



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

Assessment based on data as of 1 July 2025

28 July 2025

Key points

At the present time, based on available information, FAO-WHO-WOAH assess the global public health risk of influenza A(H5) viruses to be low, while the risk of infection for occupationally or frequently exposed (e.g., with backyard poultry) persons is low to moderate depending on the risk mitigation and hygiene measures in place and the local avian influenza epidemiological situation. Transmission between animals continues to occur and, to date, a growing yet still limited number of human infections are being reported. Although additional human infections associated with exposure to infected animals or contaminated environments are expected to occur, the overall public health impact of such infections at a global level, at the present time, is considered minor. The assessment could change if and when additional epidemiological or virological information becomes available.

This risk assessment from FAO, WHO and WOAH updates the assessment of the risk of zoonotic transmission (for example, animal to human) considering additional information made available since the previous [assessment of 17 April 2025](#). This update is limited to the inclusion of additional information being made available globally. Due to the potential risk to human health and the far-reaching implications of the disease on the health of wild birds, poultry, livestock and other animal populations, timely notification to global authorities and the use of a One Health approach are essential to tackle avian influenza effectively, to monitor and characterize virus circulation, to prevent transmission within species and to new species to reduce spread among animals, and to prevent human infections from exposure to animals.

Infections in animals

To date, H5 avian influenza viruses have been detected in birds and/or mammals across all continents except Oceania. The predominant H5 virus clades currently circulating worldwide include clades 2.3.2.1 and 2.3.4.4.

Between 1 March and 1 July 2025, an additional 807 A(H5N1) outbreaks in animals (including bird and mammal species) have been reported to WOAH. Of these, 268 outbreaks occurred in poultry (of any farming system), 389 outbreaks in wild bird and 92 outbreaks occurred in mammalian species. In Cambodia, 9 out of 14 outbreaks in poultry occurred in the vicinity of reported human cases.

H5 clade 2.3.2.1 viruses

Since 1 March 2025, clade 2.3.2.1a and 2.3.2.1e (previously classified as a 2.3.2.1c¹) viruses have been detected in poultry in Bangladesh and Cambodia, respectively. Influenza A(H5N1) infections in felids were reported in January 2025 in a wildlife rescue centre in Maharashtra State, India, causing

the death of one leopard and three tigers.² Influenza A(H5N1) clade 2.3.2.1a infections were reported in domestic cats and in samples from a live bird market in January 2025 in Madhya Pradesh, India.³ The viruses were closely related to A/Victoria/149/2024, a sample identified in a traveller from India to Australia in 2024, which was characterized as a previously unreported reassortant virus consisting of clade 2.3.2.1a, 2.3.4.4b, and wild bird low pathogenicity avian influenza gene segments.⁴

In April 2025, influenza A(H5N1) infections were reported in two captive Serval cats (*Leptailurus serval*) in Dhaka Division, Bangladesh.⁵

Influenza A(H5N1) outbreaks observed in captive felines in Thailand during 2003-2004 were characterized by severe pneumonia and high mortality and have been associated with the feeding of infected poultry and likely tiger-to-tiger transmission.^{6,7}

H5 clade 2.3.4.4b viruses

Detections of A(H5) in mammals and wild and domestic birds continue to be reported in many countries worldwide. Clade 2.3.4.4b A(H5) viruses are circulating in wild and domestic birds, have been involved in multiple spillover events affecting wild carnivorous and marine mammals as well as domestic cats and dogs. Clade 2.3.4.4b virus infections reported in mammals in the Americas, Asia and Europe have resulted in severe clinical presentation (e.g., pneumonia, myocardial necrosis), with neurological signs (e.g., meningoencephalitis) in some species.^{8, 9} Amino acid changes potentially associated with increased virulence, transmission, or adaptation to mammalian hosts have been sporadically identified.^{10,11}

In March 2024, a clade 2.3.4.4b influenza A(H5N1) virus of the B3.13 genotype was detected in unpasteurized milk samples and oropharyngeal swabs from dairy cattle for the first time in the United States of America (USA).^{12,13} Since then, influenza A(H5N1) virus detections have continued to be reported through the testing of dairy cattle and bulk milk samples.¹⁴

