



# Updated joint FAO/WHO/WOAH public health assessment of recent high pathogenicity avian influenza A(H5) virus events in animals and people

Assessment based on data as of 1 March 2026

18 May 2026

## Key points

Based on currently available information, Food and Agriculture Organization of the United Nations (FAO)/World Health Organization (WHO) / World Organisation for Animal Health (WOAH) assess the global public health risk posed by Gs/Gd-like high pathogenicity avian influenza (HPAI) A(H5) viruses as low. The risk of infection for occupationally or frequently exposed persons (e.g., with backyard poultry) is assessed as low to moderate depending on local epidemiologic conditions and the risk mitigation and hygiene measures in place. Transmission among animals continues and sporadic human infections at the human-animal-environment interface continue to be reported. While additional human infections associated with exposure to infected animals or contaminated environments are expected, the overall global public health impact of such infections is currently considered minor. The assessment may change rapidly as new epidemiological or virological information becomes available.

This joint FAO/WHO/WOAH risk assessment updates the transmission risk using new global information available since the previous assessment of [28 July 2025](#). Given the potential risk to human health and the wide-ranging impacts on wild birds and mammals, poultry, livestock and other animal populations, timely notification to global authorities and the application of a One Health approach remain essential to monitor and characterize virus circulation, limit transmission within species and between species, reduce spread among animals, and prevent human infections.

## Infections in animals

To date, HPAI A(H5) viruses have been detected in birds and/or mammals across all continents except Oceania. The predominant H5 virus clades currently circulating worldwide derive from clades 2.3.2.1 and 2.3.4.4. Between 1 July 2025 and 1 March 2026, an additional 185 A(H5N1) events<sup>i</sup> in animals (including birds and bovines) have been reported to WOAH. Of these, 1204 outbreaks occurred in poultry (of any farming system), 6326 outbreaks in wild birds and nine outbreaks occurred in bovines.

## H5 clade 2.3.2.1 viruses

Between 1 July 2025 and 1 March 2026, A(H5N1) clade 2.3.2.1a viruses were detected in poultry in Bangladesh and India, while A(H5N1) clade 2.3.2.1e viruses were detected in poultry in Cambodia

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<sup>i</sup> An event includes all related epidemiologically related outbreaks reported from the time of the immediate notification through to the final report. Separately the total number of outbreaks is also stated.

and Lao People's Democratic Republic. Clade 2.3.2.1g A(H5N1) viruses were detected in poultry on several islands of Indonesia, where they are believed to be endemic.<sup>1</sup>

#### **H5 clade 2.3.4.4b viruses**

Detections of A(H5) in wild and domestic mammals and wild and domestic birds continued to be reported in many countries worldwide. During the period of September–November 2025, Europe experienced an exceptional and early season and a high incidence of HPAI A(H5) activity in wild birds, with more than 3200 detections reported across 28 countries. This represents a ten-fold increase compared to the same period in 2024. Based on genetic data available so far, the A(H5N1) HPAI viruses identified in Europe all fall into clade 2.3.4.4b, and the majority belong to the genotype EA-2024.DI2.1<sup>2,3</sup> This surge has disproportionately affected migratory waterfowl and colonial species, with widespread A(H5N1) virus infections confirmed in key migratory hosts (e.g., Eurasian wigeons, Northern pintails, Mute swans, Greylag geese) and severe mass mortality events in Eurasian cranes (*Grus grus*).<sup>4</sup>

In Africa, poultry outbreaks of A(H5N1) clade 2.3.4.4b viruses have been reported in Nigeria and South Africa since September 2025. Several other countries in sub-Saharan Africa consider HPAI to be present in their territories. Detections of A(H5N1) were also made in wild birds in Namibia and South Africa. A(H5N1) clade 2.3.4.4b viruses are considered endemic in Egypt's poultry populations.

In Asia, clade 2.3.4.4b viruses have been reported in several countries. In India, recent poultry outbreaks have involved A(H5N1), while in Kazakhstan, A(H5N1) was detected in wild birds. In the Republic of Korea, detections include A(H5N1), A(H5N6), and A(H5N9), while in Japan A(H5N1) and A(H5N5) viruses have been reported.

