

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 March 2025

17 April 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 exposed persons is low to moderate depending on the risk mitigation 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 from 20 December 2024](#). 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, the use of a One Health approach is 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

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 USA.^{1,2} Since then, influenza A(H5N1) virus detections have continued to be reported through the testing of dairy cattle and bulk milk samples.³

Until January 2025, analyses of virus sequence data from infected dairy cattle in the USA indicated that the detections in dairy herds since January 2024 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 2024.⁴ On 31 January 2025, the USDA APHIS National Veterinary Services Laboratories (NVSL) confirmed the first detection of clade 2.3.4.4b A(H5N1) virus of the D1.1 genotype in dairy cattle in the state of Nevada, indicating a second bird-to-dairy cow transmission event.^{5, 6} Shortly after, on 13 February 2025, clade 2.3.4.4b A(H5N1) virus, also of the D1.1 genotype, was detected in dairy cattle in the state of Arizona. Phylogenetic analysis indicated that this was another, distinct transmission event marking the third bird-to-cow transmission event reported.⁷ The genotype D1.1 is currently

the most frequently detected genotype across North America and has affected wild birds, poultry and been detected in mammals, including wild and domestic felids and a marine mammal. Presently, to our knowledge, viruses from clade 2.3.4.4b A(H5N1) and genotypes B3.13 and D1.1 have not been detected outside of North America in field conditions.

As of 1 March 2025, 979 dairy cattle herds in 15 states of the USA have tested positive for A(H5N1), with a significant surge of confirmed outbreaks in dairy cattle in the State of California reaching 383 herds since the first detection in California in late August 2024.⁸

The average incidence of clinical disease on affected farms ranges between 10 and 20% with the predominant clinical signs including decreased milk production with abnormal milk, decreased feed intake, fever, dehydration, altered faecal consistency, respiratory distress and abortions.^{9,10,11} Studies have shown that commercial milk pasteurization inactivates the virus making it safe for human consumption.^{12,13,14}

The routes and modes of transmission between cattle, the duration of virus shedding as well as the infectious period remain under investigation. A preliminary modelling study indicates the duration of infectiousness could range from 2.8 to 13.1 days with a median of 6.2 days.¹⁵ Transmission between farms and states in the USA has been linked to cattle movements or possibly through feed and manure handling equipment, or on clothing or footwear of people working or visiting farms.¹⁶ While there have been advancements in our understanding, transmission dynamics remain poorly understood.¹⁷

Experimental studies of lactating dairy cattle and non-lactating heifers have been published and have provided some insight into receptor distribution, viral replication kinetics, and infection routes (see the previous [assessment from 20 December 2024](#)).

No further detections in swine have been reported in the USA since October 2024, which marked the first detection of H5N1 virus in swine in the USA.¹⁸ A preliminary experimental study in swine indicated limited replication of a bovine-derived B3.13 genotype A(H5N1) virus and no transmission via direct contact from infected pigs to naïve pigs. Experimental infections studies conducted in pigs with other genotype A(H5N1) clade 2.3.4.4b viruses showed that mammalian-derived A(H5N1) virus strains demonstrated higher potential for replication, pathogenicity, and transmissibility as compared to avian-derived A(H5N1) virus strains.^{19,20} This warrants vigilance and testing for avian influenza virus in pigs due to the genetic diversity and extent of avian influenza virus circulation as pigs act as "mixing vessels" for genetic reassortment of avian and human influenza viruses, potentially creating new strains with pandemic potential.

Detections of A(H5) in mammals, other than dairy cattle, and wild and domestic birds continue to be reported in the USA and in other 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.^{21, 22} Amino acid changes potentially associated with increased virulence, transmission, or adaptation to mammalian hosts have been sporadically identified.^{23,24}

Since 2022, at least 88 cases of A(H5N1) infections in domestic cats have been reported in the USA. Some of these domestic cat infections have been linked to the consumption of raw, unpasteurized milk from affected dairy farms as well as contaminated raw pet food.^{25,26,27} Ingestion of wild birds while hunting or scavenging on carcasses is another possible route of infection, as observed in wild animal species (predators and scavengers). However, humans can carry the virus on contaminated clothing, equipment, or fomites and infect other animals such as cats. Similarly, cats may become infected from wild birds and could carry contaminated materials to their household, such as those originating from an infected wild bird, and expose people indirectly to the virus. Influenza A(H5N1) virus was detected in two indoor domestic cats with respiratory and neurologic illness that lived in homes of dairy workers but had no known direct exposure to influenza A(H5N1)-affected farms.²⁸

