The Changing Dynamics of Highly Pathogenic Avian Influenza H5N1: Next Steps for Management & Science in North America

Johanna A. Harvey[1,2], Jennifer M. Mullinax[1], Michael C. Runge[2], Diann J. Prosser[2*]

[1]Department of Environmental Science and Technology, University of Maryland, College Park, MD 20742, USA.
[2]U.S. Geological Survey, Eastern Ecological Science Center, Laurel, MD, USA

[*]Correspondence: Diann J. Prosser, U.S. Geological Survey, Eastern Ecological Science Center, Laurel, MD, USA
Email: dprosser@usgs.gov

ORCID
Johanna A. Harvey https://orcid.org/0000-0003-4504-6777
Jennifer Mullinax https://orcid.org/0000-0003-4695-059X
Michael C. Runge https://orcid.org/0000-0002-8081-536X
Diann Prosser https://orcid.org/0000-0002-5251-1799

ABSTRACT

Highly pathogenic avian influenza virus (HPAIV) H5N1 was introduced in North America in late 2021 through trans-Atlantic pathways via migratory birds. These introductions have resulted in an unprecedented epizootic, a widespread disease event in animals, heavily affecting poultry, wild birds, and recently mammals. The North American incursions occurred during the largest epidemic season (2021 – 2022) in Europe where H5N1 may now be endemic (i.e., continuously present). The continuing outbreak includes expansion into Mexico, Central and South America beginning in late 2022. Here, we provide an overview of the Eurasian origin H5N1 introduction to the Americas, including a significant shift in virus dynamics and severe disease in wild birds. Then, to investigate the global changes in confirmed detections in wild birds and poultry across time and geographic regions, we analyzed FAO’s EMPRES-i+ database. To examine the 2021 introduction and spread in North American wild birds and poultry, we collated publicly available data across USA and Canadian federal sources. Based on our assessment, the unique magnitude of the North American H5N1 spread indicates the need for effective decision framing to prioritize management needs and scientific inquiry, particularly for species at risk and interface areas for wildlife, poultry, and humans. We illustrate the rapidly occurring and likely increasing detrimental effects that this One Health issue has on wildlife, agriculture, and potentially human health, and we offer a reframing of HPAIV disease response towards a decision analytical context to guide scientific prioritization as a potentially valuable change in focus.

Keywords: avian influenza; disease management; H5N1; highly pathogenic avian influenza virus; poultry; Clade 2.3.4.4b; structured decision making; wild birds

INTRODUCTION

In 2021 and 2022, unprecedented outbreaks of highly pathogenic avian influenza virus (HPAIV) have resulted in a large number of detections and mass mortalities in wild birds as well as effects on domestic poultry across Europe, parts of Asia, Africa and now the Americas (CMS & FAO 2022). In late 2021, North America began to experience its largest and most deadly incursion of H5 HPAIV to date, with a range of signs across wild bird species from generally asymptomatic infections in dabbling ducks to large scale die-offs in colonial nesting or gregarious birds such as northern gannets *(Morus bassanus)* and black vultures *(Coragyps atratus)* ("WHISPers" 2023). As part of the current outbreak, Eurasian-origin H5N1 belonging to the clade 2.3.4.4b viruses, was first detected in Newfoundland, Canada, in captive poultry at an exhibition farm in December of 2021 and retrospectively in a free-living great black-backed gull *(Larus marinus)* in late November 2021 (Caliendo et al. 2022). By January 2022, H5N1 was detected in North and South Carolina in the United States (Bevins et al. 2022). Since the re-introduction of this viral lineage into North America, it has rapidly spread across the continental United States (USDA APHIS 2023a) and all Canadian provinces and territories ("National Avian Influenza - Wild Positives" 2022). As of February 2023, there have been 41 wild bird mass mortality events (MMEs) reported (impacting > 100 individuals per species, range 100-3,390) in the United States since the current outbreak began in December of 2021. There have been ~28,190 impacted H5N1 wild birds, including sick and mortality estimates, ("WHISPers" 2023) reported and over 58 million domestic poultry have been infected or culled in the United States (USDA APHIS 2023b). In late 2022, H5N1 began spreading into Mexico, Central and South America including 22,000 estimated seabird mortalities off of the coast of Peru (Ministerio de Salud 2022; Gamarra-Toledo et al. 2023a). While endemicity of HPAIV has already occurred in Asia, Africa, and most recently Europe (Pohlmann et al. 2022), in the Americas the degree of asymptomatic infection in wild birds and migratory species is unknown. So, increased virus fitness and dissemination may be occurring. High levels of uncertainty remain in what future highly pathogenic avian influenza disease dynamics will look like, although signs of future endemism exist. Particularly concerning are the widespread geographic range and number of free-living species affected, which portends eventual disease endemism. This uncertainty confounds disease management responses.

Large-scale animal disease data synthesis and management is challenging for a variety of reasons, including complicated and uncertain disease dynamics, diverse groups of authorities (e.g., local, state, indigenous, and federal agencies; transnational authorities; and non-governmental research groups) and stakeholders (e.g., human health, wildlife, poultry), and limited resources. Where resources and capacity exist for implementation of management, standardized recommendations exist for domesticated poultry ("Chapter 10.4 Infection with high pathogenicity avian influenza viruses" 2021) as provided by the World Organization for Animal Health (WOAH). HPAIV priorities for the industry are to reduce transmission to and within domestic poultry by improving biosecurity measures and wildlife deterrence practices, which also reduce the incidence of spillback (i.e., transmission from poultry back to wildlife). However, no suite of organized responses currently exists for HPAIV in wild birds. A cohesive One Health approach could address better understanding of disease dynamics, disease management response, and help reduce future negative HPAIV impacts.

In other such highly complex environmental issues with competing objectives, uncertain dynamics, many stakeholders, and a complex array of management options, decision analysis processes such as structured decision making are increasingly cited as an effective model-based decision support tool for managers (Conroy & Peterson 2013; Runge et al. 2020). Decision analytical tools are increasingly being employed in response to disease management in amphibians (Grant et al. 2017; Bernard & Grant 2019) livestock (Shea et al. 2014; Probert et al. 2018), cervids (Tyshenko et al. 2016), and COVID-19 in humans and bats (Shea et al. 2020; Cook et al. 2022). Decision theory and corresponding analytical tools, e.g., structured expert elicitation (Hemming et al. 2018), value of information methods (Runge et al. 2011), and multi-criteria decision analysis (Sarah J. Converse 2020), provide a transparent and systemic framework for addressing and reducing uncertainty and risk along with other challenges common to complex multi-objective One Health disease systems.

In this perspective we provide a brief overview of the disease system, a novel synthesis of the current state of the HPAIV H5N1, address changing disease dynamics, warn of pending endemism, and examine the challenges to effective disease management response. We then make a case for a shift in focus towards decision making to provide a valuable framework to guide coordinated collaborative work of management agencies and scientists for the benefit of wild bird conservation and agricultural production. The complexity of migratory bird conservation and poultry production (e.g., scale complexity, governance structures, limited resource availability), coupled with the high degree of uncertainty regarding HPAIV disease dynamics, makes the process of data collection and management decisions in the face of HPAIV extremely challenging. We suggest that formal methods of decision analysis can aid in allocating scarce resources and prioritization of scientific inquiry to inform management and conservation actions.

AVIAN INFLUENZA ORIGIN AND EVOLUTION OF CLADE 2.3.4.4b H5NX HPAIV

Avian influenza viruses (AIV), belonging to the influenza A viruses (family: Orthomyxoviridae; genus: *Orthomyxovirus*), which are enveloped viruses with eight gene segments that may infect a diversity of vertebrate hosts, primarily birds, and less frequently mammals and humans. Currently, 16 hemagglutinin (HA) and 9 neuraminidase (NA) antigenic surface proteins have been found in birds, and these combinations are used to characterize AIVs into subtypes (e.g., H5N1, H7N8) (Webster et al. 1992). Phenotypically, AIVs are often described based on their pathogenicity in chickens. Highly pathogenic avian influenza viruses (HPAIV), historically termed fowl plague, cause high mortality; low pathogenic avian influenza viruses (LPAIV) may produce asymptomatic infections or mild to severe respiratory disease often presenting as weight loss and a drop in or loss of egg production in poultry (Suarez, 2008). Most HA subtypes result in LPAIV, with only H5 and H7 currently known to have HPAIV strains.

Historically, HPAIV infections occurred in domestic poultry and did not circulate in wild birds, except for an isolated large outbreak in common terns (*Sterna hirundo*) in South Africa in 1961 (Rowan 1962). Wild birds began to be affected by HPAIV beginning with the highly pathogenic H5N1 virus lineage A/Goose/Guangdong/1/96 (Gs/GD), which was first isolated in a domestic goose in China in 1996 (Xu et al. 1999). Increased diversification of Gs/GD via mutations and repeated genetic reassortments with common and globally distributed LPAIV subtypes has resulted in maintenance of Gs/GD viral lineages. Those descendants of Gs/GD have demonstrated an aptness to continually reassort (H5Nx, with different NA subtypes) (de Vries et al. 2015). For example, clade 2.3 caused infections in birds with some human spillover throughout Asia from 2003-2008 (Neumann et al. 2010). Viral clade 2.3.4.4 emerged in Asia in 2013 and increased circulation via wild birds and notably improved the ability to infect wild waterfowl (i.e., asymptomatic infection and high shedding rates for certain species) (Kang et al.