In North America, substantial activity of clade 2.3.4.4b A(H5) viruses has continued since the last assessment. In the United States of America, more than 3700 A(H5) detections in wild birds and over 400 A(H5) HPAI outbreaks in poultry were reported, while Canada reported nearly 500 A(H5N1) detections in wild birds and over 80 A(H5) HPAI outbreaks in poultry.<sup>5,6</sup> A(H5N1) detections in terrestrial and marine mammals have also been reported. Notably, A(H5N1) clade 2.3.4.4b was detected for the first time in northern elephant seals in February 2026 in California, involving a virus of the A3 genotype.<sup>7</sup>

In central America, Mexico reported H5N1 outbreaks in backyard poultry in October 2025 and A(H5N1) detections in wild birds in November. A(H5N1) detections of American genotype D1.1 viruses were reported in domestic birds in the Cayman Islands and Guatemala during the second half of 2025. Genotype D1.1 was the most frequently detected A(H5N1) genotype in North America in 2025, affecting wild birds, poultry and multiple mammalian species, including wild and domestic felids and marine mammals. A(H5N2) clade 2.3.4.4b viruses belonging to the K.5 genotype were detected in poultry in Mexico.

In South America, A(H5N1) has continued to spread, with detections in both poultry and wild birds across multiple countries. In late 2025, A(H5N1) outbreaks were reported from Argentina, Brazil and Colombia. Where sequence data are available, viruses belong to clade 2.3.4.4b.<sup>8</sup> In 2026, additional outbreaks occurred across the region. HPAI A(H5) outbreaks occurred in Peru in backyard poultry

and in Uruguay in wild birds, although detailed genetic information for these events is not yet available. Between 1 February and 1 March 2026, Argentina detected at least 12 A(H5N1) events across domestic and wild birds, while further A(H5N1) outbreaks occurred in backyard and wild birds in Brazil, and in backyard birds in Colombia and Peru.

Although the full extent of ongoing circulation and establishment in wild bird populations across South America remains uncertain, evidence suggests that A(H5N1) viruses circulating have continued to diversify through reassortment. Viruses detected in Brazil in mid- to late 2025 belonged to two distinct genotypes, K.8 and N.1. The K.8 genotype is related to “triple reassortant” viruses<sup>9</sup> identified in Argentina in early 2025, combining North American B3.6- and B3.13-like genomes but with multiple internal gene segments derived from South American low pathogenicity avian influenza viruses (LPAIVs).<sup>10,11</sup> Its continued presence is consistent with sustained regional spread. In contrast, the N.1 genotype clusters with recent North American B3.2 viruses but contains a PB2 segment derived from South American low pathogenicity avian influenza viruses. This suggests a separate, more recent introduction of A(H5N1) viruses to South America, followed by reassortment with locally circulating viruses.<sup>12</sup>

In the Antarctic peninsula and sub-Antarctic islands, A(H5N1) clade 2.3.4.4b viruses have been repeatedly detected in the region, including in sea birds such as skuas and penguins, following their introduction during the 2023–2024 austral summer.<sup>13</sup> Detections in wild birds and mammals in the region have continued through 2025–2026. This includes outbreaks in additional sub-Antarctic territories, such as Heard Island, where A(H5N1) was detected in Antarctic fur seals, gentoo penguins and southern elephant seals.<sup>14,15</sup> This follows initial detections in southern elephant seals on an earlier voyage in October 2025. There was no further evidence of ongoing mass mortality detected on this second voyage in January 2026. Further sequencing and phylogenetic analysis are being undertaken.

The extensive circulation of clade 2.3.4.4b A(H5) viruses in wild and domestic bird populations has resulted in multiple spillover events into wild terrestrial mammals, both carnivorous and omnivorous, wild marine mammals, and domestic cats and dogs.<sup>16</sup> Amino acid changes potentially associated with increased virulence, transmission, or adaptation to mammalian hosts have been sporadically identified.<sup>17,18,19</sup>

Since 2024 and as of 1 March 2026, 1088 dairy herds in 19 states of the United States of America have tested positive for A(H5N1). Since the last assessment of 28 July 2025, 14 additional A(H5N1) detections have been reported in the country, with the latest detection confirmed in December 2025 in Wisconsin.<sup>20</sup> Analyses of virus sequence data suggest that there have been at least four independent spillovers of A(H5N1) into dairy cattle with the most recent occurring in December 2025.<sup>21</sup>

In January 2026, Netherlands (Kingdom of the) reported the detection of A(H5N1) HPAI antibodies in the milk of a dairy cow at a dairy farm in Friesland Province, following the investigation of a cat living on that dairy farm that died from an A(H5N1) infection.<sup>22</sup> The virus detected in the cat belonged to clade 2.3.4.4b genotype EA-2024.DI2.1—which is distinct from the B3.13 and D1.1 genotypes detected in dairy cattle in the United States of America. No evidence of active infection was found in

the herd, but antibodies were later detected in four additional cows on the same farm, therefore, they do not constitute a case according to the WOAHA case definition.