Domestic and wild felids have been reported infected with influenza A(H5) virus belonging to other clades as well. In 2024, avian influenza outbreaks were reported in captive wild felines in two zoos in southern Viet Nam. These led to the death of at least 47 tigers, three lions and a leopard, and were confirmed to be caused by clade 2.3.2.1e A(H5N1) viruses, previously classified as a 2.3.2.1c clade A(H5) viruses.^{29,30} Additional 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.³¹ Influenza A(H5N1) clade 2.3.2.1a infections were reported in domestic cats in January 2025 in Madhya Pradesh, India.³² Previous A(H5N1) outbreaks in captive felines, characterized by severe pneumonia and high mortality, have been associated with the feeding of infected poultry and likely tiger-to-tiger transmission.^{33,34}

Whilst limited cat-to-human transmission has previously been reported in the USA with A(H7N2) viruses³⁵, studies have not yet shown that the currently circulating H5N1 viruses have gained the ability to effectively transmit between humans and cats.

Other A(H5) virus clades such as 2.3.2.1e and 2.3.2.1a continue to circulate and evolve in poultry in geographically restricted regions.

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 December 2024 and as of 1 March 2025, an additional 17 human cases of infection with A(H5) viruses have been reported. Of these, 12 were reported from the USA: six in persons with exposure to A(H5N1)-infected dairy cattle in California (five) and Nevada (one), three in persons with exposure while working at or involved in depopulation of A(H5N1)-infected commercial poultry farms in Iowa, Ohio and Wisconsin, two in persons with exposure to sick and dead backyard poultry in Louisiana and Wyoming, and one in a person from California with unknown exposure at the time of reporting. Samples from three cases related to exposure to dairy

cattle in California were confirmed to be clade 2.3.4.4b A(H5N1) viruses of the genotype B3.13. Viruses from two cases with exposure to poultry in Louisiana and Wyoming were confirmed to be clade 2.3.4.4b A(H5N1) viruses of the D1.1 genotype, while one virus from the case in Nevada with exposure to dairy cattle was also of the D1.1 genotype. All but three of the detected cases in the USA have reported mild symptoms, including conjunctivitis and mild respiratory symptoms, and recovered without hospitalization. The cases detected in Wyoming and Ohio were hospitalized but have recovered while the case detected in Louisiana died.

A serological study in 115 persons in Colorado and Michigan working on dairy farms during A(H5N1) outbreaks among dairy cattle found that eight (7.0%) had serologic evidence of recent infection (seropositive, ≥ 40 antibody titres to H5 2.3.4.4b by both micro-neutralization and hemagglutination inhibition assays). These seropositive individuals reporting working with dairy cattle or in the milking parlour, and four reported being ill when A(H5) was detected among the dairy cattle.³⁶ Another serosurvey conducted in September 2024 among 150 bovine veterinary practitioners found three (2%; 95% CI = 0.7%–5.7%) survey participants with antibodies to HPAI A(H5).³⁷

Two human cases of clade 2.3.2.1e³⁸ A(H5N1) virus infection were reported from Cambodia since the last update of December 2024. Both cases were fatal and had exposure to sick or dead backyard poultry.

One detection of A(H5) was reported by the United Kingdom of Great Britain and Northern Ireland in January 2025. The detection was in a specimen from an individual recruited to a zoonotic influenza surveillance study while working at farms where birds were infected with A(H5N1) viruses. The individual had mild symptoms, and the virus was determined via whole genome sequencing to be an A(H5N1) virus belonging to the clade 2.3.4.4b of A(H5) viruses and the DI.2 genotype which was predominant in Europe in the 2024/25 winter season. This genotype is distinct from the genotypes of A(H5) 2.3.4.b detected in North America.³⁹

One case of A(H5) infection was reported in an individual in Viet Nam in November 2024. The individual had contact with sick and dead poultry and developed severe disease but recovered. Further information on the virus from this case is not available.

