

Wild passerines as potential carriers and sources of avian influenza viruses in Ukraine, *Front Microbiol* (2026), Muzyka N *et al.*, doi:10.3389/fmicb.2025.1736454

This study investigates the role of wild passerine birds in the ecology and transmission of avian influenza viruses (AIVs) in Ukraine. Through extensive field sampling and virological analyses, the researchers examined the prevalence and diversity of influenza viruses circulating among a wide range of passerine species. The findings demonstrate that these birds can harbor multiple AIV subtypes and may contribute to virus maintenance and dispersal across ecosystems. By highlighting the potential epidemiological importance of passerines alongside traditionally recognized waterfowl hosts, the study improves our understanding of avian influenza dynamics and provides valuable information for wildlife surveillance and early-warning systems aimed at preventing the emergence and spread of zoonotic influenza viruses.

Avian raptors are indicator species and victims of high pathogenicity avian influenza virus HPAIV H5N1 (clade 2.3.4.4b) in Germany, *Sci Rep* (2024), Günther, A *et al.*, doi.org/10.1038/s41598-024-79930-x

This study investigates the impact of highly pathogenic avian influenza virus (HPAIV) H5N1 clade 2.3.4.4b on raptor populations in Germany and evaluates their role in disease surveillance. Combining retrospective and prospective monitoring data, the researchers demonstrate that birds of prey are both highly susceptible to HPAIV infection and valuable indicator species for detecting virus circulation and genetic diversity in wild bird populations. The study documents fatal infections in several raptor species, including white-tailed sea eagle nestlings, during major outbreak years and assesses potential consequences for reproduction and population health. At the same time, serological evidence suggests the emergence of immunity in some populations. The findings highlight the importance of integrating wildlife monitoring with disease surveillance and emphasize the role of raptors as sentinels for the early detection and tracking of highly pathogenic avian influenza viruses in European ecosystems.

Global economic impacts of Highly Pathogenic Avian Influenza: A systematic review and impact framework, *Preventive Veterinary Medicine* (2026), Nisaa, Z *et al.*, doi.org/10.1016/j.prevetmed.2026.106827

This study provides the first comprehensive global assessment of the economic consequences of Highly Pathogenic Avian Influenza (HPAI) outbreaks. Through a systematic review of 85 studies covering 27 countries, the authors quantify the financial burden of HPAI across the poultry sector, government services, public health systems, businesses, and the environment. The review develops a novel impact framework encompassing 135 economic, social, and environmental impact parameters, enabling more standardized and comparable assessments of disease costs across regions and outbreak scenarios. The findings reveal that while direct outbreak-related costs such as culling and surveillance are well documented, broader indirect and non-financial impacts remain poorly quantified. By highlighting major knowledge gaps and methodological inconsistencies, the study provides a robust foundation for future economic evaluations and



cost–benefit analyses of prevention and control strategies. The framework supports evidence-based policy development and strengthens One Health approaches to managing the growing global threat posed by HPAI.

Genesis and Spread of Novel Highly Pathogenic Avian Influenza A(H5N1) Clade 2.3.4.4b Virus Genotype EA-2023-DG Reassortant, Western Europe, Emerg Infect Dis. (2025), Van Borm S *et al.*, doi.org/10.3201/eid3106.241870

This study investigates the emergence, evolution, and geographic spread of the novel highly pathogenic avian influenza virus (HPAIV) H5N1 genotype EA-2023-DG in Western Europe. Using whole-genome sequencing and advanced phylogeographic analyses, the researchers reconstructed the virus's origin and transmission pathways across wild and domestic bird populations. The findings indicate that EA-2023-DG emerged through a reassortment event in the southwestern Baltic Sea region during the summer of 2023, combining genomic segments from the dominant H5N1 genotype circulating in Europe with segments derived from low pathogenic avian influenza viruses. Following its emergence, the virus spread rapidly across northwestern Europe, reaching at least eleven countries within months. By integrating genomic, spatial, and temporal data, the study demonstrates the value of phylodynamic approaches for tracing virus evolution and dispersal. The results provide important insights for avian influenza surveillance, outbreak preparedness, and risk assessment in the context of the ongoing global H5N1 panzootic.

A vaccine central in A(H5) influenza antigenic space confers broad immunity, Nature (2025), Kok, A *et al.*, <https://doi.org/10.1038/s41586-025-09626-3>

This study investigates the emergence and dissemination of the novel highly pathogenic avian influenza virus (HPAIV) H5N1 genotype EA-2023-DG across Western Europe. Using whole-genome sequencing and phylogeographic analyses, the researchers traced the origin of this reassortant virus to the southwestern Baltic Sea region, where genetic exchange between circulating H5N1 viruses and low pathogenic avian influenza viruses likely occurred during the summer of 2023. The study demonstrates how the newly emerged genotype rapidly spread across multiple European countries through wild bird populations, becoming one of the dominant H5N1 genotypes detected during subsequent outbreaks. By combining genomic, spatial, and temporal data, the authors provide valuable insights into the evolutionary processes driving HPAIV diversification and spread. The findings highlight the importance of international surveillance, real-time genome sequencing, and cross-border collaboration for the early detection and monitoring of emerging avian influenza variants.

Attachment and replication of clade 2.3.4.4b influenza A (H5N1) viruses in human respiratory epithelium: an in-vitro study, Lancet Microbe (2026), Bauer, L *et al.*, doi: 10.1016/j.lanmic.2025.101230. Epub 2025 Dec 15. PMID: 41412143

This study investigates the ability of contemporary clade 2.3.4.4b H5N1 avian influenza viruses to attach to and replicate within human respiratory epithelial tissues. Using advanced in vitro



models, the researchers assessed key biological characteristics associated with host adaptation and zoonotic potential. The results provide important insights into how these viruses interact with human respiratory cells and help to evaluate their capacity to infect humans. By improving our understanding of the mechanisms underlying cross-species transmission, the study contributes valuable evidence for pandemic risk assessment and supports ongoing efforts to monitor the public health threat posed by highly pathogenic avian influenza viruses.

All Kappa-Flu related publications can be found here:

<https://zenodo.org/communities/kappaflu/records?q=&l=list&p=1&s=10&sort=newest>

