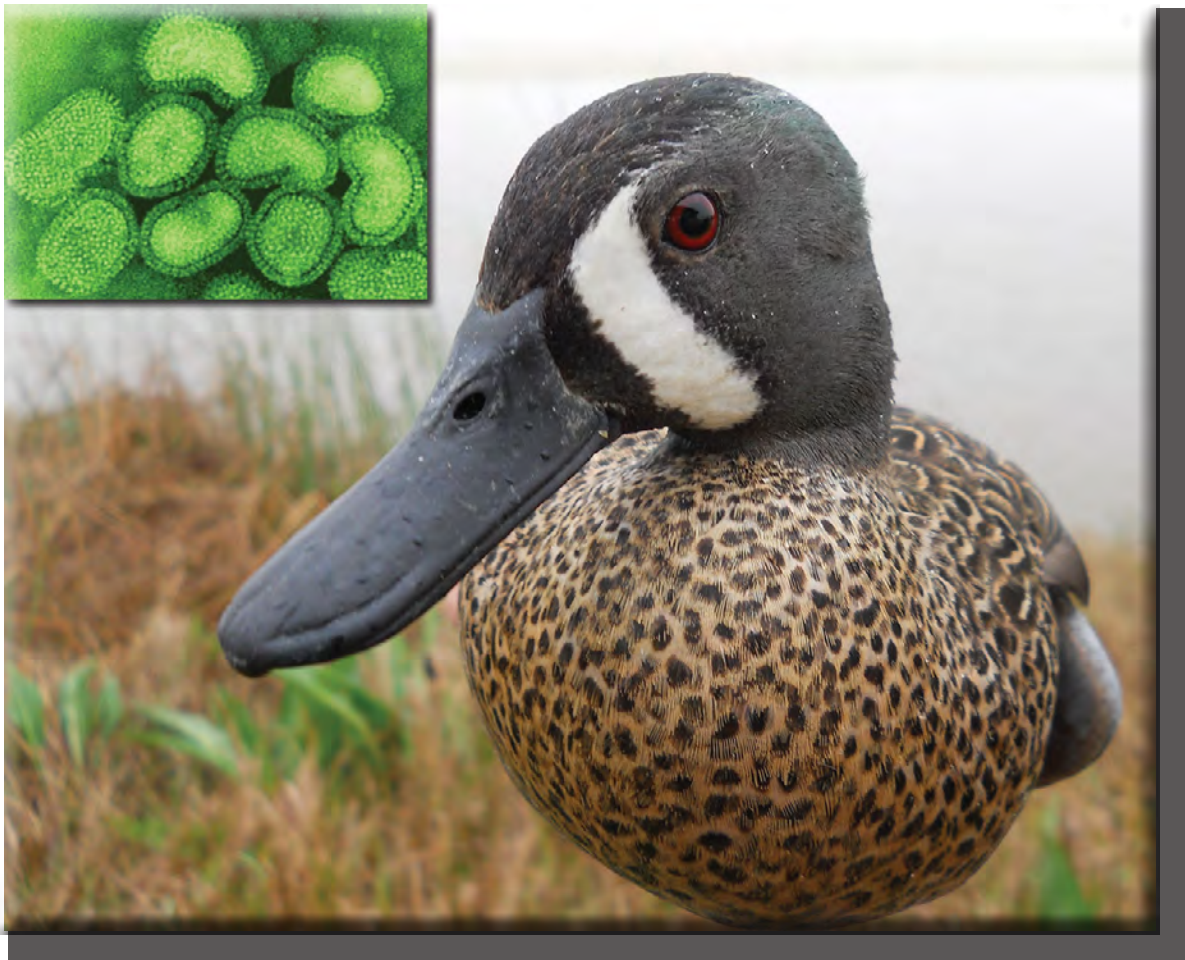


Coordinated by the Interagency Steering Committee for Avian Influenza Surveillance in Wild Migratory Birds

Proceedings of the Highly Pathogenic Avian Influenza and Wild Birds Webinar Series, August 2–5, 2021



Open-File Report 2022–1066

Cover: Blue-winged teal (*Spatula discors*) in Texas. Inset shows avian influenza virus. The first U.S. 2022 wild bird detections of highly pathogenic avian influenza (H5N1) were in South Carolina hunter-harvested blue-winged teal and American wigeon (*Mareca americana*). Photograph by Andrew Ramey, U.S. Geological Survey.

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By M. Camille Hopkins, J. Russ Mason, Giavanna Haddock, and
Andrew M. Ramey

Coordinated by the Interagency Steering Committee for Avian Influenza
Surveillance in Wild Migratory Birds

Open-File Report 2022–1066

U.S. Department of the Interior
U.S. Geological Survey

U.S. Geological Survey, Reston, Virginia: 2022

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Preface

In light of ongoing and geographically widespread highly pathogenic avian influenza (HPAI) outbreaks in wild birds throughout much of Eurasia during 2020–21, the Interagency Steering Committee for Avian Influenza Surveillance in Wild Migratory Birds disseminated an informational memorandum (appendix 1) in January 2021 to highlight the need for enhanced surveillance and heightened awareness in North America. This was followed by coordination of an August 2021 international HPAI webinar series facilitated by the U.S. Department of Agriculture (USDA) Animal and Plant Health Inspection Service (APHIS) Veterinary Services Training Program. Diverse international participation included more than 125 attendees from State and Federal agencies within the United States, Provincial and Federal agencies of Canada, the North American poultry industry, and academic institutions from both within the United States and abroad. This report includes author-submitted abstracts for most of the presentations (that is, all those received) and notes from three guided discussion sessions led by U.S. Federal agency representatives with participation from invited speakers and diverse attendees.

The three sessions of the open webinar series were as follows:

- Update on Global HPAI Situation
- Lessons Learned from North American HPAI Outbreak (2014–15)
- HPAI Challenges and Opportunities

A final closed-door session was held with U.S. Fish and Wildlife Service (USFWS) representatives and State agency members of the four Flyway Councils (Pacific, Central, Mississippi, Atlantic). Designees from each of the specific Flyway Councils serve on the National Flyway Council. Led by Russ Mason of the Michigan Department of Natural Resources, participants in this session were given an overview of the previous days' technical sessions, coupled with suggested steps that member State agencies might take in preparation for a possible HPAI outbreak in migratory waterfowl in 2022 or 2023. Subsequently, these steps were discussed by the Flyway Councils during annual late summer meetings.

Following the webinar series, videos of the three open sessions were posted online for broad dissemination on the USDA APHIS VStep YouTube Channel (https://www.youtube.com/playlist?list=PL2_jEtoY8jj11GMnDwlvDXQGVlbT8-BF).

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Abbreviations

AI	avian influenza
APHIS	Animal and Plant Health Inspection Service
HPAI	highly pathogenic avian influenza
USDA	U.S. Department of Agriculture
USFWS	U.S. Fish and Wildlife Service
USGS	U.S. Geological Survey

Proceedings of the Highly Pathogenic Avian Influenza and Wild Birds Webinar Series, August 2–5, 2021

By M. Camille Hopkins, J. Russ Mason, Giavanna Haddock, and Andrew M. Ramey

Webinar Series Agenda

In light of ongoing and geographically widespread highly pathogenic avian influenza (HPAI) outbreaks in wild birds throughout much of Eurasia during 2020–21, the Interagency Steering Committee for Avian Influenza Surveillance in Wild Migratory Birds disseminated an informational memorandum (appendix 1) in January 2021 to highlight the need for enhanced surveillance and heightened awareness in North America. This was followed by coordination of this

August 2021 international HPAI webinar series facilitated by the U.S. Department of Agriculture (USDA) Animal and Plant Health Inspection Service (APHIS) Veterinary Services Training Program. In addition to heightening awareness, the webinars provided an opportunity for information exchange and facilitated virtual discussions between Federal, State, academic, and international partners on the ongoing Eurasian outbreak, lessons learned from the 2014–15 North American HPAI outbreak, and associated challenges and opportunities.

Agenda for Highly Pathogenic Avian Influenza and Wild Birds Webinar Series, August 2–5, 2021.

