

The epizootic situation of avian influenza in the Kaluga region

D.M. Evstafyev¹, P.V. Dudin¹, T.A. Spasskaya¹, A.Ya. Bondarev^{1,}, and E.A. Vodolazov²*

¹ Russian State Agrarian University - Moscow Timiryazev Agricultural Academy, Kaluga, Russia

² Veterinary Committee under the Government of the Kaluga Region, Kaluga, Russia

Abstract. The article discusses the problems associated with increased virulence of strains due to the high representativeness of the sample of susceptible organisms, the spread of avian influenza and its natural reservoirs. Currently, avian influenza virus strains are divided into HPAI (highly pathogenic) and LPAI (low pathogenic). Registered outbreaks among wild and domestic birds and cases of human infection with influenza viruses of subtypes H5N8, H7N9 and H9N2 indicate an active mutation of the virus and the appearance of "aggressive" strains that can infect not only poultry, but also humans. This article analyzes the current epizootic situation of avian influenza in the Kaluga region for 2022-2023.

1 Introduction

Avian influenza strains, especially lines belonging to the H5 and H7 categories, pose a real danger to the health of the world's population and cause significant losses at enterprises related to poultry breeding [1,2,3]. The pathogen contains an RNA chain consisting of eight fragments, which increases its ability to change through mutations and recombinations, leading to the continuous emergence of new and diverse forms.

Currently, there are two new strains of the virus isolated from bats: H17N10 and H18N11, but they have not been sufficiently studied, and therefore it is impossible to talk about strict specificity to these fauna representatives [4,5,6].

Wild migratory birds are the main reservoir of highly and low pathogenic strains of avian influenza virus, which are transmitted to domestic and synanthropic bird species. These organisms can carry viruses with any of the sixteen possible types of hemagglutinin and nine different neuraminidases known today, making them potential sources of future more aggressive strains [7]. A wide range of diverse genetic lines of the virus is supported by the active exchange of sections of genetic material of virus strains and their genes among wild birds, mainly from the orders of anseriformes and charadriiformes [8,9].

Intensive transmission of the pathogen occurs during periods of migration, therefore, when a reconvalescent bird meets with a healthy population, infection and spread of the virus to certain nesting regions occur. These phenomena contribute to the selection of numerous subtypes of Highly Pathogenic Avian Influenza, which can create more resistant strains to continue the chain of infection both within the species and for various animal species. The

* Corresponding author: alexander200104@gmail.com

substitution of an amino acid in a protein molecule when encoded by various sites of neuraminidase (N1–N9), even in low-pathogenic strains of avian influenza virus, led to infection of not only poultry, but also humans [10,11,12]. There come moments when the mutational variability of the virus slows down, which leads to an outbreak of the disease among susceptible poultry, as a result of which the virus spreads over long distances from the infection spot.

The emergence of new strain variants is inevitable due to the high genetic variability of the virus. Over the past two years, a wave of avian influenza outbreaks among poultry has swept through the territory of the Russian Federation. With prolonged circulation of different strains of the virus, low-pathogenic strains occur that do not cause pronounced clinical symptoms in birds. The appearance of various modifications of the virus occurs under the influence of two main factors: antigenic shift and antigenic drift. The antigenic drift of avian influenza occurs under the action of virus polymerase, which leads to the emergence of new antigenic properties. The antigenic shift provokes the exchange of segments of the virus genome and the emergence of combinations that increase its virulence. This reassortment leads to the formation of strains that have the characteristics of two parent lines and cause infection of new hosts. The mutations occurring in the virus genome not only give it new features, but also contribute to the emergence of new genetic clades and subclades. Let's take for example the highly pathogenic influenza A/H5 virus, which has managed to form an entire network of sublines. These sublines were formed as a result of numerous, sometimes insignificant differences in amino acid sequences, which made it possible to classify them in a strictly defined clade system.