2015; Lee et al. 2017). Moreover, clade 2.3.4.4, which emerged in China in 2013, broadened the geographic spread into Asia, the Middle East, Africa, and Europe, and increased numbers of outbreaks since 2014 (Cui et al. 2022). The descendant viruses from Gs/Gd belonging to clade 2.3.4.4b emerged in October 2020 and have been associated with increasing deaths and transcontinental spread to over 80 countries causing outbreaks and circulation in domestic poultry and wild birds (Lee et al. 2017; Caliendo et al. 2022; Pohlmann et al. 2022).

Conventionally, aquatic birds of the Anseriformes (ducks, geese, and swans, here-after termed waterfowl) and Charadriiformes (gulls, terns, and shorebirds) are natural reservoirs for avian influenza viruses (Webster et al. 1992). Waterfowl and charadriiform species have commonly been asymptomatic carriers of LPAIV, presenting with mild intestinal infections, which circulate among wild birds. Transmission of LPAIVs primarily occurs via an indirect fecal-oral route involving an environmental exposure, which provides opportunity for spread via shared waterbodies along migratory routes or wintering areas (Ramey et al. 2020; Ahrens et al. 2022). The Gs/GD H5Nx viruses, however, have also evolved to replicate within the respiratory tract and can thus transmit directly through a respiratory route (i.e., respiratory droplets). Historically, HPAIV outbreaks in poultry have almost exclusively resulted from spillover of LPAIV from wild aquatic birds into poultry where the viruses mutate to HPAIV (Suarez, 2008). However, the dynamics of the current HPAIV outbreak differ from this historical pattern as a broader diversity of wild birds are being impacted by the disease at a disproportionate rate, with wild birds now actively transmitting HPAIV (Pohlmann et al. 2022; Ramey et al. 2022).

SPREAD OF HPAIV CLADE 2.3.4.4b AND INCREASING DISEASE IN WILD BIRDS

Eurasian H5 viruses descended from Gs/GD had not been detected in North America prior to 2014. North America’s first H5 HPAIV outbreak to affect wild birds was caused by H5 viruses belonging to clade 2.3.4.4b in 2014/2015, with dispersal of H5N8 via migratory birds moving from Asia to the Pacific Flyway then spreading to the Central and Mississippi Flyways (Fig. 1A) (Bevins et al. 2016; Ramey et al. 2016). In that outbreak, over 50 million domestic poultry were affected across 15 US states (Ramos et al. 2017), and wild birds were affected in 13 US states (Animal and Plant Health Inspection Service et al. 2016; Bevins et al. 2016). Some short-term circulation and viral persistence occurred until 2016, but H5 was successfully eradicated from poultry via culling control measures and was rarely detected in wild birds indicating minimal circulation. HPAIV was not detected in wild birds in North America again until the winter of 2021 in the province of Newfoundland, Canada (Caliendo et al. 2022). Genetic analysis of the Newfoundland detection suggests the transatlantic spread into North America likely occurred via migration from Northwestern Europe via Iceland, Greenland, or pelagic routes (Fig. 1B) (Bevins et al. 2022; Caliendo et al. 2022), the opposite side of the continent from the 2014/15 incursion. However, a separate transpacific incursion was detected infecting a bald eagle (*Haliaeetus leucocephalus*) recovered from British Columbia, Canada in early 2022 whose viral lineage was found to be most closely genetically similar to a white-tailed eagle (*Haliaeetus albicilla*) from Hokkaido, Japan (Alkie et al. 2022), though no additional Hokkaido related detections in the Americas have been reported. Since the initial detections in Newfoundland, H5N1 has spread throughout most of Canada and the continental United States and most recently (late October – November, 2022) has been detected in Mexico, and expanding into Central America (Costa Rica, Panama, Honduras) and South America (Colombia, Chile, Peru, Ecuador, Venezuela, Bolivia) by February of 2023 (EMPRES-i+ 2023).

CHANGING HPAIV DYNAMICS

Understanding changing disease dynamics is complicated by limitations of detection, testing, reporting, and collation across national and international non-governmental organizations and governmental agencies. We examined the shifts in HPAIV H5NX detections temporally, geographically, and by bird groupings, from 2014 – 2023, using the FAO's EMPRES-i+ open source database which is one of the primary collations of international regional/county-level data including data from non-governmental organizations and cooperating institutions, which according to FAO captures ~30% of H5N1 disease events (EMPRES-i+ 2023). Our synthesis emphasized that with the emergence of the current Eurasian origin H5N1, the dynamics of HPAIV have changed in two important ways for the Americas: symptomatic infections widely circulating in wild birds; and a distinct shift in seasonality of disease. Prior to the December 2021 North American HPAIV incursion, Europe experienced repeated incursions from 2005-2020, with outbreaks, or increases in disease prevalence increasingly affecting wild birds and poultry particularly in the last two years (Verhagen et al. 2021). Notably, the 2016 incursion of clade 2.3.4.4b in Europe, dominated by the H5N8 circulating strain, resulted in an increase in number of affected wild birds (Figs. 1A; 1E). The current European outbreak has resulted in the largest European HPAIV season (2021-2022) thus far (Pohlmann et al. 2022), with detections in a much broader range of wild birds, including terrestrial species and colonially nesting seabirds that had previously been minimally affected (Figs. 1C; 1D-F) (European Food Safety Authority et al. 2022a). Prior to 2021-2022, European HPAIV outbreaks followed a cycle of high intensity outbreaks in the fall/winter and sharp declines in the summer (European Food Safety Authority et al. 2022b; Pohlmann et al. 2022). However, changes in seasonality dynamics began in the Europe during the summer of 2021 with increased detections in spring/summer including several large-scale MMEs in colonially nesting birds (European Food Safety Authority et al. 2022b).

Compared to historical patterns, North American wild bird mortality due to HPAIV has been much higher than expected during the typically low AIV transmission periods of spring and summer of 2022 (Fig. 1F; Pohlmann et al. 2022). A similar temporal pattern of higher than expected transmission and outbreaks was also seen in Europe during the summer of 2022 (European Food Safety Authority et al. 2022b). We recognize that different evolutionary dynamics are exhibited by different AIV lineages (Hill et al. 2022). For example, transmission and infection dynamics of HPAIV viral clades prior to 2.3.4 resulted in limited spread due to reduced host movement and reduced host range (Antigua et al. 2019). Unfortunately, there has been a shift in the range and distribution of affected species beginning with clade 2.3.4 and increasing with clade 2.3.4.4 (Antigua et al. 2019).

Asymptomatic infections may have increased undetected dissemination and dispersal of HPAIV via long-distance migrants, such as waterfowl and gulls, as symptomatic birds are less likely to successfully migrate long distances (Fig. 1D-F). A recent study predicted that different taxonomic groups contribute to the spread of HPAIV at different rates, with gulls and swans exhibiting the highest rates of H5 viral diffusion as compared to terrestrial or domestic species (Hill et al. 2022). Furthermore, asymptomatic infections can result in increased circulating viruses, which may result in reassortment events and changing viral fitness as previously seen with the evolution of the Gs/GD viral lineages.

ASSESSING THE CURRENT NORTH AMERICAN HPAIV OUTBREAK

To examine the spatial spread of H5N1 across North America, we collated disease surveillance data and mortality data from publicly available federal sources for North American poultry (US: USDA-APHIS; CA: CFIA) and wild birds (US: USDA-APHIS, USGS-WHISPers; CA: CFIA/ACIA) for the period between December 2021 to January 2023 (Fig. 2). We note that in the US, not all sick and dead wild birds that are detected and reported to local authorities are captured in the USA databases. No federal source of mortality data for Canada was available, although efforts are underway to estimate wild bird mortality (pers. comm. Avery-Gomm, S.). No publicly available country level databases for wild bird detections or estimates were available for Mexico, Central and South America and these are omitted from further examination outside of EMPRES-i+ reports. All Canada and USA data were merged, and duplicates were removed by matching institution testing accession numbers, dates, species, and location where possible, via direct communication with the agencies. By synthesizing these disparate data sources, we have illustrated how the North American HPAIV outbreak has resulted in rapid geographic spread (Fig. 2) and affected a broad diversity of wild birds. Wild waterfowl, seabirds, a variety of wetland birds and shorebirds, some previously known to be reservoirs and asymptomatic carriers of LPAIV, are susceptible to HPAIV, resulting in mortalities and asymptomatic infections across all groups. It is well known that disease surveillance data can be an inaccurate proxy for wild bird mortality as only a subset of sick or dead wild birds that are reported are sent for testing. Additionally, many mortalities are likely to go undetected due to issues with detectability, surveillance, carcass persistence, and birds drowning at sea (Ford 2006; Ward et al. 2006) and efforts are underway to employ citizen science platforms such as iNaturalist (https://www.inaturalist.org/projects/beached-birds) to aid in detection and surveillance of beached bird mortalities.