Analyses of virus sequence data from infected dairy cattle in the USA indicated that the detections in dairy herds until February 2025 were linked to a single wild bird-to-dairy cow transmission event of a B3.13 genotype clade 2.3.4.4b A(H5N1) virus that occurred in late 2023 or early 2024.¹⁵ During January-February 2025, the United States Department of Agriculture (USDA) Animal and Plant Health Inspection Service (APHIS) National Veterinary Services Laboratories (NVSL) confirmed the detection of a genotype D1.1 H5N1 clade 2.3.4.4b virus in dairy cattle in the states of Nevada and Arizona, representing two additional separate spillover events from birds to cattle.^{16,17} The exact mode of the virus introductions into dairy cattle remains unclear.¹⁸ The genotype D1.1 virus has been the most frequently detected H5N1 genotype across North America in 2025 and has affected wild birds, poultry and mammals, including wild and domestic felids and a marine mammal. Presently, to our knowledge, viruses from the clade 2.3.4.4b A(H5N1) B3.13 and D1.1 genotypes have not been detected outside of North America in field conditions.

Between March 2024 and 1 July 2025, 1074 dairy cattle herds in 17 states of the USA have tested positive for A(H5N1). Since the last joint assessment of 17 April 2025, the number of H5N1 detections in dairy herds has significantly decreased despite a surge in the State of Idaho during the

month of April.¹⁹ The exact routes of transmission between dairy cattle, and the roles of viremia and protective immunity remain unclear. While virus shedding in milk seems to be consistently linked with clinical disease, viral RNA has also been found in respiratory and urine samples intermittently and earlier in infection. Also, while transmission to new herds has been linked with movement of lactating cows, in multiple instances herds without a link to recent movement of lactating cattle have been affected. Some results indicate seroconversion in non-lactating cattle.²⁰ Experimental intra-mammary infection and re-infection of lactating cows with an A(H5N1) B3.13 virus indicated that while the primary inoculation led to mastitis and viral shedding in milk, secondary inoculation in an unaffected quarter, following resolution of infection from the primary inoculation, resulted in neither clinical manifestations nor virus shedding in milk.²¹ Further studies are needed to understand the continued transmission of A(H5N1) in dairy cattle.

In 2025, over 70 confirmed cases of A(H5) infection were reported in domestic cats in the USA across 19 states. Many cases were presumably linked to raw food diets, exposure to dairy farms, or they occurred in indoor-only cats with unknown exposure routes. Infections frequently resulted in severe respiratory and neurological illness, with high mortality. Detections in other mammals continued to be reported as well.²²

On 11 February 2025, an outbreak in a mixed backyard flock (chickens, ducks and turkeys) in Chaco province, Argentina was reported to the Servicio Nacional de Sanidad y Calidad Agroalimentaria (SENASA). The SENASA reference laboratory deposited the sequences in GISAID database (EPI_ISL_19752381 and EPI_ISL_19823059–68). The phylogenies showed that the A(H5N1) viruses from Argentina collected in 2025 are triple reassortants; the genome resembles that of North American genotypes B3.6 and B3.13, but with the Eurasian PA segment replaced by one from South American low pathogenicity avian influenza viruses.²³

On 4th March 2025, A(H5N1) virus infection was confirmed in domestic cats on a poultry farm in Belgium. The cats showed severe disease and were euthanized. They were likely infected by consuming contaminated eggs or drinking infected water, although the precise transmission route remains unconfirmed.²⁴

On 24 March 2025, the Department for Environment, Food & Rural Affairs (DEFRA) of the United Kingdom reported their first detection of influenza A(H5N1) clade 2.3.4.4b virus in a milk sample from a single sheep in Yorkshire. The case was identified on a premises where high pathogenicity avian influenza (HPAI) viruses had been confirmed in domestic birds in February 2025. This H5N1 virus is different from the ones being detected in dairy cattle in the US.²⁵ A(H5)-specific antibodies were also detected in multiple samples from the sheep who lived in close proximity to the infected poultry and on a premises likely heavily contaminated with the virus.²⁶

On 12 May (confirmed on 15 May) 2025, A(H5N1) clade 2.3.4.4b viruses were detected on a commercial breeder farm in Montenegro, Rio Grande do Sul, Brazil. Over 17,000 birds on the premises either died or were culled. Subsequently, several suspected cases were reported, and H5 detections in wild birds were confirmed in several states.

