

How to cite: Abdrakhmanov, S.K., Irene Iglesias, Ibanez-Porras, P., Mukhanbetkaliyev, Y.Y., Mukhanbetkaliyeva, A.A., Ruzmatov, S.I., Kadyrov, A.S., Balgabekova, K.T. (2026). Development of a dashboard for monitoring and risk assessment of highly pathogenic avian influenza in Kazakhstan. *Central Asian J. Vet. Science*, 2(014), 63-70. DOI: [https://doi.org/10.51452/cajvs.2026.2\(014\).2224](https://doi.org/10.51452/cajvs.2026.2(014).2224)

Research article

Development of a dashboard for monitoring and risk assessment of highly pathogenic avian influenza in Kazakhstan

Sarsenbay K. Abdrakhmanov¹ , Irene Iglesias² , Pablo Ibanez-Porras² 
Yersyn Y. Mukhanbetkaliyev¹ , Aizada A. Mukhanbetkaliyeva¹ , Saidulla I. Ruzmatov¹ 
Ablaikhan S. Kadyrov³ , Kamila T. Balgabekova¹ 

¹Institute of Animal Science and Veterinary Medicine

S. Seifullin Kazakh Agrotechnical Research University, Astana, Kazakhstan

²National Institute for Agricultural and Food Research and Technology, Madrid, Spain

³Institute of Physical and Technical Sciences, L.N. Gumilyov Eurasian National University
Astana, Kazakhstan

Corresponding author: Yersyn Y. Mukhanbetkaliyev: ersyn_1974@mail.ru

Co-authors: (1: SA) s_abdrakhmanov@mail.ru; (2: II) irene_iglesias@yahoo.es
(3: PE) pablo.ibanez@inia.csic.es

(4: AM) aizada.1970@mail.ru; (5: SR) saidulla.ruzmatov@mail.ru

(6: AK) kadyrov.ablaikhan@gmail.com; (7: KB) kamila_balgabekova@mail.ru

Received: 22 April 2026 **Accepted:** 19 June 2026 **Published:** 30 June 2026

Copyright: Abdrakhmanov, S.K., et al. This article is an open access article distributed under the terms of the Creative Commons Attribution 4.0 International License (<https://creativecommons.org/licenses/by/4.0/>)

Abstract

Background and Aim. Highly pathogenic avian influenza (HPAI) remains one of the most significant transboundary avian diseases, affecting affecting farmed, synanthropic, and wild bird populations. Migratory wild birds play a crucial role in the long-distance spread of avian influenza viruses across continents. The aim of this study is to develop an interactive geospatial dashboard for monitoring and assessing risk factors associated with HPAI along migration routes in Kazakhstan.

Materials and Methods. Relevant spatial datasets related to the risk of avian influenza spread were integrated into an interactive geospatial dashboard. The analysis included bird migration and ringing data from EURING and the Institute of Zoology, georeferenced wild bird observations from the eBird platform (25,828 records representing 137 species), and outbreak data from the FAO EMPRES-i and WOAHA WAHIS databases. Spatial analysis and data processing were performed using ArcGIS Pro, ArcGIS Online, and the R statistical environment, while species spatial distribution modeling was performed using the MaxEnt algorithm.

Results. Through the integration and analysis of heterogeneous spatial datasets, an interactive geospatial dashboard was developed to assess the spatial distribution and potential spread of highly pathogenic avian influenza (HPAI) in Kazakhstan. The platform combines wild bird observation data from the eBird database, bird ringing and migration data, water body and wetland data, poultry density information, and officially recorded disease outbreaks. Interactive filtering tools allow data to be analyzed by geographic region, taxonomic group, and risk level. Spatial overlay analysis revealed overlap between areas of high wild bird activity and regions with intensive poultry farming, indicating potential ecological interfaces for virus transmission. The developed dashboard provides multi-layered visualization of epizootological data and supports rapid analysis of potential HPAI risk zones in Kazakhstan.

Conclusion. The developed geospatial dashboard is an effective decision-support tool for veterinary surveillance and epidemiological risk assessment. The integration of environmental and epidemiological data enables the rapid identification of potential high-risk areas for the introduction and spread of highly pathogenic avian influenza, facilitating the development of evidence-based surveillance strategies.

