Summary

The initial detection and subsequent spread of A(H5N1) in dairy cattle in the United States of America represents a key event in the ongoing evolution of highly pathogenic avian influenza (HPAI) viruses. On 25 March 2024, authorities in the United States of America reported the detection of A(H5N1) in lactating dairy cattle. The virus affecting dairy cattle is a reassortant virus with both Eurasian HPAI H5N1 2.3.4.4b and North American gene segments. To date, it has not been detected outside the United States of America. This detection was in the context of a global surge in HPAI cases that started in America. This detection was in the context of the ongoing evolution of highly pathogenic virus (HPAI) that causes more severe disease. Influenza viruses are constantly evolving and can infect a variety of species. Categorized into four groups (A, B, C and D), influenza viruses A have the widest host range. In animals, they are named after their dominant host species. Examples include avian influenza virus (AIV) (also known as bird flu), swine influenza virus (SIV) and equine influenza virus (EIV). They are also named based on their surface proteins, Hemagglutinin (HA), and Neuraminidase (NA), used to classify the virus into broad subtypes. While influenza viruses continually evolve through mutation (antigenic drift), they can also recombine or reassort (antigenic shift) due to their segmented genome. This process produces new subtypes (HA/NA) and genotypes (considering all eight gene segments), posing ongoing challenges to their control.

As of 11 July 2024, 145 dairy operations in twelve American states have been identified with the virus. On 1 April 2024, the same virus was detected in a farm worker in the state of Texas with presumed exposure to affected dairy cattle. This was followed by three additional cases among farm workers in the state of Michigan in May 2024, and Colorado in July 2024. Two of these cases were mild with only symptoms of conjunctivitis, while the case in Michigan developed upper respiratory tract symptoms more consistent with the typical acute respiratory illness that is associated with influenza virus infection. No additional cases in humans associated with exposure to infected cattle have been reported at the time of writing.

Clinical signs in cattle are varied and include a decline in milk production with thickened milk consistency. Affected cattle appear to recover and reduce virus shedding after 2–3 weeks. Globally, scientists are working to address the numerous gaps that currently exist in our knowledge of the disease. The spillover event’s effects on dairy cattle health and milk production are still unfolding, with variable financial impacts at both the cattle and dairy market levels.

The World Health Organization (WHO) assesses the overall public health risk posed by A(H5N1) to be low. Still, individuals who may be exposed to infected birds or livestock should take appropriate precautions (FAO, WHO and WOAH, 2024). Countries are encouraged to increase their preparedness for HPAI outbreaks and work towards early detection and rapid response to spillover events in non-avian species. In areas at increased risk of HPAI outbreaks or viral circulation, enhanced biosecurity and surveillance are needed among all susceptible animals.

Background: global situation with HPAI H5N1 2.3.4.4b

Influenza viruses are constantly evolving and can infect a variety of species. Categorized into four groups (A, B, C and D), influenza viruses A have the widest host range. In animals, they are named after their dominant host species. Examples include avian influenza virus (AIV) (also known as bird flu), swine influenza virus (SIV) and equine influenza virus (EIV). They are also named based on their surface proteins, Hemagglutinin (HA), and Neuraminidase (NA), used to classify the virus into broad subtypes. While influenza viruses continually evolve through mutation (antigenic drift), they can also recombine or reassort (antigenic shift) due to their segmented genome. This process produces new subtypes (HA/NA) and genotypes (considering all eight gene segments), posing ongoing challenges to their control.

The majority of AIVs that can be found in migratory wild birds are known as low pathogenicity avian influenza (LPAI) as they often produce little to no clinical signs in domestic species such as chickens (Lee et al., 2024). However, subtypes H5 and H7 viruses have the ability to mutate into a more pathogenic virus (HPAI) that causes more severe disease. Clinical signs with HPAI can be variable and depend on both the avian species and the virus strain. However, typically, HPAI infection results in high mortality in poultry with severe consequences to animal health, livelihoods, economies and food security (Pantin-Jackwood et al., 2023). Some AIVs also pose a potential threat to

1 The designation of high or low pathogenicity refers to an index determined in chickens only.
human health. Although human infections are rare, they can be serious or even fatal. For these reasons, HPAI is listed by the World Organization for Animal Health (WOAH) as a notifiable disease. Control of the disease is primarily through quarantine and/or culling of affected flocks, combined with movement restrictions, which pose a great strain on the poultry industry globally. At the local level, the direct and indirect impacts of HPAI can be acute, particularly among smallholder farmers in low- and middle-income countries that rely on poultry and their products for income and as a nutritional source, with potential disproportional impacts on women (Alders et al., 2013).