[HPAI, highly pathogenic avian influenza; AI, avian influenza; USGS, U.S. Geological Survey; USDA, U.S. Department of Agriculture; USFWS, U.S. Fish and Wildlife Service]

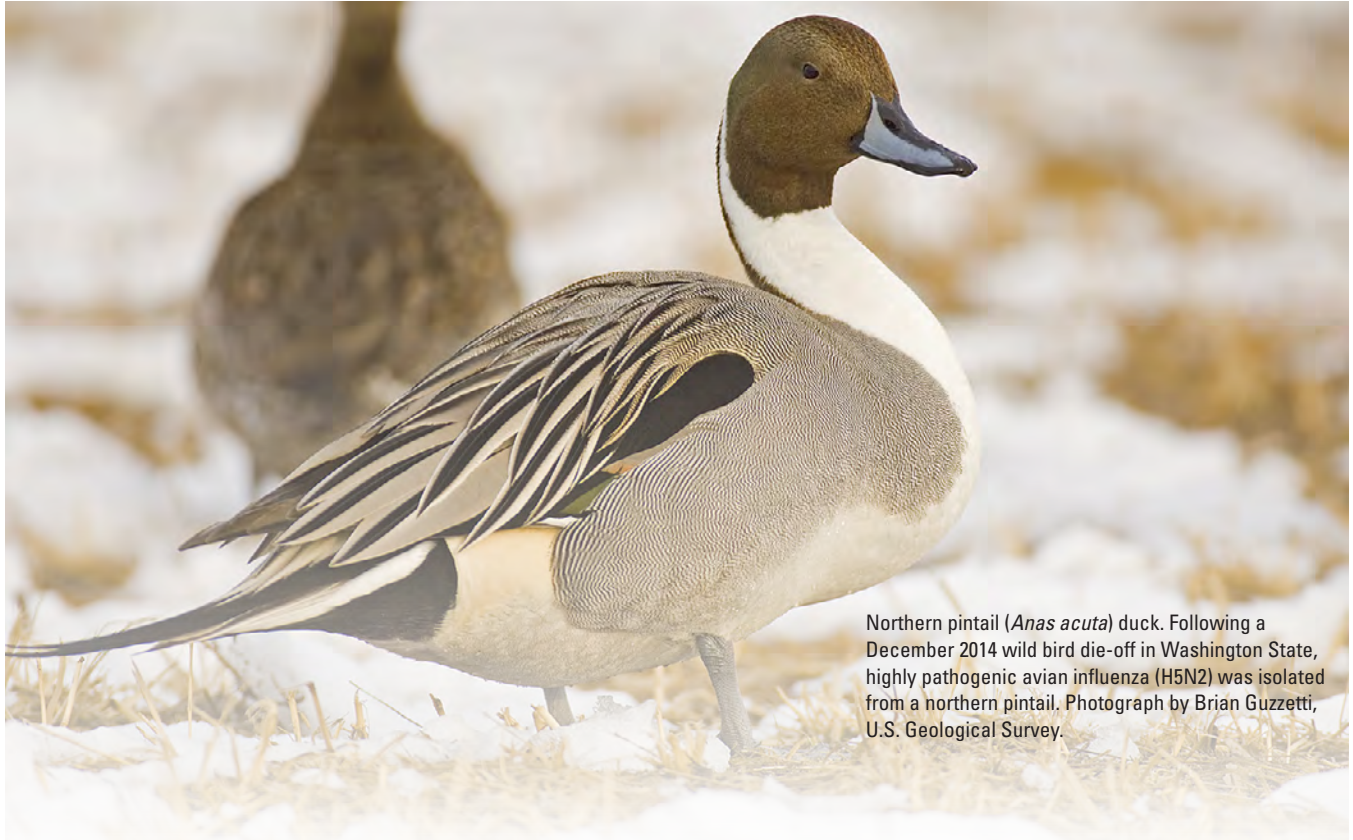
Topic or title	Estimated time on recording	Presenter (affiliation)
Session 1 (August 2, 2021): Update on Global HPAI Situation Recording available at https://www.youtube.com/watch?v=klowKJNYJvk&list=PL2_jEtoY8jij11GMnDwlvDXQGVlbT8-BF&index=2		
Overview: Why HPAI is a concern for wild bird managers in North America	0:00	Camille Hopkins (USGS Ecosystems Mission Area, United States)
Brief introduction on the Global HPAI situation (No abstract provided)	4:20	Jonathan Sleeman (USGS National Wildlife Health Center, United States)
HPAI in wild birds: situational update from Asia	7:30	Yoshihiro Sakoda (Hokkaido University, Japan)
HPAI in wild birds: situational update from Europe (No abstract provided)	29:00	Josanne Verhagen (Erasmus Medical Center, Netherlands)
Infectivity of contemporary HPAI viruses among waterfowl hosts	51:00	Mary Pantin-Jackwood (USDA Agricultural Research Service, Southeast Poultry Research Laboratory, United States)
Migratory birds disperse AI viruses between East Asia and North America via Alaska	1:13:10	Andrew Ramey (USGS Alaska Science Center, United States)
Facilitated discussion for Session 1 topics: Flyway management implications (focus on biosurveillance and early detection)	1:31:45	Jonathan Sleeman (USGS National Wildlife Health Center, United States)

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Agenda for Highly Pathogenic Avian Influenza and Wild Birds Webinar Series, August 2–5, 2021.—Continued

[HPAI, highly pathogenic avian influenza; AI, avian influenza; USGS, U.S. Geological Survey; USDA, U.S. Department of Agriculture; USFWS, U.S. Fish and Wildlife Service]

Topic or title	Estimated time on recording	Presenter (affiliation)
Session 2 (August 3, 2021): Lessons Learned from North American HPAI Outbreak (2014–15) Recording available at https://www.youtube.com/watch?v=Nw4YLaITSfA&list=PL2_jEtoY8jj11GMnDwlvDXQGVlbT8-BF&index=3		
Brief recap of Session 1 and short introduction of North American outbreak of HPAI during 2014–15	0:00	Julianna Lenocho (USDA Animal and Plant Health Inspection Service, National Wildlife Disease Program, United States)
Lessons learned from research and surveillance directed at HPAI viruses in wild birds inhabiting North America	4:00	Thomas DeLiberto (USDA Animal and Plant Health Inspection Service, National Wildlife Research Center, United States)
2014–15 HPAI incursion into the United States	27:25	Hon Ip (USGS National Wildlife Health Center, United States)
Canada lessons learned: 2014–15 wild bird HPAI surveillance (No abstract provided)	46:40	Yohannes Berhane (Canadian Food Inspection Agency, Avian Diseases Unit, Canada)
Canada lessons learned: 2014–15 environmental HPAI surveillance	1:19:35	Chelsea Himsforth (Canadian Wildlife Health Cooperative, Canada)
Facilitated discussion for Session 2 topics: Flyway management implications (importance of vigilance to passive surveillance, rapid response upon detection in North America, interagency coordination, communication strategies, personal protection and biosecurity implications, and characterization of outbreak events)	1:41:50	Julianna Lenocho (USDA Animal and Plant Health Inspection Service, National Wildlife Disease Program, United States)
Session 3 (August 4, 2021): HPAI Challenges and Opportunities Recording available at https://www.youtube.com/watch?v=bDw90f_9mMU&list=PL2_jEtoY8jj11GMnDwlvDXQGVlbT8-BF&index=3		
Brief recap of Session 2 and short introduction of HPAI challenges and opportunities	0:00	Samantha Gibbs (USFWS National Wildlife Refuge System, Wildlife Health Office, United States)
Persistence of AI viruses in the environment	2:50	David Stallknecht (University of Georgia, Southeastern Cooperative Wildlife Disease Study, United States)
Using genetic information from wild bird surveillance to understand transmission of AI viruses between wild birds and poultry	30:45	Dong-Hun Lee (University of Connecticut, United States)
Emerging technologies: Enhancing AI surveillance and risk reduction efforts	49:50	Daniel Walsh (USGS National Wildlife Health Center, United States)
Wild bird movements and AI viruses— Relationships at the wild bird-domestic poultry interface	1:07:20	Diann Prosser (USGS Eastern Ecological Science Center, United States)
Facilitated discussion for Session 3 topics: Flyway management implications and potential mitigation strategies	1:30:40	Samantha Gibbs (USFWS National Wildlife Refuge System, Wildlife Health Office, United States)
Closing comments	2:27:15	Camille Hopkins (USGS Ecosystems Mission Area, United States)
Session 4 (August 5, 2021): Closed-Door Session for USFWS Flyway Representatives and Flyway Council Members		
Discussion of questions and concerns from the webinar series	Not recorded	Russ Mason (Michigan Department of Natural Resources, United States)
Presentation of information to be delivered at Flyway Council meetings	Not recorded	Russ Mason (Michigan Department of Natural Resources, United States)
Discussion of any outstanding questions and concerns following the presentation	Not recorded	Russ Mason (Michigan Department of Natural Resources, United States)



Northern pintail (*Anas acuta*) duck. Following a December 2014 wild bird die-off in Washington State, highly pathogenic avian influenza (H5N2) was isolated from a northern pintail. Photograph by Brian Guzzetti, U.S. Geological Survey.