Since 2021, increased HPAIV MMEs world-wide have occurred, primarily in colonial-nesting species where transmission may be increased due to proximity of birds and nest sites or behaviors of birds that may facilitate viral spread, e.g., vultures feeding on HPAI infected carcasses. Large die-offs can impact populations of these species for decades and may contribute to species collapse and further ecosystem damage, particularly given the critical declines seen in North American bird biodiversity over the last half century (Rosenberg et al. 2019). We collated a list of impacted North American wild birds, these species were either impacted by MMEs (> 100 total individuals sick or dead estimated) and/or are a species that is listed as endangered, threatened, or of conservation concern (Table 1). Not surprisingly, most MMEs in North America have been in colonially nesting species. A number of those colonial nesting populations or species are listed as sensitive and species of concern due to habitat loss and anthropogenic pressures. However, many colony species are data deficient as monitoring of these populations can be difficult (Rosenberg et al. 2019). For example, Caspian terns (*Hydroprogne caspia*) have nesting colonies in the Great Lakes region of North America and are listed as endangered in Wisconsin and threatened in all other Great Lakes US states. It is estimated that 62% of the Caspian tern population in Lake Michigan died of HPAIV in the summer of 2022 (“Bird flu has killed nearly 1,500 threatened caspian terns on Lake Michigan islands” 2022; “WHISPers” 2022). Additionally, the Canadian media reported thousands of northern gannets (*Morus bassanus)*, along with common murres (*Uria aalgae*), razorbills (*Alca torda*), and great black-backed gulls have been reported washing up on coastlines in the Gulf of St. Lawrence region of Canada (Ann 2022). This region is home to the largest breeding colony of northern gannets in North America, this species has historically faced repeated anthropogenic impacts, like DDT contamination, bycatch, and the Deepwater Horizon oil spill (Chardine et al. 2013). Additionally, some scavenging species have been severely impacted, such as the high nest failure and adult mortalities seen in North American bald eagles (Nemeth et al. 2023). Overall, numerous potentially susceptible species have been identified that may be a starting point for vulnerability and prioritization assessments (Table 1).

FUTURE OF HPAIV IN NORTH AMERICA

Based on previous HPAIV dynamics across other regions, we expect a continued increase in transmission and mortality in North America birds (Verhagen et al. 2021). Yet, some level of immunity to the circulating HPAIVs may also be expected given the high number of detections that occurred from winter 2021 to summer 2022. The length of immunity and degree of cross-immunity for reassorted strains is unknown; however, clade 2.3.4.4b H5 in Europe has demonstrated increased reassortment activity and outbreak events as compared to previous clades (European Food Safety Authority et al. 2022a). Further increases in transmission and mortality events could have major implications for sensitive colonially nesting bird populations which have been disproportionately affected and includes populations and species of already heightened conservation concern.

HPAIV IMPACTS ON MAMMALS AND ONE HEALTH DISEASE

The effects of HPAIV are not limited to birds; marine mammal and sporadic terrestrial mammal H5N1 infections have been detected in the Americas since 2022. An increasing diversity of mammalian species are being affected by disease (Table 2). Additionally several MME in mammals have been reported, there was a MME of infected harbor and gray seals (*Phoca vitulina* and *Halichoerus grypus*) across the state of Maine Coast (n = 157) (Puryear et al. 2022) and in the Gulf of St. Lawrence (n = 100; (Virginie Ann 2022). There was a MME of endangered South American sea lions (*Otaria flavescens*, n = 630) and South American fur seals (*Arctocephalus australis*, n = 4) along the coast of Peru in January to February of 2023 (Gamarra-Toledo et al. 2023b). These detections are likely indicative of marine mammals becoming infected by ingestion or environmental transmission and food chain transmission such as carnivorous mammals becoming infected after ingesting infected birds (Reperant et al. 2008). Additionally, a single mink (*Neovision vision*) farm in Spain experienced a large H5N1outbreak, affecting 50,000 individuals, with suspected onward viral transmission occurring between minks (Agüero et al. 2023). Since 2020 to February 2022 there have been seven human spillover cases due to H5N1 clade 2.3.4.4b exposure from infected poultry: China (n = 1), Spain (n = 2), United Kingdom (n = 1), USA (n = 1), Vietnam (n = 1), and Ecuador (n = 1) (World Health Organization 2022; Pan American Health Organization/WHO 2023). Several genetic mutations associated with possible mammalian adaptation have been identified (Puryear et al. 2022; Agüero et al. 2023) indicating mammalian spillover potential and additional One Health implications if adapted viruses persist.

DECISION ANALYSIS FRAMEWORK TO AID EMERGENT DISEASE RESPONSE

The current HPAIV outbreak, as presented above, has created unique issues and immediate needs across various contexts. The high uncertainty of future North American HPAIV disease dynamics coupled with the diversity of species impacted and differences in migratory distance, behavior, and ecological context (e.g., habitat types, population size, conservation priority) create extensive biological uncertainty around any proactive disease management decisions. Effective disease management responses depend on improved systems for decision making. Challenges to those decisions for HPAIV include complex governance structures with conflicting or overlapping authorities, limited resources and capacity, great uncertainty around the zoonotic disease, and the effective management of it. Given these issues, a One Health focused decision-based framework encompassing wildlife, poultry, and humans may provide the tools necessary to address HPAIV.

Decision analysis provides a structured framework for characterizing, decomposing, and analyzing a management decision (Hammond et al. 2015; Runge et al. 2020). The analysis helps identify the vital scientific questions which can inform and improve proactive and reactive decision making (Nicol et al. 2019) and guide management decisions in urgent and emergent disease outbreaks (Probert et al. 2018). The process begins with identification of the actors, managers, scientists, and relevant stakeholders, as inclusive engagement is essential to fully capture all problem facets and ultimately to have a successful process. The PrOACT acronym is often used to identify the key elements of the decision analysis: **Pr**oblem framing to identify the decision maker and their authority to act; articulation of the decision maker's fundamental **O**bjectives; generating feasible **A**lternatives that may meet the objectives; building models to predict the **C**onsequences and outcomes of the alternatives in terms of meeting the objectives; and examining **T**radeoffs to identify a preferred alternative, which may require optimization before a finalized decision and action steps can be taken (Fig. 3; Hammond et al. 2015). These steps often are not linear and are often iterative, which is necessary as the understanding and needs of disease problems such as HPAIV are evolving and require adaptive management as the situations unfold and change.

DECISION ANALYSIS ACROSS GOVERNANCE SCALES

While decision analysis can help create a structured process for deliberation, the appropriate scale can vary from agency-level priority setting to local population management. A proper assessment of the problem and objectives needs to incorporate both science and value-based judgements and determine which scale is best equipped to address the issue. Federal, state, and province agencies are already invested in managing bird populations. Although priorities may be set more broadly, conservation actions and implementation typically occur at local scales. Yet, addressing detections and spread of HPAIV, along with researching specific areas of uncertainty, will require decision making and coordination across multiple scales (ranging from a single property to global migratory connections). Here, we provide example triggers for HPAIV management along with challenges specific to North America that range across governance scales and prompt a management response that could benefit from a formal decision making process (Table 3). These examples include localized triggers such as a detection of HPAIV in an area with a threatened colony nesting population. A detection in that situation may trigger a management response that could range from known viral reservoir species targeted deterrence to habitat manipulation to deter species use, and the range of options would be identified through the decision making process. The decision-focused process may help improve effectiveness across scales by bringing together agencies with separate authorities to improve coordination (Converse & Grant 2019).

Our synthesis supports North America facing a future with increased probability of recurrent HPAIV epizootics affecting wildlife, captive species, and poultry and the potential for continued major economic damage and impacts on food security. Wildlife agencies, industry managers, and public health officials need to make informed, timely decisions in the face of uncertainty including addressing species of conservation concern, sensitive management areas, and high poultry production areas. A structured decision analysis framework for response to HPAIV mitigation and management across scales would provide tools to identify actions which will best reduce the glaring uncertainties of the HPAIV disease system.

SPECIFIC TOOLS OF DECISION ANALYSIS TO DRIVE SCIENTIFIC INQUIRY

As discussed previously, much of the complexity of emergent disease systems is the inherent degree of uncertainty (biological or ecological) due to the dynamic nature of viral disease ecology as well as host ecology. Implementation of decision analytical tools in other challenging emerging wildlife diseases have included rapid problem prototyping to identify optimal management responses for white-nose syndrome (*Pseudogymnoascus destructans*) in cave hibernating bats (Bernard et al. 2019), and a simulation exercise in emergency detection of Bsal (*Batrachochytrium salamandrivorans*) introduction to US amphibians (Canessa et al. 2020). Management driven scientific inquiry is urgently needed to establish recommended disease response protocols. Value of information methods can be used within a decision framework to identify the science that should most improve management and conservation actions (Shea et al. 2014). Additionally, expert elicitation can be used to inform performance predictions of management options along with prior probability weights to determine how much management could be improved if a given uncertainty were resolved (Runge et al. 2011). Thus, scientific inquiry can be targeted to reduce uncertainties that are most relevant to decision makers. Examples of uncertainties for management have been identified (Table 3), such as whether carcass removal will reduce HPAI transmission, a question that has come up during interactions with federal managers. In this example, increases in HPAIV mortalities in scavenging species (i.e., raptors, gulls, and corvids) have been seen (Fig 1F; Kleyheeg et al. 2017), and there is some indication that carcass removal may positively impact seabird colony survival (Rijks et al. 2022). However, carcass removal as a response protocol in reducing HPAIV wild bird mortalities has not yet been studied for effectiveness in reducing transmission, possible negative ramifications such as enabling spread through carcass movement, prioritization of limited funds or person-power. So, value of information methods could be an ideal way to assess whether resources should be allocated for further study of carcass removal. Such rapid response protocols are needed but must be robust and require transparency and defensibility that can provided by a decision analytical approach.