Keywords: Highly pathogenic avian influenza; geographic information systems; migratory birds; epidemiological surveillance; spatial analysis; Kazakhstan.

Introduction

Poultry farming is an important sector of Kazakhstan's agricultural economy, ensuring domestic supplies of poultry meat and eggs and contributing significantly to the country's export revenues. In recent years, substantial investment and government development programs have supported the growth of the poultry industry. According to official data, poultry production in Kazakhstan from January to November 2024 reached 326.3 thousand tons, an increase of 9.4% compared to the same period in 2023 [1, 2]. Currently, 67 industrial poultry farms operate throughout the country, including enterprises specializing in broiler, egg, and breeding production [3]. At the same time, the poultry industry is constantly exposed to various risks that can potentially negatively impact the economic performance of the enterprise and issues of ensuring biological safety. One of these risks is the emergence and spread of especially dangerous avian diseases, including highly pathogenic avian influenza [4].

Highly pathogenic avian influenza (HPAI) is a highly contagious transboundary avian disease with zoonotic potential caused by the influenza A virus, which meets the criteria for high pathogenicity [5]. The disease affects both domestic and wild birds and can be episodically transmitted to mammals, including humans [6, 7, 8]. In addition to affecting domestic and wild birds, the virus is increasingly detected in mammals, including foxes, mink, cats, and cattle. The international organizations FAO and WOAH call for strengthened epidemiological surveillance, improved early warning systems, and coordinated international control measures [9].

At the same time, the geographic spread of highly pathogenic avian influenza A(H5N5) viruses among wild birds, whose numbers have increased in greylag geese in recent years, should continue to be closely monitored worldwide [10]. Migratory wild birds, particularly aquatic species, are widely recognized as natural reservoirs of avian influenza viruses and play a crucial role in their intercontinental and continental spread [11].

Kazakhstan occupies a strategically important geographic position at the crossroads of several major migration routes. Specifically, the country lies at the crossroads of three major migration routes: the West Asian-East African, Black Sea-Mediterranean, and Central Asian [12]. These migration routes include important regional corridors such as the West Siberian and Caspian-Black Sea routes. Millions of migratory birds, including geese, ducks, swans, flamingos, herons, and waders, travel along these routes annually. The Central Asian Flyway alone is home to at least 279 populations of migratory waterfowl, representing 182 species [13].

In this regard, spatial epidemiological modelling tools in the form of dashboards integrating data on wild bird migration and environmental factors, as well as expanded international collaboration with organisations such as the Food and Agriculture Organization of the United Nations (FAO) and EURING [14], are needed to strengthen early warning capabilities for the emergence and spread of HPAI. Understanding the spatiotemporal dynamics of wild bird species that may act as reservoirs or vectors of highly pathogenic avian influenza is important for predicting outbreak risks and improving early detection systems [15, 16].

Despite growing interest in spatial avian influenza risk assessment, integrated analytical platforms for veterinary surveillance in Central Asia remain limited. Therefore, developing tools that integrate wildlife observations, environmental data, and disease outbreak information is essential for enhancing regional surveillance capacity. The aim of this study was to develop an interactive geospatial dashboard integrating multiple environmental and epidemiological datasets to assess spatial risk factors associated with highly pathogenic avian influenza along migration routes in Kazakhstan.

Materials and Methods

To develop an interactive geospatial analytical dashboard, relevant spatial data directly related to the assessment of the epizootic risk of HPAI infection was integrated.

The integrated database included information on migration activity and key ornithological locations, including migration routes, ringing sites, stopover sites, and breeding areas of migratory birds whose migration routes pass through the territory of Kazakhstan. The information was provided by the Institute of Zoology of the Ministry of Education and Science of the Republic of Kazakhstan and was also extracted from the international FAO EMPRES-i and EURING databases [17]. Georeferenced observations of species composition aggregated from the eBird citizen science crowdsourcing platform were also used [18]. The total sample size was 25,828 georeferenced records representing 137 wild bird species. These species were classified as "risk taxa" based on an analysis of global data on the spread of highly pathogenic avian influenza (HPAI), a set of ecological features, and taxonomic similarity to documented vectors of the infection.