Virus characteristics

Regular monitoring and screening of viral sequences from birds has rarely found markers of mammalian adaptation in clade 2.3.4.4b viruses. Those that have been detected are mainly in the polymerase proteins of the virus. Sporadic events of changes in polymerase proteins have been observed more frequently detected in viruses from mammals. As of 1 March 2025, none of the virus sequences from dairy cattle in the USA have well-recognized markers in the HA gene associated with increased human receptor binding. Additional studies on some B3.13 A(H5N1) viruses indicate no differences in receptor binding, pH fusion or thermostability compared to other non-B3.13 avian A(H5N1) viruses, and that these viruses retain their avian influenza virus phenotype.⁴⁰ Some of the D1.1 viruses detected in dairy cattle have the change D701N in the PB2 protein, which has been associated with increased activity in mammalian cells. This change was also observed in the genetic sequence of the virus isolated from a patient infected with A(H5N1) clade 2.3.4.4b D1.1 genotype virus in Nevada.⁴¹ As of 1 March 2025, this change had not been observed in D1.1 viruses detected in

wild birds nor 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 efficient virus replication in people and mammals.⁴² This change has not been observed in any D1.1 viruses which have been detected in dairy cattle.

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.⁴³

Experimental studies with A(H5N1) clade 2.3.4.4b viruses, including a B3.13 virus from the human case in Texas, have shown variable transmission between ferrets by direct contact, but no or inefficient transmission via respiratory droplets in most studies.^{44,45,46,47,48,49} Ferrets infected with a non-B3.13 A(H5N1) clade 2.3.4.4b virus via the ocular route did experience severe disease and were able to transmit the virus to other ferrets via direct contact; these contact animals also developed severe disease.⁵⁰ 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.⁵¹ 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.⁵²

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](#).

Data which has not yet been peer reviewed revealed that vaccination of 39 persons with two doses of an adjuvanted inactivated A/Astrakhan/3212/2020 H5N8 virus elicited functional antibodies against European and North American A(H5N1) clade 2.3.4.4b viruses.⁵³

Assessment of current public health risk posed by influenza A(H5N1) viruses⁵⁴

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) clade 2.3.4.4b in animals and increasing 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 recent cases reported by the USA had mild illness. Thus far, among these 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 adaptations to mammalian hosts and have not acquired the capacity for sustained transmission between humans.

The epidemiological situation has changed with the ongoing spread of A(H5) virus in the USA dairy cattle population and two additional spillover events from birds to dairy cattle identified. 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 (poultry and dairy cattle), and close monitoring in animals and humans. It remains essential that, while farmers enhance biosecurity on their farms, governments focus efforts on strengthening surveillance in susceptible animal populations and in persons exposed to infected animals, to prevention and mitigation efforts to reduce and/or stop animal to animal transmission and reduce environmental contamination, to prevention efforts to stop animals to human transmission and to improve communication with at risk persons and provide occupationally exposed persons with and train in the use of personal protective equipment.

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. At the present time sustained human-to-human transmission has not been reported of A(H5) viruses.⁵⁵

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 obtained amino acid mutations in polymerase proteins, there is still limited evidence for adaptation to mammals and humans even when transmission in mammals has been suspected.⁵⁶ No changes in receptor binding tropism have been consistently observed that would increase binding to receptors in the human upper respiratory tract which would 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(H5N1) 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.

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),⁵⁷ 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.⁵⁸ WHO has published the case definition for human infections with avian influenza A(H5) virus requiring notification under IHR (2005).⁵⁹

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 mammals⁶⁰;
- 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^{61,62};
- promptly report high pathogenicity avian influenza (HPAI) events in all animal species, including cattle (according to the WOAAH case definition⁶³) and other domestic and wild mammals, to WOAAH 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;

- 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](#)
- 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.⁶⁴

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.⁶⁵ 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.⁶⁶

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.⁶⁷ 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.⁶⁸

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 WOAHA advise consuming pasteurized milk. Due to the potential health risks from many dangerous zoonotic pathogens, raw/unpasteurized milk consumption should be avoided.⁶⁹ If pasteurized milk is not available, heating raw milk until it boils makes it safer for consumption.⁷⁰

More information will be available as investigations are actively ongoing in the USA and elsewhere. WHO and GISRS, jointly with FAO, WOAHA 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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