CONCLUSIONS

The future of HPAIV in North America is of urgent concern and may be impacted by continued reassortment of HPAIV H5N1. North America has seen a high amount of mortality in the first infection season of 2021-2022 with expansion into Central and South America in late 2022 and early 2023. The changing dynamics of HPAIV along with possibility of clade 2.3.4.4b HPAIV persistence in North America through continued asymptomatic circulation and environmental persistence is unknown. This lack of knowledge is compounded by the fact that a broad range of host species with diverse migratory and life history strategies are being impacted, which all indicate likely endemism in the future. Additionally, HPAIV management in North America must occur across multiple scales, jurisdictions, and agencies. The impacts of future North American HPAIV dynamics are of broad concern from a One Health perspective and as a biodiversity crisis, that could benefit from an inclusive decision making approach. Outcomes may benefit from specific processes and tools aimed at increasing the effectiveness of decision making and conservation prioritization strategies. Given the novel behavior of HPAIV and the high levels of uncertainty, SDM could be an effective framework to inform the prioritization of funds and actions for the research and management agenda for the organizations at the helm.

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References

Agüero, M., Monne, I., Sánchez, A., Zecchin, B., Fusaro, A., Ruano, M.J., del Valle Arrojo, M., Fernández-Antonio, R., Souto, A.M., Tordable, P., Cañás, J., Bonfante, F., Giussani, E., Terregino, C. & Orejas, J.J. (2023). Highly pathogenic avian influenza A(H5N1) virus infection in farmed minks, Spain, October 2022. *Eurosurveillance*, 28.

Ahrens, A.K., Selinka, H.-C., Mettenleiter, T.C., Beer, M. & Harder, T.C. (2022). Exploring surface water as a transmission medium of avian influenza viruses – systematic infection studies in mallards. *Emerg Microbes Infect*, 11, 1250–1261.

Alkie, T.N., Lopes, S., Hisanaga, T., Xu, W., Suderman, M., Koziuk, J., Fisher, M., Redford, T., Lung, O., Joseph, T., Himsworth, C.G., Brown, I.H., Bowes, V., Lewis, N.S. & Berhane, Y. (2022). A threat from both sides: Multiple introductions of genetically distinct H5 HPAI viruses into Canada via both East Asia-Australasia/Pacific and Atlantic flyways. *Vir Evol*, 8, veac077.

Animal and Plant Health Inspection Service, Veterinary Services & National Preparedness and Incident Coordination. (2016). *Final Report for the 2014–2015 Outbreak of Highly Pathogenic Avian Influenza (HPAI) in the United States*. USDA.

Ann, V. (2022). Strain of highly pathogenic avian influenza kills thousands of birds in Quebec. *CBC News*. URL https://www.cbc.ca/news/canada/montreal/strain-highly-pathogenic-avian-influenza-quebec-1.6474289

Antigua, K.J.C., Choi, W.-S., Baek, Y.H. & Song, M.-S. (2019). The Emergence and Decennary Distribution of Clade 2.3.4.4 HPAI H5Nx. *Microorganisms*, 7, 156.

Bernard, R.F., Evans, J., Fuller, N.W., Reichard, J.D., Coleman, J.T.H., Kocer, C.J. & Campbell Grant, E.H. (2019). Different management strategies are optimal for combating disease in East Texas cave versus culvert hibernating bat populations. *Conservat Sci and Prac*, 1.

Bernard, R.F. & Grant, E.H.C. (2019). Identifying Common Decision Problem Elements for the Management of Emerging Fungal Diseases of Wildlife. *Soc Nat Resour*, 32, 1040–1055.

Bevins, S.N., Dusek, R.J., White, C.L., Gidlewski, T., Bodenstein, B., Mansfield, K.G., DeBruyn, P., Kraege, D., Rowan, E., Gillin, C., Thomas, B., Chandler, S., Baroch, J., Schmit, B., Grady, M.J., Miller, R.S., Drew, M.L., Stopak, S., Zscheile, B., Bennett, J., Sengl, J., Brady, C., Ip, H.S., Spackman, E., Killian, M.L., Torchetti, M.K., Sleeman, J.M. & Deliberto, T.J. (2016). Widespread detection of highly pathogenic H5 influenza viruses in wild birds from the Pacific Flyway of the United States. *Sci Rep*, 6, 28980.

Bevins, S.N., Shriner, S.A., Jr, J.C.C., Dilione, K.E., Douglass, K.E., Ellis, J.W., Killian, M.L., Torchetti, M.K. & Lenoch, J.B. (2022). Intercontinental Movement of Highly Pathogenic Avian Influenza A(H5N1) Clade 2.3.4.4 Virus to the United States, 2021. *Emerg Infect Dis*, 28, 6.

Caliendo, V., Lewis, N.S., Pohlmann, A., Baillie, S.R., Banyard, A.C., Beer, M., Brown, I.H., Fouchier, R.A.M., Hansen, R.D.E., Lameris, T.K., Lang, A.S., Laurendeau, S., Lung, O., Robertson, G., van der Jeugd, H., Alkie, T.N., Thorup, K., van Toor, M.L., Waldenström, J., Yason, C., Kuiken, T. & Berhane, Y. (2022). Transatlantic spread of highly pathogenic avian influenza H5N1 by wild birds from Europe to North America in 2021. *Sci Rep*, 12, 11729.

Canadian Food Inspection Agency Government of Canada. (2022). Status of ongoing avian influenza response by province. https://inspection.canada.ca/animal-health/terrestrial-animals/diseases/reportable/avian-influenza/hpai-in-canada/status-of-ongoing-avian-influenza-response/eng/1640207916497/1640207916934

Canessa, S., Spitzen-van der Sluijs, A., Stark, T., Allen, B.E., Bishop, P.J., Bletz, M., Briggs, C.J., Daversa, D.R., Gray, M.J., Griffiths, R.A., Harris, R.N., Harrison, X.A., Hoverman, J.T., Jervis, P., Muths, E., Olson, D.H., Price, S.J., Richards-Zawacki, C.L., Robert, J., Rosa, G.M., Scheele, B.C., Schmidt, B.R. & Garner, T.W.J. (2020). Conservation decisions under pressure: Lessons from an exercise in rapid response to wildlife disease. *Conservat Sci and Prac*, 2.

Chapter 10.4 Infection with high pathogenicity avian influenza viruses. (2021). In: *OIE Terrestrial Animal Health Code*. World Organization for Animal Health.

Chardine, J.W., Rail, J.-F. & Wilhelm, S. (2013). Population dynamics of Northern Gannets in North America, 1984-2009: Northern Gannet Population Dynamics. *J Field Ornithol*, 84, 187–192.

Claus O. Wilke. (2022). ggridges: Ridgeline Plots in "ggplot2."

CMS & FAO. (2022). *Scientific Task Force on Avian Influenza and Wild Birds statement. H5N1 Highly Pathogenic Avian Influenza in poultry and wild birds: Winter of 2021/2022 with focus on mass mortality of wild birds in UK and Israel*. Scientific Task Force on Avian Influenza and Wild Birds.

Conroy, M.J. & Peterson, J.T. (2013). *Decision making in natural resource management: a structured, adaptive approach*. Wiley, Hoboken, NJ.

Converse, S.J. & Grant, E.H.C. (2019). A three-pipe problem: dealing with complexity to halt amphibian declines. *Biol Conserv*, 236, 107–114.

Converse, S.J., Moore, C.T. & Armstrong, D.P. (2013). Demographics of reintroduced populations: Estimation, modeling, and decision analysis: Demographics of Reintroduced Populations. *Jour. Wild. Mgmt.*, 77, 1081–1093.

Cook, J.D., Campbell Grant, E.H., Coleman, J.T.H., Sleeman, J.M. & Runge, M.C. (2022). Evaluating the risk of SARS-CoV-2 transmission to bats in the context of wildlife research, rehabilitation, and control. *Wild Soc Bull*, 46.

Cui, P., Shi, J., Wang, C., Zhang, Y., Xing, X., Kong, H., Yan, C., Zeng, X., Liu, L., Tian, G., Li, C., Deng, G. & Chen, H. (2022). Global dissemination of H5N1 influenza viruses bearing the clade 2.3.4.4b HA gene and biologic analysis of the ones detected in China. *Emerging Microbes & Infections*, 11, 1693–1704.

EMPRES-i+. (2023). *Disease reports of avian influenza H5N1 from January 2014 - February 2023*. FAO United Nations.

European Food Safety Authority, European Centre for Disease Prevention and Control, European Union Reference Laboratory for Avian Influenza, Adlhoch, C., Fusaro, A., Gonzales, J.L., Kiuiken, T., Marangon, S., Niquex, É., Staubach, C., Terregino, C., Aznar, I., Muñoz Guajardo, I. & Baldineli, F. (2022a). Avian influenza overview December 2021 – March 2022. *EFS2*, 20, 7289.

European Food Safety Authority, European Centre for Disease Prevention and Control, European Union Reference Laboratory for Avian Influenza, Adlhoch, C., Fusaro, A., Gonzales, J.L., Kuiken, T., Marangon, S., Niqueux, É., Staubach, C., Terregino, C., Aznar, I., Guajardo, I.M. & Baldinelli, F. (2022b). Avian influenza overview March – June 2022. *EFS2*, 20.

Ford, R.G. (2006). Using Beached Bird Monitoring Data for Seabird Damage Assessment: The Importance of Search Interval. *Mar Ornithol* 34: 91-98.

Gamarra-Toledo, V., Plaza, P.I., Gutiérrez, R., Luyo, P., Hernani, L., Angulo, F. & Lambertucci, S.A. (2023a). Avian flu threatens Neotropical birds. *Science*, 379, 246–246.