The integration of these heterogeneous spatial data within a single user interface paved the way for the consolidation of spatial visualization tools and subsequent analytical modeling to assess the seasonality of migration processes and associated epizootic risks. Bird ringing data were used to reconstruct migration routes connecting Kazakhstan with other regions of Eurasia. The EURING database (EDB) contains a significant portion of the ringing return data [19].

Information on HPAI outbreaks (H5N1, H5N8) in wild and domestic birds was obtained from the FAO EMPRES-i and WOA (WAHIS) databases [20]. These data provide insight into long-range ecological relationships and potential routes of virus spread.

Analytical data processing was performed using ArcGIS Pro (ESRI, USA), ArcGIS Online [21], and the R statistical environment [22]. The MaxEnt environment was used to model species distribution. MaxEnt is based on georeferenced points of species locations and raster layers of environmental factors significant for the species [23]. The following environmental covariates were used as predictor raster layers: bioclimatic variables (BIO1–BIO19 from WorldClim v2.1), proximity to open water bodies and wetlands (derived from the Global Surface Water dataset), normalized difference vegetation index (NDVI), and spatial density of poultry farming enterprises. The dataset was partitioned into training (75%) and testing (25%) subsets using random spatial blocking to minimize spatial autocorrelation. Model performance was evaluated using the area under the receiver operating characteristic curve (AUC); the mean AUC across 10 replicate model runs was 0.89 (SD = 0.02), indicating high discriminatory capacity.

All datasets were georeferenced and standardized within a single spatial coordinate system. Duplicate and incomplete records were removed, and spatial verification of observation coordinates was performed.

Results

As a result of the research, an interactive geospatial dashboard was developed through the integration, visualization, and analysis of existing data into a single user interface. This dashboard supports multilayered display and assessment of the spatial distribution and potential spread of highly pathogenic avian influenza (HPAI) in Kazakhstan. Interactive filtering tools allow data exploration by geographic area, taxonomic group, and risk level.

Specifically, the developed unified geospatial analytical platform integrates multiple heterogeneous spatial datasets. These include wild bird observation data from the eBird database, bird ringing and migration data, waterbody and wetland data, and poultry density data obtained from databases, enabling the visualization, exploration, and assessment of risks in near real time.

The platform is designed as a multi-layered geospatial system that allows users to combine and visualize multiple data sets relevant to HPAI transmission dynamics (Figure 1).