Author-Submitted Abstracts

Overview: Why Highly Pathogenic Avian Influenza Is a Concern for Wild Bird Managers in North America

Camille Hopkins
U.S. Geological Survey Ecosystems Mission Area, Reston, Virginia, United States

In January 2021, the Interagency Steering Committee for Avian Influenza Surveillance in Wild Migratory Birds disseminated an informational memorandum (appendix 1) regarding the increasing global highly pathogenic avian influenza (HPAI) activity in poultry and wild birds. The committee includes representatives from the U.S. Department of Agriculture, the U.S. Department of the Interior, the Association of Fish and Wildlife Agencies, the National Flyway Council, and the U.S. Agency for International Development. This overview presentation compared the historical perspective of HPAI to the paradigm shift evident during the U.S. 2014–15 HPAI outbreak. Recognizing that migratory bird flyways link global avian influenza dynamics to those in North America, the Steering Committee coordinated this 3-day webinar series to (1) enhance our situational awareness of international avian influenza dynamics, (2) reflect on lessons learned from the 2014–15 U.S. HPAI outbreak, and (3) close with discussions on HPAI challenges and opportunities.

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Highly Pathogenic Avian Influenza in Wild Birds: Situational Update From Asia

Yoshihiro Sakoda

Hokkaido University, Faculty of Veterinary Medicine,
OIE Reference Laboratory for Highly Pathogenic
Avian Influenza and Low Pathogenic Avian Influenza,
Sapporo, Japan

Global dispersion of highly pathogenic avian influenza (HPAI), especially that caused by H5 clade 2.3.4.4, has threatened poultry industries and, potentially, human health. In October 2020, an HPAI virus, A/northern pintail/Hokkaido/M13/2020 (H5N8) (NP/Hok/20) belonging to clade 2.3.4.4b, was isolated from a fecal sample collected at a lake in Hokkaido, Japan, where migratory birds rested. In the phylogenetic trees of all eight gene segments, NP/Hok/20 fell into the cluster of European isolates in 2020 but was distinct from the isolates in eastern Asia and Europe during the winter season of 2017–18. These data imply that HPAI virus clade 2.3.4.4b would have been delivered by bird migration despite the intercontinental distance, although it was not defined whether NP/Hok/20 was transported from Europe via Siberia, where migratory birds nest in the summer season. Given the probability of perpetuation of transmission in the northern territory (set of four islands off the northeastern coast of Hokkaido, Japan), periodic updates of intensive surveys on avian influenza at the global level are essential to prepare for future outbreaks of the HPAI virus.

Control measures in the case of HPAI outbreaks in poultry include culling, surveillance, and biosecurity; wild birds in captivity may also be culled, although some rare bird species may be rescued for conservation. In this study, two anti-influenza drugs, baloxavir marboxil (BXM) and peramivir (PR), used in humans were examined in treating HPAI in birds, using chickens as a model. Chickens were infected with H5N6 HPAI virus and were treated immediately or 24 hours from challenge with 20 milligrams per kilogram (mg/kg) BXM or PR twice a day for 5 days. When treated immediately, BXM significantly reduced virus replication in organs and provided full protection to chickens compared with that induced by PR. In the 24-hour-delayed treatment, neither drug completely inhibited virus replication nor ensured the survival of infected chickens. A single administration of 2.5 mg/kg of BXM was determined as the minimum dose required to fully protect chickens from HPAI virus; the concentration of baloxavir acid, the active form of BXM, in chicken blood at this dose was sufficient for a 48-hour antiviral effect post-administration. Thus, these data can be a starting point for the use of BXM and PR in treating captive wild birds infected with HPAI virus.

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Infectivity of Contemporary Highly Pathogenic Avian Influenza Viruses Among Waterfowl Hosts

Mary Pantin-Jackwood

U.S. Department of Agriculture, Agricultural Research Service, U.S. National Poultry Research Center, Southeast Poultry Research Laboratory, Exotic and Emerging Avian Viral Disease Research Unit, Athens, Georgia, United States

Highly pathogenic avian influenza (HPAI) viruses are a threat to poultry worldwide. The most important natural reservoir of avian influenza viruses are wild waterfowl. Avian influenza viruses, including HPAI viruses, do not usually cause disease in ducks and other wild aquatic birds, the exception being the Goose/Guangdong (Gs/GD) lineage H5 subtype HPAI viruses, some of which can cause moderate to severe disease in waterfowl species. With the continuous occurrence of HPAI outbreaks in poultry it is important to address the role of wild waterfowl in the transmission and spread of these viruses. For many years we have conducted studies examining the pathobiology in different waterfowl species of many strains of HPAI viruses. Infectivity (dose of the virus required to infect the birds), pathogenesis (clinical signs, lesions), presence of the viruses in tissues, duration and titer of virus shed, transmission to contact birds, and seroconversion to the viruses are evaluated. We have found that the pathobiology of HPAI viruses in waterfowl is affected by the strain of the virus and the species, age, health, and immune status of the birds. For most HPAI viruses examined, ducks and geese became infected and transmitted the viruses to contact birds without showing clinical signs. Viruses were also shed for many days by both the oropharyngeal and cloacal routes, which increases the probability of virus spread and transmission. Some of the

Gs/GD H5 lineage viruses, including the clade 2.3.4.4 viruses, replicated to high titers causing systemic disease and mortality in waterfowl. These results help in understanding the role of wild waterfowl in the spread of HPAI viruses around the world, since many of these species are migratory.

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Migratory Birds Disperse Avian Influenza Viruses Between East Asia and North America Via Alaska

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The purpose of this presentation is to convey that there is substantial evidence for the dispersal of avian influenza (AI) viruses by wild birds between East Asia and North America via Alaska and why this pathway of viral dispersal is ecologically and economically relevant. Extensive research and surveillance for AI viruses since approximately 2006 provide us with a clear understanding of common wild bird hosts in Alaska. On one hand, common wild bird hosts of AI viruses in Alaska are generally similar to those reported elsewhere. For example, dabbling ducks and gulls are common hosts of AI viruses in Alaska and across much of the globe. On the other hand, some of the specific species that are most important to viral ecology in Alaska, particularly western portions of the State, have not typically been recognized as the most important hosts of AI viruses elsewhere. Example taxa include northern pintails (*Anas acuta*), emperor geese (*Anser canagicus*), glaucous (*Larus hyperboreus*) and glaucous-winged gulls (*Larus glaucescens*), and common (*Uria aalge*) and thick-billed murres (*Uria lomvia*). Identification of the most common hosts of AI viruses in Alaska is important because some individuals of these taxa make migratory movements between East Asia and North America including northern pintails, emperor geese, and glaucous gulls. These intercontinental movements facilitate the dispersal of viruses between continents. Through the targeted sampling of wild birds for AI viruses in western Alaska, including these common viral hosts with intercontinental migratory tendencies, we have detected the bi-directional exchange of AI viruses between East Asia

and North America. Collective evidence from investigations of host movements and viral ecology affirms that AI viruses are sporadically dispersed by wild birds across the Bering Strait. Thus, western Alaska represents a point of entry for foreign-origin AI viruses into North America, as well as a gateway through which viruses are dispersed to East Asia. Understanding viral dispersal between East Asia and North America is ecologically and economically relevant because it informs us on the risk of introduction of foreign-origin highly pathogenic AI (HPAI) viruses. Introductions of HPAI viruses by wild birds may lead to outbreaks of disease among domestic poultry and wild birds. For example, in 2014, wild birds introduced HPAI viruses from East Asia to North America via Alaska, the same trans-Beringian pathway we have been investigating for approximately 15 years. This introduction resulted in the largest outbreak of HPAI in U.S. history, and the only outbreak that has thus far affected wild birds in North America. This outbreak extended into the summer of 2015 in poultry with sporadic detections in wild birds continuing into the summer of 2016. This outbreak resulted in the death or destruction of approximately 50 million domestic birds in the United States and an unknown number of wild birds with economic losses estimated to total approximately \$3 billion.