In 1996, the first appearance of the Gs/Gd line occurred, since then the genetic code of this line has undergone significant changes. The grouping of genomic segments, which are responsible for the creation of virus internal proteins, led to the fact that the H5 gene split into ten different clades, each with its own unique characteristics. [13,14]. These discoveries are key for the development of new vaccines and medicines, as they allow for a deeper understanding of the mechanisms of virus adaptation and evolution [15,16,17]. Monitoring the genetic diversity of influenza viruses is important to ensure a rapid response to epizootics, as well as to preserve human health [18].

The purpose of the study is to analyze the causes of avian influenza in the Kaluga region, to assess the effectiveness of preventive and liquidation measures, to determine the forecast of the situation with Highly Pathogenic Avian Influenza for 2024-2025.

2 Materials and methods

The research was carried out using materials provided by the Veterinary Committee under the Government of the Kaluga Region, including the order of the Ministry of Agriculture dated 03/24/2021 No.158 "On approval of Veterinary rules for the implementation of preventive, diagnostic, restrictive and other measures, the establishment and cancellation of the quarantine and other restrictions aimed at preventing the spread and elimination of highly pathogenic avian influenza foci"; an action plan to eliminate the epizootic focus of highly pathogenic avian influenza; a plan to prevent the spread of the pathogen highly pathogenic avian influenza in the Kaluga region.

Kaluga Region is a part of the Central Federal District, bordered by the Moscow, Bryansk, Oryol, Tula and Smolensk regions. The region has 24 municipal districts and 2 urban districts. A number of large poultry enterprises are located in the region.

3 Results and discussion

In 2022, 12 cases of poultry infection with H5N1 and H7N9 strains, wild - H5N8 were recorded in the Kaluga region. The foci of the disease were located in 7 districts of the region (Fig.1).

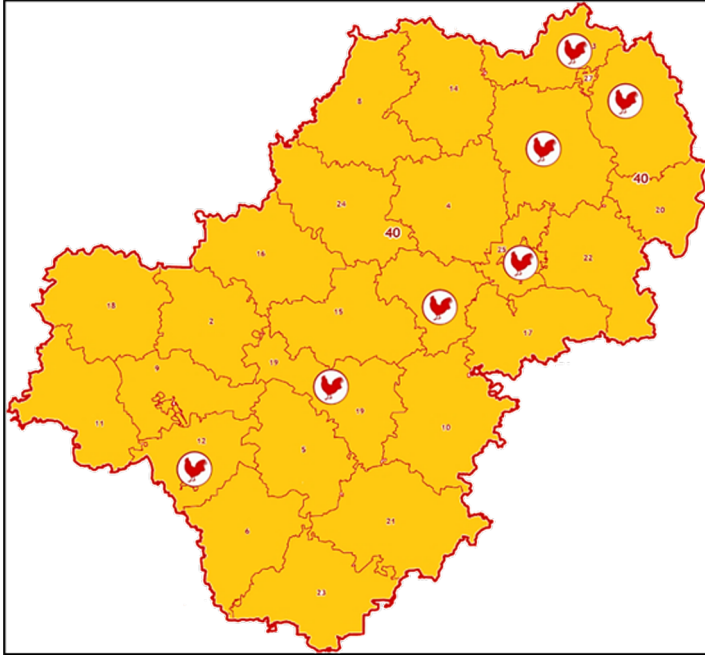


Fig.1. Infection foci detected in the Kaluga Region in 2022.

Poultry kept in private households and backyards of citizens were infected. Large poultry enterprises were not affected. The outbreak of infection began with the purchase of infected young poultry by farm owners at the fair, which allowed the virus to spread to other areas of the region. The infected young birds were brought from the Kursk region, which was previously unfavorable according to Highly Pathogenic Avian Influenza.

A distinctive feature of the disease was its lightning-fast development. There were no usual clinical signs of influenza, but there was a refusal to feed, a decrease in activity. During the examination of the dead individuals, hidden pathologies were revealed: minor hemorrhages, pancreas inflammation, its consistency is flabby, collapsing with the least contact; the spleen is enlarged, with spot hemorrhages on the surface; the presence of exudate in the duodenum, edematous mucosa with hemorrhages. Areas of hemorrhages were found on the organs of the reproductive system and lungs. Some of the dead individuals had serous discharge from the nasal openings.