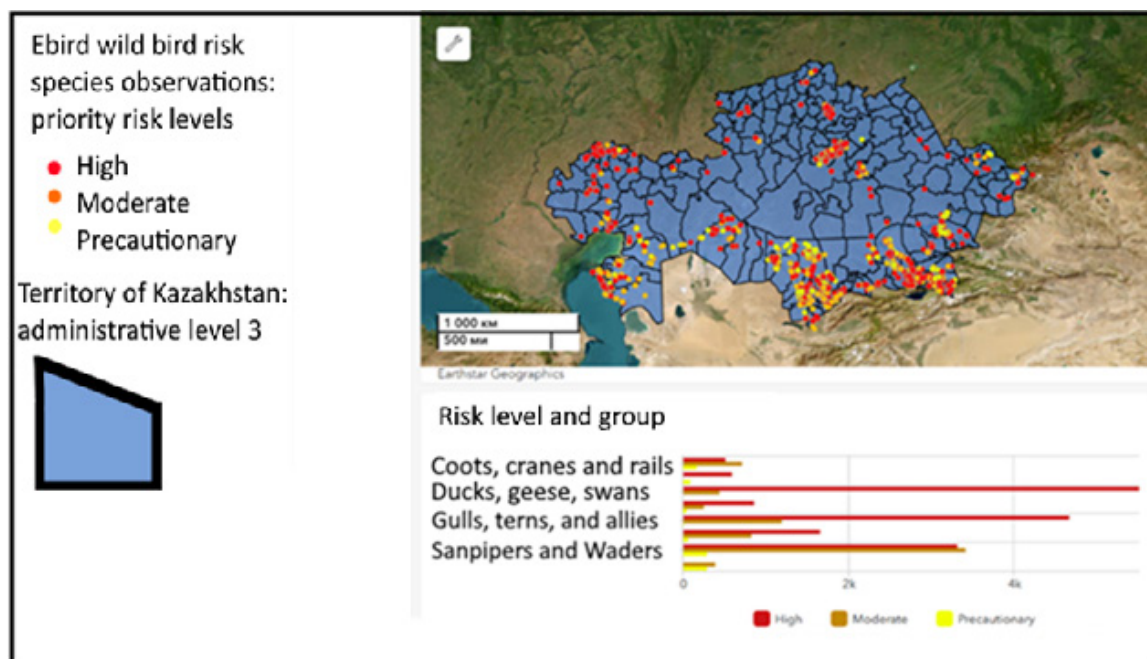


Figure 1. Distribution of wild bird observations by avian influenza risk groups in Kazakhstan, obtained from the eBird database

The dashboard includes several interactive components presenting key categories of wild bird observation risk data, derived from the eBird database. Observations are grouped according to taxonomic and ecological risk categories, including waterfowl, shorebirds, gulls, and other species known to play a role in maintaining and spreading the virus.

Data on bird ringing sites and migration routes make it possible to track the connections and routes of cross-border movement of potential carriers of the avian influenza virus. Thus, migration routes reconstructed based on bird ringing data demonstrate extensive ecological interconnections between Kazakhstan and many regions of Eurasia, indicating potential routes for the long-distance spread of avian influenza viruses (Figure 2).

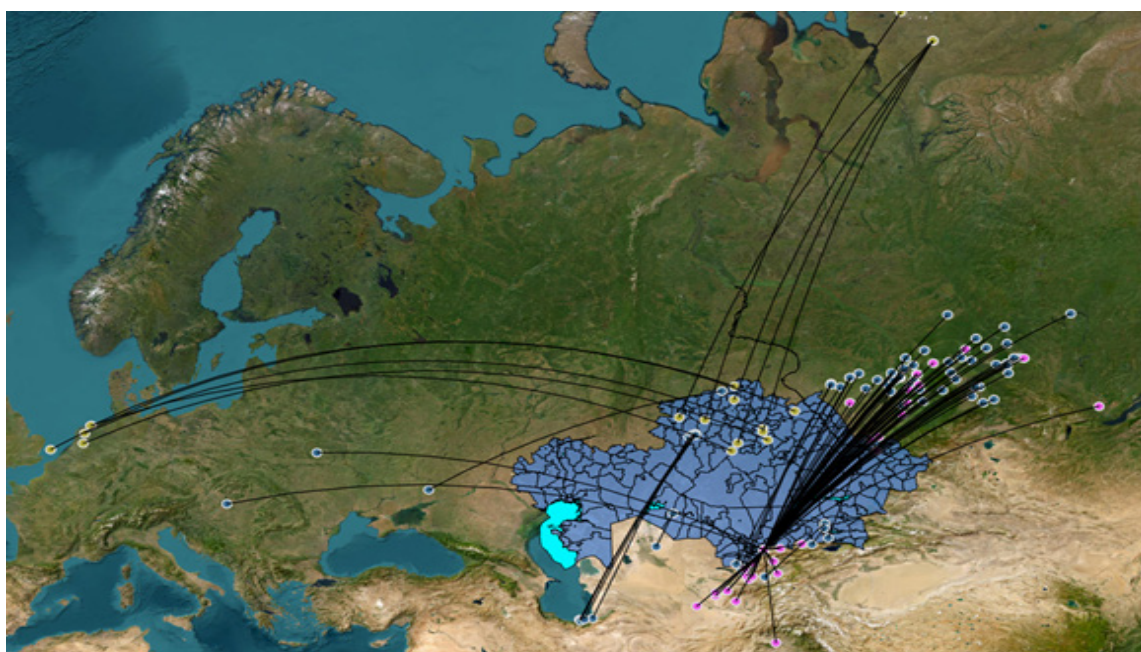


Figure 2. Migratory connection of wild birds with Kazakhstan, obtained on the basis of bird ringing data

The platform also allows for comparison of observed disease outbreaks, i.e., the current epizootic situation, with spatial patterns of predicted disease spread risk. This is additionally accomplished by using data on officially registered cases of highly pathogenic avian influenza outbreaks among wild and domestic birds (Figure 3).