Gamarra-Toledo, V., Plaza, P.I., Inga, G., Gutiérrez, R., García-Tello, O., Valdivia-Ramírez, L., Huamán-Mendoza, D., Nieto-Navarrete, J.C., Ventura, S. & Lambertucci, S.A. (2023b). First Mass Mortality of Marine Mammals Caused by Highly Pathogenic Influenza Virus (H5N1) in South America. bioRxiv 2022.

Gerber, B.D., Converse, S.J., Muths, E., Crockett, H.J., Mosher, B.A. & Bailey, L.L. (2018). Identifying Species Conservation Strategies to Reduce Disease-Associated Declines: Optimal conservation strategy. *Conserv Lett*, 11, e12393.

Graham, L. (2022). Bird flu has killed nearly 1,500 threatened Caspian terns on Lake Michigan islands. *Michigan Radio*. https://www.michiganradio.org/environment-climatechange/2022-06-29/bird-flu-has-killed-nearly-1-500-threatened-caspian-terns-on-lake-michigan-islands

Grant, E.H.C., Muths, E., Katz, R.A., Canessa, S., Adams, M.J., Ballard, J.R., Berger, L., Briggs, C.J., Coleman, J.T., Gray, M.J., Harris, M.C., Harris, R.N., Hossack, B., Huyvaert, K.P., Kolby, J., Lips, K.R., Lovich, R.E., McCallum, H.I., Mendelson, J.R., Nanjappa, P., Olson, D.H., Powers, J.G., Richgels, K.L., Russell, R.E., Schmidt, B.R., Spitzen-van der Sluijs, A., Watry, M.K., Woodhams, D.C. & White, C.L. (2017). Using decision analysis to support proactive management of emerging infectious wildlife diseases. *Front Ecol Environ*, 15, 214–221.

Hammond, J.S., Keeney, R.L. & Raiffa, H. (2015). *Smart Choices: a practical guide to making better decisions*. Harvard Business School: McGraw-Hill, Boston, Mass., London.

Hemming, V., Burgman, M.A., Hanea, A.M., McBride, M.F. & Wintle, B.C. (2018). A practical guide to structured expert elicitation using the IDEA protocol. *Methods Ecol Evol*, 9, 169–180.

Hill, N.J., Bishop, M.A., Trovão, N.S., Ineson, K.M., Schaefer, A.L., Puryear, W.B., Zhou, K., Foss, A.D., Clark, D.E., MacKenzie, K.G., Gass, J.D., Borkenhagen, L.K., Hall, J.S. & Runstadler, J.A. (2022). Ecological divergence of wild birds drives avian influenza spillover and global spread. *PLoS Pathog*, 18, e1010062.

Kang, H.-M., Lee, E.-K., Song, B.-M., Jeong, J., Choi, J.-G., Jeong, J., Moon, O.-K., Yoon, H., Cho, Y., Kang, Y.-M., Lee, H.-S. & Lee, Y.-J. (2015). Novel Reassortant Influenza A(H5N8) Viruses among Inoculated Domestic and Wild Ducks, South Korea, 2014. *Emerg. Infect. Dis.*, 21, 298–304.

Kleyheeg, E., Slaterus, R., Bodewes, R., Rijks, J.M., Spierenburg, M.A.H., Beerens, N., Kelder, L., Poen, M.J., Stegeman, J.A., Fouchier, R.A.M., Kuiken, T. & van der Jeugd, H.P. (2017). Deaths among Wild Birds during Highly Pathogenic Avian Influenza A(H5N8) Virus Outbreak, the Netherlands. *Emerg Infect Dis*, 23, 2050–2054.

Lee, D.-H., Bertran, K., Kwon, J.-H. & Swayne, D.E. (2017). Evolution, global spread, and pathogenicity of highly pathogenic avian influenza H5Nx clade 2.3.4.4. *J Vet Sci*, 18, 269.

Ministerio de Salud. (2022). *Alerta epidemiológica: Epizootia de influenza aviar, tipo A, subtipo H5 en aves silvestres y aves de traspatio en el país* (No. CODIGO: AE 029-2022). Centro Nacional de Epidemiología, Prevención y Control de Enfermedades, Lima, Peru.

National Avian Influenza - Wild Positives. CFIA (2022). https://cfia-ncr.maps.arcgis.com/apps/dashboards/89c779e98cdf492c899df23e1c38fdbc

Nemeth, N.M., Ruder, M.G., Poulson, R.L., Sargent, R., Breeding, S., Evans, M.N., Zimmerman, J., Hardman, R., Cunningham, M., Gibbs, S. & Stallknecht, D.E. (2023). Bald eagle mortality and nest failure due to clade 2.3.4.4 highly pathogenic H5N1 influenza a virus. *Sci Rep*, 13, 191.

Neumann, G., Chen, H., Gao, G.F., Shu, Y. & Kawaoka, Y. (2010). H5N1 influenza viruses: outbreaks and biological properties. *Cell Res*, 20, 51–61.

Nicol, S., Brazill-Boast, J., Gorrod, E., McSorley, A., Peyrard, N. & Chadès, I. (2019). Quantifying the impact of uncertainty on threat management for biodiversity. *Nat Commun*, 10, 3570.

Pan American Health Organization/WHO. (2023). *Epidemiological Alert: Outbreaks of avian influenza and human infection caused by influenza A(H5) public health implications in the Region of the Americas*. PAHP/WHO, Washington, D.C.

Pohlmann, A., King, J., Fusaro, A., Zecchin, B., Banyard, A.C., Brown, I.H., Byrne, A.M.P., Beerens, N., Liang, Y., Heutink, R., Harders, F., James, J., Reid, S.M., Hansen, R.D.E., Lewis, N.S., Hjulsager, C., Larsen, L.E., Zohari, S., Anderson, K., Bröjer, C., Nagy, A., Savič, V., van Borm, S., Steensels, M., Briand, F.-X., Swieton, E., Smietanka, K., Grund, C., Beer, M. & Harder, T. (2022). Has Epizootic Become Enzootic? Evidence for a

Fundamental Change in the Infection Dynamics of Highly Pathogenic Avian Influenza in Europe, 2021. *mBio*, e00609-22.

Probert, W.J.M., Jewell, C.P., Werkman, M., Fonnesbeck, C.J., Goto, Y., Runge, M.C., Sekiguchi, S., Shea, K., Keeling, M.J., Ferrari, M.J. & Tildesley, M.J. (2018). Real-time decision-making during emergency disease outbreaks. *PLoS Comput Biol*, 14, e1006202.

Puryear, W., Sawatzki, K., Hill, N., Foss, A., Stone, J.J., Doughty, L., Walk, D., Gilbert, K., Murray, M., Cox, E., Patel, P., Mertz, Z., Ellis, S., Taylor, J., Fauquier, D., Smith, A., DiGiovanni, R.A., van de Guchte, A., Gonzalez-Reiche, A.S., Khalil, Z., van Bakel, H., Torchetti, M.K., Lenoch, J.B., Lantz, K. & Runstadler, J. (2022). Outbreak of Highly Pathogenic Avian Influenza H5N1 in New England Seals. biorRxiv 2022.

Ramey, A.M., Hill, N.J., DeLiberto, T.J., Gibbs, S.E.J., Camille Hopkins, M., Lang, A.S., Poulson, R.L., Prosser, D.J., Sleeman, J.M., Stallknecht, D.E. & Wan, X.F. (2022). Highly pathogenic avian influenza is an emerging disease threat to wild birds in North America. *J Wildl Manag*, 86, 1–21.

Ramey, A.M., Reeves, A.B., Drexler, J.Z., Ackerman, J.T., De La Cruz, S., Lang, A.S., Leyson, C., Link, P., Prosser, D.J., Robertson, G.J., Wight, J., Youk, S., Spackman, E., Pantin-Jackwood, M., Poulson, R.L. & Stallknecht, D.E. (2020). Influenza A viruses remain infectious for more than seven months in northern wetlands of North America: IAVs in wetlands. *Proc Royal Soc B*, 287.

Ramey, A.M., Reeves, A.B., TeSlaa, J.L., Nashold, S., Donnelly, T., Bahl, J. & Hall, J.S. (2016). Evidence for common ancestry among viruses isolated from wild birds in beringia and highly pathogenic intercontinental reassortant H5N1 and H5N2 influenzaA viruses. *Infec Genet Evol*, 40, 176–185.

Ramos, S., MacLachlan, M. & Melton, A. (2017). *Impacts of the 2014-2015 Highly Pathogenic Avian Influenza Outbreak on the U.S. Poultry Sector* (No. LPDM-282-02).

Reperant, L.A., van Amerongen, G., van de Bildt, M.W.G., Rimmelzwaan, G.F., Dobson, A.P., Osterhaus, A.D.M.E. & Kuiken, T. (2008). Highly Pathogenic Avian Influenza Virus (H5N1) Infection in Red Foxes Fed Infected Bird Carcasses. *Emerg. Infect. Dis.*, 14, 1835–1841.

Rijks, J.M., Leopold, M.F., Kühn, S., in 't Veld, R., Schenk, F., Brenninkmeijer, A., Lilipaly, S.J., Ballmann, M.Z., Kelder, L., de Jong, J.W., Courtens, W., Slaterus, R., Kleyheeg, E., Vreman, S., Kik, M.J.L., Gröne, A., Fouchier, R.A.M., Engelsma, M., de Jong, M.C.M., Kuiken, T. & Beerens, N. (2022). Mass Mortality Caused by Highly Pathogenic Influenza A(H5N1) Virus in Sandwich Terns, the Netherlands, 2022. *Emerg. Infect. Dis.*, 28, 2538–2542.