During the health measures for the period 2022, 12 foci of avian influenza were eliminated in seven administrative districts of the region and in the city of Kaluga. Measures to eliminate foci of the disease were carried out in accordance with the order of the Ministry of Agriculture of the Russian Federation "On approval of Veterinary rules for the implementation of preventive, diagnostic, restrictive and other measures, the establishment and cancellation of the quarantine and other restrictions aimed at preventing the spread and elimination of highly pathogenic avian influenza foci". For each disease case, the governor of the region imposed quarantine and approved a plan of liquidation measures.

To prevent further infection, drastic measures had to be taken: to destroy all birds not only in 12 foci of infection, but also within a radius of 5-10 km around them. In total, 21 thousand poultry from private farms were seized and slaughtered during the events.

In accordance with the orders of the Veterinary Committee under the Government of the Kaluga Region, veterinary specialists organized a walkover for private subsidiary farms, towns, villages, garden non-profit associations and other settlements. During the walkover, an explanatory conversation was held with citizens, counting poultry, familiarizing owners who contain poultry about measures to prevent avian influenza. Upon detection of dead wild, synanthropic and domestic poultry, pathological materials were hermetically packed and sent to the State Budgetary Institution of the Kaluga Region "Regional Animal Disease Station and Veterinary Laboratory" for research on Highly Pathogenic Avian Influenza. Preventive and liquidation measures were carried out on the territory of epizootic foci.

By the decision of the special anti-epizootic commission in the Kaluga region, buffer zones were created around poultry farms in 2022. At a distance of at least 5 km from large farms, it is recommended not to engage in poultry farming without providing a high level of biological protection. At the same time, compensation measures are provided for the complete abandonment of poultry. This has made it possible to increase the level of biosafety of enterprises. The use of vaccination as a preventive measure for large poultry farms is not recommended.

In 2023, 1 case of avian influenza virus in seagulls was registered in the Kaluga Region. This suggests that as a result of virus mutations, seagulls have become more susceptible, thereby becoming the main sources of infection (Fig.2).

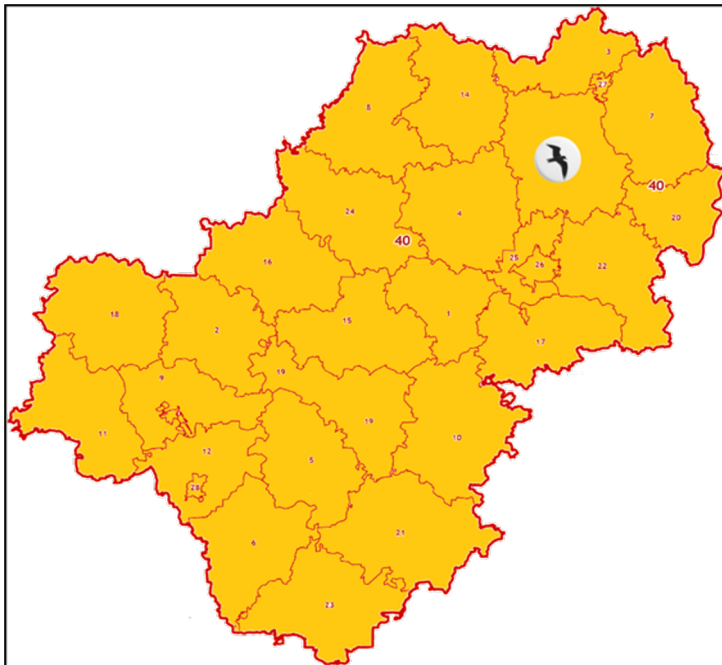


Fig. 2. The outbreak of infection detected in the Kaluga region in 2023.

