not simply “treat or slaughter”; it is a risk-based disease-control decision designed to protect animal health, public health and prevent further spread.

10. Scientific Advances in the Control and Prevention of H5N1

Control of H5N1 is increasingly moving from reactive outbreak management towards early detection, targeted vaccination and integrated surveillance. Advances in molecular diagnostics and genomic sequencing allow faster identification of infections and help track viral evolution and spread. Vaccination of poultry is also receiving greater attention as a complementary control measure. WOAHA recognises vaccination as one possible component of a broader strategy, alongside surveillance, biosecurity and rapid outbreak response.

New surveillance approaches are expanding beyond poultry to include wild birds, livestock, wildlife and environmental interfaces. In 2026, WOAHA also issued updated guidance for HPAI surveillance in smallholder poultry systems, highlighting the importance of early detection and One Health collaboration. Together, these advances support a more sustainable approach: detect early, understand the virus, prevent transmission and respond rapidly.

11. Biosecurity: Prevention Is the First Defence

Good biosecurity is the first line of protection against H5N1. Key measures include:

- Minimize contact between domestic animals and wild birds.
- Protect feed and water from contamination.
- Maintain proper cleaning and disinfection.
- Restrict unnecessary animal and equipment movement.
- Prevent pets from hunting or scavenging birds.
- Use appropriate PPE when handling suspected cases.
- Report unusual illness or mortality promptly.

Simple, consistent biosecurity can protect animals, veterinarians and the wider community.

12. What Every Veterinarian Should Remember

H5N1 has changed from being primarily an avian disease to a wider One Health concern.

Veterinarians should:

- Think beyond birds when assessing unusual disease.
- Ask about exposure to birds, wildlife, livestock and contaminated environments.
- Recognize respiratory and neurological red flags.
- Use appropriate PPE and biosecurity measures.
- Report and investigate unusual cases promptly.



Early recognition in animals can provide an important opportunity to protect animal health, human health and the environment.

Conclusion

H5N1 is no longer a story confined to birds. Its detection in wildlife, companion animals, livestock and humans demonstrates the ability of influenza viruses to cross species boundaries and emerge in unexpected hosts. For veterinarians, this changing landscape calls for greater clinical awareness, strong biosecurity, timely diagnosis and effective surveillance. Equally important is collaboration among veterinary, medical, wildlife and environmental sectors. The future of H5N1 preparedness depends not only on detecting the virus early, but also on understanding the connections between animals, people and their shared environment.

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