The current panzootic HPAI H5N1 goose/Guangdong lineage virus emerged over 25 years ago and has continually evolved, giving rise to several different H5 hemagglutinin genetic clades. This evolution has significantly expanded its host range in wild birds and its geographical distribution (Hall, Dusek and Spackman, 2015; Smith, Donis and WHO/OIE/FAO H5 Evolution Working Group, 2015; WHO/OIE/FAO H5N1 Evolution Working Group, 2008, 2014). Since 2021, clade 2.3.4.4b viruses have spread transcontinentally across Eurasia, Africa, the Americas, and Antarctica, facilitated by long-distance migratory wild bird movement. The virus has also established itself in native wild bird populations, reassorting with local low pathogenicity viruses to create new genotypes with slightly different characteristics (Fusaro et al., 2024). The expanded wild bird host range of the clade 2.3.4.4b viruses has contributed to increased spillover into poultry, as opportunities for interfaces between production poultry and infected wild birds increased (Kandeil et al., 2022). Strengthening biosecurity measures, surveillance, vaccination and compartmentalization are prevention measures taken by countries to reduce the impact of this virus. That said, outbreaks in poultry continue to be reported, with backyard, small-scale and commercial poultry sectors significantly affected in some regions (EFSA et al., 2024).

Furthermore, the typical epidemiological patterns of 2.3.4.4b viruses have changed, with unprecedented numbers of viral detections in the northern hemisphere during the summer months (instead of the usual decline), and multiple mass die-offs of wild bird species globally. In the past, wild birds primarily served as reservoirs, but these new patterns indicate a significant shift in virus transmission, pathogenicity and impact. Since 2022, there has been an upsurge in reports of different mammalian species being affected. These mammals include scavenger species, marine mammals, carnivorous domestic pets, and farmed ruminants.

**HPAI in the United States of America**

Like other parts of the world, North America has seen multiple introductions of the Eurasian HPAI (H5N1) clade 2.3.4.4b, originally through the Pacific (Alkie et al., 2022) and the North Atlantic flyways (Youk et al., 2023). The majority of H5N1 clade 2.3.4.4.4.b viruses there are derived from an introduction via the North Atlantic Flyway in late 2021, which has subsequently reassorted with North American avian influenza viruses (Caliendo et al., 2022). Since 2022, the United States Department of Agriculture (USDA) Animal and Plant Health Inspection Service (APHIS) has identified A(H5N1) detections in more than 299 individual mammals (USDA APHIS, 2024a). Figure 1 shows a timeline of the A(H5N1) detection events in animals in the United States of America since December 2021.

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**Figure 1. Timeline of A(H5N1) events in animals in the United States of America from 1 December 2021 to 11 July 2024 by type of animal. Includes data published by USDA APHIS and events reported to WOAH via the WAHIS platform and by national authorities gathered by FAO EMPRES-i**


On 25 March 2024, the USDA reported the first occurrence of the virus in American dairy cattle (USDA APHIS, 2024b). Tests indicate the virus to be HPAI H5N1 clade 2.3.4.4b, a previously minor genotype (a four gene Eurasian-North American reassortant) that had been detected only in wild birds and one mammal in the country. Following this initial detection, investigations and dairy producer reporting resulted in the identification of additional cases. As of 11 July 2024, USDA APHIS has confirmed A(H5N1) clade 2.3.4.4b on 145 dairy cattle premises in twelve American states (Colorado, Idaho, Iowa, Kansas, Michigan, Minnesota, New Mexico, North Carolina, Ohio, South Dakota, Texas, and Wyoming) (see Figure 2). Phylogenetic analysis suggests that following a single interspecies spillover event, likely in a Texas herd, the virus spread rapidly interstate through cattle movement (Nguyen et al., 2024).