In total, 192 dead seagulls were detected and destroyed during the quarantine period, 175 laboratory diagnostic studies were conducted. After the elimination of disease outbreak in seagulls, no cases of avian influenza were detected in other species (ducks, geese and others). To date, the H5N1 strain has undergone changes, which has made it easier for seagulls to infect resident bird species. It was a matter of concern that seagulls can spread this virus both

on poultry farms and among remote seabird colonies, creating a universal threat. For most regions of the Russian Federation, this bird species has become a synanthrope. The migration of seagulls causes the spread of infection and infection of resident birds. The main nesting sites of seagulls are ponds, lakes, floodplains and river deltas, swamps. Due to the occurrence of outbreaks among the livestock of wild near-water birds, it is worth monitoring the number of birds, especially representatives belonging to hunting sites. Wild bird registration should be carried out 3 times a year - in spring, summer and autumn. This will help to track spring migration, nesting processes after hatching, and autumn migration. The registration sheet reflects the type of bird, the number of individuals encountered in a given area, a description of the route or observation platform. Since 2023, this measure has been applied in some regions of the Russian Federation.

The main tasks in case of Highly Pathogenic Avian Influenza outbreaks is to carry out work to increase the biosecurity level of enterprises operating in closed mode and strengthen control over the implementation of veterinary legislation; the application of the principle of regionalization; ensuring traceability of products using information systems.

The possibility of susceptible livestock vaccination is controversial. There are several problems that every veterinary specialist will have to face. First, the emergence of new infection foci among vaccinated poultry. The vaccine uses one of the field strains circulating in the area. During vaccination, there is a possibility of circulation of another field strain, which leads to the emergence of a potentially new strain of the virus in the bird's body. Second, it is difficult to diagnose Highly Pathogenic Avian Influenza in poultry, because when a vaccinated bird is infected, clinical signs of the disease will not appear, but a reservoir of infection is created. Mechanical transfer of the pathogen is also possible.

The main preventive measures remain to increase the biosafety level of poultry enterprises, active monitoring of infection among wild migratory birds. The decision to use vaccines should be based on an assessment of all possible risks, only in emergency cases. Large enterprises must operate in a "closed" mode, use barrier systems, and carry out mandatory disinfection of premises after each batch of poultry and containers is released for product acceptance.

4 Conclusion

The active circulation of several highly pathogenic strains of avian influenza virus observed in the Kaluga Region in 2022-2023 has caused serious concern among veterinary specialists. Significant interest in this topic is explained by the fact that the variants of the virus identified in this region can have a noticeable impact on the health of both animals and humans. It is important to note that registered outbreaks of avian influenza have occurred among owners of private subsidiary farms. Outbreaks of avian influenza at large poultry farms in the region have not been recorded, which indicates a high level of biosafety. Through the work of the State Veterinary Service and owners of large poultry enterprises, the information and explanatory work carried out with citizens in the region, it was possible to minimize the risk of infection of poultry livestock.

Based on the data of the antiepidemic situation in the territory of the Russian Federation, it is worth noting that the forecast for 2024-2025 may be unfavorable for the Highly Pathogenic Avian Influenza. A possible peak of infection should be expected during the period of mass migration of wild migratory birds (April-May, September-October). The detection of human infection with new strains of influenza viruses is added to the list of alarming factors. It is necessary to strengthen control over compliance with veterinary rules for poultry both at large poultry enterprises and in personal subsidiary and farms. The current situation with the Highly Pathogenic Avian Influenza requires additional study and development of measures to prevent future epidemics. Monitoring the spread of infection,

carrying out effective sanitary and antiepidemiological measures will be key in ensuring public health.