In May 2025, A(H5N1) clade 2.3.4.4b viruses were detected in harbour seals and sea otters in Hokkaido, Japan, during investigations of their mortality. The viral sequences, including the hemagglutinin gene, were very similar or identical to clade 2.3.4.4b viruses detected in wild birds in the region, suggesting likely spillover from avian sources.

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 [WOAH situation reports on HPAI](#), as well as [WOAH's World Animal Health Information System](#).

Detections in humans

Since the last joint assessment of April 2025 and as of 1 July 2025, an additional 16 human cases of infection with A(H5N1) viruses have been detected. Of these, nine were detected in Cambodia, two were detected in Bangladesh and India, and single cases were detected in China, Mexico and Viet Nam. Of the nine cases detected in Cambodia, four died. The cases detected in India and Mexico were also fatal. All but two cases reported direct or indirect exposure to domestic birds. The source of infection of the case in Mexico was determined as likely indirect exposure to either domestic or wild birds and the exposure information for one case in India was not available. No human-to-human transmission was suspected associated with these confirmed cases. The viruses from the case in India and from both cases in Bangladesh belong to HA clade 2.3.2.1a viruses. Viruses from all the cases from Cambodia belong to clade 2.3.2.1e viruses. The viruses from the cases in China and Mexico belong to clade 2.3.4.4b viruses.

Virus characteristics

Regular monitoring and screening of viral sequences from birds has rarely found markers of mammalian adaptation in A(H5) viruses. Those that have been detected are mainly in the polymerase proteins of the virus. Sporadic mutations in polymerase proteins have been observed more frequently in viruses from mammals. Additional studies on A(H5N1) genotype B3.13 viruses indicate no differences in receptor binding (retaining a preference for binding to avian-like sialic acid receptors).²⁷ Some of the D1.1 genotype viruses detected in dairy cattle have the amino acid mutation D701N in the PB2 protein, which has been associated with increased polymerase activity in mammalian cells. As of 1 March 2025, this mutation has neither been observed in D1.1 viruses detected in wild birds nor in poultry. The virus from the patient in Wyoming infected with A(H5N1) clade 2.3.4.4b genotype D1.1 had the E627K mutation in the PB2 protein which is associated with more efficient virus replication in mammalian cells.²⁸ This change has not been observed in any D1.1 viruses which have been detected in dairy cattle, but the E627K mutation has been found in some B3.13 viruses detected in dairy cows.

Available virus sequences from human cases have shown some genetic markers that may reduce susceptibility to neuraminidase inhibitors (antiviral medicines such as oseltamivir) or endonuclease inhibitors (such as baloxavir marboxil). While these changes may reduce antiviral susceptibility in laboratory testing, the clinical impact of these genetic changes requires further studies.²⁹

Experimental studies with A(H5N1) clade 2.3.4.4b viruses, including a B3.13 virus from the human case in Texas and a human case from Michigan, have shown variable transmission between ferrets

by direct contact, but no or inefficient transmission via respiratory droplets in most studies.^{30,31,32,33,34,35,36} An unpublished study in ferrets done by the US CDC with a D1.1 A(H5N1) virus (A/Washington/239/2024) did not show transmission via respiratory droplets.³⁷

Currently circulating A(H5N1) viruses would need further genetic changes to gain the ability to spread efficiently among humans via respiratory droplets, consistent with the current level of risk to public health, which is low.

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.³⁸ Experimental studies suggest prior A(H1N1) immunity reduced virus replication and disease severity of bovine-derived B3.13 genotype A(H5N1) virus in ferrets and that ferrets with this pre-existing immunity expressed A(H5N1) cross-reacting antibodies to the neuraminidase protein.³⁹ However, the effectiveness of quadrivalent seasonal influenza vaccine (QIV) against influenza A(H5N1) virus remains a speculation, as a recent study observed no cross-neutralisation of H5N1 viruses by sera from patients vaccinated against seasonal influenza with QIV.⁴⁰

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) and others), 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 2025 following the WHO Consultation on the Composition of Influenza Virus Vaccines for Use in the 2025-2026 Northern Hemisphere Influenza Season.