Also on 25 March 2024, three sick domestic cats on an affected Texas dairy farm tested positive for A(H5N1) virus. Additional cases continue to be identified. Illness or death in cats on dairy farms may be suggestive of A(H5N1) infection. In the United States of America, A(H5N1) virus has been previously detected in domestic cats in 2022 and 2023 (Sillman et al., 2023), with their susceptibility to this subtype previously reported as well (Rabalski et al., 2023). USDA and Centers for Disease Control and Prevention (CDC) officials have issued guidance for farm workers, pet owners and veterinarians (CDC, 2024a, 2024b, 2024c).

On 1 April 2024, A(H5N1) virus was detected in a farm worker with exposure to presumed infected dairy cattle in Texas (CDC, 2024d). The genome for the human isolate had a single previously seen molecular change known to be associated with viral adaptation to mammalian hosts. There was no evidence however of onward spread among people. No markers known to be associated with influenza antiviral resistance were found.

On 24 April 2024, it was reported that A(H5N1) virus was detected in the lung tissue of a culled dairy cow from an infected herd. The cow was not showing clinical signs of influenza infection (USDA, 2024).

On 29 April 2024, a federal order was issued by USDA APHIS requiring the testing of lactating dairy cattle before interstate movement in the United States of America, as well as mandatory reporting of all positive influenza A nucleic acid detection diagnostic results (e.g. polymerase chain reaction [PCR] or genetic sequencing) in livestock. These requirements are aimed at preventing the spread and improving understanding of the epidemiologic situation (USDA, 2024).

On 22 May 2024, a second human case related to the ongoing outbreak was identified in Michigan. The individual was a worker from a dairy farm where the A(H5N1) virus had been detected in cows. Although their nasal swab tested negative, an eye swab tested positive for the influenza A(H5) virus. The patient reported only eye symptoms (CDC, 2024e).

On 30 May 2024, the CDC reported a third human case, also in Michigan. As with the previous case, the individual is a dairy farm worker with known exposure to infected cows. The patient reported upper respiratory tract symptoms, including a cough without fever and eye discomfort with watery discharge. This is the first American human case of H5 to report symptoms that are more typical of acute respiratory illness associated with influenza virus infection. None of the three cases are connected epidemiologically to each other (CDC, 2024f).

On 3 July 2024, an additional human case with mild symptoms was reported in a Colorado cattle farm worker (CDC, 2024g). A new cluster of four human cases and one with test results still pending were reported on 12 July 2024 in workers involved in poultry flock depopulation activities. Their connection to the virus affecting dairy farms is unknown at the time of writing.

Figure 2. Influenza A(H5N1) detections in cattle in the United States of America, from 25 March 2024 until 11 July 2024, with background estimated cattle density layer from GLW4 model v4 adjusted to FAOSTAT 2015


Note: For more information on Gridded Livestock of the World v4 (GLW4) see Gilbert et al., 2018.
Clinical Signs and Epidemiology

The clinical picture of affected cattle remains under investigation. Early epidemiologic investigations suggest cattle may exhibit various clinical signs including changes in milk production and appearance (Box 1).

Infections with influenza A virus in cattle in the past have been rarely reported (Brown et al., 1998; Campbell, Easterday and Webster, 1977), but the involvement of the mammary gland, as well as subclinical infection with subclinical shedding of the virus, has been previously described (Crawshaw et al., 2008; Kalthoff et al., 2008; Mitchell, Nordland and Walker, 1958; Mitchell, Walker and Bannister, 1956). In the current outbreak, affected dairy cattle have generally recovered, returning to milk production with no further clinical signs, and appear to stop shedding the virus after 2–3 weeks. Subclinical infection has also been reported (Nguyen et al., 2024). According to the case definition used by USDA APHIS in April 2024, the virus has been found in high concentration in milk secretions of infected, lactating cattle (USDA APHIS, 2024c). The virus is strongly localized to the mammary gland of infected cattle, with infection of alveolar epithelial cells. High concentrations of the virus are found in the milk (Burrough et al., 2024). The virus may infect one or more quarters of the udder. In one Texas dairy herd, the virus was detected in 29 percent of nasal swabs, but with a low virus concentration (Oguzie et al., 2024).