Overlap analysis revealed partial spatial overlap between areas with high wild bird observation densities and regions characterized by intensive poultry farming. These ecological boundaries may represent potential hotspots for virus spread between wild and domestic bird populations.

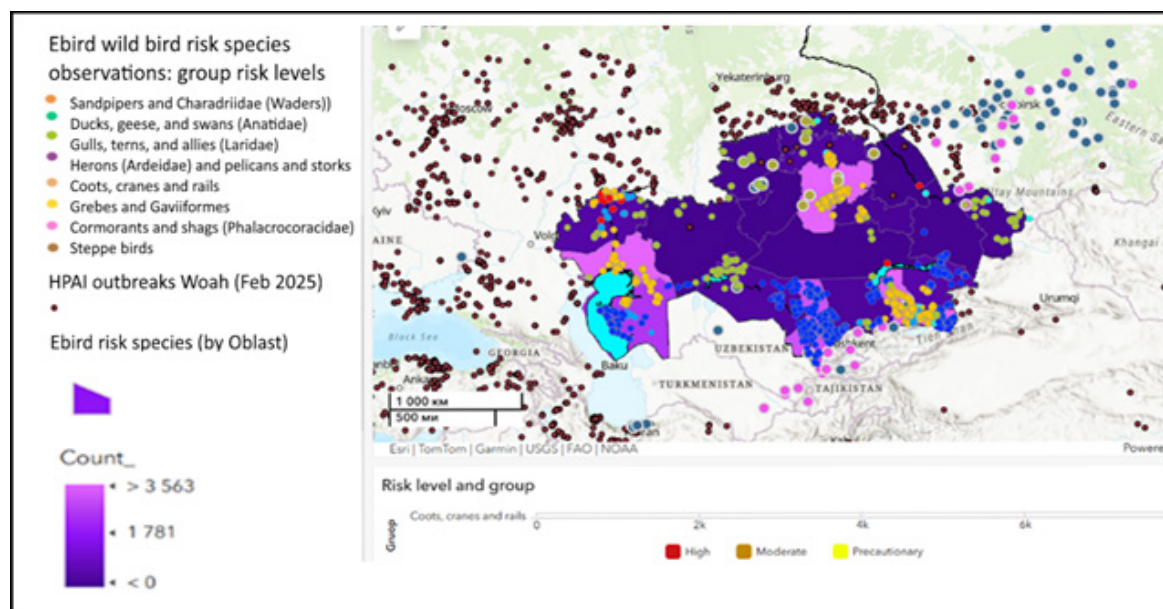


Figure 3. Spatial relationship between wild bird observations, poultry density and reported outbreaks of highly pathogenic avian influenza (HPAI)

Overall, the developed geospatial information dashboard represents an effective digital tool for risk monitoring and early warning of the emergence and spread of HPAI in Kazakhstan, contributing to a better understanding of the spatial interactions between wild bird reservoirs and poultry farming systems.

Discussion

The dominant factor determining the epizootic risk of the emergence and spatial spread of highly pathogenic avian influenza (HPAI) in the Republic of Kazakhstan is the large number and taxonomic diversity of migratory ornithocomplexes that annually cross the country's territory [24]. According to existing estimates, approximately 50 million individuals of waterfowl and semi-aquatic birds stopover in Kazakhstan's water bodies during the spring and autumn migration periods, confirming the country's status as one of the key and natural continental hubs for the concentration of migration flows [25, 26].

A key functional element of the developed geospatial analytical panel is the ability to differentiate risk assessment based on the species of birds present in a specific geographic region. Of fundamental importance here is the fact that different species demonstrate varying degrees of involvement in the circulation and transmission of the HPAI virus. In the context of this study, based on an analysis of global epizootological data, a set of ecological characteristics, and taxonomic similarity with verified carriers of the infection, 137 avifauna species found in Kazakhstan were identified as potentially dangerous taxa (risk species) [27].