Rosenberg, K.V., Dokter, A.M., Blancher, P.J., Sauer, J.R., Smith, A.C., Smith, P.A., Stanton, J.C., Panjabi, A., Helft, L., Parr, M. & Marra, P.P. (2019). Decline of the North American avifauna. *Science*, 366, 120–124.

Rowan, M.K. (1962). Mass mortality among European Common Terns in South Africa in April-May 196. *British Birds*, 55, 103–114.

Runge, M.C., Converse, S.J. & Lyons, J.E. (2011). Which uncertainty? Using expert elicitation and expected value of information to design an adaptive program. *Biological Conservation*, 144, 1214–1223.

Runge, M.C., Grand, J.B. & Mitchell, M.S. (2013). Structured Decision Making. In: *Wildlife Management and Conservation: Contemporary Principles and Practices*. Johns Hopkins University Press, Baltimore, MD, pp. 51–72.

Runge, M.C., Sarah J. Converse, James E. Lyons, & David R. Smith (eds.). (2020). *Structured decision making: case studies in natural resource management*. Wildlife management and conservation. Johns Hopkins University Press, Baltimore.

Sarah J. Converse. (2020). Introduction to Multi-criteria decision analysis. In: *Structured decision making: Case studies in natural resource management* (eds. Runge, M.C., Sarah J. Converse, Lyons, J.E. & Smith, D.R.). Johns Hopkins University Press, pp. 51–61.

Shea, K., Runge, M.C., Pannell, D., Probert, W.J.M., Li, S.-L., Tildesley, M. & Ferrari, M. (2020). Harnessing multiple models for outbreak management. *Science*, 368, 577–579.

Shea, K., Tildesley, M.J., Runge, M.C., Fonnesbeck, C.J. & Ferrari, M.J. (2014). Adaptive Management and the Value of Information: Learning Via Intervention in Epidemiology. *PLOS Biology*, 12, e1001970.

Suarez, D.L. (2008). Influenza A Virus. In: *Avian influenza* (ed. Swayne, D.E.). Blackwell Pub, Ames, Iowa.

Tyshenko, M.G., Oraby, T., Darshan, S., Westphal, M., Croteau, M.C., Aspinall, W., Elsaadany, S., Krewski, D. & Cashman, N. (2016). Expert elicitation on the uncertainties associated with chronic wasting disease. *Journal of Toxicology and Environmental Health, Part A*, 79, 729–745.

USDA APHIS. (2023a). 2022-2023 Detections of Highly Pathogenic Avian Influenza in Wild Birds. https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/avian/avian-influenza/hpai-2022/2022-hpai-wild-birds

USDA APHIS. (2023b). 2022-2023 Confirmations of Highly Pathogenic Avian Influenza in Commercial and Backyard Flocks. https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/avian/avian-influenza/hpai-2022/2022-hpai-commercial-backyard-flocks

USDA APHIS. (2023c). 2022-2023 Detections of Highly Pathogenic Avian Influenza in Mammals. https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/avian/avian-influenza/hpai-2022/2022-hpai-mammals

Verhagen, J.H., Fouchier, R.A.M. & Lewis, N. (2021). Highly Pathogenic Avian Influenza Viruses at the Wild–Domestic Bird Interface in Europe: Future Directions for Research and Surveillance. *Viruses*, 13, 212.

Virginie Ann. (2022). Highly pathogenic avian influenza believed to be killing seals in Quebec. *The Canadian Press*.

de Vries, E., Guo, H., Dai, M., Rottier, P.J.M., van Kuppeveld, F.J.M. & de Haan, C.A.M. (2015). Rapid Emergence of Highly Pathogenic Avian Influenza Subtypes from a Subtype H5N1 Hemagglutinin Variant. *Emerg. Infect. Dis.*, 21, 842–846.

Ward, M.R., Stallknecht, D.E., Willis, J., Conroy, M.J. & Davidson, W.R. (2006). Wild Bird Mortality and West Nile Virus Surveillance: Biases Associated with Detection, Reporting, and Carcass Persistence. *J Wildl Dis*, 42, 92–106.

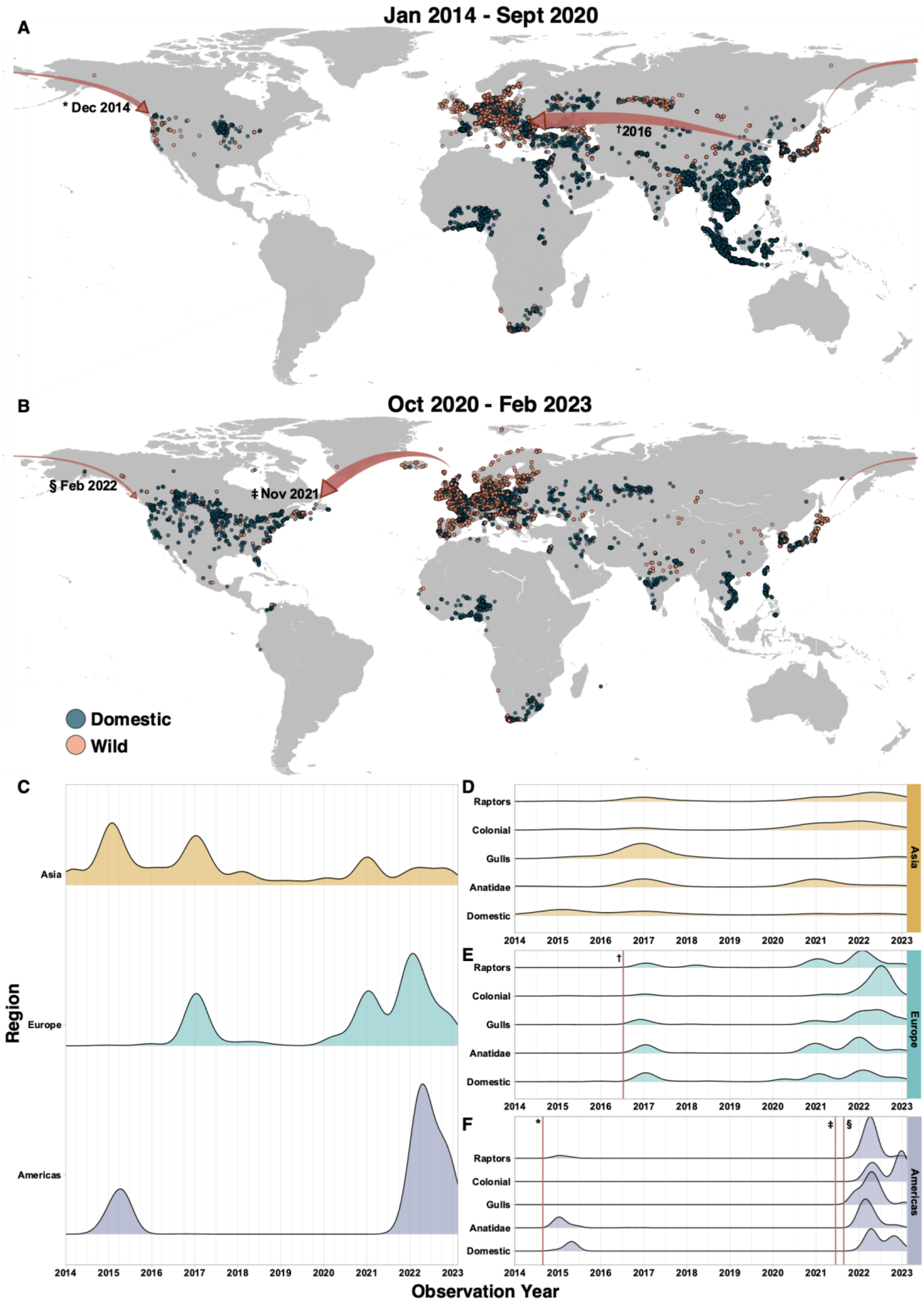
Webster, R.G., Bean, W.J., Gorman, O.T., Chambers, T.M. & Kawaoka, Y. (1992). Evolution and ecology of influenza A viruses. *Microbio. Rev*, 56, 28.

WHISPers [WWW Document]. (2023). https://whispers.usgs.gov/home

World Health Organization. (2022). *Rapid Risk Assessment: Assessment of risk associated with recent influenza A(H5N1) clade 2.3.4.4b viruses*.

Xu, X., Subbarao, K., Cox, N.J. & Guo, Y. (1999). Genetic Characterization of the Pathogenic Influenza A/Goose/Guangdong/1/96 (H5N1) Virus: Similarity of Its Hemagglutinin Gene to Those of H5N1 Viruses from the 1997 Outbreaks in Hong Kong. *Virology*, 261, 15–19.