The majority of circulating clade 2.3.4.4b viruses reacted well to at least one of the post-infection ferret antisera raised against the existing CVVs. The majority of the clade 2.3.2.1e viruses characterized antigenically reacted well to ferret antisera raised against the existing and CVV proposed in September 2024. Clade 2.3.2.1a viruses detected recently in poultry and felines in India were not characterized antigenically but had HA genes similar to that of the A(H5N1) virus detected in a traveller returning to Australia from India. This virus reacted poorly with ferret antisera raised against available CVVs, thus a new clade **2.3.2.1a** CVV was proposed. A new clade **2.3.4.4h** CVV was also proposed due to the ongoing detections of this clade of viruses in poultry in China and continued genetic evolution leading to reduced reactivity to existing CVVs. The updated list of available zoonotic influenza candidate vaccine viruses (CVVs) which include A(H5N1) viruses and potency testing reagents is updated on the WHO [website](#).

Assessment of current public health risk posed by influenza A(H5N1) viruses⁴¹

1. What is the global public health risk of additional human cases of infection with avian influenza A(H5) viruses?

Despite the continued detections of A(H5) viruses in animals and continued human exposures to the virus at the human-animal-environment interface, there have been relatively few human infections reported to date.

Of the human cases of A(H5) detections reported since the beginning of 2021, the vast majority were infections in people associated with exposure to A(H5) viruses through direct or indirect contact with infected animals, or contaminated environments, such as live poultry markets or other premises with infected animals. Severity of illness has ranged from mild to fatal, with the majority of mild cases reported by the USA associated with exposure to infected dairy cattle. Thus far, among the cases, there has been no reported or identified human-to-human transmission through follow up epidemiologic, virologic and serologic investigations. Investigations for some of the cases continue.

Current virologic and epidemiologic information indicates that these viruses remain avian influenza viruses without established adaptation to mammalian hosts and have not acquired the capacity for sustained transmission between humans.

The epidemiological situation changed in 2024 with the spread of A(H5) virus in the USA dairy cattle population following an initial spillover event from birds to dairy cattle in 2023/24 followed by two additional spillover events identified in 2025. Persons exposed to affected dairy cattle and other infected animals may be in prolonged and close contact with potentially contaminated surfaces and animal products. As long as A(H5) viruses continue to be detected in wild and domestic birds and mammals, including dairy cattle, and related environments, including in unpasteurized/raw milk, further human cases are expected, particularly amongst exposed individuals not wearing appropriate personal protective equipment and/or in environments where mitigation measures are not in place.

Based on currently available information, FAO-WHO-WOAH assesses the global public health risk of influenza A(H5) viruses as low. Although additional human infections associated with exposure to infected animals or contaminated environments are expected to occur, they remain limited in the general population and the overall current public health impact of such infections at a global level is minor, considering the surveillance, response, mitigation and control measures in place.

However, while the risk of infection to the general public is low, among persons with exposure to infected birds or mammals or contaminated environments, the risk of infection can range from low to moderate, depending on nature of the exposure, the duration of exposure, the consistent and appropriate use of personal protective equipment, and the use of other response, mitigation and control measures particularly in environments where animals are kept.

The pandemic potential of these viruses requires enhanced vigilance, especially in animal populations where animal to animal transmission is known to occur, and close monitoring in animals and humans. It remains essential that, while farmers enhance biosecurity on their farms, governments should focus efforts on strengthening surveillance in susceptible animal populations and in persons exposed to infected animals. In addition to prevention and mitigation

efforts to reduce and/or stop animal to animal transmission and reduce environmental contamination. Furthermore, prevention efforts to stop animals to human transmission and to improve risk communication and community engagement in particular to those occupationally exposed or with backyard poultry and training in the use of personal protective equipment are key to preventing new human infection with these viruses.

2. What is the likelihood of human-to-human transmission of avian influenza A(H5) viruses?

There has been no reported human-to-human transmission of A(H5) viruses since 2007, although there may be knowledge gaps in investigations around identified human infections. In 2007 and the years prior, small clusters of A(H5) virus infections in humans were reported, including limited human to human transmission from patients to health care workers. Since then, sustained human-to-human transmission of A(H5) viruses has not been reported.⁴²

The A(H5) viruses currently detected in mammals, including in human cases, largely retain genomic and biological characteristics of avian influenza viruses and remain well-adapted to spread among birds. Except for within-host acquired amino acid mutations in polymerase proteins, there is still limited evidence for adaptation to mammals and humans even when transmission in non-human mammals has been suspected.⁴³ No changes in receptor binding tropism have been consistently observed that would increase binding to receptors in the human upper respiratory tract which is one of several adaptations required to increase the probability of transmission to and among people. In addition, available preliminary sero-studies and sero-investigations have not identified human-to-human transmission of A(H5N1) in the USA. Therefore, sustained human-to-human transmission of the currently circulating A(H5) viruses is considered unlikely without further genetic changes in the virus. This is actively being assessed by agencies in affected Member States, FAO, WHO, WOAH and partners.