The incubation period has been estimated to vary between 12 and 21 days, with the variability due to multiple factors including the route of exposure, viral dose, production phase of the animal and other unknown factors (USDA APHIS, 2024c). There is some evidence that lateral transmission among cattle likely occurred, although the exact mechanism of spread remains under investigation; viral transmission through contaminated fomites or mechanical means is also being investigated, while recent evidence suggests that subclinically infected animals may play an important role in the spread (Nguyen et al., 2024). The average herd level morbidity has been reported as less than 10 percent, but it may vary (USDA APHIS, 2024d).

Evidence from viral sequencing suggests that the virus can spread from affected dairy herds to nearby poultry premises, although further investigation is required to confirm the likely routes of transmission in these instances. The frequency of cattle-to-bird transmission is also unknown. Many knowledge gaps remain around the pathogenesis and risk factors associated with A(H5N1) in dairy cattle (Box 2).

Box 1. List of clinical signs in dairy cattle infected with Influenza A(H5N1)

- Decreased milk production
- Thickened, concentrated, colostrum-like milk
- Decrease in feed consumption with a simultaneous drop in rumen motility
- Abnormal tacky or loose feces
- Lethargy
- Fever
- Dehydration


Potential impacts

Meat and milk production

Impacts of A(H5N1) virus infection on milk production are under investigation. Dairy cattle appear to recover within a few weeks (National Milk Producers Federation, 2024), though the negative impact on milk production in individual cows may vary. Dramatic reductions in milk production in dairy herds have been reported, with some herds experiencing large losses in milk production for a week or more until clinical signs subside (Texas Department of Agriculture, 2024).

In March 2024, the number of milk cows on farms in the United States of America was estimated to be 9.33 million head, spread across over 20,000 dairy operations. Milk production during February 2024 totalled 18.1 billion pounds (about 8.2 billion kg) (USDA NASS, 2024). While the impacts of infection on individual dairy producers may be severe, the current number of cases is unlikely to result in a significant impact on national milk production.

As of 11 July 2024, no beef cattle have been identified as infected with A(H5N1) virus. However, dairy cattle are an important contributor to beef production in the United States of America, with dairy and beef crossbreeds, dairy-finished steers, cull cows and finished heifers all contributing to the total supply. All animals entering slaughter in the United States must pass ante- and post-mortem inspection. Sick cattle are not permitted to enter the food chain. Based on the apparent ability of cattle to recover from infection, A(H5N1) is unlikely to significantly impact national beef supplies.

Box 2. Knowledge gaps

Knowledge gaps in A(H5N1) pathogenesis in cattle include:
- Viral virulence and transmissibility associated with viral changes;
- Animal and herd level incubation periods;
- Tissue distribution of the virus and presence/absence of viraemia;
- Duration of infectiousness;
- Time to and extent of recovery and return to milk production;
- Duration of viral shedding in milk and other routes; and
- Differential impacts of HPAI infection on cattle based on age, production phase and other variables.

Knowledge gaps in risk factors for A(H5N1) infection and subsequent spread in cattle, including:
- Routes and modes of transmission into and among dairy cattle;
- Probability of transmission associated with contaminated fomites;
- Probability of transmission via mechanical means, including milking and the use of milking equipment; and
- Frequency and risk factors associated with cattle-to-bird transmission and bird-to-cattle transmission.

Source: Authors’ own elaboration.
Global trade
Unlike the global pig meat trade which was heavily affected by the introduction of African swine fever into China in 2018, it is unlikely that the global milk trade will be affected by the avian influenza infection in dairy cattle. Considering that the total American exports of “raw milk of cattle” represent just one percent of its global trade (FAO, 2024), an impact on global raw milk prices is not expected. Pasteurization is required for any milk entering interstate commerce for human consumption in the United States of America, which exports an average of 3 million metric tonnes of pasteurized milk and milk products annually (USDA APHIS, 2024f). Since import risk management measures should be scientifically justified and in line with the WOAH International Standards to avoid implementing unjustified trade restrictions, there is currently no reason for disruptions in international trade.

However, the uncertainty about how the situation might evolve has already impacted the beef and milk Chicago Mercantile Exchange (CME) futures markets. From 22 March to 2 May, the price of June 2024 CME contracts for live cattle decreased by 3.3 percent only; however, the expected risk associated to live cattle contracts increased by 24 percent, as measured by the CME Group Volatility Index (CVOL). In contrast, the price of June 2024 contracts for milk (class III) was 12.1 percent higher (22 March to 2 May), with a clear upward trend over the preceding month.