References

1. V.N. Irza, M.S. Volkov, A.V. Varkentin, Effective animal husbandry, **5**, 180 (2022). URL: <https://cyberleninka.ru/article/n/o-tekushey-panzootii-vysokopatogennogo-grippa-ptits> (date of application: 01/25/2024)
2. O.I. Zakharova, O.A. Burova, N.N. Toropova et al., Agrarian science of the Euro-North-East., **23(3)**, 295-306 (2022). DOI 10.30766/2072-9081.2022.23.3.295-306, EDN HMLRJQ.
3. V.N. Irza, Avian influenza. The epizootic situation of avian influenza in the world and the Russian Federation. Measures for avian influenza, Proceedings of the All-Russian Research Institute of Experimental Veterinary named after Y.R. Kovalenko, **82** 250-254 (2021). EDN XPSPOC.
4. A.Ya. Bondarev, D.M. Evstafiev, *Highly pathogenic avian influenza: current state, virus spread and control measures*, The role of agrarian science in sustainable rural development: Collection of the VIII All-Russian (national) scientific conference with international participation, Novosibirsk, December 20, 2023 (Novosibirsk: IC NGAU "Zolotoy Kolos", 2023) 331-335, EDN PCYLCX.
5. V.Yu. Marchenko, N.I. Goncharova, E.V. Gavrilova, R.A. Maksyutov, A.B. Ryzhikov, Review of the epizootological situation of highly pathogenic avian influenza in Russia in 2020, *Problems of particularly dangerous infections*, **2** (2021). URL: <https://cyberleninka.ru/article/n/obzor-epizootologicheskoy-situatsii-po-vysokopatogennomu-grippu-ptits-v-rossii-v-2020-g> (date of application: 01/25/2024).
6. V.Yu. Marchenko, S.V. Svyatchenko, G.S. Onkhonova et al., Problems of particularly dangerous infections, **1**, 48-55 (2023). DOI 10.21055/0370-1069-2023-1-48-55, EDN WEIXQX.
7. R.S. Gonzalez, Unravelling the pathobiological diversity of highly pathogenic avian influenza in birds: specialty 03/14/02 "Pathological anatomy": dissertation for the degree of Candidate of Veterinary Sciences, (Belaterra, 2019) 212. EDN AXIYVG.
8. M.R. Abayeva, B.S. Userbayev, S.K. Kendirbayeva, K.T. Sultankulova, Science, new technologies and innovations of Kyrgyzstan, **2**, 30-33 (2023). DOI 10.26104/NNTIK.2023.51.31.006, EDN ZRVFLK.
9. V.Yu. Marchenko, N.I. Goncharova, T.N. Tran et al., Problems of particularly dangerous infections, **2**, 31-37 (2020). DOI 10.21055/0370-1069-2020-2-31-37, EDN RNIOIO.
10. M. Volkov, Animal husbandry of Russia, **S3**, 50-54 (2021). EDN JKTONY.
11. V. N. Irza, E. D. Javadov, I. M. Sazhaev et al., Avian influenza, BIO, **1(244)**, 24-30 (2021). EDN EYZFGO.
12. S.A. Zykov, Efficient animal husbandry, **4(152)**, 78-79 (2019). EDN SSFWRW.
13. A.A. Pechenkina, Bulletin of Modern Research, **5-1(35)**, 16-20 (2020). EDN HIDKEZ.
14. D. Karo-Karo, R. Bodewes, R. Restuadi et al., Viruses, **14(10)**, 2216 (2022). DOI 10.3390/v14102216, EDN YQTORO.
15. E. Boravleva, A. Gambaryan, Microbiology Independent Research Journal, **5(1)**, 22-28 (2018). DOI 10.18527/2500-2236-2018-5-1-22-28 EDN YTGZRJ.
16. A.Yu. Selyutina, T.A. Spasskaya, *Agronomy, animal husbandry, economics*, **1** Moscow-Berlin, (Moscow: Publishing House: Directmedia Publishing LLC, 2021) 117-119.

17. A.V. Frolov, S.V. Pankratov, T. N. Rozhdestvenskaya, S.N. Norkina, A.M. Shestopalov, Avian influenza. Specific prevention, *Veterinary medicine and feeding*, 64-66 (2020).
18. Highly pathogenic avian influenza (review of literature and current legislation), Bulletin of Veterinary Medicine, **2(105)**, 42-49 (2023). EDN MJGXHL.