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Lessons Learned From Research and Surveillance Directed at Highly Pathogenic Avian Influenza Viruses in Wild Birds Inhabiting North America

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Following detections of HPAI viruses in wild birds inhabiting East Asia after the turn of the millennium, the intensity of sampling of wild birds for AI viruses increased throughout much of North America. The objectives for many research and surveillance efforts were directed towards detecting Eurasian-origin HPAI viruses and understanding the potential of such viruses to be maintained and dispersed by wild birds. In this review, we highlight six important lessons learned from research and surveillance directed at HPAI viruses in wild birds inhabiting North America: (1) wild birds may disperse AI viruses between North America and adjacent regions via migration, (2) HPAI viruses can be introduced

to wild birds in North America, (3) HPAI viruses may cross the wild bird-domestic poultry interface in North America, (4) the probability of encountering and detecting a specific virus may be low, (5) population immunity of wild birds may influence HPAI virus outbreaks in North America, and (6) proactive disease surveillance empowers agencies, producers, and conservationists to be prepared to develop solutions that will protect humans, agriculture, and wildlife by understanding the epidemiology of specific infectious diseases and zoonotic outbreaks. We review empirical support derived from research and surveillance efforts for each lesson learned and, furthermore, identify implications for future surveillance efforts, biosecurity, and population health. We conclude our review by identifying five additional areas in which we think future mechanistic research relative to AI viruses in wild birds in North America are likely to lead to other important lessons learned in the years ahead.

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2014–15 Highly Pathogenic Avian Influenza Incursion Into the United States

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Novel Eurasian lineage avian influenza A (H5N8) virus has spread rapidly and globally since January 2014. In December 2014, H5N8 and reassortant H5N2 viruses were first detected in wild birds in Washington State, and subsequently in backyard birds in the Pacific Flyway. Wild birds had minimal role in subsequent spread into commercial poultry, especially in the Midwest, where the negative impact on the economy was particularly significant.

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Canada Lessons Learned: 2014–15 Environmental Highly Pathogenic Avian Influenza Surveillance

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Wild waterfowl are the reservoir for AI (shedding virus in their feces) and the focus of AI surveillance programs around the world. Thus far, these programs have been centered on testing of individual wild birds—an approach that has significant limitations stemming from the practical and financial impediments to collecting a representative sample of wild waterfowl. These programs were in place in the United States and Canada in 2014–15 and failed to predict outbreaks in either country. In a 2015–16 pilot study, we used targeted resequencing (a genomics technology in which a specific set of viral genes are isolated and sequenced) to identify the 2014–15 outbreak AI virus in wetland sediments. We also found that the outbreak virus was widespread in wetlands throughout the Fraser Valley and likely could have been detected in advance of the outbreak had this approach been available. We subsequently embarked on a longitudinal study to refine and validate the technology. We found that targeted resequencing of sediment was able to detect a greater diversity of AI virus sequences in wetland sediment samples compared

to samples from birds. For example, 434 unique clusters of N1 sequences (that is, N1 strains) were identified, of which 85 were found in both birds and sediment, 43 were found only in birds, and 306 were found only in sediment. We also found that AI virus strains were detected in sediment up to a year prior to being detected in birds and that there was no evidence that AI viruses persist in sediment between years. Targeted resequencing of wetland sediment is current being operationalized for the 2021–22 AI virus surveillance season in British Columbia.

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Persistence of Avian Influenza Viruses in the Environment

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In aquatic habitats, AI viruses are transmitted within wild waterfowl populations through a fecal-oral route. These viruses can maintain infectivity through extended periods of time in water and resulting environmental transmission may be a critical component of AI virus maintenance within and between waterfowl migratory seasons. The chemical and physical characteristics of water, such as temperature, pH, and salinity, can greatly influence the duration of AI virus infectivity with ideal conditions including low temperature, neutral pH, and low salinity. These relationships have been documented in laboratory studies using distilled water models and surface water obtained from waterfowl habitats throughout the United States. Although results from these studies

have demonstrated the potential persistence of AI viruses for extended periods of time (months to years), translation of these results to field conditions have been problematic owing to the biological, physical, and chemical complexity of natural aquatic habitats. More recent studies have attempted to bridge this gap using field collected samples and (or) conducting field-based experiments. These studies have demonstrated that potential AI virus persistence varies greatly between waterfowl habitats and that long-term persistence of AI viruses can occur under natural cold water conditions in the field. In these field studies, it was demonstrated that AI virus infectivity can be maintained in waterfowl habitats for periods of time extending from early migration to late spring and summer. Currently, there are still many unknowns related to environmental persistence of AI viruses which need to be understood. We do not fully understand how or if the biotic community within aquatic environments (insects, filter-feeders, aquatic vegetation, bacteria, and biofilms) affect AI virus infectivity and limited studies. Likewise, we do not know if AI virus is associated with specific fractions of the aquatic environment such as sediments or aquatic vegetation. Such associations may not only affect transmissibility in these environments but also AI virus detectability. Finally, there are questions related to how these viruses associate in these environments especially related to virus aggregation. If AI viruses exist as aggregates in aquatic habitats, this also could be an important consideration related to transmissibility and detectability as well as a factor that could enhance the maintenance of infectivity. At present, there are no proven strategies to reduce environmental transmission of AI viruses by manipulation of waterfowl habitats, but with an improved understanding of mechanisms that enhance or reduce AI virus persistence in these aquatic environments, future management options cannot be discounted.

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Using Genetic Information From Wild Bird Surveillance to Understand Transmission of Avian Influenza Viruses Between Wild Birds and Poultry

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Recent advances in genome sequencing through next-generation sequencing (NGS) have been transforming how laboratories diagnose and further characterize the viruses. Full-length viral genome sequencing can provide detailed information for virus discovery, diagnosis, characterization, and genotypic classification. NGS of AI viruses can reveal the approximately 13,500 nucleotide sequences of all the gene segments, including PB2, PB1, PA, HA, NP, NA, M, and NS segments. Continuous increments in viral evolution of AI viruses require enhanced genomic surveillance to further the epidemiologic understandings and design of improved outbreak prevention strategies. Phylogenetic analyses have been widely applied to the analysis of viral genome sequence datasets (Lam and others, 2010), which has been used extensively to describe the molecular epidemiology, immunological, and transmission of the evolving epidemiology of influenza viruses (Lam and others, 2010; Faria and others, 2011). Maximum-likelihood trees are the most commonly used method to demonstrate tree topologies showing genetic distances between genome sequences based on their nucleotide substitutions. Recent Bayesian phylodynamic approaches, however, use posterior probability of the tree, which is calculated from prior probability of the phylogeny and tree likelihood by Bayesian inferences (Lam and others, 2010). Such methods allow estimation of viral diffusion histories over time in greater detail (Faria and others, 2011; Volz and others, 2013). This approach could estimate the most probable origin and transmission dynamics between host species and (or) geographic regions (Holmes and Grenfell, 2009; Lam and others, 2010). For example, this approach has been used to determine the evolution and spread patterns of the 2014–15 U.S. H5N2 viruses by performing a comparative genomic study using 268 full-length genome sequences and data from outbreak investigations (Lee and others, 2018). The analysis suggests that multiple introductions of H5N2 viruses into Midwest States occurred during March–June 2015; transmission to Midwest poultry farms from Pacific wild birds occurred about 1.7 to 2.4 months before detection. Once established in poultry, the virus rapidly spread between turkey and chicken farms in neighboring States.

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Emerging Technologies: Enhancing Avian Influenza Surveillance and Risk Reduction Efforts

Daniel Walsh

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Recent developments in modeling techniques have led to new quantitative tools that can be leveraged to improve wildlife health. In particular, machine learning approaches are creating new opportunities to examine wildlife data to inform and enhance surveillance and risk reduction efforts. For example, surveillance for known and novel influenza A viruses involves active surveillance within wild bird populations.

This information is critical for understanding viral evolution forming the basis of risk assessments and countermeasure development; however, surveillance programs are resource intensive, so there is a need to improve efficiency. We use a form of machine learning, gradient boosted trees, to estimate the probability of isolating AI viruses during wild bird surveillance using historic surveillance data for AI viruses from 2006 to 2011. The resulting model had high predictive power and included the matrix gene rRT-PCR (real-time reverse-transcriptase polymerase chain reaction) results and the geographic location of collection for each sample as important predictors. Additionally, we estimated that there is a 16-percent probability of isolating an AI virus from a sample declared negative (that is, ≥ 35 Ct-value [cycle threshold]) under current protocols. This model can be used to help inform AI virus surveillance designs that will maximize the likelihood of collecting and testing samples that will yield an AI virus isolation, thereby conserving limited resources and laboratory capacity. An ongoing study provides a second example of leveraging machine learning approaches to help reduce the risk of transboundary transmission of AI viruses to domestic poultry. It is known that one of the most effective actions for minimizing risk of AI virus transmission at the wildlife-livestock interface is separation, which is achieved through biosecurity measures implemented by individual livestock producers; however, maintaining high levels of biosecurity to reduce AI transmission risk over long periods of time is often not economically feasible and leads to “biosecurity fatigue.” Therefore, there is a desperate need for a tool that poultry producers can use to evaluate AI virus transmission risk associated with migratory bird movements and allow them to increase their biosecurity activities and awareness above baseline levels according to real-time distribution of migratory flocks. We are developing a web visualization tool to meet this need that uses machine learning approaches to harness and integrate the information gathered by NEXRAD, the network of 143 Doppler weather radars across the continental United States operated by the National Weather Service, with citizen science bird observations contained in the eBird database, to create near real-time maps of migratory bird locations. The tool can be used to ascertain the movements of migratory birds in relation to a producer’s location. Similar to the well-known radar graphics that show weather, the most exciting aspect of our tool is the real-time nature of these maps of migratory birds that would permit the creation of “personalized” AI risk assessments that are dynamic rather than static. These assessments are intended to overcome biosecurity fatigue, and most importantly allow producers to maintain biosecurity awareness. This awareness may reduce the transboundary transmission of AI between poultry and migratory birds, improving the health of both domestic and wild populations.