While speculation is an important driver of futures markets, we cannot discard some impacts on the milk and beef markets in the United States of America, particularly in the short term. Trade restrictions, like those announced by Colombia on fresh or frozen beef from infected American states, and the requirement of the Canadian Food Inspection Agency (CFIA) for an addendum to export certificates certifying negative test results for influenza virus (Canadian Food Inspection Agency, 2024) contribute to the volatility of the American cattle market.

The potential impact of rumours or misinformation on both dairy producers and consumers who rely on the critical nutrients that milk provides should not be underestimated. Numerous uncertainties surrounding HPAI spillover and spill-back, prompting researchers to work diligently to disseminate timely and accurate scientific information.

Public health
On 26 April 2024, FAO, WHO and WOAH published a preliminary situation assessment on recent A(H5N1) viruses. The report notes that given the ongoing circulation of H5N1 viruses, further sporadic human cases among exposed individuals are expected, and active case finding should continue to rapidly identify any human-to-human transmission. The assessment found that “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.” However, the overall public health risk posed by A(H5N1) is considered low, and for those exposed to infected birds, animals or contaminated environments, the risk of infection is considered low to moderate (FAO, WHO and WOAH, 2024).

Since the virus is shed in the milk from infected dairy cattle, the potential role of consumption and handling of milk and milk products in transmission, as well as the role of pasteurization in mitigating the potential risk, are being investigated. The United States Food and Drug Administration (FDA) initiated a commercial milk sampling study using retail samples purchased from 17 states. Other dairy products, including cultured dairy products such as yoghurt and sour cream, were also tested. Results shared as of 12 June 2024 found that all dairy products except yoghurt had at least one sample test positive for segments of A(H5N1) viral nucleic acid through reverse transcription-quantitative polymerase chain reaction (RT-qPCR). These samples underwent gold-standard egg inoculation testing to determine the presence of live virus and were all confirmed negative for viable A(H5N1) virus. The current data demonstrate that pasteurization is effective in deactivating the A(H5N1) virus in bovine milk. All samples of retail powdered infant formula and powdered milk products marketed as toddler formula were qPCR negative, indicating no detection of influenza A viral nucleic acid segments or the virus itself (FDA, 2024). Research is ongoing to support more specific, science-based pasteurization treatment parameters for A(H5N1) in bovine milk and other dairy products (FDA, 2024).

Similarly, research studies related to beef are underway, including sampling ground beef in retail stores and sampling muscle tissue from sick cows that have been culled from their herd and not allowed to enter the food supply (condemned). Results were shared on 30 May 2024, indicating that of the 109 muscle samples tested, viral particles were detected in tissue samples, including diaphragm muscle, from one cow. No meat from the condemned dairy cattle entered the food supply. Complete results of the 30 retail ground beef samples from states with affected dairies were shared on 1 May 2024, and no PCR positives were detected (USDA APHIS, 2024e). Researchers also examined the impact of cooking temperature on virus inactivation in beef, and results were shared on 30 May 2024. Ground beef patties were inoculated with a very high concentration of an H5N1 virus surrogate. The ground beef patties did not previously contain any virus particles before inoculation for the study. Results confirmed the inactivation of the virus in samples cooked to 62.7°C (145°F) and above, in line with USDA Food Safety and Inspection Service (FSIS) recommendations, with substantial inactivation at 48.9°C (120°F). All evidence to date suggests that thorough cooking will inactivate influenza A virus, and A(H5N1) is not considered a food safety concern (USDA APHIS, 2024e).

1 Formally “milk and cream, not concentrated nor containing added sugar or other sweetening matter – of a fat content, by weight, not exceeding 1 percent;” (HS code 02211).
When possible, restrict access of wild livestock include:

- Important biosecurity practices to protect fully understood.
- And transmission routes are not yet emerging issue, and the risk factors chain actors are informed about the risks and health services providers, and other value should ensure that livestock owners, animal government sectors, veterinary services cattle, and other ruminants, and humans from focus on protecting wild and domestic birds, appropriate.