Fig. 1) **Spread of Clade 2.3.4.4b in domestic and wild birds.** A-B) Map of HPAIV detections in domestic (blue circles) and wild (coral circles) birds from A) December 2014 – September 2020 with red arrows demonstrating the incursion from Asia to North America in December of 2014 (* symbol), and incursion from Asia to Europe in 2016 († symbol); B) October 2020 - November 15, 2022 with a red arrows demonstrating the transatlantic incursion from Europe to North America in November 2021(‡ symbol), and incursion from Japan to British Columbia in February 2022 (§ symbol). C-F) Ridgeline plots, created using the ggridges package (Claus O. Wilke 2022) in R v.4.1.0, of C) of the combined wild and domestic bird HPAIV detections across Asia, Europe, and North America from 2014 – February 2023; D-F) Density of detections across raptors, colonially nesting species, gulls, wild species within the taxonomic family of Anatidae, and domestic bird which are scaled across: D) Asia; E) Europe, with † symbol indicating timing of incursion of from Asia in 2016; and F) the Americas, with the * symbol indicating the incursion from Asia in December of 2014, the ‡ symbol indicating the incursion from Europe in December of 2021, and the § symbol indicating the trans-Pacific incursion in February of 2022. Maps and all plots contain all high pathogenicity H5NX confirmed detections in wild and domestic birds from the FAO’s EMPRES-i+ database for each date range.


A
Jan 2014 - Sept 2020
* Dec 2014
†2016
B
Oct 2020 - Feb 2023
§ Feb 2022
‡ Nov 2021
Domestic
Wild
C
Region
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2014
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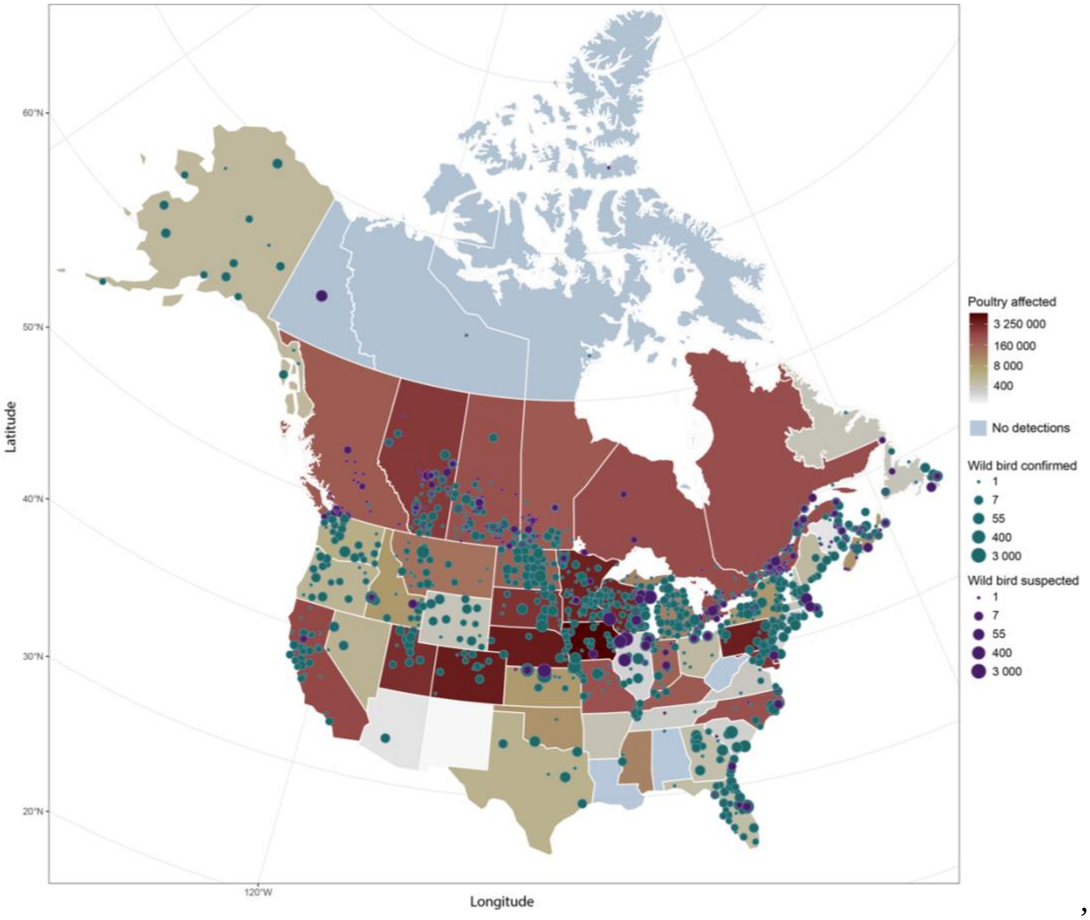

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Fig. 2). Map of the density of poultry (log transformed) affected by HPAIV H5N1from December 2021 to October 2022 across Canadian provinces/territories/US states (Canadian Food Inspection Agency Government of Canada 2022; USDA APHIS 2023b).The darkest red corresponds to the highest number of birds affected and tan/grey corresponds to the lowest number of birds affected. Slate blue indicates no poultry detections were reported for that province/territory/state. Circles (blue = confirmed; purple = suspected) indicate wild bird detections (log transformed) per US county/Canadian census subdivisions (plotted to centroid), circle diameter is scaled by number of detections. Wild bird data collected from USDA and WHISPers (USDA APHIS 2023a; "WHISPers" 2023) current as of October 26, 2022; Canada wild bird data collected from CFIA ("National Avian Influenza - Wild Positives" 2022) current as of October 7, 2022. Base layers downloaded from the United States Census Bureau and the Canada Statistics Agency and are displayed using Lambert canonical projection (Esri: 102009) in R V 4.1.3 and RStudio 2022.02.0.

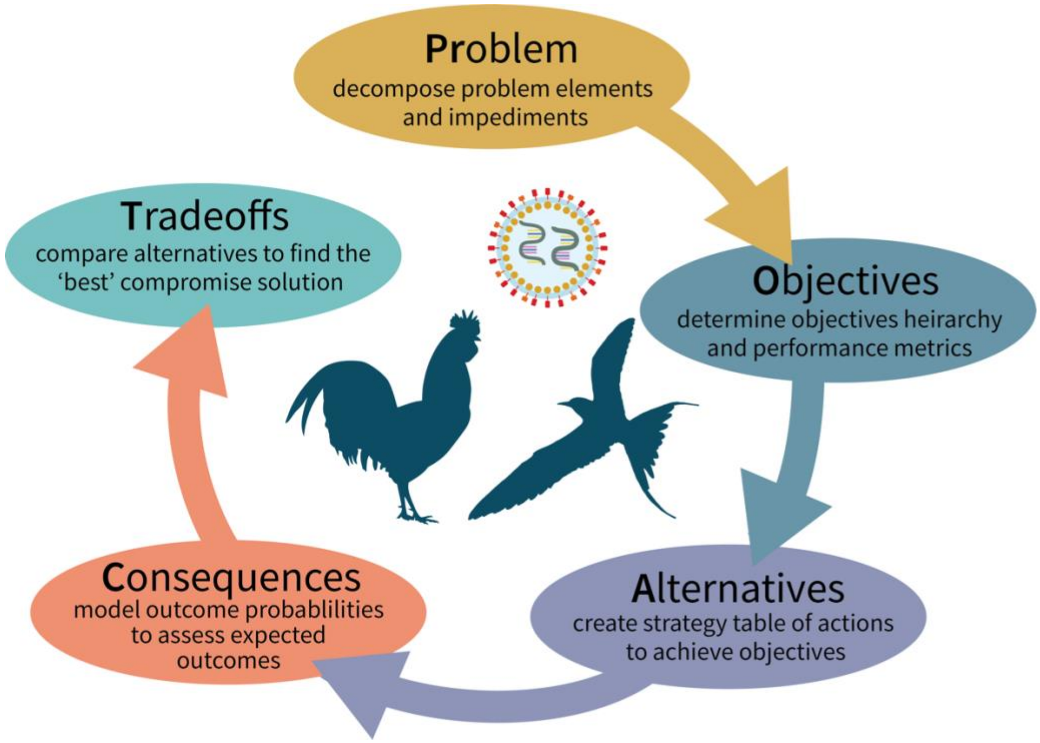


Fig. 3. Structured decision making process steps: Problem, Objective, Alternatives, Consequences and Tradeoffs, for addressing high pathogenicity avian influenza virus (HPAIV) impact on poultry and wild birds in North America. Figure adapted from (Converse et al. 2013; Runge et al. 2013).

Table 1. List of North America wild birds affected by H5N1 clade 2.3.4.4b with either a mass mortality events (MMEs) of >100 individuals per species AND/OR is a species that is threatened/listed of conservation concern. Common and species names, taxonomic order, Total *N* = number of individuals (sick and mortality estimates), MMEs listed (* indicates known MME not represented in data but from media report; Ann 2022), nesting behavior and non-breeding behavior ([1]Billermn et al. 2022). This list is not meant to be exhaustive but demonstrative of the impacts across wild birds and species of conservation concern. Data merged and collated from December 2021 to February 2023 and sourced from US: USDA-APHIS, USGS-WHISPers; and CA: CFIA/ACIA. Threat level and listing including designations by: [2] BCC = Birds of Conservation Concern 2021 (*Birds of Conservation Concern 2021 Migratory Bird Program* 2021) as continental listed (C) or regionally listed (R); [3]ESA = listed under the USA Endangered Species Act as endangered (E) or threatened (T); [4]SARA = listed under the Canada Species at Risk Act under Schedule 1 (Legislative Services Branch Canada 2022) as endangered (E), threatened (T) or of special concern (SC); US State (ST: State abbrev.) listed as endangered (E) or threatened (T).