Mammalian detections of A(H5N5) clade 2.3.4.4b viruses have also been reported in recent years, particularly those belonging to the A6 genotype. Since 2023, detections have been reported in terrestrial carnivora (northern racoon, striped skunk, red fox, Eurasian lynx, Eurasian Otter, American mink, Arctic fox and domestic cats) across North America and Europe and in marine mammals.

For the latest information on avian influenza situation in animals worldwide, see the FAO [Global Avian Influenza Viruses with Zoonotic Potential situation update](#) and the [WOAHA situation reports on HPAI](#), as well as [WOAHA's World Animal Health Information System](#).

### **Detections in humans**

Since the last joint assessment of July 2025 and as of 1 March 2026, nine additional human cases of A(H5N1) virus infections, and single cases of A(H5), A(H5N2), A(H5N5) virus infections have been detected (based on date of reporting) in Bangladesh, Mexico and the United States of America. Eight A(H5N1) cases were detected in Cambodia, and one was detected in Bangladesh. All cases reported direct or indirect exposure to domestic birds or contaminated environments. No human-to-human transmission was suspected associated with these confirmed cases. The viruses from two cases in Bangladesh belong to clade 2.3.2.1a viruses, viruses from six of the cases from Cambodia belong to clade 2.3.2.1e, and viruses from the cases in Mexico and the United States of America belong to clade 2.3.4.4b.

### **Virus characteristics**

Routine monitoring and screening of viral sequences from birds have rarely identified markers of mammalian adaptation in A(H5) viruses, and when detected, these have primarily involved the polymerase proteins. Such mutations have been observed more frequently in viruses isolated from mammals. The PB2 D701N amino acid mutation has been identified in genotype D1.1 viruses detected in poultry (including chickens and turkeys), wild birds, cats, dairy cattle and wild mammals such as red foxes.<sup>23</sup> The PB2 E627K mutation has been detected in some B3.13 viruses identified in dairy cattle and in clade 2.3.2.1 and 2.3.4.4 A(H5) viruses detected in poultry, cats and wild birds across multiple regions.

Some genetic markers in A(H5N1) virus sequences from human cases have been linked to potentially lower lab-based susceptibility to common antivirals like oseltamivir or baloxavir marboxil; the clinical significance of some of these markers remains uncertain.<sup>24</sup>

Experimental studies with A(H5N1) clade 2.3.4.4b viruses have generally not demonstrated efficient transmission via respiratory droplets.<sup>25,26,27,28,29,30,31</sup> Ferret studies conducted by the US CDC using a D1.1 A(H5N1) virus (A/Washington/239/2024) did not show respiratory droplet transmission.<sup>32</sup> Overall, currently circulating A(H5N1) viruses would require additional genetic changes to acquire efficient human-to-human transmission via respiratory droplets, consistent with the current low public health risk.

Based on limited seroprevalence information available on A(H5) viruses, human population immunity against the HA of A(H5) viruses is expected to be minimal; human population immunity targeting the N1 neuraminidase is found to be present although the impact of this immunity is yet to be understood.<sup>33</sup>

### **Candidate vaccine viruses (CVV)**

The WHO Global Influenza Surveillance and Response System (GISRS), in collaboration with animal health partners (FAO, WOA, OFFLU (Joint WOA-FAO network of expertise on animal influenza)), continue to evaluate candidate vaccine viruses for pandemic preparedness purposes both bi-annually and on an *ad hoc* basis. Regular genetic and antigenic characterization of contemporary zoonotic influenza viruses are published [here](#) with the most recent update on A(H5) CVVs published in February 2026 following the WHO Consultation on the Composition of Influenza Virus Vaccines for Use in the 2026-2027 Northern Hemisphere Influenza Season.

### **Assessment of current public health risk posed by influenza A(H5N1) viruses<sup>34</sup>**

Despite continued detections of A(H5) viruses in animals and ongoing human exposure at the human-animal-environment interface, relatively few human infections have been reported to date. Since the beginning of 2021, the vast majority of reported human A(H5) infections have been associated with direct or indirect exposure to infected animals such as milking cows on an infected dairy farm or participating in mass culling and disposal events at poultry farms, or contaminated environments, such as live poultry markets, or beaches with sick and dying wild birds and marine mammals.<sup>35,36</sup> Illness severity has ranged from mild to fatal. To date, no human-to-human transmission has been identified through epidemiologic, virologic and serologic investigations, although investigations for some of cases are ongoing. Current evidence indicates that these viruses remain avian-adapted, without established mammalian adaptive mutations or the capacity for sustained human-to-human transmission.