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Wild Bird Movements and Avian Influenza Viruses—Relationships at the Wild Bird-Domestic Poultry Interface

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Southeast Asia has historically been the epicenter for the emergence of HPAI viruses, which have shown the capacity to spread around the globe and have caused major concern over a potential human pandemic and serious economic loss within the poultry industry. This region, especially southeastern China, has been identified as an area of frequent transmission between wild and domestic birds owing to overlap where rice-paddy agriculture, domestic duck farming, and wild birds convene. Such regular interaction between wild and domestic birds allows for a unique viral ecology with sustained cross species transmission and viral mixing. Conversely, whereas wild birds have been shown to play a role in the spread and persistence of avian influenza into and within the United States, our agricultural practices differ from those in Southeast Asia. This necessitates study of differences in factors that enable interaction across the wild bird-domestic poultry interface. Understanding the role wild birds play in HPAI transmission, both in Asia and the United States, is critical for planning response to HPAI spread and understanding the ecology of this threat. This presentation reviews efforts to understand the role of wild waterfowl in the transmission, persistence, and amplification of AI viruses around the globe, and highlights ongoing efforts to incorporate the numerous relevant variables into models that can identify spatiotemporal trends in transmission risk across the wild bird-domestic poultry interface.

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Closed-Door Session for U.S. Fish and Wildlife Service Flyway Representatives and Flyway Council Members

Russ Mason

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On the final day of the webinar, a closed-door session was held with U.S. Fish and Wildlife Service Flyway Council personnel and key State agency members of the four Flyway Councils (Pacific, Central, Mississippi, Atlantic). The aim of this session was to increase managers' awareness of the science indicating an emerging HPAI North American threat as well as to provide information and discussion points for presentation to annual meetings of the Flyway Councils and their technical committees in late August and early September.

Russ Mason of the Michigan Department of Natural Resources provided a brief overview of the previous sessions. Emphasis was placed on the increasing likelihood that HPAI would cross into North America and that migrating waterfowl might distribute virus across the United States via the spring and fall migrations in 2022.

Participants then discussed the feasibility and practical utility of enhanced surveillance, tabletop response exercises, strategies to enhance communications among State fish and wildlife agencies, and the ability of the respective agencies to mount direct management activities if requested. Overall, there was a willingness to assist in surveillance and management efforts if Federal resources were provided to support the work. Already, State wildlife health resources are stretched thin by extensive and costly efforts to manage chronic wasting disease (CWD), tuberculosis, and other diseases affecting fish and wildlife resources. There was consensus that establishing a national wildlife disease surveillance network was increasingly important in order to proactively mount effective, efficient, and economic responses to HPAI and other emerging diseases.



Lesser scaup (*Aythya affinis*). The first U.S. 2022 live wild bird highly pathogenic avian influenza (H5N1) detection was from this diving duck species in Maryland. Photograph by Jennifer Wall, U.S. Geological Survey.

Facilitated Discussion Summaries

Summaries for the facilitated discussion sessions are intended to serve as supplements to the recorded talks available at the uniform resource locators (URLs) indicated. They are to direct readers to topics of potential interest and to help facilitate understanding. They may or may not accurately represent the ideas put forth by participants.

Facilitated Discussion for Session 1: Update on Global Highly Pathogenic Avian Influenza Situation

Topic: Flyway management implications (focus on bio-surveillance and early detection)

Moderator: Jonathan Sleeman

Panelists: Camille Hopkins, Yoshihiro Sakoda, Josanne Verhagen, Mary Pantin-Jackwood, Andrew Ramey

Participants: Webinar attendees from State and Federal agencies within the United States, Provincial and Federal agencies of Canada, the poultry industry within North America, and academic institutions from both within the United States and from abroad

Recording available at https://www.youtube.com/watch?v=klowKJNYJvk&list=PL2_jEtoY8jj11GMnDwIvDXQGVLbT8-BF&index=1

*Note: Topics are discussed throughout the video. Timestamps are approximate of where the most discussion for a topic occurs

Discussion starts at 1:31:45

- What do we do well in North America?
 - Mix of active and passive surveillance (1:34:37)
 - Passive surveillance is important for mortality events and documenting outbreaks
 - Active surveillance is important for subclinical infections and what may be “under the radar”
 - Formation of the interagency steering committee (1:41:25)
 - At the State and Federal level
 - Helps leverage resources
- What do we need to improve? Where are our knowledge gaps?
 - Experimental support of surveillance is lacking
 - Full sequencing of viruses genomes
 - Pertaining to outside the United States (1:36:50)

- Japan experienced a delay between detecting the virus and actually being able to implement or increase biosecurity measures after several years of no detections
- Extend surveillance into northeastern Europe
- Efforts and funding are currently sporadic. More consistent and systematic data would answer important questions (1:40:00)
- We lack a national surveillance capacity and sustained infrastructure
 - Current surveillance efforts are decoupled from managers, leading to wasteful spending as we attempt to respond. Time is wasted trying to coordinate and gather funds at all levels of jurisdiction.
- Improve communicating that no detection is important data to be collected
- Current surveillance systems tend to be individual pathogen-based, which presents challenges as the number of pathogens of interest increase. A possible solution could be to shift towards an intelligence-based approach that assessed changes in epidemiological or ecological situations, not just the pathogen. (1:47:15)
- Heightened sense of a need for surveillance going into this migratory cycle because of the trends seen in Asia, but: (1:51:55)
 - No active surveillance by State agency in Washington since 2017
 - What is it that people want exactly to determine? What are we after?
 - This helps determine where to focus efforts and funding for sampling
 - Live captures versus hunter harvest
- Don't know how to influence or reduce the transmission of the virus between wild birds and domestic poultry. No guidance is available.
- Need to identify what is the focus of sampling and surveillance efforts to determine what kinds of sampling to do
- How do we achieve this consistent and continuous surveillance?
 - Using National Animal Health Laboratory Network (NAHLN) labs as surveillance nodes across the country for wildlife disease surveillance. (1:44:30)
 - Then work with the State and Tribal governments that are associated with each node
 - Leads to communities that work together internally and then feed into a national effort.
 - Potentially studying low pathogenic viruses to learn more about epidemiology
 - Approach from a decision support view: (1:58:06)
 - First step is determining what you can change
 - Poultry farmers will not change behaviors based on virus alone, need more information
 - Need to shift from surveillance focusing on pathogen to what will support decision making
- What technologies could help us move into the direction of intelligence-based models and continuous surveillance?
 - Machine learning to enhance surveillance (2:02:25)
 - Using radar data to capture biological data to track migratory birds across the landscape
 - Using machine learning to determine the species
 - Goal to potentially develop a “migratory bird forecast” for poultry farmers
- Active swabbing plan in Alaska (1:49:40)
 - Swabbing birds that are not dabbling ducks is still being explored
 - In Alaska, unable to isolate the virus in hunter-shot geese except during the spring harvest.
 - Trying something new: sampling only hatch-year geese because maybe they are more immunologically naïve and the viruses can be isolated
 - Dabbling ducks provide the “most information per dollar” at this point
 - Autumn 2021 (2:01:00)
 - Swab as many hunter-harvested dabbling ducks as possible (~400 birds)
 - Look for hatch-year geese swabs through hunter harvest (~500 birds)
 - Collect fecal swabs from emperor geese and glaucous-winged gulls (~500 birds), not strictly hunter harvested

- Are we doing a good job with early detection? Is it a realistic goal? How can we enhance it? (2:03:50)
 - Could model after *Batrachochytrium salamandrivorans* (Bsal) approach
 - Risk-based spatial surveillance efforts (Richgels and others, 2016)
 - Current plan is surveillance in Atlantic and Pacific Flyways with thought that if worried about introductions from the United Kingdom or Eurasia, they most likely will be in the Atlantic of Pacific Flyways
 - Question: Or should efforts be focused in the Central or Mississippi Flyways because there are higher poultry densities?
 - Maybe a baseline surveillance number across the country would be helpful (2:07:30)
 - Need to determine “How early is an early enough warning to change actions?” and “What are the warning signs that would change the actions?” (2:08:12)
 - Looking at the importance of Pre-Border Surveillance (Horizon scanning)
 - Detecting patterns in East Asia even before it gets to North America
 - Need to ask managers these questions. How much time do they need or prefer?
 - What are the actions they could take? (2:16:50)
 - Not clearly defined what potential management actions agencies are interested in pursuing
 - It is possible to conduct research to help inform management and decision making if managers and management agencies ask for specific information
 - Working to determine where the higher risk areas are from wild birds to domestic birds to make a risk map (2:09:58)
 - To work on these models, need lots of information:
 - The movement and ecology of wild birds
 - Species that are more susceptible
 - Length of virus shedding period and asymptomatic period
 - Surveillance within different flyways
 - Genetic mapping
 - Determine how high are the risks? What is the probability of a spillover happening? How often? (2:13:46)
 - Challenges include a dynamic situation and a changing landscape
 - Recognize we are looking for “needles in a haystack,” so there will be imperfections and areas to improve
 - Logistical challenge of properly timed sampling in coordination with movement. Not always coinciding, but: (2:14:52)
 - Reliance upon hunter-harvested birds and banding efforts
 - Timing isn’t perfect, but not so bad
 - Efforts will be ramping up in the next month or two at the same time that there is movement in birds between North America and East Asia
 - Reaching out to managers hasn’t happened yet but needs to (2:18:22)
 - Hasn’t been considered a wildlife management issue before or yet because there haven’t been notable wild population effects from HPAI beside H5N1
 - Consider and address the poultry industry as well (backyard and factory farm)
- Summary of discussion from Jonathan Sleeman (2:24:50)
 - Need to have sustained, robust wildlife disease systems on a national level with connection between agencies and nodes
 - One of the biggest impediments for disease surveillance in general
 - Think more broadly and creatively about what surveillance is
 - Not just pathogen detection
 - Surveillance is information to make decisions and to take proper and effective actions
 - Look for other streams, sources, or kinds of information that could be used to inform
 - What does “early detection” mean? How early is early enough? What are we detecting early? What are the signs? Are there novel data sources we could be using (other countries, environmental data)?
 - Potential for new technologies:

- Machine learning
- Field-based kits to sequence virus for rapid detection in the field as a complement to brick and mortar labs
- Logistical challenges of working with wild birds:
 - Timing
 - Acquiring samples (hunter harvested versus live sampling and the need to use fecal samples)
 - Not perfect
- Need to effectively understand HPAI in wild birds and domestic
 - The movement and ecology of wild birds
 - Species that are more susceptible
 - Length of virus shedding period and asymptomatic period
 - Surveillance within different flyways
 - Genetic mapping
- Three key questions:
 - What are our capabilities to detect these viruses?
 - How can we prevent a repeat of the 2014 outbreak?
 - Could highly pathogenic viruses become endemic in North America and what are those implications? Would this be a significant new wild-life disease?
- From the wildlife manager perspective:
 - What is their responsibility if there haven't been any wild die-offs?
 - What can managers do or influence?
 - Possibly influence habitat and water
 - Minimize captive release scenarios
 - Need to communicate and be on the same page regarding responsibilities

Facilitated Discussion for Session 2: Lessons Learned from North American Highly Pathogenic Avian Influenza Outbreak (2014–15)

Topic: Flyway management implications (importance of vigilance to passive surveillance, rapid response upon detection in North America, interagency coordination, communication strategies, personal protection and biosecurity implications, and characterization of outbreak events)

Moderator: Julianna Lenocho

Panelists: Thomas DeLiberto, Hon Ip, Yohannes Berhane, Chelsea Himsworth

Participants: Webinar attendees from State and Federal agencies within the United States, Provincial and Federal agencies of Canada, the poultry industry within North America, and academic institutions from both within the United States and from abroad

Recording available at https://www.youtube.com/watch?v=Nw4YLaTSfA&list=PL2_jEtoY8jjj11GMnDwIvDXQGVLbT8-BF&index=2

*Note: Topics are discussed throughout the video. Timestamps are approximate of where the most discussion for a topic occurs

Discussion starts at 1:42:07

- Given the recent outbreak of HPAI in Eurasia, how is the Federal Government ramping up or modifying the wild bird surveillance in Canada for the upcoming year?
 - Canada-wide wild bird surveillance like in 2005
 - Hunter-harvested duck sample collection
 - About 500 birds per Province
- Comments on the recent low pathogenic H5 activities in the last few years after the 2014–15 outbreak. Would it be possible that these have a higher risk of introduction and spread like the H5? (1:44:46)
 - Advantage of long-term surveillance:
 - A picture at a national scale of low pathogenic viruses circulating in wild bird populations
 - Because of surveillance for ~18 years, there's a good picture of the occurrence of different hemagglutinin and neuraminidase subtypes in wild bird populations
 - Observing periodic increases and decreases of certain hemagglutinin types in wild populations
 - H5 exhibits cycles of peaks and valleys of prevalence

- Certain H5 viruses are largely confined to the Pacific Flyway while others are largely confined to the Atlantic Flyway
 - There are observable spatiotemporal patterns
- Questions:
 - As we see H5 viruses increase in wild birds, is the immunity building as well?
 - Will this provide some level of population immunity?
 - On the contrary, when in troughs of H5 cycles, are populations of birds more susceptible to epidemics?
 - Currently in a trough of H5. What might this mean if an intercontinental H5 virus enters the population?
 - Does exposure to other subtypes contribute to resistance to highly pathogenic avian influenza viruses?
 - Are swabs from wild waterfowl collected through surveillance only being used to determine if HPAI is present? Is it a binary (HPAI positive or negative) or are we subtyping? (1:50:48)
- Lots of discussion about low pathogenic viruses, but is this information being derived from all samples?
- The U.S. Department of Agriculture (USDA) perspective:
 - Focus is first to determine if there is any influenza in the sample
 - If yes, immediately test for H5 and H7 influenza
 - If positive, shipped to USDA's National Veterinary Services Laboratories (NVSL) for a determination of subtype
 - Take all non-H5 or non-H7 positives and ship them back to the archive in Fort Collins
 - Lower priority of getting these sequenced, but sequencing is conducted within financial and time constraints
 - Goal is to use the samples as an emerging disease warning system
- How do we improve the timing for information from the laboratory results and detections and communicating them to stakeholders and managers? (1:55:25)
 - Results for H5 and H7 are within 7 to 10 days and try to get the information out as fast as possible
 - For other metrics, it depends on the current workload and how many positives for how quickly information is distributed
- In the past, there have been funds for U.S. State wildlife agencies to conduct surveillance, typically through hunter harvest, but there are individual-bird mortalities (especially raptor mortalities) as well. Are there potential funds and a process for collecting samples on these birds? Is sediment testing being considered? (1:58:18)
 - Just established the 2021–22 surveillance plan (live bird and hunter harvest) (U.S. Department of Agriculture and others, 2021)
 - No plans right now for sediment surveillance or sampling but this technology is of interest
 - Get in touch with USDA National Wildlife Disease Program if there are mortality events
 - Current U.S. strategy:
 - Goal: Sample as many birds recovered through morbidity and mortality investigations that are suggestive of influenza and test at the USGS National Wildlife Health Center
 - Interagency protocol for large die-offs regardless of influenza signs
 - Samples go to USGS National Wildlife Health Center to be tested for AI
 - For one-offs:
 - Cannot test every single bird for everything but a few mechanisms can be utilized:
 - (1) Document mortalities into open source, publicly accessible website: <https://whispers.usgs.gov/home>. Gives everyone an idea of whether a pattern is emerging
 - (2) It is always worth talking to NWHC epidemiologists (<https://www.usgs.gov/staff-profiles/epidemiology-team>) because they have information from adjacent States and countries and can give an idea of what may be going on in your area.
 - They also are familiar with the patterns of the area and can help identify differences and possible signs of an outbreak

- In regard to reporting out results, what is the plan for communication with State wildlife agencies? Seems like in the past there was closer coordination with the States during large AI surveillance programs but that is different this year (2:06:20)
 - Wild bird surveillance
 - Samples are handled at NAHLN labs
 - Any nonnegative H5 or H7 are forwarded to NVSL for confirmation
 - Still working on specifics of the messaging with goal of the notification getting to the USDA National Wildlife Disease Center and to the State animal health officials and State wildlife agencies at the same time
- Guidelines for testing singleton raptors (2:09:25)
 - USGS National Wildlife Health Center has submission criteria for what they will and will not accept
 - It is a balance of how many resources are available with how sensitive the system can be
 - Try to modify submission criteria depending on the perceived level of risk
 - Example: In 2020, there was a large uptick in cases in wild birds in Europe and Asia
 - Alerted people to this issue and liberalized their criteria for mortality samples
 - Could be helpful to become more robust, scientific, and systematic in how to assess the risks and subsequent modification of surveillance and testing to match
 - Deciding on what the high-risk signals are
 - Is an uptick in cases in East Asia sufficient?
- Are there plans with USDA Animal and Plant Health Inspection Service to increase collaboration with wildlife rehabilitation centers? Especially during peaks of H5 in wild birds. (2:12:44)
 - Wildlife rehabilitation facilities will receive raptors that test negative for West Nile Virus
 - By the time they die, they are no longer eligible to be sent to the USGS National Wildlife Health Center for testing
 - Samples are taken from wildlife rehabilitation facilities and individuals
 - Have detected some important diseases from these samples
- Greater collaboration is possible but requires coordination with the State agencies that permit the wildlife rehabilitation activities
- Challenges of samples from wildlife rehabilitation facilities
 - If animals have been in captivity for an extended period of time, could they have contracted a disease during then?
 - Would therapeutics mask disease?
- Could be an important source of samples that should be considered in the future
- In British Columbia: (2:22:55)
 - Avoid testing in wildlife rehabilitation centers because if there is a positive, there could be a depopulation of the facilities
 - What does a detection in the facility mean? Depopulation of the entire facility?
- Will there be a program or messaging to wildlife rehabilitation centers when a higher activity of H5 is detected to have a more coordinated sampling? (2:15:00)
 - Work closely with rehabilitation community to develop guidelines to mitigate zoonotic risks
 - Could be a model for how to work with that community to develop a program for HPAI
 - Coordinated effort where the communication goes through the State agency is important rather than direct Federal to individual contact
- If environmentally sampled influenza ribonucleic acid (RNA) is not persisting between collections how does that explain the subsequent detection in wild birds? (2:17:38)
 - Birds may not have been infected in the Fraser Valley
 - Hypotheses:
 - One may be less likely to capture a bird infected with AI than to find it in the sediment
 - Birds may have brought avian influenza from areas further north such as Alaska
 - Goal is to pilot sediment sampling and live trapping and hunter mortality samples over time
 - The weather could also cause changes in disease prevalence

- Water tables and high rainfall can cause congregation
- These may be altered by climate change

Facilitated Discussion for Session 3: Highly Pathogenic Avian Influenza Challenges and Opportunities

Topic: Flyway management implications and potential mitigation strategies

Moderator: Samantha Gibbs

Panelists: David Stallknecht, Dong-Hun Lee, Daniel Walsh, Diann Prosser

Participants: Webinar attendees from State and Federal agencies within the United States, Provincial and Federal agencies of Canada, the poultry industry within North America, and academic institutions from both within the United States and from abroad

Recording available at https://www.youtube.com/watch?v=bDw9Of_9mMU&list=PL2_jEtoY8jj11GMnDwIvDXQGVLbT8-BF&index=3

*Note: Topics are discussed throughout the video.

Timestamps are approximate of where the most discussion for a topic occurs

Discussion starts at 1:30:44

- Peak prevalence of influenza occurs prior to migration in Minnesota in resident birds. If we only monitor migration, how do resident birds fit into the monitoring? Does migration really translate to big changes in influenza on the ground? (1:32:53)
 - Coming from the perspective that migratory birds bring novelty to the influenza patterns and focusing on the risks associated with migration
 - Can see resident information from eBird data, but radar data would not necessarily capture resident birds
 - Assume that migratory waterfowl bring novel viruses to the resident birds
 - A possible weakness: not looking at how resident birds affect the risk for poultry producers
 - Are we not looking broadly enough? (1:42:29)
 - Waterfowl may not be showing up in March, but other birds are and can concentrate easily. How hard is it to expand migratory surveillance to other species?
 - We can develop all these new applications that could be very useful, but does anyone have the funding or the resources to sustain them?
- Recommendation: an increasingly pressing need for sustainable funding for a variety of purposes (surveillance, genomics, tool applications)
- Poultry industry seeks refined information on when to increase biosecurity. Could we be giving them a false sense of security with our current risk assessment practices? (1:35:47)
 - In the past, outbreaks occurred outside of migration period; care and caution may be prudent when providing recommendations
 - Biosecurity fatigue is a concern. People naturally become complacent over time. Goal is to overcome this fatigue by refreshing people on practices and keep up diligence
 - Important to convey that humans play a role in introduction of avian influenza from wild birds to domestic poultry
- When modeling to try and understand the migratory bird patterns and events, the environment is important (1:39:29)
 - Transmission risk models are hybrid models trying to understand the poultry and wild populations in time and space while adding the environment component
 - How does it get into turkey farms in March? A lapse in biosecurity?
 - A possible gap: more sampling across the year to better understand the environmental factors and seasonal effects
 - Hard because funding has subsided (possibly until a new large event)
 - Currently sampling can be biased
- Looking at ecological factors in Washington in 2014, the response and detection was based on Aspergillosis die-off which occurred in December. (2:01:41)
 - Birds located in Washington in December are typically not migrating, and therefore HPAI may have been in Washington prior to detection when no surveillance was occurring.
 - If we want to have a competent and robust system, solely pointing at wild birds and managers is not effective
 - Asking bird banders to “pick up the slack” should be rethought

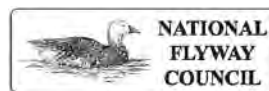
- How do we enhance mitigation measures in the field for surveillance crews? What are some recommendations for the on-the-ground crews in regard to personal protective equipment and cleaning? (1:46:16)
 - Currently working in a surveillance mode and trying to keep close ties with agricultural departments to protect all levels of the resource (backyard to large facilities)
 - Biggest challenge: how to integrate surveillance and management strategies in wild birds into domestic programs
 - No fluid coordination currently
 - The connection between wild surveillance and agriculture biosecurity is lacking
- The poultry industry has made changes to increase biosecurity, like bringing birds indoors to reduce the transmission from wild birds. (1:58:15)
 - Not everyone is diligent about biosecurity
 - Newcastle outbreaks in 2002 and 2003 were traced back to workers who wore dirty boots or clothes and “walked” the disease onto the farm
 - Education of personnel is necessary to better understand why the need to practice biosecurity
 - There's a difference between demanding biosecurity practices and teaching them why they are important
- How do we explicitly connect all the research presented with why HPAI is a concern for wild bird managers in North America? (1:58:10)
 - There is an assumption that there is something that waterfowl managers can actually control to reduce the risk of spillover
 - Not as clear or straightforward as we hope it is
 - Be wary of vilifying the wild birds; a human component adds to this transmission
 - Wild bird State manager authority includes:
 - Monitoring wild populations
 - Setting regulatory seasons
 - Responding to events in public domain that are controllable
 - So, when asking questions like “Are there mitigation practices to implement out on the landscape?”
 - Assuming that waterfowl managers control wetlands, which is not always accurate
 - Most are private so there is very little authority for State managers to control this
 - There are already conditions on the landscape that are beyond control that cannot be controlled (drought cycles leading to more concentration of birds)
- Encourage people to expand idea of “manager” when having these discussions (2:08:23)
 - A private individual managing a rice field is still a manager
 - This person may be seeking input for sound management during outbreaks
- Wildlife managers not only manage wildlife but also people and their access to wetlands
 - Limiting access, monitoring access, and instituting disinfection protocols may be management options
- The landscape is changing with regard to HPAI in wild birds (2:10:19)
 - It is a dynamic situation that has become an issue for wild birds in the past two decades
 - We don't know where HPAI in wild birds is going and what we see today may not be what we see in 5 years.
 - It may be important consider out what could happen and to prepare in order to avoid reactive management scenarios.
- There is a lack of implementation science and human dimensions research in wildlife disease work. (2:04:02)
 - Acquisition of new knowledge and information does very little to change human behavior
 - So how do we affect the behaviors that people make?
 - Lack of understanding of what people are able to do, willing to do, and how to change what they do limits our conversation of how science can influence decisions.
 - Need for structured decision-making conversation and research
 - Risk assessment framework is lacking
 - How high of a risk is this to North American wildlife? What is our level of uncertainty?
 - Can we develop a risk assessment tool to help guide decisions?

- There's a lot of effort to upregulate private land management
 - They are not there for the health of wildlife, but rather for hunting
 - How do we work with these stakeholders to explain what our concerns are and why?
 - Asking them to do things for the benefit of waterfowl only may not be effective
- There are cycles of die-offs due to other pathogens that are predictable every year in certain parts of the country (for example, Florida). How do we deal with possible comorbidity and dual testing of these pathogens and HPAI? (2:11:57)
- Large die-off of Muscovy ducks every year that became “old-hat”
 - May not be testing for HPAI
 - Should testing for HPAI in these die-offs be increased?
- How do we communicate to the public about less concerning diseases (in regard to human health), like botulism, differently than HPAI, which is of greater threat?
- There is a North America Waterfowl Management plan (<https://nawmp.org>), but it does not have a wildlife disease section. (2:14:14)
 - This is an opportunity to engage and to get language regarding disease into this plan
 - The Association of Fish and Wildlife Agencies plan to discuss establishing the National Fish and Wildlife Health Initiative in September.
 - The intent is to work with Federal agencies to secure funding for a national surveillance effort

References Cited

- Richgels, K.L.D., Russell, R.E., Adams, M.J., White, C.L., and Campbell Grant, E.H., 2016, Spatial variation in risk and consequence of *Batrachochytrium salamandrivorans* introduction in the USA: Royal Society Open Science, v. 3, no. 2, article 150616, 9 p., accessed June 22, 2022, at <https://doi.org/10.1098/rsos.150616>.
- U.S. Department of Agriculture, U.S. Geological Survey, U.S. Fish and Wildlife Service, and National Flyway Council, 2021, Implementation plan for avian influenza surveillance in waterfowl in the United States, summer FY 2021 – winter FY 2022 (ver. 1.0, March 2021): U.S. Department of Agriculture, Animal and Plant Health Inspection Service, 8 p., accessed June 22, 2022, at https://www.aphis.usda.gov/animal_health/downloads/animal_diseases/ai/2021-22-wild-bird-ai-surveillance-implementation-plan.pdf.

Appendix 1. Interagency Steering Committee for Avian Influenza Surveillance in Wild Migratory Birds Information Memorandum, January 11, 2021



INTERAGENCY STEERING COMMITTEE FOR AVIAN INFLUENZA SURVEILLANCE IN WILD MIGRATORY BIRDS
 INFORMATION MEMORANDUM

DATE: January 11, 2021

TO:

FROM: Interagency Steering Committee for Avian Influenza Surveillance in Wild Migratory Birds
(see end of document for members)

SUBJECT: Increasing global highly pathogenic avian influenza (HPAI) activity in poultry and wild birds

I. KEY FACTS:

- a. Emerging avian influenza viruses can present a significant threat to human and animal health.
- b. Outbreaks of Eurasian (EA) lineage highly pathogenic avian influenza (HPAI) H5 subtype (e.g., EA HPAI: H5N8, H5N2, H5N6, etc.) have been increasing rapidly in Europe and Asia in both domestic poultry and wild birds since August of 2020. (See Fig. 1)
- c. EA HPAI H5N8 and its reassortants have been particularly successful, reaching endemic status in Asia and exhibiting subsequent seasonal spread to Europe since 2014. In 2014-2015, EA HPAI H5N8 reached North America presumably via wild migratory waterfowl and reassorted to form Eurasian/North American (EA/NA) HPAI H5N2 which precipitated devastating outbreaks in the United States and Canada both in domestic poultry and wild birds. Over 50 million chickens and turkeys died or were destroyed to stop the spread of the outbreak and billions of dollars were lost due to loss of export and recovery. The economic losses to the U.S. were estimated at \$3.3 billion.
- d. While human cases of EA HPAI H5N8 have not been reported previously, both EA HPAI H5N1 and EA HPAI H5N6 viruses have spilled over into human populations in the recent past, causing illness and death.
- e. The Interagency Steering Committee for Avian Influenza Surveillance in Wild Migratory Birds was formed in 2006 to coordinate surveillance for HPAI in wild birds. The Committee has a lead role in planning and implementing the U.S. wild bird HPAI surveillance activities.

II. BACKGROUND:

Select species of wild waterfowl and shorebirds are the natural reservoirs of low pathogenic avian influenza viruses. They are classified into subtypes based on their two primary surface proteins, H (hemagglutinin) and N (neuraminidase). Low pathogenicity avian influenza (LPAIs) naturally circulate in select wild waterfowl and shorebirds. LPAIs can spill into the domestic poultry compartment where they may cause asymptomatic or mild disease. However, when

LPAI H5 and H7 subtypes infect domestic poultry, they can evolve into HPAI viruses that cause high mortality in poultry and devastating economic losses to commercial operations. Highly pathogenic viruses in poultry can spill back into wild birds, resulting in further geographic spread of the virus by migratory birds. Some subtypes of avian influenza viruses are zoonotic, i.e., can infect people, causing morbidity and mortality.

During the month of December 2020, 74 new outbreaks of Eurasian HPAI in domestic poultry in 14 countries in Asia and Europe were reported to the World Organisation for Animal Health (OIE). For the same time period, 298 new outbreaks were reported in other captive and wild birds in 17 countries in Asia and Europe. This is a significant increase from the previous (October-November) OIE reporting period. Evidence shows that the EA HPAI H5N8 subtype is circulating widely across this geography. Even more concerning, viral reassortants (recombinations of the HPAI H5N8 with other avian influenza viruses to form new subtypes such as H5N5 and H5N1) have also been detected. The outbreaks are affecting domestic poultry, other captive avian species, as well as wild birds. Please see <https://www.oie.int/en/animal-health-in-the-world/update-on-avian-influenza/2020/> for the latest updates.

III. POSITION OF AFFECTED STAKEHOLDERS/PUBLIC LANDS AFFECTED

State and federal agencies charged with protecting the health of wildlife, domestic animals, and public health will all be impacted by the (re)introduction of HPAI. Working together using the One Health approach, and striving to prevent and mitigate the introduction and spread of these novel HPAI strains are essential to minimizing health and economic impacts.

Enhanced avian influenza surveillance in wild birds by state wildlife management agencies, U.S. Department of Agriculture (USDA), and the U.S. Geological Survey through cooperative agreements and federal funding during the 2006-2015 HPAI outbreaks provided an early warning for the entry of HPAI viruses into North America via migratory flyways. This work also provided viral genomic data that was used for poultry outbreak trace-back investigations. While HPAI viruses are known to occasionally cause clinical disease in individual wild birds (e.g., raptors), the extent to which many of these emerging HPAI viruses impact waterfowl and raptor population health, as well as associated impacts on hunter participation due to health concerns with consuming HPAI-infected game are largely unknown.

Surveillance of agricultural animal imports into the country is conducted by the USDA. The USDA, State agricultural agencies, and the poultry industry conduct surveillance for avian influenza viruses in poultry within the U.S. These efforts are designed to prevent HPAI introduction and spread through commercial channels. For agricultural agencies, the detection of H5 and H7 viruses in poultry requires placing restrictions of bird movement and often depopulation of affected flocks. This leads to economic impacts as well as animal welfare concerns associated with illness and death from the virus or culling requirements.

Public health agencies at all levels are responsible for monitoring and responding to influenza activity in the human population. This includes surveillance for novel strains of HPAI that have spilled over into the human population, improvement of treatments, application of preventive social measures, and vaccine development.

IV. RECOMMENDATION

Because both trade in HPAI-infected poultry products and wild bird migration likely contribute to the local and long-distance spread of HPAI viruses, proactive measures to detect and limit the impacts of virus introduction and spread in all sectors are imperative. The Interagency Steering Committee for Avian Influenza Surveillance in Wild Migratory Birds stands ready to provide expertise, planning, and surveillance as requested to fill existing gaps in HPAI response capabilities.

PREPARED BY: The Interagency Steering Committee for Avian Influenza Surveillance in Wild Migratory Birds - Samantha Gibbs DVM PhD MPH (*committee chair*), U.S. Fish and Wildlife Service; Tom DeLiberto PhD DVM, Tom Gidlewski VMD MS, Darrel Styles DVM PhD, U.S. Department of Agriculture; Jonathan Sleeman MA VetMB Dipl. ACZM Dipl. ECZM MRCVS, M. Camille Hopkins DVM MS PhD, U.S. Geological Survey; Russ Mason PhD, National Flyway Council; Colin Gillin DVM, Association of Fish and Wildlife Agencies; Patti Bright MS DVM Dipl.ACVP, U.S. Agency for International Development.

Figure 1. Spatial distribution of highly pathogenic avian influenza, provided by the World Organisation for Animal Health (OIE).