Common name	**Species**	**Order**	**Total *N***	**MMEs**	**Nesting behavior[1]**	**Non-breeding behavior[1]**	**Threat level/listing**
American coot	*Fulica americana*	Gruiformes	178	160	Paired solitary	Large flocks, mixed	-
Atlantic puffin	*Fratercula arctica*	Pelecaniformes	5	-	Colonial	Colonial	ST: ME (T)
Artic tern	*Sterna paradisaea*	Charadriiformes	4	-	Colonial	Colonial	ST: ME (T)
American white pelican	*Pelecanus erythrorhynchos*	Pelecaniformes	2350	1025; 1050	Colonial	Gregarious, flocking	ST: WA (T)
Bald eagle	*Haliaeetus leucocephalus*	Accipitriformes	382	-	Paired solitary	Social groups	ST: CA, NJ, RI, (E); CT, GA, NC, NM, NY, SC, SD, (T)
Black vulture	*Coragyps atratus*	Accipitriformes	1605	230; 200; 100	Colonial	Gregarious, communal roosts	-
Caspian tern	*Hydroprogne caspia*	Charadriiformes	1517	255; 1231	Colonial	Large flocks	ST: WI (E); NC, MI (T)
Common eider	*Somateria mollissima*	Anseriformes	137	-	Often colonial	Large flocks	-
Common tern	*Sterna hirundo*	Charadriiformes	18	-	Colonial	Colonial	BCC (R)[2]; ST: DE, IL, MD, NC, OH, PA, VT, WI (E); MI, MN, NH, NY (T)

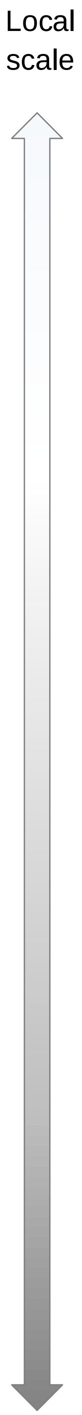
Common name	Species	Order	Total *N*	MMEs	Nesting behavior[1]	Non-breeding behavior[1]	Threat level/listing
Double-crested cormorant	*Phalacrocorax auritus*	Pelecaniformes	2813	301; 979; 200; 849	Colonial	Gregarious	-
Great egret	*Ardea alba*	Pelecaniformes	119	115	Often colonial	Solitary or flocks	
Horned grebe	*Podiceps auritus*	Podicipediformes	2	-	Paired solitary	Flocks	SARA (SC)[4]; ST: MN (E)
Lesser scaup	*Aythya affinis*	Anseriformes	1502	1007; 470	Mostly solitary	Large flocks	-
Northern gannet	*Morus bassanus*	Pelecaniformes	89	> 1000*	Colonial	Small, loose flocks	-
Northern harrier	*Circus hudsonius*	Accipitriformes	2	-	Paired or polygynous, often loose assemblages	Communal roosts	ST: CT, DE, IA, IL, IN, MO, NH, NJ, OH, RI (E); KY, MA, NY, PA (T)
Osprey	*Pandion haliaetus*	Accipitriformes	3	-	Paired solitary	Solitary	ST: IL (E); NJ, SD (T)
Peregrine falcon	*Falco peregrinus*	Falconiformes	26	-	Paired solitary or spaced cavity aggregates	Often paired	ST: KY, ME, MI, MS, NC, NJ, NY, RI, SD, WI (E); CT, NH, TX, VA (T)
Red-shouldered hawk	*Buteo lineatus*	Accipitriformes	5	-	Paired solitary	Solitary or in pairs	ST: IA, NJ (E); MI, WI (T)
Ross's goose	*Anser rossii*	Anseriformes	610	101; 325	Colonial	Large flocks, mixed	-
Royal tern	*Thalasseus maximus*	Charadriiformes	5	-	Dense colonies	Compact large flocks year-round	ST: MD (E)
Sandhill crane	*Antigone canadensis*	Gruiformes	8	-	Paired solitary	Large flocks	ESA (E)[3]; ST: WA (E); CA (T)
Snow goose	*Anser caerulescens*	Anseriformes	6284	1200; 1000; 800; 500; 392;	Colonial	Gregarious, flocking	-

Common name	Species	Order	Total *N*	MMEs	Nesting behavior[1]	Non-breeding behavior[1]	Threat level/listing
				300; 200; 150 - (x5); 107; 102; 100			
Snowy owl	*Bubo scandiacus*	Strigiformes	21	-	Paired solitary	Solitary	BCC (C)[2]
Trumpeter swan	*Cygnus buccinator*	Anseriformes	45	-	Paired or families	Paired birds and family groups	ST: IN (E); MI, OH (T)
Willet	*Tringa semipalmata*	Charadriiformes	2	-	Paired solitary	Small groups	BCC (C)[2]

Table 2. Total number of HPAIV H5 infections reported through testing in North America mammals where data is available for Canada and the United States (*indicates captive non-native species). Data collected from the CFIA (“National Avian Influenza - Wild Positives” 2022) and the USDA (USDA APHIS 2023c) for the period between January 2021 to February 2023.

Common name	Species	Canadian provinces	US states
Amur leopard*	*Panthera pardus orientalis*	-	New York = 1
Amur tiger*	*Panthera tigris altaica*	-	Nebraska = 1
Black bear	*Ursus americanus*	Alberta = 1; Quebec = 2	Alaska = 1
Bobcat	*Lynx rufus*	-	California = 1, Washington =1, Wisconsin =2
Bottlenose dolphin	*Tursiops truncatus*	-	Florida = 1
Coyote	*Canis latrans*	-	Michigan =1
Fisher	*Pekania pennant*	-	Wisconsin =1
Grey seal	*Halichoerus grypus*	Quebec = 1	Maine = 1
Harbor seal	*Phoca vitulina*	Quebec = 17	Maine = 16
Grizzly bear	*Ursus arctos horribilis*	-	Montana = 2
Harbour porpoise	*Phocoena phocoena*	Quebec = 1	-
Kodiak brown bear	*Ursus arctos middendorffi*	-	Alaska = 1
Mink	*Neovison vison*	Ontario = 1	-
Mountain lion	*Puma concolor*	-	Nebraska = 1
Racoon	*Procyon lotor*	Ontario = 2	Michigan = 1, Oregon = 1, Washington = 6
Red fox	*Vulpes vulpes*	Alberta = 6, British Columbia = 3, Manitoba = 6, Nova Scotia = 2, Ontario = 12, Prince Edward Island = 6, Quebec = 1, Saskatchewan = 3, Yukon = 2	Alaska = 2, Iowa =2, Michigan = 14, Minnesota = 8, Montana = 1, New York = 12, North Dakota =2, South Dakota = 1, Utah = 1
Striped skunk	*Mephitis mephitis*	Alberta = 22, British Columbia = 1, Manitoba =1, Ontario =1, Saskatchewan = 6	Colorado = 1, Idaho = 7, Minnesota = 1, Montana =1, Oregon = 2, Wisconsin = 2
Skunk	*Species not specified*	-	Montana =1, Oregon =6
Virginia opossum	*Didelphis virginiana*	-	Illinois = 1, Iowa = 2

Table 3. Examples of potential triggers and the associated decision makers and decision contexts that could benefit from a structured decision making approach, including the challenges associated, for HPAIV application in North America. Gradient arrow indicates an increase in scale from local to regional scale.



Potential Triggers	Decision Maker	Problem Framing	Challenges
HPAIV mortalities detected within a National Wildlife Refuge (NWR)	Refuge manager	Should carcasses be removed?	Uncertain if carcass removal mitigates AIV transmission? Uncertain if carcass handling increases human exposure?
HPAIV detection in wild birds near a poultry farm	Poultry farm manager	Can increased levels of biosecurity be enacted when disease threats are increased?	Wetlands adjacent to a farm may provide habitat for wildlife. How can that risk be mitigated?
HPAIV detected in area with a threatened colony nesting population	Landowner where the population occurs/ agency responsible for threatened species	What actions can be taken to protect sensitive species?	Do actions favorably impact all nesting species in a mixed species nesting site?
Prior loss or decline due to HPAIV in a sensitive species/population	State wildlife agency	Can future population decline due to HPAIV be prevented? Can populations be managed independently to protect species persistence?	Level of immunity and cross-immunity in species not known Lack of information on population sizes or stability for many sensitive populations/species
HPAIV impact on multi-use and public access areas (state park, National Forest, NWR)	State Park manager, National Forest superintendent, or Refuge manager	Should public use be curtailed to decrease disease spread?	Disease mitigation may undermine ability to achieve public use objectives (i.e., difficult tradeoffs need to be navigated).
HPAIV detected in wild birds or poultry during waterfowl hunting season	U.S. Fish and Wildlife Service, or state wildlife agency	What measures or restrictions within the area of detection will reduce spread? Can hunting continue safely?	Uncertainty about how hunting contributes to disease transmission and dispersal.

	Potential Triggers	Decision Maker	Problem Framing	Challenges
	HPAIV detection during fall waterfowl banding	U.S. Fish and Wildlife Service, Canadian Wildlife Service	Should banding be stopped, to prevent aggregation of birds and transmission at banding sites?	Banding is essential for long term population monitoring. Uncertain if banding impacts transmission?
	Limited capacity/funding for disease surveillance and response	Multiple agencies that need to coordinate	How can capacity and resources best be used for effective disease management/response?	Funding and capacity are multi-scale problems, and the responsive agencies might not have a governance structure that allows or promotes collaboration and sharing of resources
Regional scale	Continued HPAIV persistence in North American flyway	North American Flyway Councils	Can sensitive species be protected? Can surveillance strategies improve prioritization objectives?	Impacts on birds are geographically widespread