The integration of heterogeneous ecological and epizootological datasets within a single interactive geospatial monitoring platform represents a methodologically promising approach aimed at improving the epidemiological surveillance system for highly pathogenic avian influenza. The spatial patterns identified during the study correlate with known migratory routes and the habitats of wetland ecosystems that support large populations of waterfowl. The spatial overlap of wild avifauna habitats and industrial poultry farming sites forms an epizootically significant ecological cluster within which HPAI virus transmission events from wild reservoir hosts to poultry are highly likely to occur. The implementation

of interactive monitoring systems based on geographic information systems (GIS) technologies creates the preconditions for increasing situational awareness and information and analytical support for epizootological surveillance strategies for transboundary animal and bird infections based on risk assessment principles.

From a practical standpoint, the developed dashboard can be actively operationalized within the targeted active surveillance frameworks of state veterinary inspectorates. Specifically, risk zone maps generated by the platform can serve as the basis for scheduling preventive inspections of commercial poultry farms located within high-risk buffer zones identified by spatial overlay analysis. During peak spring and autumn migration periods, inspectorates may use the dashboard's real-time filtering tools to prioritize biosecurity audits and intensify clinical and virological monitoring in farms situated within 10–15 km of major stopover wetlands or ringing recovery hotspots. Integration of the platform's outputs into national animal health information systems (e.g., the electronic veterinary reporting module of the Ministry of Agriculture of the Republic of Kazakhstan) would further enhance the timeliness and evidence-based nature of surveillance responses to emerging HPAI threats.

Conclusion

The developed geospatial dashboard represents an effective analytical and decision-making support tool for monitoring the risk of highly pathogenic avian influenza in Kazakhstan. By integrating multiple spatial datasets related to wild bird ecology, environmental conditions, and poultry farming, the system enables the rapid identification of areas where conditions may favor the introduction and spread of the virus. The approach presented in this study can contribute to the development of advanced veterinary surveillance systems and can be adapted for monitoring other transboundary animal and avian diseases.

Authors' Contributions

SA developed the concept and design of the study. II, PP, AM, SR, YM, AK and BK: conducted a comprehensive literature search, analyzed the collected data, and drafted the manuscript. SA and YM: Performed final revision and proofreading of the manuscript. All authors have read, reviewed, and approved the final manuscript.

Acknowledgements

This research was funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan, Grant No. AP23489183 “Epidemiology of avian influenza and development of preventive measures based on methods of quantitative epidemiology and information and communication technologies”.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

References

- 1 Bekshin, Z., Temirbekova, A., Nurbekova, Z., Amirkhanova, N., Satenova, A., Askarov, A., Zakarya, K., Abduraimov, Y., Rsaliyev, A. (2025). Epidemiology, Virology, and Control of Highly Pathogenic Avian Influenza in Kazakhstan. *Pathogens*, 14(11), 1084. DOI: 10.3390/pathogens14111084.
- 2 Sultankulova, K.T., Argimbayeva, T.U., Aubakir, N.A., Bopi, A., Omarova, Z.D., Melisbek, A.M., Karamendin, K., Kydyrmanov A., Chervyakova, O.V., Kerimbayev, A.A., Burashev, Y.D., Kasymbekov, Y.T., Orynbayev, M.B. (2024). Reassortants of the Highly Pathogenic Influenza Virus A/H5N1 Causing Mass Swan Mortality in Kazakhstan from 2023 to 2024. *Animals (Basel)*, 14(22), 3211. DOI: 10.3390/ani14223211.
- 3 Abenova, A.Z., Mukhanbetkaliyev, Y.Y., Kadyrov, A.S., Sytnik, I.I., Shevtsov, A.B., Korennoy, F.I., Martin, I.I., Perez, A.M., Abdrakhmanov, S.K. (2025). Environmental Suitability of Kazakhstan to Highly Pathogenic Avian Influenza Using Data on Eurasian Outbreaks, 2020-2024. *Viruses*, 17(4), 574. DOI: 10.3390/v17040574.