Based on currently available information, FAO/WHO/WOA assess the global public health risk posed by currently circulating influenza A(H5) viruses as low and unchanged from the [previous risk assessment](#), while the risk of infection for occupationally or frequently exposed persons remains low to moderate depending on local epidemiological conditions and mitigation measures in place. However, as influenza viruses are constantly evolving and spreading in animal populations, zoonotic influenza risk assessments require continuous review and may change rapidly.

WHO, together with FAO and WOA, continues to evaluate A(H5) viruses closely and will re-assess the risk associated with the currently circulating A(H5) viruses as more information becomes available. Further antigenic characterization of A(H5) viruses, including in relation to the existing CVVs, and development of specific reagents are being prioritized at the WHO Collaborating Centres and Essential Regulatory Laboratories of GISRS in collaboration with public health, animal health, and veterinary sector colleagues.

### **Recommended actions**

It is recommended that Member States and national authorities:

- increase surveillance and vigilance, and assess the risk in human populations, especially amongst occupationally exposed persons, for the possibility of zoonotic infections,

particularly through National Influenza Centres (NICs) and other influenza laboratories associated with GISRS, using such methods as active case finding and molecular and serologic methods;

- reduce the risk among occupationally exposed persons by reducing environmental exposures and providing adequate and appropriate personal protective equipment; and
- conduct epidemiological investigations including case finding around suspected and confirmed human cases to determine if there are additional cases or indications of human-to-human transmission.

Under the International Health Regulations (IHR) (2005),<sup>37</sup> States Parties are required to notify WHO within 24 hours of any laboratory-confirmed case of human influenza caused by a new subtype according to the WHO case definition.<sup>38</sup> WHO has published the case definition for human infections with avian influenza A(H5) virus requiring notification under IHR (2005).<sup>39</sup>

Avian influenza is a WOAHL-listed disease. Based on [Chapter 10.4<sup>40</sup> of the Terrestrial Animal Health Code, three categories of avian influenza](#) should be notified to WOAHL by national Veterinary Authorities through WAHIS. It includes infection with HPAI in poultry<sup>ii</sup>, infection of birds other than poultry including wild birds, and infection of domestic and captive wild birds with low pathogenicity avian influenza (LPAI) viruses having proven natural transmission to humans associated with severe consequences.

Member States and national authorities are also recommended to:

- conduct joint epidemiological investigations in and around suspected and confirmed outbreak areas in animals to determine the extent of spillover;
- increase surveillance, including joint/collaborative genomic surveillance, and sharing surveillance data applying One Health principles;
- timely reporting efforts for the early detection of A(H5) influenza viruses in domestic birds, wild birds and wild mammals<sup>41</sup>;
- include infection with an A(H5) influenza virus as a differential diagnosis, in non-avian species, including cattle, swine and other livestock and farmed domestic and wild animal populations, with high likelihood of exposure to A(H5) viruses;
- implement preventive and early response measures to break the chain of infection among domestic animals (for example, poultry and dairy cattle), including considering the use of vaccination to reduce circulation in poultry as per national policies and according to guidance provided by animal health organizations<sup>42,43</sup>;
- promptly report high pathogenicity avian influenza (HPAI) events in all animal species, including cattle (according to the WOAHL case definition<sup>44</sup>) and other domestic and wild mammals, to WOAHL and other international organizations such as FAO;

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<sup>ii</sup> All birds reared or kept in captivity for the production of any commercial animal products or for breeding for this purpose, fighting cocks used for any purpose, and all birds used for restocking supplies of game or for breeding for this purpose, until they are released from captivity. Birds that are kept in a single household, the products of which are used within the same household exclusively, are not considered poultry, provided that they have no direct or indirect contact with poultry or poultry facilities. Birds that are kept in captivity for other reasons, including those that are kept for shows, racing, exhibitions, zoological collections and competitions, and for breeding or selling for these purposes, as well as pet birds, are not considered poultry, provided that they have no direct or indirect contact with poultry or poultry facilities.