Strong collaboration between animal health, human health and the environment from protecting agricultural production systems, Biosecurity is an integrated approach to analysing and managing risks to health that includes policy, regulation, and practices to protect agricultural production systems, human health and the environment from biological risks (FAO, 2003).

FAO recommends that countries rapidly assess potential biosecurity risks related to HPAI in wild and domestic birds, but also in cattle, particularly considering how the current practices in place along the value chain may enhance or mitigate the risk of introduction and/or spread of the virus. Strong collaboration between animal health, human health and wildlife management professionals is critical, including the involvement of authorities responsible for occupational health and safety when appropriate.

In the short term, biosecurity efforts should focus on protecting wild and domestic birds, cattle and other ruminants, and humans from the A(H5N1) virus. In collaboration with other government sectors, veterinary services should ensure that livestock owners, animal health services providers, and other value chain actors are informed about the risks and the recommended practices to mitigate these risks. The spillover of A(H5N1) into cattle is an emerging issue, and the risk factors and transmission routes are not yet fully understood.

Given the information available, the most important biosecurity practices to protect livestock include:

1. When possible, restrict access of wild birds and other wildlife to livestock and their environment. Reduce wild bird attractants in livestock housing areas such as feed spillage, uncovered waste piles and standing water due to poor drainage.

2. Report increased numbers of dead birds or other wildlife in your area to animal health authorities.

3. Do not house poultry with other livestock species.

4. Poultry litter should be completely composted to inactivate viruses and bacteria before further use.

5. Change into clean outerwear and footwear when going between barns, poultry houses or animal handling areas. Establishing clean/dirty areas separated by a line or other demarcation can help ensure that pathogens are not brought into animal areas or transferred between animal groups. Wash hands frequently with soap and water.

6. Limit the unnecessary movement of animals, visitors and vehicles onto the farm. Limit access to animal areas for any non-essential persons, including visitors, salespeople or technicians.

7. Purchase replacement animals from herds/flocks with known health status. If possible keep new animals separated from the rest of the herd/flock for at least three weeks.

8. Closely monitor cattle for clinical signs consistent with A(H5N1) infection, including a sudden decrease in milk production, and contact a veterinarian promptly if any are observed.

9. Avoid sharing equipment between farms. When sharing equipment is necessary, ensure cleaning and disinfection of all items, including animal handling and treatment equipment, milk sampling and testing equipment, and breeding and hoof trimming equipment. Pay particular attention to proper disinfection of milking equipment.

10. If an A(H5N1) outbreak is confirmed:
   a. Sick cattle should be isolated from healthy cattle and other animal species (particularly swine) for at least 28 days after the onset of the disease. They should be milked after the healthy part of the herd, and the equipment should be thoroughly cleaned and disinfected afterwards. The farm should not move cattle to other farms until 28 days after the onset of the disease in the last clinical case. The deaths of any other animals on the farm (wild or domestic birds, domestic cats, etc.) should be investigated, including laboratory testing with all proper precautions.
   b. Do not feed raw milk or raw colostrum to any animals. Consider routinely feeding pasteurized colostrum or milk to calves or using colostrum/milk replacers.
   c. Do not allow personnel to move between infected farms to other farms, regardless of the species of livestock present.
   d. Take precautions when discarding milk, especially from affected cows, to ensure that the discarded milk does not become a source of further spread. Such precautions could include heat treatment or pasteurization of discarded milk, as well as biosecurity measures to ensure that other animals do not have access to discarded milk (USDA APHIS, 2024g).

While it is uncommon for A(H5N1) to spill over into humans, those who work directly with poultry and livestock should take additional precautions and follow all public health guidelines. This includes using recommended personal protective equipment (PPE), appropriate personal hygiene, and risk-based biosecurity measures when handling any animal suspected of being exposed or infected with HPAI, as well as sick or dead wild birds. Milk and other dairy products should only be consumed after heat treatment, such as high-temperature short time (HTST), traditional pasteurization or ultra-high temperature (UHT) processing. Do not consume raw milk or raw milk products. To kill bacteria and viruses, meat and viscera should be thoroughly cooked to the recommended temperatures before consumption. Individuals with possible symptoms of influenza should follow guidance from public health authorities.