- 4 Zikibayeva, K.B., Svanbayev, A.A., Akhmetsadykov, N.N., Kudaibergenova, K.N., Akhmetsadykova, S.N., Nurolda, E.N., Kydyrmanov, A.I. (2025). Epidemiological investigation of poultry infectious in Kazakhstan (2021–2024). *Front. Vet. Sci.*, 11, 1520606. DOI: 10.3389/fvets.2024.1520606.
- 5 Alexakis, L., Buczkowski, H., Ducatez, M., Fusaro, A., Gonzales, J. L., Kuiken, T., Ståhl, K., Staubach, C., Svartström, O., Terregino, C., Willgert, K., Melo, M., Kohnle, L. (2025). Avian influenza overview December 2024–March 2025. *EFSA Journal*, 23(4). DOI: 10.2903/j.efsa.2025.9352.
- 6 Su, Y., Wu, R., Liu, P., Li, Z., Pu, J., Wang, L. (2026). Integrated region-specific modeling of H5 avian influenza in Asia using ENSO-based forecasts. *One Health*, 22, 101322. DOI: 10.1016/j.onehlt.2026.101322.
- 7 Behravesh, C.B., Charron, D.F., Liew, A., Becerra, N.C., Machalaba, C., Hayman, D.T., Mettenleiter, T.C. (2024). An integrated inventory of One Health tools: Mapping and analysis of globally available tools to advance One Health. *CABI One Health*, 3(1).
- 8 Burdakov, A.V., Ukharov, A.O., Wahl, T.G. (2013). One Health Surveillance with Electronic Integrated Disease Surveillance System. *Online Journal of Public Health Informatics*, 5(1), e199.
- 9 WHO/OIE/FAO H5N1 Evolution Working Group. (2012). Continued evolution of highly pathogenic avian influenza A (H5N1): updated nomenclature. *Influenza and Other Respiratory Viruses*, 6, 1–5. DOI:10.1111/j.1750-2659.2011.00298.x.
- 10 Abdrakhmanov, S.K., Mukhanbetkaliyev, Y.Y., Ruzmatov, S.I., Mukhanbetkaliyeva, A. A.. (2025). Spread of highly pathogenic avian influenza in Kazakhstan: investigating the role of bird migration and threats to poultry farming. *Herald of science of S. Seifullin Kazakh Agrotechnical Research University: Veterinary Sciences*, 3(011), 52–60. DOI:10.51452/kazatuvc.2025.3(011).2013.
- 11 Dupas, M.C., Vincenti-Gonzalez, M.F., Dhingra, M., Guinat, C., Vergne, T., Wint, W., Dellicour, S. (2024). Global risk mapping of highly pathogenic avian influenza H5N1 and H5Nx in the light of epidemic episodes occurring from 2020 onward. *bioRxiv*, 2024–11. DOI:10.7554/eLife.104748.4.
- 12 Iglesias, I., Ruzmatov, S., Ibañez-Porras, P., Kadyrov, A., Bakishev, T., Korennoy, F., Abdrakhmanov, S. (2025). Risk assessment of highly pathogenic Avian Influenza (HPAI) in wild bird species in Kazakhstan. *German Journal of Veterinary Research*, 5(3), 76–93.
- 13 Bakishev, T.G., Bakisheva, Z.S., Yessembekova, G.N., Shirobokova, D.S., Kairzhanova, A.D., Syzdykova, A.S., Akzhunussova, I. (2025). Epizootic situation and comprehensive diagnosis of equine salmonellosis-associated abortion in the Republic of Kazakhstan. *Herald of science of S. Seifullin Kazakh Agrotechnical Research University: Veterinary Sciences: Veterinary Sciences*, 2(010), 93–100. DOI:10.51452/kazatuvc.2025.2(010).1952.
- 14 Nisaa, Z., Häsler, B., Bennani, H., Jorquera, R., Scolamacchia, F., Alarcon, P. (2025). Global Economic Impacts of High Pathogenic Avian Influenza: A Systematic Review and Impact Framework. DOI:10.2139/ssrn.5641855.
- 15 Rehman, S., Batool, K., Lokapirnasari, W.P., Ullah, S., Khan, M.S., Abubakar, A.A., Jamal, M. (2024). The evolution of H5N1 influenza viruses in Indonesia to mammalian hosts: a review of molecular markers. *World's Poultry Science Journal*, 80(2), 349–370. DOI:10.1080/00439339.2023.2294268.
- 16 Pak, S.-I., Jheong, W.-H., Lee, K.-N. (2019). A GIS-Based Spatial Analysis for Enhancing Classification of the Vulnerable Geographical Region of Highly Pathogenic Avian Influenza Outbreak in Korea. *Journal of Veterinary Clinics. The Korean Society of Veterinary Clinics*, 36(1), 15.22. DOI:10.17555/jvc.2019.02.36.1.15.
- 17 Davis, C.T., Chen, L.M., Pappas, C., Stevens, J., Tumpey, T.M., Gubareva, L.V., Katz, J.M., Villanueva, J.M., Donis, R.O., Cox, N.J. (2014). Use of highly pathogenic avian influenza A(H5N1) gain-of-function studies for molecular-based surveillance and pandemic preparedness. *mBio*, 5(6), e02431-14. DOI:10.1128/mBio.02431-14.
- 18 Sayseng, J.O., Chuang, T.-W. (2025). Integrating citizen science and remote sensing data to identify key environmental factors influencing H5N1 avian influenza virus potential spillover risk in the Philippines. *GeoHealth*, 9, e2025GH001405. DOI:10.1029/2025GH001405.
- 19 Orkara, Sh., Khamzina, A., Sandybayev, N., Sattarova, R., Davletova, A., Khamzin, K., Pokharel, K., Ibragimov, P., Burambayeva, N., Smagulov, D. (2025). Epidemiological landscape and