- conduct genetic sequencing and share genetic sequences of influenza viruses and associated metadata in publicly available databases in a timely manner;
- protect animals by mitigating the risk of introduction and spread of the disease through implementation and/or strengthening biosecurity in livestock holdings/premises and along the value chain;
- protect persons by employing good production and hygiene practices when handling animals and animal products; and
- protect persons in contact with suspected/infected animals by providing appropriate personal protective equipment and communicating and educating on the importance and proper use of personal protective equipment and providing information and access to testing.

Additional sets of recommendations related to avian influenza viruses with zoonotic potential can be found here:

- [FAO and WOAHA Global strategy for the prevention and control of high pathogenicity avian influenza \(2024–2033\)](#)
- [Recommendations from the FAO Global Dialogue - Tackling high pathogenicity avian influenza together. Foz do Iguaçu, Brazil – 11 September 2025](#)
- [FAO recommendations for Global Avian Influenza Viruses with Zoonotic Potential](#)
- [FAO Recommendations for the surveillance of influenza A\(H5N1\) in cattle. With broader application to other farmed mammals](#)
- [WOAHA Surveillance of High Pathogenicity Avian Influenza for Smallholder Poultry Systems in Resource-Limited Settings](#)
- [WHO Practical interim guidance to reduce the risk of infection in people exposed to avian influenza viruses](#)
- [WHO Surveillance for human infections with avian influenza A\(H5\) viruses: objectives, case definitions, testing and reporting](#)
- [WHO Considerations for the use of human A\(H5\) influenza vaccines during non-pandemic period](#)
- [WHO guidance on the use of licensed human influenza A\(H5\) vaccines for the inter-pandemic and emergence periods](#)

Additional studies/surveillance, applying One Health principles are warranted, which could provide information to enhance confidence in the risk assessment. These may include serological studies in high-risk animal populations, in high-risk human populations, and epidemiological investigations.

Anyone who may have been exposed to infected or potentially infected animals or contaminated environments should be advised to promptly seek health care if they feel unwell, and to inform their health care provider of their possible exposure. Following prompt testing, early and appropriate clinical management should be initiated, and precautionary measures put in place to assess and prevent potential further spread among humans and animals.

Clinicians should also be alerted to potential zoonotic infection in patients with an exposure history to birds or animals especially in areas where A(H5) viruses are known or suspected to be circulating in animals but also in areas where surveillance in animals may be limited.

Routine epidemiologic and virologic surveillance for influenza should be conducted ideally year-round using a standard case definition in health care facilities according to WHO guidance.<sup>45</sup>

Timely sharing of information and sequence data from both the human and animal health sectors from all regions should continue to be strongly recommended and is critical for rapid and robust joint risk assessment. The rapid sharing of virus materials with WHO Collaborating Centres of GISRS continues to be essential to conduct a thorough risk assessment and develop or adjust targeted response measures. The Tool for Influenza Pandemic Risk Assessment (TIPRA) provides an in-depth assessment of risk associated with some zoonotic influenza viruses – notably the likelihood of the virus gaining human-to-human transmissibility, and the impact should the virus gain such transmissibility. TIPRA maps relative risk amongst viruses assessed using multiple elements.<sup>46</sup> Data pertaining to the risk elements within TIPRA should be generated and shared with WHO.

Efforts to reduce human exposure to birds, livestock, and other mammals infected with or potentially infected with avian and other animal influenza viruses should be implemented and enhanced to minimize the risk of zoonotic infections. Individuals with activities that involve exposure to infected animals and/or contaminated environments are at higher risk and should take necessary precautions to prevent infection.

Those who are exposed to potentially infected animals should have access to, be trained in their use under different environmental conditions, and wear personal protective equipment including eye protection.<sup>47</sup> If they develop respiratory symptoms or conjunctivitis, they should be rapidly tested, and precautionary infection control measures should be put in place to prevent potential further spread among humans and to animals. For detailed guidance on treatment, refer to relevant global and national guidance.<sup>48</sup>

Some manufacturers have initiated production of an A(H5) human vaccine that matches current circulating strains. Updated WHO guidance on the use of licensed human influenza A(H5) vaccines for the interpandemic and emergence periods were published in December 2025.<sup>49</sup>

FAO, WHO and WOAHA advise consuming pasteurized milk, instead of raw/unpasteurized milk. Due to the potential health risks from many dangerous zoonotic pathogens, raw/unpasteurized milk consumption should be avoided.<sup>50</sup> If pasteurized milk is not available, heating raw milk until it boils makes it safer for consumption.<sup>51</sup>

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