In the medium to long term, initiatives to strengthen biosecurity in the poultry and livestock value chains may be needed. The Progressive Management Pathway for Terrestrial Animal Biosecurity (FAO PMP-TAB) (FAO, 2023) is a stepwise framework to sustainably improve biosecurity along the terrestrial animal value chains under a One Health approach.
Surveillance

Surveillance is a crucial tool for the early detection and rapid response to HPAI viruses. It aids in the understanding of the evolution and spread of the virus and helps assess the subsequent risks to human and animal health. Countries are encouraged to implement or maintain surveillance of wild and domestic birds and to monitor and investigate any suspect cases in non-avian species, including livestock. Passive surveillance, where a producer or animal owner notices something unusual and contacts a veterinarian or animal health worker, remains a cost-effective method to identify disease. Sensitization of veterinarians and animal health workers, slaughterhouse workers, border inspection points, farmers and other value chain actors may be needed to support HPAI surveillance goals. Countries should develop and regularly update a suspect case definition for influenza A(H5N1) for cattle, which can help ensure that suspect cases are quickly identified and investigated. The USDA case definition is available online (USDA APHIS, 2024c), though countries are encouraged to develop their own robust case definition that fits their national context.

Risk-based surveillance approaches can target animals in areas with known infections or those recently imported from affected regions. These methods can also enhance surveillance designs in situations where passive reporting is insufficient. These approaches should be based on risk assessments to address the geographical areas and specific populations at risk of HPAI introduction and spread. Wastewater monitoring has shown potential as a cost-effective option for monitoring AIVs in large populations of humans or animals, although the research is still ongoing for animal populations (Lee et al., 2023; Wolfe et al., 2024). Testing of bulk tank milk or retail milk samples may also be used to assess the possibility of AIVs circulating in dairy animals. Similarly, countries may elect to test banked or stored samples of sera or milk to better understand historically when and if HPAI may have been circulating in a cattle population. Serological surveys could also have some application to quantify or monitor the burden of infection over time.

Ultimately, the choice of surveillance method and design should be based on clear objectives. These methods should support the early detection of poultry outbreaks and spillover events from birds to non-avian species, including livestock.

Emergency preparedness and contingency planning

Countries are encouraged to develop or update contingency plans for HPAI events, including spillover into non-avian species. FAO has published guidelines for countries and relevant local, national or regional organizations to strengthen their capability and capacity to manage any animal health emergency using good emergency management practices (GEMP) (Gary et al., 2021). Preparing for HPAI outbreaks requires the development of plans and institutional arrangements to engage and guide the efforts of public and private sectors in a systematic, comprehensive and coordinated way. Given the nature of HPAI, contingency plans should be developed, reviewed, communicated and evaluated using a One Health approach to ensure that all relevant partners are prepared to support a response. To support the mobilization and allocation of resources for contingency planning and surveillance, an estimation of the costs of outbreaks can be estimated through FAO’s Outbreak Costing Tool (Casal et al., 2022).

Information sharing

The WOAH/FAO Network of Expertise on Animal Influenza (OFFLU) urges the scientific community to continue to monitor influenza events in animals, report cases and relevant epidemiologic data to WOAH, and to deposit and share whole genome genetic sequence data and associated metadata in publicly available databases promptly. Research organizations are also encouraged to coordinate studies to better understand the pathogenesis, transmission and adaptation of virus lineages and to share the results with OFFLU. This supports national and international risk managers and contributes to risk mitigation measures, such as assessments of the need to update vaccines for humans and poultry.

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The Emergency Prevention System (EMPRES) is a FAO programme founded in 1994 with the goal of enhancing world food security, fighting transboundary animal and plant pests and diseases, and reducing the adverse impact of food safety threats. EMPRES-Animal Health is the component dealing with the prevention and control of transboundary animal diseases (TADs).

For information about EMPRES-Animal Health send an e-mail to empres-animal-health@fao.org

For more information visit us at https://www.fao.org/animal-health

EMPRES-Animal Health can assist countries in the shipment of samples for TAD diagnostic testing at a FAO reference laboratory and reference centre. Please contact Empres-Shipping-Service@fao.org for information prior to sampling or shipment. Please note that sending samples out of a country requires an export permit from the Chief Veterinarian’s Office of the country and an import permit from the receiving country.

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