WHO, together with FAO and WOAH, 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.

Confidence level of the assessment

The overall confidence in the risk assessment is considered medium. The information used is derived from reports from national animal and human health authorities. There may be biases in surveillance, testing and reporting. Although the results and conclusions from peer-reviewed publications, pre-print publications and unpublished data informed this risk assessment, no systematic literature review was undertaken. Critical knowledge gaps remain in the understanding of the epidemiology.

Recommended actions

It is recommended that Member States and national authorities:

- increase surveillance and vigilance, 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;
- assess and reduce the risk among occupationally exposed persons using methods such as active case finding and molecular and serologic methods, reducing environmental exposures, providing adequate and appropriate personal protective equipment;
- conduct active case finding around suspected and confirmed human cases to determine if there are additional cases or indications of human-to-human transmission; and
- work with national agencies and partners to better understand the exposure to and risk from raw/unpasteurized milk and milk products.

Under the International Health Regulations (IHR) (2005),⁴⁴ 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.⁴⁵ WHO has published the case definition for human infections with avian influenza A(H5) virus requiring notification under IHR (2005).⁴⁶

Member States and national authorities are also recommended to:

- increase surveillance and timely reporting efforts for the early detection of A(H5) influenza viruses in domestic birds, wild birds and mammals⁴⁷;
- 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^{48,49};
- promptly report high pathogenicity avian influenza (HPAI) events in all animal species, including cattle (according to the WOAHP case definition⁵⁰) and other domestic and wild mammals, to WOAHP and other international organizations such as FAO;
- conduct genetic sequencing and share genetic sequences of influenza viruses and associated metadata in publicly available databases;
- 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:

- [Global strategy for the prevention and control of high pathogenicity avian influenza \(2024–2033\)](#)
- [WOAH Statement on High Pathogenicity Avian Influenza in Cattle](#), updated 6 December 2024
- FAO [Recommendations for the surveillance of influenza A\(H5N1\) in cattle with broader application to other farmed mammals](#), published 27 November 2024
- FAO alert on avian influenza: Risk of upsurge and regional spread through wild birds in Latin America and the Caribbean in [English](#) and [Spanish](#)
- [FAO recommendations for Global Avian Influenza Viruses with Zoonotic Potential](#)
- FAO EMPRES Watch entitled '[A\(H5N1\) influenza in dairy cattle in the United States of America](#)'
- [WHO Practical interim guidance to reduce the risk of infection in people exposed to avian influenza viruses](#)
- [Surveillance for human infections with avian influenza A\(H5\) viruses: objectives, case definitions, testing and reporting](#)
- [Considerations for the use of human A\(H5\) influenza vaccines during non-pandemic period](#)
- CDC [Information for Workers Exposed to H5N1 Bird Flu](#)

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(H5N1) 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 healthcare facilities according to WHO guidance.⁵¹

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.⁵² 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.⁵³

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.⁵⁴ 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.⁵⁵

Some manufacturers have initiated production of an A(H5) human vaccine that matches current circulating strains. Although a few countries are procuring vaccine to vaccinate occupationally exposed persons, this is not currently being recommended as a global strategy considering the limited number of human infections with A(H5N1) 2.3.4.4b viruses.

Investigations are ongoing to understand the risk to humans from consuming raw/unpasteurized milk contaminated with A(H5N1) virus. FAO, WHO and WOAH 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.⁵⁶ If pasteurized milk is not available, heating raw milk until it boils makes it safer for consumption.⁵⁷

More information will be available as investigations are actively ongoing in the USA and elsewhere. WHO and GISRS, jointly with FAO, WOAH and OFFLU are working closely together to continuously assess the avian influenza situation. This includes increased surveillance and testing to monitor the evolution and geographic spread of avian influenza viruses, including A(H5N1) viruses, to provide timely and updated joint risk assessments.

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