

## REVIEW



# Highly pathogenic avian influenza is an emerging disease threat to wild birds in North America

Andrew M. Ramey<sup>1</sup> | Nichola J. Hill<sup>2</sup> |  
 Thomas J. DeLiberto<sup>3</sup> | Samantha E. J. Gibbs<sup>4</sup> |  
 M. Camille Hopkins<sup>5</sup> | Andrew S. Lang<sup>6</sup> |  
 Rebecca L. Poulson<sup>7</sup> | Diann J. Prosser<sup>8</sup> |  
 Jonathan M. Sleeman<sup>9</sup> | David E. Stallknecht<sup>7</sup> |  
 Xiu-Feng Wan<sup>10</sup>

<sup>1</sup>U.S. Geological Survey Alaska Science Center, 4210 University Drive, Anchorage, AK 99508, USA

<sup>2</sup>Department of Infectious Disease & Global Health, Cummings School of Veterinary Medicine, Tufts University, 200 Westboro Road, North Grafton, MA 01536, USA

<sup>3</sup>National Wildlife Disease Program, Wildlife Services, Animal and Plant Health Inspection Service, U.S. Department of Agriculture, 4101 LaPorte Avenue, Fort Collins, CO 80521, USA

<sup>4</sup>Wildlife Health Office, Natural Resource Program Center, National Wildlife Refuge System, U.S. Fish and Wildlife Service, 16450 NW 31st Place, Chiefland, FL 32626, USA

<sup>5</sup>U.S. Geological Survey Ecosystems Mission Area, 12201 Sunrise Valley Drive, MS 300 (Room 4A100F), Reston, VA 20192, USA

<sup>6</sup>Department of Biology, Memorial University of Newfoundland, 232 Elizabeth Avenue, St. John's, Newfoundland, A1B 3X9, Canada

<sup>7</sup>Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, 589 D.W. Brooks Drive, Athens, GA 30602, USA

## Abstract

Prior to the emergence of the A/goose/Guangdong/1/1996 (Gs/GD) H5N1 influenza A virus, the long-held and well-supported paradigm was that highly pathogenic avian influenza (HPAI) outbreaks were restricted to poultry, the result of cross-species transmission of precursor viruses from wild aquatic birds that subsequently gained pathogenicity in domestic birds. Therefore, management agencies typically adopted a prevention, control, and eradication strategy that included strict biosecurity for domestic bird production, isolation of infected and exposed flocks, and prompt depopulation. In most cases, this strategy has proved sufficient for eradicating HPAI. Since 2002, this paradigm has been challenged with many detections of viral descendants of the Gs/GD lineage among wild birds, most of which have been associated with sporadic mortality events. Since the emergence and evolution of the genetically distinct clade 2.3.4.4 Gs/GD lineage HPAI viruses in approximately 2010, there have been further increases in the occurrence of HPAI in wild birds and geographic spread through migratory bird movement. A prominent example is the introduction of clade 2.3.4.4 Gs/GD HPAI viruses from East Asia

This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2022 The Authors. *The Journal of Wildlife Management* published by Wiley Periodicals LLC on behalf of The Wildlife Society. This article has been contributed to by US Government employees and their work is in the public domain in the USA.



<sup>8</sup>U.S. Geological Survey Eastern Ecological Science Center at the Patuxent Research Refuge, 12100 Beech Forest Road, Laurel, MD 20708, USA

<sup>9</sup>U.S. Geological Survey National Wildlife Health Center, 6006 Schroeder Road, Madison, WI 53711, USA

<sup>10</sup>Center for Influenza and Emerging Infectious Diseases (CIEID), Department of Molecular Microbiology and Immunology, Bond Life Sciences Center, Department of Electronic Engineering and Computer Science, University of Missouri, Columbia, MO 65211, USA

#### Correspondence

Andrew M. Ramey, U.S. Geological Survey Alaska Science Center, 4210 University Drive, Anchorage, AK 99508, USA.  
Email: [aramey@usgs.gov](mailto:aramey@usgs.gov)

#### Present address

Nichola J. Hill, Biology Department, University of Massachusetts Boston, 100 Morrissey Blvd, Boston, MA 02125, USA.

#### Funding information

U.S. Geological Survey

to North America via migratory birds in autumn 2014 that ultimately led to the largest outbreak of HPAI in the history of the United States. Given the apparent maintenance of Gs/GD lineage HPAI viruses in a global avian reservoir; bidirectional virus exchange between wild and domestic birds facilitating the continued adaptation of Gs/GD HPAI viruses in wild bird hosts; the current frequency of HPAI outbreaks in wild birds globally, and particularly in Eurasia where Gs/GD HPAI viruses may now be enzootic; and ongoing dispersal of AI viruses from East Asia to North America via migratory birds, HPAI now represents an emerging disease threat to North American wildlife. This recent paradigm shift implies that management of HPAI in domestic birds alone may no longer be sufficient to eradicate HPAI viruses from a given country or region. Rather, agencies managing wild birds and their habitats may consider the development or adoption of mitigation strategies to minimize introductions to poultry, to reduce negative impacts on wild bird populations, and to diminish adverse effects to stakeholders using wildlife resources. The main objective of this review is, therefore, to provide information that will assist wildlife managers in developing mitigation strategies or approaches for dealing with outbreaks of Gs/GD HPAI in wild birds in the form of preparedness, surveillance, research, communications, and targeted management actions. Resultant outbreak response plans and actions may represent meaningful steps of wildlife managers toward the use of collaborative and multi-jurisdictional One Health approaches when it comes to the detection, investigation, and mitigation of emerging viruses at the human-domestic animal-wildlife interface.

#### KEYWORDS

avian influenza, bird flu, disease, highly pathogenic, influenza, outbreak, North America, wildlife

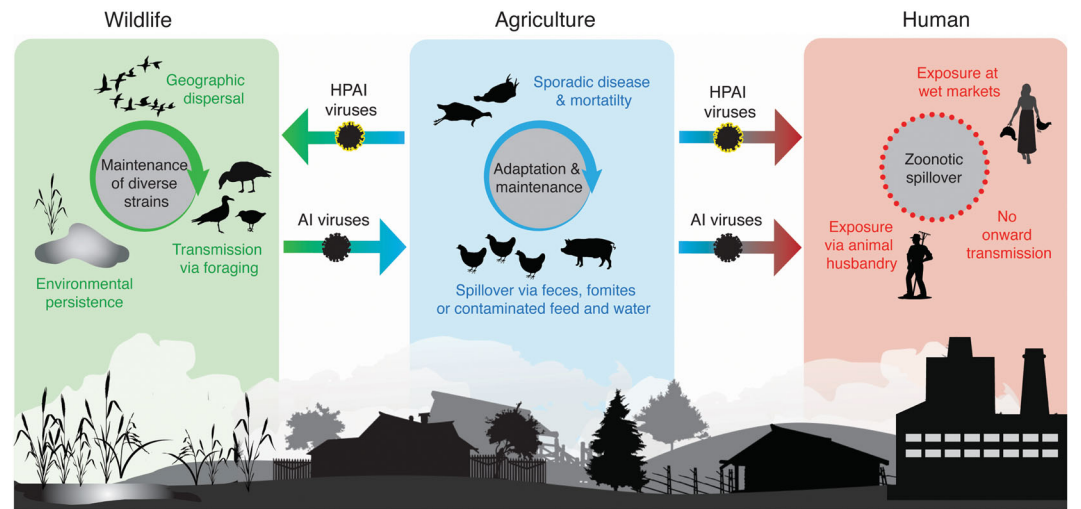
All influenza A viruses, including those that cause bird flu, swine flu, and (human) seasonal influenza, belong to the same viral taxonomic species. The greatest genetic and antigenic diversity of influenza A viruses is maintained in birds. This review is focused on avian-origin influenza A (AI) viruses in birds, specifically those considered to be highly pathogenic (HP) in poultry. Prior to 2002, highly pathogenic avian-origin influenza (HPAI) viruses were limited almost exclusively to poultry and disease resulting from such an infection had only been documented once in wild birds (Rowan 1962, Becker 1966). The situation has since changed. Following the emergence of a specific viral lineage in domestic geese in Guangdong, China in 1996, there have been increasing detections of HPAI viruses, often associated with mortality in wild birds. In this review our objective is to provide basic background information on AI viruses with an emphasis on those affecting wild birds, a brief history of the emergence and evolution of

goose/Guangdong (Gs/GD) lineage HPAI viruses that have recently affected wild birds including those inhabiting North America, a perspective on the ongoing maintenance of Gs/GD lineage HPAI viruses in a global avian reservoir as it pertains to the potential for future outbreaks of HPAI in North American wildlife, and information that wildlife agencies or managers can use to prepare for and respond to future outbreaks of HPAI in wild birds.

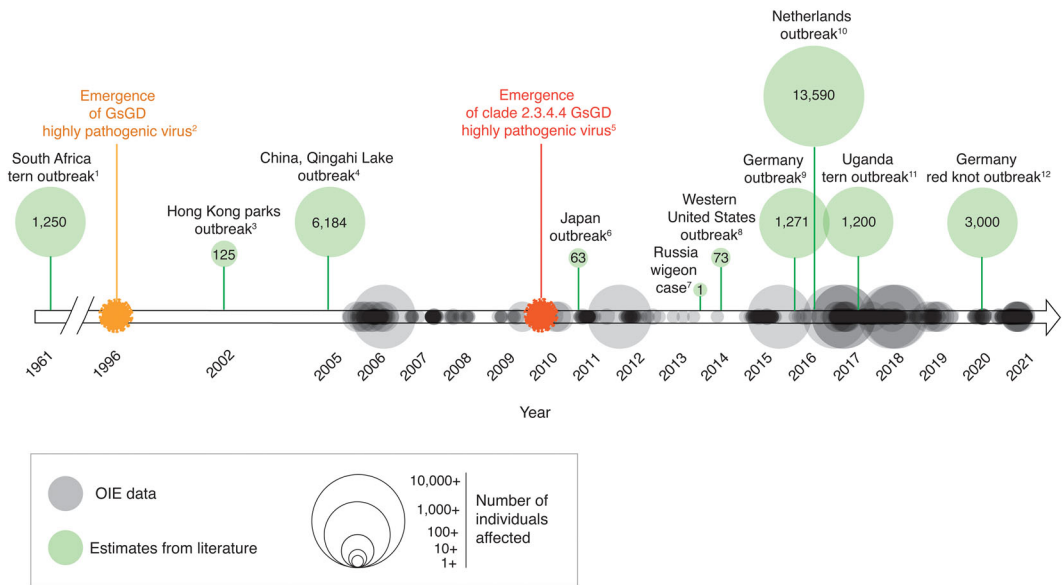
## BACKGROUND ON AVIAN-ORIGIN INFLUENZA A VIRUSES

Wild aquatic birds including waterfowl, shorebirds, gulls, and seabirds are the primary or primordial reservoir hosts of the greatest genetic and antigenic diversity of influenza A viruses (Olsen et al. 2006, Lang et al. 2016). Influenza A viruses maintained in wild birds are not typically associated with disease in these hosts; however, disease sometimes occurs when wild bird-origin viruses spread to other vertebrate species. For example, outbreaks of influenza in wild harbor seals (*Phoca vitulina*) and farmed mink have been attributed to viruses of wild-bird origin (Hinshaw et al. 1984, Klingeborn et al. 1985, Berg et al. 1990, Anthony et al. 2012, Zohari et al. 2014). Evidence for human exposure to AI viruses maintained in wild birds is sparse (Gill et al. 2006). Conversely, there is substantial evidence that AI viruses maintained in wild birds are sporadically introduced to domestic poultry (Figure 1) where they sometimes adapt to and are maintained among domestic birds (Swayne 2008). On rare occasions, viruses are again transmitted between species, this time from domestic poultry to humans (Figure 1) where they may cause clinical disease (Lam et al. 2013). Other times, as part of the host adaptation process, AI viruses that have a hemagglutinin gene of the H5 or H7 subtype may develop a HP phenotype in domestic birds. That is, viruses develop the propensity to cause mortality in chickens as assessed through a standardized pathogenicity index involving experimentally inoculated 6-week-old specific-pathogen-free chickens (Allan et al. 1977, Swayne and Suarez 2000).

Historically (i.e., prior to 2002), HPAI infections were only associated with domestic birds with the exception of a single outbreak among terns (*Sterna* spp.) in South Africa in 1961 (Becker 1966, Rowan 1962; Figure 2). The complete epidemiological context of this wild bird mortality event is not clear from published accounts, but the HPAI viruses leading to disease in terns may have developed pathogenicity in domestic poultry (e.g., chickens, ostriches) raised within this region. Since 2002, the detection of HPAI viruses in wild birds has become more



**FIGURE 1** Conceptual diagram depicting the generalized ecology of avian-origin influenza A (AI) viruses. Arrows depict common directionality of cross-species transmission events for AI viruses, including those with a highly pathogenic (HP) phenotype among wildlife, agricultural, and human sectors



**FIGURE 2** Timeline depicting occurrence and magnitude of outbreaks of highly pathogenic avian influenza (HPAI) in wild and captive birds (i.e., non-poultry), as reported to the World Organisation for Animal Health (OIE) and in representative published reports, relative to the evolution of goose/Guangdong (GsGD) lineage HPAI viruses. Apparent differences in reported outbreak magnitudes between OIE data and published accounts reflect different methods for outbreak characterization and reporting among organizations and administrative regions. Data courtesy of the World Organisation for Animal Health (OIE 2021a) and references reported in literature cited (<sup>1</sup>Rowan 1962, <sup>2</sup>Guo et al. 1998, <sup>3</sup>Ellis et al. 2004, <sup>4</sup>Chen et al. 2006, <sup>5</sup>Smith et al. 2015, <sup>6</sup>Sakoda et al. 2012, <sup>7</sup>Marchenko et al. 2015, <sup>8</sup>Bevins et al. 2016, <sup>9</sup>Pohlmann et al. 2018, <sup>10</sup>Kleyheeg et al. 2017, <sup>11</sup>Abolnik et al. 2019, <sup>12</sup>European Food Safety Authority et al. 2021)

common (Figures 2–3). The majority of cross-species transmission of HPAI viruses between poultry and wild birds has involved a particular viral genetic lineage that first emerged in domestic geese in Guangdong, China.

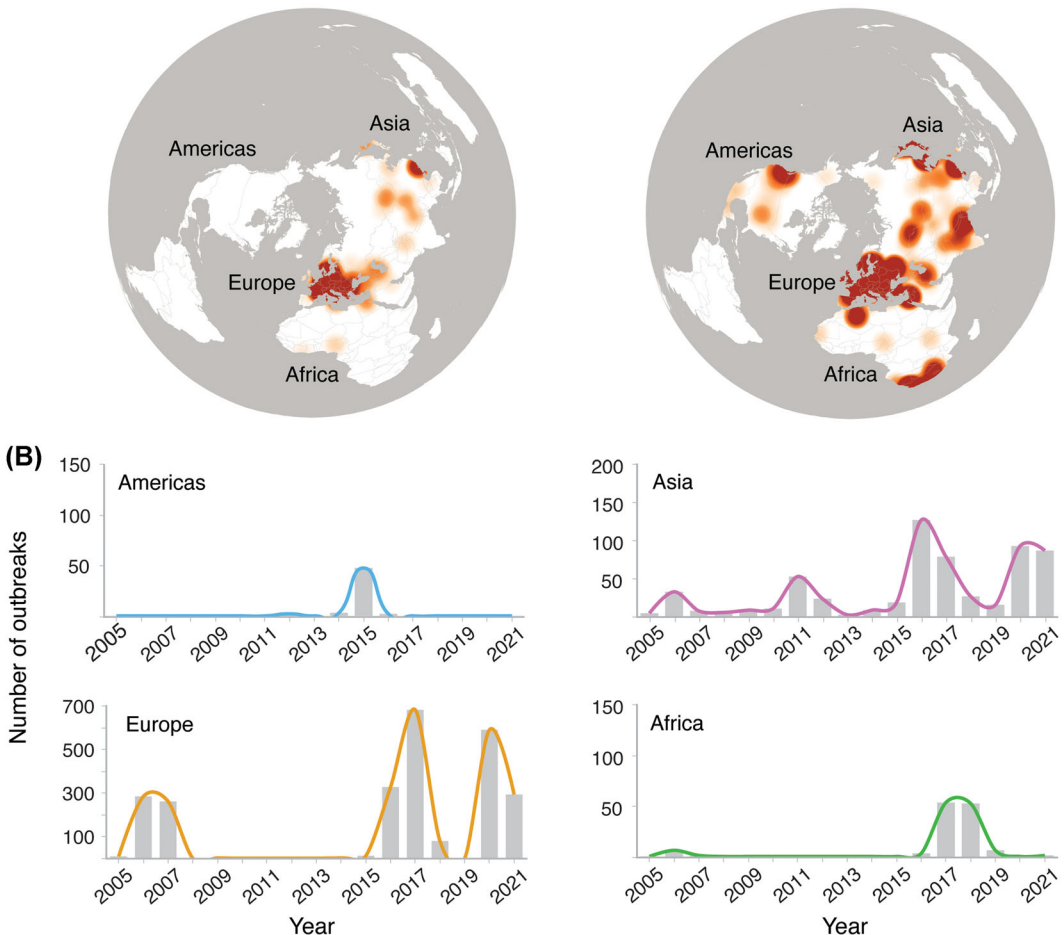
## EMERGENCE AND EVOLUTION OF GOOSE/GUANGDONG LINEAGE HPAI VIRUSES

In the spring of 1996, domestic geese in Guangdong, China were affected by HPAI associated with hemorrhagic, neurological disease and mortality exceeding 40%. The causal agent was identified as an HPAI virus strain designated as A/goose/Guangdong/1/1996 (H5N1) (Wan 2012). In 1997, viral descendants of A/goose/Guangdong/1/1996 (H5N1) were identified among domestic chickens during HPAI outbreaks in Hong Kong and from 18 human patients, 6 of whom died (Guo et al. 1998, Xu et al. 1999, Sims et al. 2003). Despite the depopulation of domestic birds on affected farms and the introduction of new controls in local poultry markets, A/goose/Guangdong/1/1996-like (Gs/GD) viruses were maintained among domestic birds within the region, leading to additional sporadic poultry outbreaks (Cauthen et al. 2000).

In late 2002 and early 2003, Gs/GD HPAI viruses were associated with the mortality of wild and captive aquatic birds (e.g., waterfowl, herons, gulls, and flamingos) in Hong Kong parklands representing the first reported detections of HPAI in wild birds since 1961 (Ellis et al. 2004; Figure 2). Though unknown at the time, these detections in 2002–2003 marked the first of many new challenges to the long-held and well-supported paradigm that HPAI was a poultry disease that could be effectively eradicated through the implementation of strict biosecurity for domestic bird production and prompt detection and depopulation of infected and exposed flocks.

**(A)** 2005–2009: Early GsGD HPAI outbreaks

2010–2021: Emergence of clade 2.3.4.4



**FIGURE 3** Occurrence of outbreak events for highly pathogenic avian influenza (HPAI) in wild and captive birds (i.e., non-poultry) from 2 August 2005–22 March 2021 as reported to the World Organisation for Animal Health (OIE). Panel A depicts the relative occurrence of detection events (red) geographically during the period following spread of emergent A/goose/Guangdong/1/1996-like (GsGD) highly pathogenic HPAI viruses to wild and captive birds (left) and subsequent to the evolution of clade 2.3.4.4 viruses (right), many of which may be adapted to wild birds. Panel B depicts the relative occurrence of HPAI outbreak detections by year. Data courtesy of the World Organisation for Animal Health (OIE [2021a](https://www.oie.int/))

By early 2004, periodic outbreaks of Gs/GD HPAI expanded beyond Hong Kong to 8 Asian countries (Sims et al. [2005](#)). Also during this time interval, Gs/GD HPAI viruses were again reported to cause fatal human disease, emphasizing the zoonotic risk of these avian-origin viruses (Peiris et al. [2004](#)).

In 2005, Gs/GD HPAI viruses were associated with an outbreak at Qinghai Lake, China that resulted in the mortality of more than 6,000 wild aquatic birds, including large numbers of bar-headed geese (*Anser indicus*), brown-headed gulls (*Chroicocephalus brunnicephalus*), and great black-headed gulls (*Larus ichthyæetus*; Chen et al. [2006](#); Liu et al. [2005](#); Figure 2). By late 2005, Gs/GD HPAI viruses had spread to wild birds in eastern Europe, purportedly through the transport of infected poultry and dispersal via wildlife (Gilbert et al. [2006](#); Ward et al. [2008, 2009](#)). During 2006–2009, Gs/GD HPAI viruses proliferated throughout at least 38 countries in Africa, Asia, Europe, and the Middle East (Figure 3) with many detections in wild and domestic birds. Affected wild bird taxa included ducks,



swans, geese, gulls, crows, and raptors (Brown 2010). It is plausible that 1 genetic lineage of viral diversity (clade 2.3.2.1) was, at least partially, maintained within, dispersed by, and adapted to wild birds during this interval. The global trade of infected domestic poultry and spread of viruses to wild birds were purported to be the most important mechanisms governing the occurrence of Gs/GD HPAI viruses within the global avian reservoir (i.e., birds in which viruses were maintained) during this period (WHO/OIE/FAO H5N1 Evolution Working Group 2012). Furthermore, human cases of disease due to infection with Gs/GD HPAI viruses continued during this time period (many of which were fatal), though exposure was generally associated with poultry contact (Wan et al. 2011). One exception was a cluster of 7 human cases in Azerbaijan during 2006 (4 of which were fatal) for which de-feathering of infected dead wild swans (*Cygnus* spp.) was considered the most likely source of infection (Gilsdorf et al. 2006).

From 2010–2013, sporadic outbreaks caused by Gs/GD HPAI viruses continued to affect wild and domestic birds in Asia and Europe (Marchenko et al. 2011, Marinova-Petkova et al. 2012, Sakoda et al. 2012, Luo et al. 2018). A specific viral lineage of Gs/GD HPAI viruses emerged during this time period, clade 2.3.4.4 viruses (Smith et al. 2015). These clade 2.3.4.4 Gs/GD HPAI viruses would ultimately become further adapted to waterfowl, sometimes causing apparent asymptomatic infections (Kwon et al. 2017, Pantin-Jackwood et al. 2017, van den Brand et al. 2018, Seekings et al. 2021), and exhibit limited capacity for transmission to mammals (Kaplan et al. 2016, Herfst et al. 2018). In early 2014, clade 2.3.4.4 Gs/GD HPAI viruses were identified as causing widespread outbreaks of disease in both wild waterfowl and domestic poultry in South Korea (Jeong et al. 2014). The detection of a clade 2.3.4.4 Gs/GD HPAI virus in an Eurasian wigeon (*Mareca penelope*) in northeastern Russia, coincident with the onset of autumn migration during September 2014 (Marchenko et al. 2015), foreshadowed an unprecedented event to follow to the east.

Concomitant with the southward migration of migratory waterfowl in late November 2014, HPAI viruses were detected in wild birds inhabiting the United States and Canada for the first time in recorded history (Lee et al. 2015). Clade 2.3.4.4 Gs/GD HPAI viruses were first detected in poultry within a region of southern British Columbia, Canada, that serves as important staging and wintering habitat for large numbers of migratory waterfowl and shorebirds (Pasick et al. 2015). Soon after, HPAI was detected in wild waterfowl and captive falcon carcasses recovered in northern Washington, USA, the latter birds having recently fed upon a captured American wigeon (*Mareca americana*) prior to expiring (Ip et al. 2015). The best available evidence suggests that Gs/GD HPAI viruses were introduced from East Asia to North America via Alaska by wild birds with extensive reassortment, or the genetic shuffling of viral genes, between these HPAI viruses and other AI viruses maintained in North American wild birds following viral introduction (Lee et al. 2016; Hill et al. 2017; Ramey et al. 2016, 2017). Subsequently, an outbreak of Gs/GD HPAI affected wild waterfowl and raptors, and domestic chickens and turkeys in areas throughout the western and central United States and Canada through June 2015 (Bevins et al. 2016, Krauss et al. 2016). This outbreak resulted in the loss of an unknown number of wild birds, >50 million domestic birds (Ramos et al. 2017), and approximately \$3 billion dollars in agricultural-related damages (indemnity payments, costs of response activities, lost revenue) in the United States alone (Greene 2015, Hagerman and Marsh 2016). No cases of human infection with clade 2.3.4.4 Gs/GD HPAI viruses were identified in North America during this outbreak. Though clade 2.3.4.4 Gs/GD HPAI viruses appeared to be eradicated in domestic poultry within the United States and Canada by early October 2015 through aggressive mitigation efforts (e.g., depopulation of poultry), there is evidence that HPAI viruses of this viral lineage continued to be maintained in wild birds and the wetland environments they inhabited within North America through at least November 2016 (Lee et al. 2017b, 2018).

Concurrent with outbreaks of HPAI in North America during 2014–2015, Europe also experienced numerous detections of Gs/GD HPAI viruses in wild, captive, and domestic birds, purportedly, at least in part, a function of wild bird-mediated viral dispersal from Asia (Harder et al. 2015, Verhagen et al. 2015, Globig et al. 2017). By 2016–2017, detections of clade 2.3.4.4 Gs/GD HPAI viruses in wild and domestic birds had become even further widespread in Europe, Africa, and Asia (Abolnik et al. 2019, Poen et al. 2019, Lycett et al. 2020). Though Gs/GD HPAI viruses have not been detected in wild birds inhabiting North America since 2016, there have been ongoing outbreaks of Gs/GD HPAI in wild birds (e.g., crows, ducks, swans, geese, gulls, and raptors) and domestic poultry in Asia and Europe, and sporadic outbreaks in Africa, throughout 2018–2020 (Figure 3) and continuing into 2021 (Poen et al. 2019,





Molini et al. 2020, Baek et al. 2021, European Food Safety Authority et al. 2021, Verhagen et al. 2021). These recent outbreaks have, at times, resulted in disease and mortality of fairly large numbers of birds (e.g., >10,000 individuals) and affected diverse species including African penguin (*Spheniscus demersus*; Molini et al. 2020), bar-headed goose, barnacle goose (*Branta leucopsis*), black-necked grebe (*Podiceps nigricollis*), brown-headed gull, Eurasian wigeon, great black-backed gull (*Larus marinus*), great black-headed gull, mute swan (*Cygnus olor*; Hill et al. 2019), red knot (*Calidris canutus*), tufted duck (*Aythya fuligula*), peregrine falcon (*Falco peregrinus*), white-tailed eagle (*Haliaeetus albicilla*; Krone et al. 2018), and white-winged terns (*Chlidonias leucopterus*; Kleyheeg et al. 2017, Li et al. 2017, Abolnik et al. 2019, European Food Safety Authority et al. 2021, World Organisation for Animal Health [OIE] 2021c). Wild bird-origin clade 2.3.4.4 Gs/GD HPAI viruses have also been implicated in recent reports of cross-species transmission to mammalian wildlife including gray seals (*Halichoerus grypus*), harbor seals (*Phoca vitulina*), and red fox (*Vulpes vulpes*; Shin et al. 2019, OIE 2021b, Rijks et al. 2021). Reports of human infection with clade 2.3.4.4 Gs/GD HPAI viruses have so far been sporadic, with exposures generally associated with domestic poultry contact (e.g., those in China and Russia; Yang et al. 2015, Bi et al. 2016, He et al. 2018, Pyankova et al. 2021).

Recent increases in detections of HPAI in wild birds and other wildlife (since 2002) do not appear to be primarily a function of increased awareness of this disease, enhancements in surveillance effort, or the development of improved molecular diagnostics. For example, following the identification of HPAI in terns in South Africa in 1961, many research and surveillance efforts had been conducted to understand ecology of AI viruses in natural reservoir wild bird species leading up to detections in Hong Kong in 2002 (Stallknecht 2003), yet none reported HPAI in wild birds, even when sampling was conducted in association with poultry outbreaks (Nettles et al. 1985). Following the detections of HPAI in captive and wild birds in Hong Kong and China in 2002–2005, large-scale active surveillance programs were established in Europe and North America. Since the establishment of these programs, most detections of HPAI in wild birds have been spatiotemporally coincident with outbreaks of poultry disease or wild bird mortality events (Hesterberg et al. 2009, Bevins et al. 2016) with few exceptions (Lee et al. 2017b), despite substantial investment in the sampling of many thousands of apparently healthy or hunter-harvested wild birds and the application of contemporary molecular diagnostics (Bevins et al. 2014). Also, well-established surveillance efforts in Australia and South America have not yet reported the detection of Gs/GD HPAI in wild birds, providing evidence that such viruses have not yet been dispersed to these continents via wild bird migration (Pereda et al. 2008, Grillo et al. 2015, Jiménez-Blum et al. 2018).

## POTENTIAL FOR FUTURE OUTBREAKS OF HPAI IN NORTH AMERICAN WILDLIFE

Though the occurrence, timing, and extent of future outbreaks of HPAI in North American wildlife are uncertain and will be determined by stochastic or unpredictable events, a number of current factors indicate that the re-emergence of clade 2.3.4.4 Gs/GD HPAI viruses in wild birds inhabiting the United States and Canada is plausible and may be probable. First, contrary to the historical (pre-2002) paradigm that HPAI is a poultry-specific disease, there is growing evidence that Gs/GD HPAI viruses are perpetuated in an avian reservoir characterized by bidirectional viral exchange between wild and domestic bird hosts (Bodewes and Kuiken 2018, Lycett et al. 2020). Bidirectional virus exchange appears to be facilitating the adaptation of Gs/GD HPAI viruses in wild bird hosts following introduction from poultry (Kwon et al. 2017, Pantin-Jackwood et al. 2017, van den Brand et al. 2018, Seekings et al. 2021) and promoting viral dispersal via migratory bird movements (Global Consortium for H5N8 and Related Influenza Viruses 2016, Lycett et al. 2020), though poultry production and trade also play a role in viral dissemination. Additionally, the frequency and geographic extent of HPAI occurrences among wild and captive birds have increased since the emergence of Gs/GD HPAI viruses (Figures 2–3) despite concerted global mitigation and control efforts targeted towards domestic poultry. Therefore, recent trends suggest that eradication of Gs/GD HPAI viruses from a global avian reservoir is unlikely to be imminent and that continued outbreaks of HPAI among wild and captive birds should be expected.



East Asia represents an important geographic area where outbreaks of HPAI have repeatedly occurred among wild and captive aquatic birds following the emergence of Gs/GD HPAI viruses (since 2002). Countries in East Asia that have repeatedly been affected by past outbreaks of HPAI in wild birds include Japan, South Korea, and Russia (Marchenko et al. 2011, 2015; Sakoda et al. 2012; Jeong et al. 2014; Baek et al. 2021). These countries provide important breeding, molting, staging, or wintering habitat for numerous species of waterfowl, shorebirds, and gulls that inhabit North America at other times of year including: dunlin (*Calidris alpina*; Winker and Gibson 2010, Gill et al. 2013), emperor goose (*Anser canagicus*; Hupp et al. 2007, Ramey et al. 2019), glaucous gull (*Larus hyperboreus*; Ahlstrom et al. 2021), king eider (*Somateria spectabilis*; Phillips et al. 2006), long-tailed duck (*Clangula hyemalis*; Petersen et al. 2003), northern pintail (*Anas acuta*; Miller et al. 2005, Flint et al. 2009), sharp-tailed sandpiper (*Calidris acuminata*; Handel and Gill 2010), and Steller's eider (*Polysticta stelleri*; Dau et al. 2000). Consequently, there is evidence for ongoing bidirectional dispersal of AI viruses by migratory birds between East Asia and North America via Alaska (Ramey et al. 2015, 2018b; Jeong et al. 2019). This is the same pathway as purported to have led to the previous introduction of Gs/GD HPAI viruses into the United States and Canada in 2014 (Lee et al. 2015, Ramey et al. 2016, Hill et al. 2017). Therefore, additional incursions of AI viruses from East Asia to North America via this pathway should be expected.

Europe also represents a region where HPAI outbreaks in wild birds have become increasingly widespread (Verhagen et al. 2021; Figure 3). Prior research indicates bidirectional viral dispersal between Europe and North America via the North Atlantic (Wille et al. 2011, Hall et al. 2014, Huang et al. 2014). The specific taxa purportedly involved in AI virus dispersal via this trans-Atlantic pathway and the frequency of introduction events have generally been less well-described as compared to the North Pacific Basin. As a result, the likelihood for future introductions of HPAI viruses from Europe into North America by wild birds remains unclear.

Should future incursions of Gs/GD HPAI viruses from East Asia or Europe into North America via wild birds occur, the economic, ecological, and cultural ramifications could be considerable. For example, the economic consequences of prior wild bird-mediated introductions to the poultry industries in the United States and Canada resulted in damages estimated at several billion United States dollars, suggesting that costs of future outbreaks could be comparable (Greene 2015, Hagerman and Marsh 2016). Large-scale mortality events affecting thousands of wild birds, such as those that have previously occurred in East Asia and Europe (Chen et al. 2006, Kleyheeg et al. 2017), could have detrimental effects to specific populations of North American wild bird species, particularly those that are threatened or endangered. Large-scale mortality events could also affect participation in culturally and economically important human uses of wildlife such as subsistence hunting of Indigenous peoples (Charania et al. 2014) and sport hunting among a broader public (Dishman et al. 2010). Future introductions of Gs/GD HPAI could also result in human illness or mortality, particularly if viruses are able to evade biosecurity and enter poultry production systems given a precedent for viral exposure via infected domestic birds (Van Kerkhove et al. 2011).

Important data gaps obscure our ability to forecast future introductions of Gs/GD HPAI viruses from East Asia or Europe into North America and the consequences thereof. For example, the geographic extent and host species in which Gs/GD HPAI viruses are enzootic remain enigmatic despite previous and ongoing research and surveillance efforts. This is, in part, a function of inconsistent sampling across space and time and the evolution and adaption of Gs/GD HPAI viruses among wild and domestic maintenance hosts comprising the global avian reservoir. Additionally, the persistence of Gs/GD HPAI viruses in the environment is poorly understood despite the recognition that this mechanism likely plays some role in recurrent epidemics among wild birds (Brebán et al. 2009). Though information is limited, previous laboratory and field experiments provide support that AI viruses, including Gs/GD HPAI viruses, may remain infectious for periods of weeks or months within environmental surface waters (Brown et al. 2007, Keeler et al. 2014, Ramey et al. 2020). Also, our understanding of how population immunity may influence the establishment of Gs/GD HPAI viruses in wild bird populations is incomplete. Laboratory experiments provide evidence that the immune status of birds, as influenced by prior infection with endemic AI viruses, influence the probability of viral transmission (Latorre-Margalef et al. 2017, Segovia et al. 2018); however, it is unclear how such heterotypic immunity (priority acquired immunity to different AI viruses) influences the establishment of





introduced AI viruses in North America. Furthermore, surveillance information regarding AI viruses maintained among wild birds inhabiting areas directly adjacent to North America, such as Far Eastern Russia (e.g., Kamchatka and Chukotka) and Greenland, have been extremely limited through both space and time (Hjulsager et al. 2012, Sivay et al. 2012, Hartby et al. 2016, Gaidet et al. 2018). Thus, information on viral threats occurring in wildlife at areas most spatially proximate to North America remain cryptic. Information on the timing, frequency, and routes of intercontinental migratory movements across the North Atlantic and North Pacific Basins is still incomplete for numerous wild bird hosts of AI viruses that may be capable of dispersing viruses from Europe or Asia into North America. This includes previously mentioned taxa for which existing data only reflects birds from specific age and sex classes, a relatively small number of marking sites, or a limited portion of the annual cycle. As a result, our ability to quantify wild bird-mediated viral dispersal is constrained by a relatively coarse understanding of routes and timing of migratory movements between North America and adjacent regions. Finally, our understanding of the susceptibility of North American wildlife species to disease on account of infection with Gs/GD HPAI viruses is limited to information for a relatively small number of individuals and species infected with a narrow range of genetic viral variants as assessed through field observation (Ip et al. 2016) and experimental challenge studies (Brown et al. 2006, Pasick et al. 2007, Hall et al. 2009, Spackman et al. 2017, Luczo et al. 2020).

## PREPARING FOR FUTURE OUTBREAKS OF HPAI IN WILD BIRDS

Until late November 2014, HPAI outbreaks in the United States and Canada were restricted to poultry and stringent biosecurity for domestic bird production, in conjunction with prompt depopulation of affected or potentially exposed poultry flocks, was sufficient for eradicating this economically important avian disease. Even during 2014–2015, this strategy was ultimately successful in eradicating HPAI in domestic poultry in the United States and Canada, albeit at significant economic cost; however, the apparent evolving role of wild birds in the maintenance and dispersal of clade 2.3.4.4 Gs/GD HPAI viruses suggests that this strategy alone may not be sufficient for limiting damages moving forward. Thus, managers of wildlife and their habitats may consider the development or adoption of mitigation strategies if future losses from HPAI outbreaks, including diseased birds and economic losses, are to be minimized.

In North America, the management of wildlife resources and their associated habitats is the responsibility of diverse local, state, provincial, territorial, tribal, and federal agencies and Indigenous organizations with different policies and mandates. Therefore, specific management strategies are not applicable or appropriate in all instances. As such, wildlife management agencies may consider 3 simple guiding principles in the consideration, development, and implementation of strategies tailored to organizational priorities and mandates that aim to mitigate direct and indirect damages of HPAI to wildlife resources. Specifically, managers and organizational units may work within their respective chains of command and with wildlife health offices, as applicable, to be informed, be prepared, and take action as appropriate for their respective agency or organization. Some organizations may already be applying these principles in existing response and management plans.

### Be informed

As a first step towards the potential development and application of management actions to mitigate damages incurred through the dissemination of HPAI via wild birds, managers and organizational units may choose to be informed. Many state, provincial, territorial, federal, and tribal wildlife management agencies and Indigenous organizations maintain some level of wildlife health expertise to provide assistance with the investigation of wildlife morbidity and mortality events and conduct disease surveillance. In some cases, organizations without these resources have established partnerships or agreements with outside agencies and laboratories to provide the



necessary support in the event of an outbreak. In either scenario, these existing support networks serve as an initial place to seek information from wildlife health experts to help guide planning for and response to HPAI outbreak events.

For those managers or organizational units lacking such support networks or for those seeking additional information, rigorous scientific summaries on the occurrence and ecology of AI viruses in wild birds are widely available through a variety of sources (Table 1). For example, situational updates and summary reports on AI viruses in wild birds can be accessed through organizational websites including those for the Food and Agriculture Organization of the United Nations, OIE, the Canadian Wildlife Health Cooperative, the United States Department of Agriculture, and the United States Geological Survey (Table 1). Alerts and reports are also sporadically issued by the United States Interagency Steering Committee for Surveillance for Highly Pathogenic Avian Influenza in Wild Birds, the United States Geological Survey National Wildlife Health Center, and the International Society for Infectious Diseases (Table 1). The latter organization offers a publicly available subscription service (ProMED) that provides frequent global updates on infectious disease outbreaks, including highly pathogenic avian influenza in wild birds (Table 1). Another source of potentially useful contemporary information is recent review articles that offer synthesis of the dynamic trends of HPAI infection in wild birds. Recent review products have been published on the changing role of wild birds in the epidemiology of AI viruses (Bodewes and Kuiken 2018), the evolution and global spread of clade 2.3.4.4 Gs/GD HPAI viruses (Lee et al. 2017a), ongoing challenges with Gs/GD HPAI in domestic and wild birds in Europe (Verhagen et al. 2021), and lessons learned from research and surveillance directed towards HPAI viruses in wild birds inhabiting North America (Ramey et al. 2018a). Reading recently published reports is another way to obtain valuable information towards the development of science-based management strategies. Example topics that are relevant towards the consideration and development of mitigation strategies for HPAI in North American wildlife include the susceptibility of common wild and peridomestic bird species to infection and clinical disease when exposed to clade 2.3.4.4 Gs/GD HPAI viruses (Pantin-Jackwood et al. 2016, Spackman et al. 2017, Kwon et al. 2018, Bosco-Lauth et al. 2019, Shearn-Bochsler et al. 2019, Luczo et al. 2020)

**TABLE 1** Useful websites for obtaining information and updates on highly pathogenic avian influenza in wild birds and use of personal protection equipment in investigations thereof

Organization	Url
Food and Agriculture Organization of the United Nations	<a href="http://www.fao.org/ag/againfo/programmes/en/empres/Global_AIV_Zoonotic_Update/situation_update.html">http://www.fao.org/ag/againfo/programmes/en/empres/Global_AIV_Zoonotic_Update/situation_update.html</a>
World Organisation of Animal Health	<a href="https://www.oie.int/en/disease/avian-influenza/">https://www.oie.int/en/disease/avian-influenza/</a>
Canadian Wildlife Health Cooperative	<a href="http://www.cwhc-rcsf.ca/avian_influenza.php">http://www.cwhc-rcsf.ca/avian_influenza.php</a>
U.S. Department of Agriculture	<a href="https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/avian/avian-influenza/ai">https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/avian/avian-influenza/ai</a>
U.S. Geological Survey	<a href="https://www.usgs.gov/ecosystems/fish-wildlife-disease/wildlife-diseases-and-agriculture/avian-influenza">https://www.usgs.gov/ecosystems/fish-wildlife-disease/wildlife-diseases-and-agriculture/avian-influenza</a>
U.S. Geological Survey National Wildlife Health Center	<a href="https://www.usgs.gov/centers/nwhc/science/avian-influenza">https://www.usgs.gov/centers/nwhc/science/avian-influenza</a>
International Society for Infectious Diseases (ProMED)	<a href="https://promedmail.org/">https://promedmail.org/</a>
Occupational Safety and Health Administration	<a href="https://www.osha.gov/avian-flu">https://www.osha.gov/avian-flu</a>
Department of the Interior	<a href="https://pubs.er.usgs.gov/publication/tm15C2">https://pubs.er.usgs.gov/publication/tm15C2</a>
Centers for Disease Control and Prevention	<a href="https://www.cdc.gov/flu/avianflu/groups.htm">https://www.cdc.gov/flu/avianflu/groups.htm</a>



and the persistence of infectious AI viruses in surface waters of North American wetlands (Keeler et al. 2014, Ramey et al. 2021). Other topics relevant to specific management areas include the current distribution, abundance, movement patterns, and interaction of susceptible wildlife species with domestic species in or near management areas, and understanding past outbreaks or susceptibility of infection in wildlife species that occur within a management area.

By reviewing and interpreting the scientific data on the occurrence and ecology of AI viruses in wild bird hosts through information sources, including those outlined here, wildlife managers, organizational units, and agencies within North America will be able to better assess what, if any, preparations and potential mitigation actions are appropriate for their organization and management unit. Agency and organizational personnel would benefit from being informed on the current global situation regarding Gs/GD HPAI in wild birds to make decisions to improve outbreak preparedness, participate in effective surveillance programs, contribute to research filling critical information gaps, and respond to outbreak events in wildlife through targeted actions and communications.

## Be prepared

A second possible step towards determining whether and how to develop and apply management actions to mitigate damages incurred through the dissemination of HPAI via wild birds is to be prepared. Preparations include numerous elements such as coordination and communication within a management organization and with external agricultural and public health agency partners, consideration of the appropriate use of personal protective equipment (PPE) during outbreak events, determining whether and how to document the geographic extent of HPAI outbreaks in wild birds, evaluation of management options to mitigate the dissemination or impacts of HPAI viruses, and elevating situational awareness as determined to be appropriate. Managers, organizational units, or agencies may choose to develop specific plans or decision trees in advance to guide decisions and actions (or non-actions) given the detection of HPAI in North American wild birds.

Given that the occurrence of Gs/GD HPAI viruses in wild birds inhabiting North America presents some level of health risk among wild and domestic animals and the humans that interact with them, communication among wildlife, agricultural, and public health management agencies and organizations is critical to fostering effective coordination (Sleeman et al. 2017). This coordination among wildlife management, agricultural, and public health agencies working on HPAI helps to ensure that local, state, provincial, territorial, tribal, Indigenous, and federal points of contact are up to date; organizational expertise is identified; responsibilities are assigned to key personnel; communication and surveillance plans are established and maintained; and management actions (or non-actions) are identified and agreed upon before HPAI outbreaks occur in wild birds inhabiting North America.

Internal communications (those shared within a wildlife management agency or organization) and external communications (those shared with other agencies, organizations, stakeholders, and the public) may be most effective when conducted by professional external affairs or public information experts and when initiated both prior to and early in the course of an outbreak event (Reynolds et al. 2014). Communication products can be developed prior to an outbreak and include joint agency talking points, pre-approved fact sheets, press releases, website information, social media posts, and informational brochures. Topics of these communications may include details on signs of disease in wild birds, how to report sightings of sick birds, the management responses that could be necessary, and the potential health risks for wild birds, domestic animals, and humans.

Another important component of organizational preparation is to determine whether and how to provide guidance regarding the use of PPE during an outbreak to field personnel and the public. Previous research indicates that human infection with wild bird-origin AI viruses may be a relatively low probability event (Gill et al. 2006) but also one with potentially high consequences when considering Gs/GD HPAI viruses (Gilsdorf et al. 2006). Thus, agencies may choose to critically assess what constitutes appropriate PPE given perceived risk, if such equipment is



currently available or can be readily acquired, and whether personnel are properly trained in appropriate and effective use. Guidance for personnel investigating a potential avian influenza mortality event is available from the Occupational Safety and Health Administration, the Department of the Interior, and the Centers for Disease Control and Prevention (Table 1). A previous rapid risk assessment for SARS-CoV-2 may also provide helpful insight as to how inter-jurisdictional and inter-organizational efforts to assess risk helps with guidance regarding the use of PPE during an outbreak scenario (Runge et al. 2020).

Another important component of preparedness planning is to determine whether and how to document the geographic extent of HPAI outbreaks in wild birds (Preece et al. 2017). This may include quantifying the number or proportion of birds exhibiting disease or mortality, effects of disease on local bird populations, and observational effort. This hazard characterization step is critical to evaluating whether HPAI threatens North American wildlife beyond small-scale mortality events and for the early detection of changes in the level of risk to animal health. Efforts to thoroughly characterize and document wild bird mortality events may also be useful towards bolstering ongoing interagency HPAI passive surveillance efforts. Determining whether and how to document the geographic extent of HPAI outbreaks in wild birds represents a good example action for which prior intra- and inter-organizational coordination and communication may be important for promoting the efficient and effective collection of useful information.

Preparedness planning of specific management actions to mitigate the risk of viral spread among birds, from birds to other wildlife, and from birds to other potential hosts (e.g., domestic animals, companion animals, humans) is a challenging task given currently available information but an area that also warrants careful consideration. There is considerable, albeit incomplete, data to guide decisions regarding whether and how to pursue mitigation actions during an outbreak event. Example actions might include the suspension of banding or capture efforts during outbreaks, particularly those that use bait and promote the concentration of wildlife, which may facilitate increased viral prevalence (Soos et al. 2012); the restriction of public access to affected wetlands to limit human exposure and spread via fomites (virally contaminated inanimate objects such as boots, waders, or vehicles) given that Gs/GD HPAI viruses may remain infectious in water for extended periods (Brown et al. 2007, Domanska-Blicharz et al. 2010); the development and implementation of disinfection protocols for vehicles, boats, and gear used to access potentially affected sites to minimize viral dissemination through human activities (Dargatz et al. 2016); the suspension of hunting in potentially affected areas or species to limit possible human exposure and spread via virally contaminated bird carcasses or fomites (Gill et al. 2006, Gilsdorf et al. 2006); and the manipulation of water levels of small managed wetlands to facilitate faster viral inactivation (e.g., through increasing ultraviolet penetration or raising the water temperature; Sagripanti and Lytle 2007, Weber and Stilianakis 2008). Ideally, if managers or agencies decide to implement management actions during an outbreak aimed at mitigating negative consequences to animal or human health, they would be developed and applied in such a manner as to facilitate subsequent evaluation of efficacy.

Perhaps one of the most important components of preparing for potential HPAI outbreaks in North American wildlife is for managers and agencies to consider elevating their situational awareness (e.g., to be vigilant) regarding this important animal disease. For decades, the successful eradication of HPAI in domestic poultry in the United States and Canada has been dependent on early disease detection and a prompt response. Therefore, a similar approach may also be effective for facilitating mitigation actions in wild birds or their habitats. The vigilance of wildlife managers is important to early detection capabilities within wild bird populations of the United States and Canada, and the prompt detection of any future incursions of the Gs/GD HPAI viruses into North America may help reduce the risk of cross-species transmission to poultry. Given that Gs/GD HPAI has previously been detected through the investigation of morbidity and mortality in North American waterfowl and other wild birds (Ip et al. 2016, Shearn-Bochsler et al. 2019), prompt reporting of avian health issues or suspect mortality cases may ultimately inform effective response and mitigation activities in wild and domestic animal sectors. Organizational units and agencies may obtain useful information from within existing support networks (as applicable) to understand what is considered normal or baseline wild bird mortality and specific trigger points or thresholds for sick, diseased, or dead birds on managed lands that may signify abnormalities and lead to the initiation of an outbreak investigation.



## Take action (as appropriate)

A final potential step towards determining whether and how to apply management actions to mitigate damages incurred through HPAI outbreaks in wild birds is to take appropriate action, or to choose inaction, per information obtained and plans developed specifically for an organization or management unit. Potential actions include those outlined previously and the participation in or support of research and surveillance programs. Numerous agencies and academic institutions within the United States and Canada conduct limited active surveillance for HPAI in wild birds or have research programs to better understand the maintenance and dispersal of AI viruses. Representatives from these agencies and institutions often request assistance for active surveillance efforts from wildlife managers or organizational units in the form of help with field logistics or biological sampling of hunter-harvested or live wild birds for AI viruses. Passive surveillance is another important component of early detection and response (Ip et al. 2016). Wildlife managers may find it helpful to communicate within their organization and interagency network to (re-) familiarize themselves with the submission processes for HPAI-suspect bird carcasses at the Canadian Wildlife Health Cooperative, the United States Geological Survey National Wildlife Health Center, the University of Georgia Southeastern Cooperative Wildlife Disease Study, or their local, state, provincial, territorial, or federal diagnostic laboratory or wildlife agency prior to the onset of migratory periods for wild birds. Finally, though this review has focused on the introduction of Gs/GD HPAI viruses to North American wildlife via wild bird migration, the importation of exotic wildlife to the United States and Canada represents another plausible route of viral dissemination (Suetens et al. 2004). Therefore, the United States Fish and Wildlife Service is laying the groundwork for testing illegal wildlife imports for high consequence diseases including HPAI. It is expected that additional information on this program will become available as it is established.

## MANAGEMENT IMPLICATIONS

Given the apparent increasing frequency of outbreaks of HPAI among wild birds globally, including ongoing outbreaks of HPAI in Europe and Asia and the prior introduction of Gs/GD HPAI viruses into the United States and Canada, wildlife managers and agencies in North America may consider raising their situational awareness regarding this important emergent wildlife disease. Furthermore, managers, organizational units, and management agencies within North America may choose to be informed, be prepared, and take action, as appropriate, to limit impacts of HPAI to wildlife resources and the stakeholders that rely upon them.

## ACKNOWLEDGMENTS

Any use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the United States Government. We thank the World Organisation of Animal Health for making data used to generate Figures 2 and 3 publicly available. We appreciate reviews on prior versions of this manuscript provided by J. L. Dooley, J. M. Pearce, the Editor and Associate Editor of the *Journal of Wildlife Management*, and 2 anonymous reviewers. A. M. Ramey is supported by the U.S. Geological Survey through the Species Management Program of the Ecosystems Mission Area.

## CONFLICT OF INTERESTS

The authors declare that there are no conflict of interests.

## ETHICS STATEMENT

No animals were handled, observed, or otherwise potentially disturbed in the preparation of this review product.



## DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no new data were created or analyzed in this study.

## ORCID

Andrew M. Ramey  <http://orcid.org/0000-0002-3601-8400>  
 Nichola J. Hill  <http://orcid.org/0000-0003-3213-6693>  
 Thomas J. DeLiberto  <http://orcid.org/0000-0003-1115-1472>  
 M. Camille Hopkins  <http://orcid.org/0000-0003-1465-6038>  
 Andrew S. Lang  <http://orcid.org/0000-0002-4510-7683>  
 Rebecca L. Poulson  <http://orcid.org/0000-0002-8087-3295>  
 Diann J. Prosser  <http://orcid.org/0000-0002-5251-1799>  
 Jonathan M. Sleeman  <http://orcid.org/0000-0002-9910-6125>  
 David E. Stallknecht  <http://orcid.org/0000-0001-7355-8732>  
 Xiu-Feng Wan  <http://orcid.org/0000-0003-3907-5803>

## REFERENCES

- Abolnik, C., R. Pieterse, B. M. Peyrot, P. Choma, T. P. Phiri, K. Ebersohn, C. V. Heerden, A. A. Vorster, G. V. Zel, P. J. Geertsma, and A. T. Laleye. 2019. The incursion and spread of highly pathogenic avian influenza H5N8 clade 2.3.4.4 within South Africa. *Avian Diseases* 63:149–156.
- Ahlstrom, C. A., M. L. van Toor, H. Woksepp, J. C. Chandler, J. A. Reed, A. B. Reeves, J. Waldenström, A. B. Franklin, D. C. Douglas, J. Bonnedahl, and A. M. Ramey. 2021. Evidence for continental-scale dispersal of antimicrobial resistant bacteria by landfill-foraging gulls. *Science of the Total Environment* 764:144551.
- Allan, W. H., D. J. Alexander, B. S. Pomeroy, and G. Parsons. 1977. Use of virulence index tests for avian influenza viruses. *Avian Diseases* 21:359–363.
- Anthony, S. J., J. S. Leger, K. Pugliares, H. S. Ip, J. M. Chan, Z. W. Carpenter, I. Navarrete-Macias, M. Sanchez-Leon, J. T. Saliki, J. Pedersen, and W. Karesh. 2012. Emergence of fatal avian influenza in New England harbor seals. *MBio* 3: e00166-12.
- Baek, Y. G., Y. N. Lee, D. H. Lee, J. I. Shin, J. H. Lee, D. H. Chung, E. K. Lee, G. B. Heo, M. Sagong, S. J. Kye, and K. N. Lee. 2021. Multiple reassortants of H5N8 Clade 2.3.4.4b highly pathogenic avian influenza viruses detected in South Korea during the winter of 2020–2021. *Viruses* 13:490.
- Becker, W. B. 1966. The isolation and classification of tern virus: influenza virus A/tern/South Africa/1961. *Epidemiology & Infection* 64:309–320.
- Berg, M., L. Englund, I. A. Abusugra, B. Klingeborn, and T. Linne. 1990. Close relationship between mink influenza (H10N4) and concomitantly circulating avian influenza viruses. *Archives of Virology* 113:61–71.
- Bevins, S. N., R. J. Dusek, C. L. White, T. Gidlewski, B. Bodenstein, K. G. Mansfield, P. DeBruyn, D. Kraege, E. Rowan, C. Gillin, and B. Thomas. 2016. Widespread detection of highly pathogenic H5 influenza viruses in wild birds from the Pacific Flyway of the United States. *Scientific Reports* 6:1–9.
- Bevins, S. N., K. Pedersen, M. W. Lutman, J. A. Baroch, B. S. Schmit, D. Kohler, T. Gidlewski, D. L. Nolte, S. R. Swafford, T. J. DeLiberto. 2014. Large-scale avian influenza surveillance in wild birds throughout the United States. *PLoS ONE* 9: e104360.
- Bi, Y., Q. Chen, Q. Wang, J. Chen, T. Jin, G. Wong, C. Quan, J. Liu, J. Wu, R. Yin, and L. Zhao. 2016. Genesis, evolution and prevalence of H5N6 avian influenza viruses in China. *Cell Host & Microbe* 20:810–821.
- Bodewes, R., and T. Kuiken. 2018. Changing role of wild birds in the epidemiology of avian influenza A viruses. *Advances in Virus Research* 100:279–307.
- Bosco-Lauth, A. M., N. L. Marlenee, A. E. Hartwig, R. A. Bowen, and J. J. Root. 2019. Shedding of clade 2.3.4.4 H5N8 and H5N2 highly pathogenic avian influenza viruses in peridomestic wild birds in the US. *Transboundary and Emerging Diseases* 66:1301–1305.
- Breban, R., J. M. Drake, D. E. Stallknecht, and P. Rohani. 2009. The role of environmental transmission in recurrent avian influenza epidemics. *PLoS Computational Biology* 5:e1000346.
- Brown, I. H. 2010. Summary of avian influenza activity in Europe, Asia, and Africa, 2006–2009. *Avian Diseases* 54: 187–193.
- Brown, J. D., D. E. Stallknecht, J. R. Beck, D. L. Suarez, and D. E. Swayne. 2006. Susceptibility of North American ducks and gulls to H5N1 highly pathogenic avian influenza viruses. *Emerging Infectious Diseases* 12:1663.





- Brown, J. D., D. E. Swayne, R. J. Cooper, R. E. Burns, and D. E. Stallknecht. 2007. Persistence of H5 and H7 avian influenza viruses in water. *Avian Diseases* 51:285–289.
- Cauthen, A. N., D. E. Swayne, S. Schultz-Cherry, M. L. Perdue, and D. L. Suarez. 2000. Continued circulation in China of highly pathogenic avian influenza viruses encoding the hemagglutinin gene associated with the 1997 H5N1 outbreak in poultry and humans. *Journal of Virology* 74:6592–6599.
- Charania, N. A., I. D. Martin, E. N. Liberda, R. Meldrum, and L. J. Tsuji. 2014. Bird harvesting practices and knowledge, risk perceptions, and attitudes regarding avian influenza among Canadian First Nations subsistence hunters: implications for influenza pandemic plans. *BMC Public Health* 14:1–11.
- Chen, H., Y. Li, Z. Li, J. Shi, K. Shinya, G. Deng, Q. Qi, G. Tian, S. Fan, H. Zhao, and Y. Sun. 2006. Properties and dissemination of H5N1 viruses isolated during an influenza outbreak in migratory waterfowl in western China. *Journal of Virology* 80:5976–5983.
- Chen, H., G. J. Smith, S. Y. Zhang, K. Qin, J. Wang, K. S. Li, R. G. Webster, J. S. Peiris, and Y. Guan. 2005. H5N1 virus outbreak in migratory waterfowl. *Nature* 436:191–192.
- Dargatz, D., A. Beam, S. Wainwright, and B. McCluskey. 2016. Case series of turkey farms from the H5N2 highly pathogenic avian influenza outbreak in the United States during 2015. *Avian Diseases* 60:467–472.
- Dau, C. P., P. L. Flint, and M. R. Petersen. 2000. Distribution of recoveries of Steller's eiders banded on the lower Alaska Peninsula, Alaska. *Journal of Field Ornithology* 71:541–548.
- Dishman, H., D. Stallknecht, and D. Cole. 2010. Duck hunters' perceptions of risk for avian influenza, Georgia, USA. *Emerging Infectious Diseases* 16:1279.
- Domanska-Blicharz, K., Z. Minta, K. Smietanka, S. Marché, and T. V. Berg. 2010. H5N1 high pathogenicity avian influenza virus survival in different types of water. *Avian Diseases* 54:737–737.
- Ellis, T. M., R. B. Bousfield, L. A. Bissett, K. C. Dyrting, G. S. Luk, S. T. Tsim, K. Sturm-Ramirez, R. G. Webster, Y. Guan, and J. M. Peiris. 2004. Investigation of outbreaks of highly pathogenic H5N1 avian influenza in waterfowl and wild birds in Hong Kong in late 2002. *Avian Pathology* 33:492–505.
- European Food Safety Authority, European Centre for Disease Prevention and Control, European Union Reference Laboratory for Avian Influenza, C. Adlhoch, A. Fusaro, J. L. Gonzales, T. Kuiken, S. Marangon, É. Niqueux, C. Staubach, C. Terregino, and I. Muñoz Guajardo. 2021. Avian influenza overview December 2020–February 2021. *European Food Safety Authority Journal* 19:e06497.
- Flint, P. L., K. Ozaki, J. M. Pearce, B. Guzzetti, H. Higuchi, J. P. Fleskes, T. Shimada, and D. V. Derksen. 2009. Breeding-season sympatry facilitates genetic exchange among allopatric wintering populations of northern pintails in Japan and California. *Condor* 111:591–598.
- Gaidet, N., I. Leclercq, C. Batéjat, Q. Grassin, T. Daufresne, and J. C. Manuguerra. 2018. Avian influenza virus surveillance in high Arctic breeding geese, Greenland. *Avian Diseases* 62:237–240.
- Gilbert, M., X. Xiao, J. Domenech, J. Lubroth, V. Martin, and J. Slingenbergh. 2006. Anatidae migration in the western Palearctic and spread of highly pathogenic avian influenza H5N1 virus. *Emerging Infectious Diseases* 12:1650–1656.
- Gill, J. S., R. Webby, M. J. Gilchrist, and G. C. Gray. 2006. Avian influenza among waterfowl hunters and wildlife professionals. *Emerging Infectious Diseases* 12:1284.
- Gill, R. E., Jr., C. M. Handel, and D. R. Ruthrauff. 2013. Intercontinental migratory connectivity and population structuring of dunlins from western Alaska. *Condor* 115:525–534.
- Gilsdorf, A., N. Boxall, V. Gasimov, I. Agayev, F. Mammadzade, P. Ursu, E. Gasimov, C. Brown, S. Mardel, D. Jankovic, and G. Pimentel. 2006. Two clusters of human infection with influenza A/H5N1 virus in the Republic of Azerbaijan, February–March 2006. *Eurosurveillance* 11:3–4.
- Global Consortium for H5N8 and Related Influenza Viruses. 2016. Role for migratory wild birds in the global spread of avian influenza H5N8. *Science* 354:213–217.
- Globig, A., E. Starick, T. Homeier, A. Pohlmann, C. Grund, P. Wolf, A. Zimmermann, C. Wolf, D. Heim, H. Schlößer, and S. Zander. 2017. Epidemiological and molecular analysis of an outbreak of highly pathogenic avian influenza H5N8 clade 2.3.4.4 in a German zoo: effective disease control with minimal culling. *Transboundary and Emerging Diseases* 64:1813–1824.
- Greene, J. L. 2015. Update on the highly-pathogenic avian influenza outbreak of 2014–2015. <https://nationalaglawcenter.org/wp-content/uploads/assets/crs/R44114.pdf>. Accessed 2 Mar 2021.
- Grillo, V. L., K. E. Arzey, P. M. Hansbro, A. C. Hurt, S. Warner, J. Bergfeld, G. W. Burgess, B. Cookson, C. J. Dickason, M. Ferenczi, and T. Hollingsworth. 2015. Avian influenza in Australia: a summary of 5 years of wild bird surveillance. *Australian Veterinary Journal* 93:387–393.
- Guo, Y., X. Xu, and X. Wan. 1998. Genetic characterization of an avian influenza A (H5N1) virus isolated from a sick goose in China. *Chinese Journal of Experimental and Clinical Virology* 12:322–325.
- Hagerman, A. D., and T. L. Marsh. 2016. Theme overview: economic consequences of highly pathogenic avian influenza. *Choices* 31:1–2.



- Hall, J. S., H. S. Ip, J. C. Franson, C. Meteyer, S. Nashold, J. L. TeSlaa, J. French, P. Redig, and C. Brand. 2009. Experimental infection of a North American raptor, American kestrel (*Falco sparverius*), with highly pathogenic avian influenza virus (H5N1). *PLoS ONE* 4:e7555.
- Hall, J. S., G. T. Hallgrímsson, K. Suwannanarn, S. Sreevatsen, H. S. IP, E. Magnúsdóttir, J. L. TeSlaa, S. W. Nashold, and R. J. Dusek. 2014. Avian influenza virus ecology in Iceland shorebirds: intercontinental reassortment and movement. *Infection, Genetics and Evolution* 28:130–136.
- Handel, C. M., and R. E. Gill, Jr. 2010. Wayward youth: trans-Beringian movement and differential southward migration by juvenile sharp-tailed sandpipers. *Arctic* 63:273–288.
- Harder, T., S. Maurer-Stroh, A. Pohlmann, E. Starick, D. Höreth-Böntgen, K. Albrecht, G. Pannwitz, J. Teifke, V. Gunalan, R. T. Lee, and C. Sauter-Louis. 2015. Influenza A (H5N8) virus similar to strain in Korea causing highly pathogenic avian influenza in Germany. *Emerging Infectious Diseases* 21:860.
- Hartby, C. M., J. S. Krog, F. Merkel, E. Holm, L. E. Larsen, and C. K. Hjulsgager. 2016. First characterization of avian influenza viruses from Greenland 2014. *Avian Diseases* 60:302–310.
- He, J., B. Y. Liu, L. Gong, Z. Chen, X. L. Chen, S. Hou, J. L. Yu, J. B. Wu, Z. C. Xia, A. Latif, and R. Gao. 2018. Genetic characterization of the first detected human case of avian influenza A (H5N6) in Anhui Province, East China. *Scientific Reports* 8:1–6.
- Herfst, S., C. K. Mok, J. M. van den Brand, S. van der Vliet, M. E. Rosu, M. I. Spronken, Z. Yang, D. de Meulder, P. Lexmond, T. M. Bestebroer, and J. M. Peiris. 2018. Human clade 2.3.4.4 A/H5N6 influenza virus lacks mammalian adaptation markers and does not transmit via the airborne route between ferrets. *mSphere* 3:e00405-17.
- Hesterberg, U., K. Harris, D. Stroud, V. Guberti, L. Busani, M. Pittman, V. Piazza, A. Cook, and I. Brown. 2009. Avian influenza surveillance in wild birds in the European Union in 2006. *Influenza and Other Respiratory Viruses* 3: 1–4.
- Hill, N. J., I. T. Hussein, K. R. Davis, E. J. Ma, T. J. Spivey, A. M. Ramey, W. B. Puryear, S. R. Das, R. A. Halpin, X. Lin, and N. B. Fedorova. 2017. Reassortment of influenza A viruses in wild birds in Alaska before H5 clade 2.3.4.4 outbreaks. *Emerging Infectious Diseases* 23:654.
- Hill, S. C., R. Hansen, S. Watson, V. Coward, C. Russell, J. Cooper, S. Essen, H. Everest, K. V. Parag, S. Fiddaman, and S. Reid. 2019. Comparative micro-epidemiology of pathogenic avian influenza virus outbreaks in a wild bird population. *Philosophical Transactions of the Royal Society B* 374:20180259.
- Hinshaw, V. S., W. J. Bean, R. G. Webster, J. E. Reh, P. Fiorelli, G. Early, J. R. Geraci, and D. J. St Aubin. 1984. Are seals frequently infected with avian influenza viruses? *Journal of Virology* 51:863–865.
- Hjulsgager, C. K., S. Ø. Breum, R. Trebbien, K. J. Handberg, O. R. Therkildsen, J. J. Madsen, K. Thorup, J. A. Baroch, T. J. DeLiberto, L. E. Larsen, and P. H. Jørgensen. 2012. Surveillance for avian influenza viruses in wild birds in Denmark and Greenland, 2007–10. *Avian Diseases* 56:992–998.
- Huang, Y., M. Wille, J. Benkaroun, H. Munro, A. L. Bond, D. A. Fifield, G. J. Robertson, D. Ojkic, H. Whitney, and A. S. Lang. 2014. Perpetuation and reassortment of gull influenza A viruses in Atlantic North America. *Virology* 456:353–363.
- Hupp, J. W., J. A. Schmutz, C. R. Ely, E. E. Syroechkovskiy, Jr., A. V. Kondratyev, W. D. Eldridge, and E. Lappo. 2007. Moulting migration of emperor geese *Chen canagica* between Alaska and Russia. *Journal of Avian Biology* 38:462–470.
- Ip, H. S., R. J. Dusek, B. Bodenstein, M. Kim Torchetti, P. DeBruyn, K. G. Mansfield, T. DeLiberto, and J. M. Sleeman. 2016. High rates of detection of clade 2.3.4.4 highly pathogenic avian influenza H5 viruses in wild birds in the Pacific Northwest during the winter of 2014–15. *Avian Diseases* 60:354–358.
- Ip, H. S., M. Kim Torchetti, R. Crespo, P. Kohrs, P. DeBruyn, K. G. Mansfield, T. Baszler, L. Badcoe, B. Bodenstein, V. Shearn-Bochsler, and M. L. Killian. 2015. Novel Eurasian highly pathogenic avian influenza A H5 viruses in wild birds, Washington, USA, 2014. *Emerging Infectious Diseases* 21:886.
- Jeong, J., H. M. Kang, E. K. Lee, B. M. Song, Y. K. Kwon, H. R. Kim, K. S. Choi, J. Y. Kim, H. J. Lee, O. K. Moon, and W. Jeong. 2014. Highly pathogenic avian influenza virus (H5N8) in domestic poultry and its relationship with migratory birds in South Korea during 2014. *Veterinary Microbiology* 173:249–257.
- Jeong, S., D. H. Lee, Y. J. Kim, S. H. Lee, A. Y. Cho, J. Y. Noh, E. O. Tseren-Ochir, J. H. Jeong, and C. S. Song. 2019. Introduction of avian influenza A (H6N5) virus into Asia from North America by wild birds. *Emerging Infectious Diseases* 25:2138.
- Jiménez-Bluhm, P., E. A. Karlsson, P. Freiden, B. Sharp, F. Di Pillo, J. E. Osorio, C. Hamilton-West, and S. Schultz-Cherry. 2018. Wild birds in Chile Harbor diverse avian influenza A viruses. *Emerging Microbes & Infections* 7:1–4.
- Kaplan, B. S., M. Russier, T. Jeevan, M. Marathe, E. A. Govorkova, C. J. Russell, M. Kim-Torchetti, Y. K. Choi, I. Brown, T. Saito, et al. 2016. Novel highly pathogenic avian A (H5N2) and A (H5N8) influenza viruses of clade 2.3.4.4 from North America have limited capacity for replication and transmission in mammals. *mSphere* 1:e00003-16.
- Keeler, S. P., M. S. Dalton, A. M. Cressler, R. D. Berghaus, and D. E. Stallknecht. 2014. Abiotic factors affecting the persistence of avian influenza virus in surface waters of waterfowl habitats. *Applied and Environmental Microbiology* 80:2910–2917.



- Kleyheeg, E., R. Slaterus, R. Bodewes, J. M. Rijks, M. A. Spierenburg, N. Beerens, L. Kelder, M. J. Poen, J. A. Stegeman, R. A. Fouchier, and T. Kuiken. 2017. Deaths among wild birds during highly pathogenic avian influenza A (H5N8) virus outbreak, the Netherlands. *Emerging Infectious Diseases* 23:2050.
- Klingeborn, B., L. Englund, R. Rott, N. Juntti, and G. Rockborn. 1985. An avian influenza A virus killing a mammalian species—the mink. *Archives of Virology* 86:347–351.
- Krauss, S., D. E. Stallknecht, R. D. Slemons, A. S. Bowman, R. L. Poulson, J. M. Nolting, J. P. Knowles, R. G. Webster. 2016. The enigma of the apparent disappearance of Eurasian highly pathogenic H5 clade 2.3.4.4 influenza A viruses in North American waterfowl. *Proceedings of the National Academy of Sciences* 113:9033–8.
- Krone, O., A. Globig, R. Ulrich, T. Harder, J. Schinköthe, C. Herrmann, S. Gerst, F. J. Conraths, and M. Beer. 2018. White-tailed sea eagle (*Haliaeetus albicilla*) die-off due to infection with highly pathogenic avian influenza virus, subtype H5N8, in Germany. *Viruses* 10:478.
- Kwon, J. H., D. H. Lee, D. E. Swayne, J. Y. Noh, S. S. Yuk, S. Jeong, S. H. Lee, C. Woo, J. H. Shin, and C. S. Song. 2018. Experimental infection of H5N1 and H5N8 highly pathogenic avian influenza viruses in northern pintail (*Anas acuta*). *Transboundary and Emerging Diseases* 65:1367–1371.
- Kwon, J. H., Y. K. Noh, D. H. Lee, S. S. Yuk, T. O. Erdene-Ochir, J. Y. Noh, W. T. Hong, J. H. Jeong, S. Jeong, G. B. Gwon, and C. S. Song. 2017. Experimental infection with highly pathogenic H5N8 avian influenza viruses in the Mandarin duck (*Aix galericulata*) and domestic pigeon (*Columba livia domestica*). *Veterinary Microbiology* 203:95–102.
- Lam, T. T., J. Wang, Y. Shen, B. Zhou, L. Duan, C. L. Cheung, C. Ma, S. J. Lycett, C. Y. Leung, X. Chen, and L. Li. 2013. The genesis and source of the H7N9 influenza viruses causing human infections in China. *Nature* 502:241–244.
- Lang, A. S., C. Lebarbenchon, A. M. Ramey, G. J. Robertson, J. Waldenström, and M. Wille. 2016. Assessing the role of seabirds in the ecology of influenza A viruses. *Avian Diseases* 60:378–386.
- Latorre-Margalef, N., J. D. Brown, A. Fojtik, R. L. Poulson, D. Carter, M. França, and D. E. Stallknecht. 2017. Competition between influenza A virus subtypes through heterosubtypic immunity modulates re-infection and antibody dynamics in the mallard duck. *PLoS Pathogens* 13:e1006419.
- Lee, D. H., J. Bahl, M. Kim Torchetti, M. L. Killian, H. S. Ip, T. J. DeLiberto, and D. E. Swayne. 2016. Highly pathogenic avian influenza viruses and generation of novel reassortants, United States, 2014–2015. *Emerging Infectious Diseases* 22:1283.
- Lee, D. H., K. Bertran, J. H. Kwon, and D. E. Swayne. 2017a. Evolution, global spread, and pathogenicity of highly pathogenic avian influenza H5Nx clade 2.3.4.4. *Journal of Veterinary Science* 18:269.
- Lee, D. H., M. Kim Torchetti, M. L. Killian, T. J. DeLiberto, and D. E. Swayne. 2017b. Reoccurrence of avian influenza A (H5N2) virus clade 2.3.4.4 in wild birds, Alaska, USA, 2016. *Emerging Infectious Diseases* 23:365.
- Lee, D. H., M. Kim Torchetti, K. Winker, H. S. Ip, C. S. Song, and D. E. Swayne. 2015. Intercontinental spread of Asian-origin H5N8 to North America through Beringia by migratory birds. *Journal of Virology* 89:6521–6524.
- Lee, D. H., M. Kim Torchetti, J. Hicks, M. L. Killian, J. Bahl, M. Pantin-Jackwood, and D. E. Swayne. 2018. Transmission dynamics of highly pathogenic avian influenza virus A(H5Nx) clade 2.3.4.4, North America, 2014–2015. *Emerging Infectious Diseases* 24:1840–1848.
- Li, M., H. Liu, Y. Bi, J. Sun, G. Wong, D. Liu, L. Li, J. Liu, Q. Chen, H. Wang, and Y. He. 2017. Highly pathogenic avian influenza A (H5N8) virus in wild migratory birds, Qinghai Lake, China. *Emerging Infectious Diseases* 23:637.
- Liu, J., H. Xiao, F. Lei, Q. Zhu, K. Qin, X. W. Zhang, X. L. Zhang, D. Zhao, G. Wang, Y. Feng, and J. Ma. 2005. Highly pathogenic H5N1 influenza virus infection in migratory birds. *Science* 309:1206.
- Luczo, J. M., D. J. Prosser, M. J. Pantin-Jackwood, A. M. Berlin, and E. Spackman. 2020. The pathogenesis of a North American H5N2 clade 2.3.4.4 group A highly pathogenic avian influenza virus in surf scoters (*Melanitta perspicillata*). *BMC Veterinary Research* 16:351.
- Luo, K., K. Zhang, L. Liu, X. Shen, P. Jiao, Y. Song, J. Lv, M. Wang, Y. Liu, W. Qi, and T. Ren. 2018. The genetic and phylogenetic analysis of a highly pathogenic influenza A H5N6 virus from a heron, southern China, 2013. *Infection, Genetics and Evolution* 59:72–74.
- Lycett, S. J., A. Pohlmann, C. Staubach, V. Caliendo, M. Woolhouse, M. Beer, and T. Kuiken. 2020. Genesis and spread of multiple reassortants during the 2016/2017 H5 avian influenza epidemic in Eurasia. *Proceedings of the National Academy of Sciences* 117:20814–20825.
- Marchenko, V. Y., K. A. Sharshov, N. Y. Silko, I. M. Susloparov, A. G. Durymanov, A. Zaykovskaya, A. Y. Alekseev, O. V. Smolovskaya, A. P. Stefanenko, E. M. Malkova, and A. M. Shestopalov. 2011. Characterization of the H5N1 influenza virus isolated during an outbreak among wild birds in Russia (Tuva Republic) in 2010. *Molecular Genetics, Microbiology and Virology* 26:186–190.
- Marchenko, V. Y., I. M. Susloparov, N. P. Kolosova, N. I. Goncharova, A. V. Shipovalov, A. G. Durymanov, T. N. Ilyicheva, L. V. Budatsirenova, V. K. Ivanova, G. A. Ignatyev, and S. N. Ershova. 2015. Influenza A (H5N8) virus isolation in Russia, 2014. *Archives of Virology* 160:2857–2860.



- Marinova-Petkova, A., G. Georgiev, P. Seiler, D. Darnell, J. Franks, S. Krauss, R. J. Webby, and R. G. Webster. 2012. Spread of influenza virus A (H5N1) clade 2.3.2.1 to Bulgaria in common buzzards. *Emerging Infectious Diseases* 18:1596.
- Miller, M. R., J. Y. Takekawa, J. P. Fleskes, D. L. Orthmeyer, M. L. Casazza, and W. M. Perry. 2005. Spring migration of northern pintails from California's Central Valley wintering area tracked with satellite telemetry: routes, timing, and destinations. *Canadian Journal of Zoology* 83:1314–1332.
- Molini, U., G. Aikukutu, J. P. Roux, J. Kemper, C. Ntahonshikira, G. Marruchella, S. Khaibey, G. Cattoli, and W. G. Dundon. 2020. Avian influenza H5N8 outbreak in African penguins (*Spheniscus demersus*), Namibia, 2019. *Journal of Wildlife Diseases* 56:214–218.
- Nettles, V. F., J. M. Wood, and R. G. Webster. 1985. Wildlife surveillance associated with an outbreak of lethal H5N2 avian influenza in domestic poultry. *Avian Diseases* 29:733–741.
- Olsen, B., V. J. Munster, A. Wallensten, J. Waldenström, A. D. Osterhaus, and R. A. Fouchier. 2006. Global patterns of influenza A virus in wild birds. *Science* 312:384–388.
- Pantin-Jackwood, M. J., M. Costa-Hurtado, K. Bertran, E. DeJesus, D. Smith, and D. E. Swayne. 2017. Infectivity, transmission and pathogenicity of H5 highly pathogenic avian influenza clade 2.3.4.4 (H5N8 and H5N2) United States index viruses in Pekin ducks and Chinese geese. *Veterinary Research* 48:1–4.
- Pantin-Jackwood, M. J., M. Costa-Hurtado, E. Shepherd, E. DeJesus, D. Smith, E. Spackman, D. R. Kapczynski, D. L. Suarez, D. E. Stallknecht, and D. E. Swayne. 2016. Pathogenicity and transmission of H5 and H7 highly pathogenic avian influenza viruses in mallards. *Journal of Virology* 90:9967–9982.
- Pasick, J., Y. Berhane, C. Embury-Hyatt, J. Copps, H. Kehler, K. Handel, S. Babiuk, K. Hooper-McGrevy, Y. Li, Q. M. Le, and S. L. Phuong. 2007. Susceptibility of Canada geese (*Branta canadensis*) to highly pathogenic avian influenza virus (H5N1). *Emerging Infectious Diseases* 13:1821.
- Pasick, J., Y. Berhane, T. Joseph, V. Bowes, T. Hisanaga, K. Handel, and S. Alexandersen. 2015. Reassortant highly pathogenic influenza A H5N2 virus containing gene segments related to Eurasian H5N8 in British Columbia, Canada, 2014. *Scientific Reports* 5:1–4.
- Peiris, J. S., W. C. Yu, C. W. Leung, C. Y. Cheung, W. F. Ng, J. A. Nicholls, T. K. Ng, K. H. Chan, S. T. Lai, W. L. Lim, and K. Y. Yuen. 2004. Re-emergence of fatal human influenza A subtype H5N1 disease. *Lancet* 363:617–619.
- Pereda, A. J., M. Uhart, A. A. Perez, M. E. Zaccagnini, L. La Sala, J. Decarre, A. Gojman, L. Solari, R. Suarez, M. I. Craig, and A. Vagnozzi. 2008. Avian influenza virus isolated in wild waterfowl in Argentina: evidence of a potentially unique phylogenetic lineage in South America. *Virology* 378:363–370.
- Petersen, M. R., B. J. McCafferey, and P. L. Flint. 2003. Post-breeding distribution of long-tailed ducks *Clangula hyemalis* from the Yukon-Kuskokwim Delta, Alaska. *Wildfowl* 54:103–114.
- Phillips, L. M., A. N. Powell, and E. A. Rexstad. 2006. Large-scale movements and habitat characteristics of king eiders throughout the nonbreeding period. *Condor* 108:887–900.
- Poen, M. J., D. Venkatesh, T. M. Bestebroer, O. Vuong, R. D. Scheuer, B. B. Oude Munnink, D. de Meulder, M. Richard, T. Kuiken, M. P. Koopmans, and L. Kelder. 2019. Co-circulation of genetically distinct highly pathogenic avian influenza A clade 2.3.4.4 (H5N6) viruses in wild waterfowl and poultry in Europe and East Asia, 2017–18. *Virus Evolution* 5:vez004.
- Pohlmann, A., E. Starick, C. Grund, D. Höper, G. Strebelow, A. Globig, C. Staubach, F. J. Conraths, T. C. Mettenleiter, T. Harder, and M. Beer. 2018. Swarm incursions of reassortants of highly pathogenic avian influenza virus strains H5N8 and H5N5, clade 2.3.4.4b, Germany, winter 2016/17. *Scientific Reports* 8:1–6.
- Preece, N. D., S. E. