https://doi.org/10.29326/2304-196X-2026-15-1-13-19

Cross-species transmission of avian influenza A(H5N1) virus to mammals: lessons learnt from 2024–2025 outbreaks in cattle

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ABSTRACT

Introduction. In 2024–2025, a number of high pathogenicity avian influenza A(H5N1) outbreaks were reported in dairy cattle. Such an expansion of the virus' hosts range increases global risks for livestock farming and public health, which requires strengthening animal disease monitoring and control systems.
Objective. Analysis of the epizootological characteristics of avian influenza A(H5N1) virus infection in dairy cattle and other mammals in 2024–2025, as well as a summary of the response measures taken and recommendations of international organizations.
Materials and methods. Analytical research methods were used utilizing PubMed, Scopus, Web of Science, Springer, Wiley Online Library databases and materials from international organizations (FAO, EFSA, WOAH, OFFLU, CDC).
Results. Outbreaks of avian influenza A(H5N1) caused by clade 2.3.4.4b virus of genotypes B3.13 and D1.1 in dairy cattle in 2024–2025 occurred as a result of three independent confirmed cases of the pathogen transmission from wild birds. The infection was detected on 1,078 cattle farms in 17 US states. Subsequent virus transmission to poultry, wild and domestic animals, including cats, as well as to humans (70 people), mainly those working on livestock and poultry farms, was reported. Reverse transmission of the pathogen from cows back to birds was documented as well. Rapid and wide spread of the virus is associated with extensive animal movements and insufficient biosafety measures. Influenza A(H5) is recommended for the inclusion in the differential diagnosis for cattle, pigs, domestic and wild animals.
Conclusion. Avian influenza A(H5N1) epizootic in cattle and the infection transmission to other mammals pose a serious threat to livestock industry and public health. In response to the existing risks, it is necessary to strengthen biosafety measures and surveillance in epidemiologically significant animal populations, incorporate the experience of other countries and establish international cooperation to study the trends of the virus evolution.

Keywords: review, avian influenza A(H5N1), cross-species transmission, cattle, cats, pigs, biosafety, animal movement, milk, epizootological surveillance

Acknowledgements: The study was supported by the Ministry of Education and Science of the Russian Federation within the state assignment for the Federal Research Center for Virology and Microbiology (No. FGNM-2022-0004). The authors thank the reviewers for their contribution to the peer review of this paper.

For citation: Krasnova E. A., Korogodina E. V., Lunina D. A. Cross-species transmission of avian influenza A(H5N1) virus to mammals: lessons learnt from 2024–2025 outbreaks in cattle. *Veterinary Science Today.* 2026; 15 (1): 13–19. https://doi.org/10.29326/2304-196X-2026-15-1-13-19

Conflict of interests: The authors declare no conflict of interests.

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УДК 619:578.832.1:598.2:578.42:636.2

Межвидовая передача вируса гриппа птиц A(H5N1) млекопитающим: уроки вспышек среди крупного рогатого скота в 2024–2025 гг.

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РЕЗЮМЕ

Введение. В 2024–2025 гг. произошла серия вспышек высокопатогенного гриппа птиц A(H5N1) среди молочного скота. Подобное изменение круга хозяев вируса повышает глобальные риски для животноводства и общественного здравоохранения, что требует усиления систем эпизоотологического мониторинга и контроля.
Цель исследования. Анализ эпизоотологических характеристик инфекции молочного скота и других млекопитающих, вызванной вирусом гриппа птиц A(H5N1) в 2024–2025 гг., а также обобщение принятых мер реагирования и рекомендаций международных организаций.
Материалы и методы. Применялись аналитические методы исследований с использованием баз данных PubMed, Scopus, Web of Science, Springer, Wiley Online Library и материалов международных организаций (FAO, EFSA, WOAH, OFFLU, CDC).

Результаты. Вспышки гриппа птиц A(H5N1), обусловленные вирусом клады 2.3.4.4b генотипов B3.13 и D1.1, среди молочного скота в 2024–2025 гг. произошли в результате трех установленных независимых случаев передачи возбудителя из популяции дикой птицы. Инфекция была выявлена на 1078 фермах у крупного рогатого скота в 17 штатах США. Зафиксирована последующая передача вируса домашней птице, диким и домашним животным, включая кошек, и людям (70 человек), в основном работникам ферм и птицефабрик, а также обратная передача возбудителя от коров к птицам. Повсеместное быстрое распространение вируса связано с массовыми перемещениями скота и недостаточностью мер обеспечения биобезопасности. Рекомендовано проводить исследования на грипп A(H5) при дифференциальной диагностике заболеваний крупного рогатого скота, свиней, домашних и диких животных.

Заключение. Эпизоотия гриппа птиц A(H5N1) среди крупного рогатого скота и передача инфекции другим млекопитающим демонстрирует серьезную угрозу для животноводства и общественного здоровья. В ответ на существующие риски необходимо усилить меры биобезопасности и надзор в эпидемиологически важных популяциях животных, учесть опыт других стран и наладить международное сотрудничество для изучения направлений эволюции вируса.

Ключевые слова: обзор, грипп птиц A(H5N1), межвидовая передача, крупный рогатый скот, кошки, свиньи, биобезопасность, перемещение скота, молоко, эпизоотологический надзор

Благодарности: Работа выполнена при поддержке Минобрнауки России в рамках государственного задания ФГБНУ ФИЦВиМ (тема № FGNM-2022-0004). Авторы благодарят рецензентов за экспертную оценку данной работы.

Для цитирования: Краснова Е. А., Корогодина Е. В., Лунина Д. А. Межвидовая передача вируса гриппа птиц A(H5N1) млекопитающим: уроки вспышек среди крупного рогатого скота в 2024–2025 гг. *Ветеринария сегодня.* 2026; 15 (1): 13–19. https://doi.org/10.29326/2304-196X-2026-15-1-13-19

Конфликт интересов: Авторы заявляют об отсутствии конфликта интересов.

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INTRODUCTION

A highly alarming development in recent years has been the worldwide reports of high pathogenicity avian influenza virus (HPAIV) detection in mammals (Fig.). Previously considered primarily as a threat to poultry, HPAIV has established a "new normal", characterized by transmission to mammals [1, 2, 3]. Since 2022, a significant increase in the number of H5 avian influenza cases has been reported in terrestrial animals (foxes, raccoons, minks, bears, tigers, lynxes, ermines, squirrels, etc.) and aquatic mammals (dolphins, seals, sea lions, walruses, etc.) [4]. In 2023, HPAI transmission with wild virus-infected mammals from North and South America to Antarctica was first reported [5]. Mass animal mortality was reported: from hundreds to thousands of sea lions in Peru, Argentina, Uruguay, and Brazil, fur seals in Chile and Brazil, and elephant seals in Argentina [3, 6]. In early 2024, mass mortality of southern elephant seals and fur seals caused by HPAI was reported in the sub-Antarctic zone, which was probably facilitated by their colonial lifestyle and high susceptibility to the pathogen [7]. In 2024, the situation worsened regarding HPAIV infection of domestic animals (cats) and humans from livestock, including cattle. This indicates a continuing threat of mammal-to-mammal transmission of the avian influenza agent and presents a significant risk for further viral mutation and the potential acquisition of human-to-human transmissibility [8].

According to the Food and Agriculture Organization of the United Nations (FAO), in the first quarter of 2025, the H5Nx subtype influenza virus was confirmed in almost 100 mammalian species, mainly carnivorous. Thus, in a relatively short period (2021–2025) of subtype H5Nx virus spread, the number of susceptible species of mammals and wild birds has doubled[1]. The expansion of the range of susceptible mammalian species and the geographical spread of the virus increase the risk of its spillover to humans, according to the World Organisation for Animal Health (WOAH). Therefore, it is extremely important to maintain reliable surveillance and comply with biosafety measures, especially for new and atypical avian influenza virus hosts [6].

The increased risk of the interspecies HPAIV transition to new mammalian species and from mammals to humans is facilitated by the following factors: high activity of type A(H5N1) virus circulation, increase in the genetic diversity within clade 2.3.4.4, accumulation of mutations resulting in adaptation to mammals (including increased viral replication and changes in virulence, host-specific polymerase activity, *inter alia* binding to human-type α2,6-linked sialic acid receptors, etc.) in gene segments encoding the key surface protein hemagglutinin (HA), another surface protein neuraminidase (NA), matrix proteins (M1 and M2), nucleoprotein (NP) and polymerase basic protein 2 (PB2) [9, 10, 11, 12].

Cases of infection in mammals that are in close contact with humans draw particular attention to the issue of the virus overcoming the interspecies barrier and increasing its pandemic potential. Such animals include farm animals (cattle, pigs) and pets (cats) [8, 9, 13, 14, 15].

In order to study the epizootological characteristics of the infection caused by avian influenza A(H5N1) virus in dairy cattle and other mammals in 2024–2025, as well as the response measures taken and recommendations from international organizations, an analysis of available scientific publications and materials from international organizations such as WOAH, FAO, European Food Safety Agency (EFSA), Global WOAH/FAO Network of Expertise on Animal Influenza (OFFLU), US Centers for Disease Control and Prevention (CDC) was made. Examination of the current HPAI pattern and experience in its control are essential for the improvement of the comprehensive disease control.

AVIAN INFLUENZA OUTBREAKS IN DAIRY CATTLE IN THE USA

Infection of cattle with influenza A(H5) virus is a dramatic change in the range of the virus hosts and the disease pattern, that has led to the sustained pathogen transmission

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[1] Global avian influenza viruses with zoonotic potential situation update: Bird & mammal species affected by H5Nx HPAI. https://www.fao.org/animal-health/situation-updates/global-aiv-with-zoonotic-potential/bird-species-affected-by-h5nx-hpai/en

from one mammal to another and an increased risk for wild and domestic animals, as well as to agricultural workers, thus increasing global public health risks [14]. According to FAO, the detection of the virus in dairy cattle and cases of the infection in farm workers who have come into contact with the infected animals emphasize the need to strengthen the disease monitoring and control systems [16].

In March 2024, after reports of unexplained symptoms in dairy cattle in the United States, influenza A(H5N1) virus of clade 2.3.4.4b, genotype B3.13 was isolated from unpasteurized milk samples and oropharyngeal swabs collected from cattle [13]. Genotype B3.13 influenza causative agent is a reassortant of the European highly pathogenic strain of subtype H5N1 virus and the North American low pathogenic strain [1]. Sequencing and phylogenetic analysis of the isolated virus strains demonstrated that initially there was a single event of this pathogen (genotype B3.13) spillover from wild birds to cattle in late 2023 – early 2024, followed by its wide and rapid spread across the United States, mainly due to the peculiarities of cattle farming in the country. Subsequent transmission of genotype B3.13 influenza A(H5N1) virus from infected cattle to wild birds, poultry (chickens), wild mammals (raccoons), synanthropic rodents (mice), pets (cats) and humans (animal and poultry farm operators) was reported. Moreover, reverse transmission of the virus from cows to birds was registered [17].

In early 2025, the second and third independent cases of highly pathogenic clade 2.3.4.4b influenza virus spillover from wild birds to cattle were confirmed, with the pathogen belonging to genotype D1.1[2]. Currently, D1.1 genotype virus is the most commonly detected in North America and it infects wild birds and poultry, as well as mammals.

The website of the United States Department of Agriculture (USDA) features an updated map with the quantitative and territorial (by state) distribution of HPAI cases in animals (cattle, swine, alpacas)[3]. As of 01 August 2025, 1,078 cattle herds in 17 states were HPAIV infected. On the CDC website, the current situation in humans is displayed[4]. As of 07 July 2025, there were 70 confirmed cases of human infection with the avian influenza virus (mostly in animal and poultry farm employees). So far, the current public health risk is assessed as low.

The widespread transmission of highly pathogenic avian influenza A(H5N1) virus in cattle challenges long-established theories of influenza ecological dynamics and highlights substantial gaps in the global preparedness system for responding to such biological threats, necessitating immediate measures to address the identified deficiencies [14].

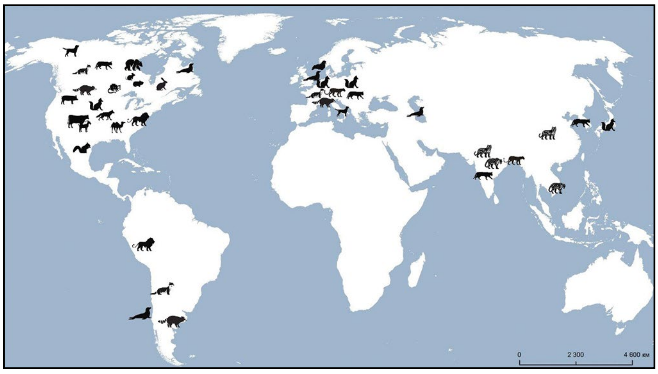

Fig. Geographic distribution of HPAI in mammals, 2022–2025 (symbols on the map indicate main mammalian families affected by HPAI outbreaks during this period; World Animal Health Information System, 01 August 2025)

Infection transmission routes and risk factors. On-farm virus transmission mainly occurred through contaminated milk and during milking procedures (shared milking equipment), rather than by respiratory route [18], while the farm-to-farm spread is mainly due to the animal movements and use of shared equipment [13]. It was demonstrated that influenza A (H5N1) virus retains its infectivity for several hours in raw milk from infected animals remaining on milking machines and is detected in environmental samples from milking parlors, which highlights the risk of indirect transmission during routine milking. However, under experimental conditions involving prolonged co-housing (14 days) of infected and control cows, as well as shared use of milking equipment, the reproduction of the virus transmission failed [19]. During the model experiment, the possibility of calves becoming infected through the alimentary route by being fed raw milk from cows infected with the highly pathogenic subtype H5N1 genotype B3.13 avian influenza virus was confirmed [20]. At the same time, the calves' clinical signs were mild (nasal discharge, mild fever and lethargy, loose stools and rapid breathing) and similar to signs of other common diseases, which would complicate the diagnosis in the field.

Specifics farming practices in the United States imply extensive animal movements, both on-farm and from farm to farm, at different production stages [9]. For example, about 40% of the young replacement dairy cows are reared outside the farm. According to the National Epidemiological Survey of the United States Department of Agriculture (USDA), the onset of clinical signs in livestock on more than 50% of affected farms was preceded by the introduction of new cattle into the herd within the previous 30 days. Furthermore, over 45% of farms continued to move cattle even after animals had begun to demonstrate clinical signs[5]. Farm animal movements are allowed in the United States and the animals were moved without prior laboratory tests, which contributed to the virus spread in the absence of clinical signs.

Another highly probable route of the infection transmission between farms and states is non-compliance with biosafety requirements: use of shared transport and equipment (including those used for cleaning and feed and waste handling), lack of their disinfection; the clothes and shoes of regular staff who are simultaneously employed on other farms or have their own livestock and poultry, as well as farm visitors, who have access to animals (including veterinarians, feed consultants, animal breeders and hoof trimming specialists, carriers, etc.) [13, 16].

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[2] 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). https://www.woah.org/app/uploads/2025/04/2025-04-17-fao-woah-who-h5n1-assessment.pdf

[3] HPAI confirmed cases in livestock. https://www.aphis.usda.gov/livestock-poultry-disease/avian/avian-influenza/HPAI-detections/HPAI-confirmed-cases-livestock

[4] H5 bird flu: Current Situation. https://www.cdc.gov/bird-flu/situation-summary/index.html

[5] Animal and Plant Health Inspection Service, U.S.D.A. Highly Pathogenic Avian Influenza H5N1 Genotype B3.13 in Dairy Cattle: National Epidemiologic Brief. https://www.aphis.usda.gov/sites/default/files/highly-pathogenic-avian-influenza-national-epidemiological-brief-09-24-2024.pdf

An additional risk factor involves mixed animal breeding and presence of pets in the animal housing areas, as well as feeding them and young cattle with unpasteurized milk. For example, cats were present on 75% of HPAI infected farms, and poultry was kept on 19% of the farms[6].

Thus, the virus widespread in the U.S. dairy herds was mainly due to asymptomatic transmission, lack of surveillance in epizootologically important populations, and insufficient compliance with biosafety measures.

Currently, the routes and means of the pathogen transmission in cattle as well as the virus shedding duration, etc. are being studied. A preliminary model study demonstrates that the duration of the infection period can vary from 2.8 to 13.1 days, with a median of 6.2 days [21].

Clinical signs were reported on average in less than 20% of cases, and mortality did not exceed 2%. The following prevailing clinical signs are described in cattle [13, 14]:

– decrease in milk production and change in milk quality (color, consistency, coagulation);

– loss of appetite and reduced rumen activity;

– fever;

– mastitis;

– dehydration;

– changed feces consistency;

– nasal discharge and respiratory distress.

During the outbreaks in the United States, clinical signs in cattle persisted for up to 21 days (an average of 6 days), with the exception of changes in milk quality. Milk production was reported to be reduced for up to 45 days (an average of 12 days). Despite the fact that viral RNA was detected in milk, nasal swabs, urine, and sera of infected cattle, the highest concentrations of the infectious virus were consistently detected in milk and mammary gland tissues [22].

Milk tests. The H5 avian influenza virus actively replicates in the mammary glands, and the infected cows shed high quantities of the virus in milk for up to 3 weeks, even in the absence of clinical signs [13]. The widespread expression of receptors for both avian and human influenza viruses in cow mammary glands combined with a high viral load in milk (from $10^{4.0}$ to $10^{8.8}$ $TCID_{50}$/mL) suggests local replication of the virus. It was experimentally demonstrated that intramammary exposure to even low doses of genotype B3.13 influenza A(H5N1) virus (from 10^1 to 10^3 $TCID_{50}$) is sufficient for stable infection establishment, shedding high titers of the virus in milk, and clinical mastitis development [19]. Intramammary exposure to influenza A(H5N1) virus in high doses leads to severe clinical outcomes and death observed in dairy cows on farms, while respiratory and oral exposure are less likely to result in productive infection and related morbidity.

During laboratory studies, various methods were used to isolate influenza virus RNA from raw milk samples, including column-based and magnetic sorbent extraction, as well as phenol-chloroform extraction method (Trizol LS). The efficiency of isolation can be influenced by pretreatment of milk samples, as well as their storage conditions [8].

Studies have shown that milk increases the thermal stability of the influenza viruses, but results of the experiments on the pathogen inactivation under different heating conditions and processing time are contradictory [23]. A number of studies indicate that industrial pasteurization of milk is a reliable method of the avian influenza virus inactivation [24]. Other studies mention that neither pasteurization at 72 °C for 15 seconds nor at 63 °C for 30 minutes can completely kill the virus in milk, whereas heat treatment at 80 °C for 15 seconds completely inactivates H5N1 influenza virus in milk [23, 25]. Despite the fact that viral RNA is detected in the samples of pasteurized dairy products, no infectious virus has been detected so far [26]. This further highlights the potential dangers of unpasteurized milk and dairy products made from it. Laboratory experiments have demonstrated that the HPAIV remains viable in raw cow and sheep milk for over 24 hours at room temperature and for more than 7 days under refrigeration [27]. Furthermore, studies of raw milk cheese showed that infectious avian influenza A(H5N1) virus can persist in such a product for several months (more than 60 days)[7]. The results obtained indicate the need to implement additional measures to reduce the risks of infection for both animals and humans during the production and consumption of raw milk products [28].

AVIAN INFLUENZA IN PIGS AND CATS

Pigs have unique anatomical and physiological characteristics of the respiratory tract, which may facilitate infections caused by influenza A virus strains that are not adapted to them [29]. Thus, in October 2024, the U.S. Department of Agriculture confirmed the presence of the avian influenza A(H5N1) pathogen in a pig on a backyard farm in Oregon[8]. On this farm, both poultry and livestock – including pigs – were kept together and shared common water sources, facilities, and equipment. The pig did not demonstrate any clinical signs of infection caused by influenza A(H5) pathogen. No specific adaptation of the virus to humans or mammals has been identified. The detection of H5N1 viral genetic material in pig tissues and excrement indicates their potential role in maintaining and amplifying the pathogen transmission [14].

A preliminary experimental study in pigs demonstrated limited replication of genotype B3.13 influenza A(H5N1) virus isolated from cattle and no pathogen transmission through direct contact from the infected pigs to the uninfected ones. Experimental intranasal and oral infection of pigs with another genotype of influenza A(H5N1) virus of clade 2.3.4.4b revealed that the strains isolated from mammals demonstrated a higher potential for replication, pathogenicity, and transmissibility compared with the strains isolated from birds [30, 31]. Thus, pigs represent a critically important element in the mechanism of interspecies transmission, especially under conditions of mixed livestock farming. This factor requires close attention and the need to test pigs for avian influenza virus due to its genetic diversity and scale of circulation, since pigs act as "mixing vessels" for genetic reassortment of avian and human influenza viruses, potentially contributing to the emergence of new strains with pandemic potential. Pigs must

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[6] Animal and Plant Health Inspection Service, U.S.D.A. Highly pathogenic avian influenza H5N1 genotype B3.13 in dairy cattle: National epidemiologic brief. https://www.aphis.usda.gov/sites/default/files/highly-pathogenic-avian-influenza-national-epidemiologicalbrief-09-24-2024.pdf

[7] United States Food and Drug Administration. Investigation of Avian Influenza A (H5N1) Virus in Dairy Cattle. https://www.fda.gov/food/alerts-advisories-safety-information/investigation-avian-influenza-h5n1-virus-dairy-cattle

[8] Federal and State Veterinary Agencies Share Update on HPAI Detections in Oregon Backyard Farm, Including First H5N1 Detections in Swine. https://www.aphis.usda.gov/news/agency-announcements/federal-state-veterinary-agencies-share-update-HPAI-detections-oregon

be incorporated into comprehensive epizootiological surveillance systems to more accurately assess the ecological characteristics of the H5N1 influenza virus as it circulates in domestic animal populations and to analyze their potential role in zoonotic outbreaks.

Importantly, in recent years there has been an increase in interspecies transmission of avian influenza A(H5N1) virus to cats. Since 2022, at least 88 cases of domestic cat infection with this subtype virus have been reported in the United States alone. In 2024–2025, infection and mortality cases were reported in domestic and wild members of the *Felidae* family in India, Vietnam, the Netherlands and other countries [32]. Cats can act as the virus carriers or intermediate hosts, as they are in close contact with humans and animals of other species. Infection of cats with both avian influenza and human influenza viruses is possible, which can lead to the virus adaptation and emergence of recombinant strains with zoonotic potential [8, 15, 32, 33].

During influenza outbreaks caused by subtype A(H5N1) virus of clade 2.3.4.4b in 2024–2025, neurological and respiratory signs, as well as high mortality, were reported in infected cats in the United States, indicating the susceptibility of the *Felidae* family members to the virus and their potential role in its transmission. Cats kept at home, as well as animals from shelters, are at increased risk of infection, especially when they come into contact with infected wild birds, consume raw infected poultry meet or unpasteurized milk from cattle infected with influenza A virus [15, 34]. For example, in raw milk consumed by cats with clinical signs of avian influenza virus infection, reverse transcription polymerase chain reaction (RT-PCR) revealed the RNA of subtype H5N1 pathogen. After consuming raw milk derived from infected cattle, about 50% of cats became diseased and died [13]. HPAI A(H5N1) virus was detected in domestic cats in the homes of dairy farm workers[9], while there was no direct contact of animals with the avian influenza affected farm, which suggests the pathogen transmission with the humans (for example, with contaminated footwear and clothing) [35]. Clinical signs in infected cats included depression, body stiffness, ataxia, blindness, circling, ocular and nasal discharge. The influenza A virus antigen was detected in the brain, lungs, heart, and retina of the diseased cats [13]. Therefore, when examining cats that have had contact with wild birds or have consumed raw poultry or dairy products, and that present with acute neurological and respiratory symptoms, veterinarians should include avian influenza in the list of differential diagnoses [34].

MEASURES TAKEN AND RECOMMENDATIONS

In response to the unprecedented HPAIV spread in cattle in the United States, the following response measures have been implemented at the governmental level: restrictions on the import of cattle with clinical signs of the disease, as well as on the movement of animals from infected states; requirements for veterinary inspection certificates prior to transport; testing of dairy cattle before interstate movement; enhanced biosafety measures; restrictions on exhibitions; and the imposition of quarantine [13, 16]. State financial support was offered to dairy producers to ensure the necessary biosafety level and to compensate for the costs associated with HPAI outbreaks. In addition to federal decrees, additional response measures were implemented at the state level.

On 06 December 2024, the USDA announced the launch of the National Milk Testing Strategy (NMTS)[10, 11]. The total number of PCR tests conducted in the first year, from April 2024 to April 2025, amounted to 210,146. The NMTS specifies that before transporting dairy cattle from one state to another, a negative test result for influenza A virus must be obtained from an accredited laboratory; the movement of cattle with influenza clinical signs and their transport for slaughter are not permitted. Milk sampling should be carried out under the supervision of a licensed or accredited veterinarian. The sample size should be from 3 to 10 mL and contain milk from each udder lobe. Milk samples can only be pooled in a laboratory. All animals moved in a group (consignment) of 30 or fewer animals must be tested. If larger numbers of animals are being moved, then a total of only 30 animals shall to be tested. Samples shall be collected and tested no later than 7 days before the movement. If positive results for influenza A are obtained, dairy cattle are not permitted to be transported for 30 days from the date of the last positive sample collected from any animal in the herd. After the 30-day period, the animals must be retested. Dairy cattle without clinical signs transported directly to slaughter are not required to be subjected to the pre-movement test, but they must have a veterinary inspection certificate.

Based on the analysis of epizootological study results of the animals infected with influenza A(H5N1) virus, the USDA recommends strengthening biosafety measures on dairy farms:

– avoid sharing equipment and vehicles, and disinfect them;

– comply with biosafety requirements during any contact between people (personnel, visitors) and animals on the farm;

– exclude open storage of feed and litter material and prevent contact of these materials with domestic and wild animals and birds;

– avoid housing animals of different species together on the farm;

– utilize advanced waste management practices to prevent infected manure from entering compost;

– carry out pasteurization, chemical, or heat treatment of dairy waste;

– disinfect raw milk (pasteurization) if it is subsequently fed to calves or other animal species;

– quarantine new animals added to the herd for minimum 30 days, and isolate any cattle displaying the disease clinical signs.

The literature also emphasizes the importance of proactive control of HPAI in wildlife [7, 12] and in domestic animals [9]. The need is emphasized for monitoring wild animal populations for subtype H5 HPAIV, based on the data on unusual morbidity levels and recorded mortality cases, as well as on the results of virological and serological

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analyses, including timely exchange of diagnostic information on the disease and viral genome sequences for the rapid detection of new incursions of the virus and tracking its evolution through phylogenetic analyses. Enhanced biosafety measures are coming to the fore for domestic and farm animals.

In light of reports of cattle and other mammalian species being infected with avian influenza virus, the FAO has published updated recommendations. These recommendations include guidance on implementing effective monitoring programs for the timely detection of avian influenza cases in cattle [16]. Among them are the following:

– strengthen epizootological surveillance and timely report with a view to early detection of influenza A(H5) virus in poultry, wild birds and mammals;

– include influenza A(H5) in differential diagnosis for cattle, pigs and farm animals, as well as for domestic and wild animals;

– promptly report HPAI cases in all animal species, including cattle and other domestic and wild mammals, to international organizations (WOAH, FAO);

– carry out active monitoring/detection of the disease cases, using *inter alia* molecular and serological tools;

– provide the persons in contact with animals with appropriate personal protective equipment, as well as provide them with the capacities for testing;

– perform genome sequencing and deposit the influenza virus genetic sequences and associated metadata in the publicly accessible databases;

– implement and/or strengthen biosafety systems on the animal farms/premises and throughout the production chain;

– take preventive measures and early response measures to interrupt the infection chain in pets.

CONCLUSION

The avian influenza A(H5N1) outbreak in dairy cattle in the United States represents a significant change in the epidemic potential of the virus and its ability to interspecies transmission. This event highlights the need to strengthen the epizootological monitoring systems and mandatory compliance with biosafety measures in animal husbandry. The atypical and vague clinical manifestations of avian influenza in cattle complicate the disease diagnosis and timely measures. It is important that the virus can be excreted in milk for several weeks even in the absence of clinical signs. This fact underscores the need for strict compliance with dairy processing protocols, including pasteurization as an effective method of virus inactivation. Pigs and cats have also been found to be susceptible to the infection caused by influenza A(H5N1) pathogen, thus raising concerns about their potential role in the virus evolution and spread.

Further efforts are needed to address gaps in the biological threat monitoring and response system. To effectively control the subtype H5N1 influenza virus spread in animals and minimize the risk of zoonotic infections, the experience of other countries should be taken into account and comprehensive measures aimed at the pathogen spread prevention should be taken. The inclusion of influenza A(H5) virus infection in the differential diagnosis for cattle, pigs and other mammals, as well as increased epizootological surveillance, are key steps in ensuring safety of animal husbandry and public health. When studying the avian influenza virus evolution and developing effective prevention strategies, it is important to carry out genomic monitoring and establish international scientific cooperation.

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Received 28.08.2025
Revised 02.10.2025
Accepted 12.01.2026

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Вклад авторов: Краснова Е. А. – концепция, поиск и анализ литературы, подготовка текста; Корогодина Е. В. – поиск и анализ литературы, корректировка текста; Лунина Д. А. – анализ литературы, визуализация, корректировка текста.