genetic prospects for marker-assisted selection in Kazakh sheep. *Frontiers in Veterinary Science*, 12. DOI:10.3389/fvets.2025.1647959.

20 Alexakis, L., Buczkowski, H., Ducatez, M., Fusaro, A., Gonzales, J.L., Kuiken, T., Mirinavičiūtė, G., Ståhl, K., Staubach, C., Svartström, O., Terregino, C., Willgert, K., Melo, M., Kohnle, L (2025). Scientific report: Avian influenza overview March–June 2025. *EFSA Journal*, 23(7): 9520, 65. DOI: 10.2903/j.efsa.2025.9520.

21 Turner, A. (2025). Environmental Risk Factors for Highly Pathogenic Avian Influenza in Pennsylvania's Commercial Poultry Industry. West Chester University Graduate Theses, Dissertations, and Final Projects. 3. https://digitalcommons.wcupa.edu/all_capstones/3

22 Plaza, P., Santangeli, A., Rosciano, N., et al. (2025). Wild Birds Affected by Highly Pathogenic Avian Influenza A (H5N1) Worldwide: Epidemiological Insights Into the Recent Panzootic. *Global Change Biology*, 31: 10, e70523. DOI:10.1111/gcb.70523.

23 Martelli, L., Fornasiero, D., Martínez-Lanfranco, J.A., Spada, A., Scarton, F., Scolamacchia, F., Manca, G., Mulatti, P. (2025). Exploring the Role of Wild Bird Species in the Transmission of Avian Influenza to Poultry. *Transboundary and Emerging Diseases*, 2025: 2288535, 15. DOI:10.1155/tbed/2288535.

24 Hay, J., Yeh, K.B., Dasgupta, D., Shapieva, Z., Omasheva, G., Deryabin, P., Richards, A.L. (2016). Biosurveillance in Central Asia: Successes and challenges of tick-borne disease research in Kazakhstan and Kyrgyzstan. *Frontiers in Public Health*, 4, 4. DOI:10.3389/fpubh.2016.00004.

25 Biyashev, K.B., Makbuz, A.Z., Biyashev, B.K. (2016). Occurrence of enteroinfectious pathogens in agricultural animals and poultry. *Biol. Med*, 8(2).

26 Tabynov, K., Kuanyshbek, A., Zharmambet, K., Yelchibayeva, L., Karibayev, T., Berdikulov, M., Tabynov, K. (2025). Evaluation of commercial vaccines for efficacy and transmission control against the emergent H5N8 (clade 2.3. 4.4 b) avian influenza virus in Kazakhstan. *Virology*, 610. DOI: 10.1016/j.virol.2025.110601.

27 Zikibayeva, K.B., Svanbayev, A.A., Akhmetsadykov, N.N., Kudaibergenova, K.N., Akhmetsadykova, S.N., Nurola, E.N, Kydyrmanov, A.I. (2025). Epidemiological investigation of poultry infectious in Kazakhstan (2021–2024). *Front. Vet. Sci.*, 11, 1520606. DOI: 10.3389/fvets.2024.1520606.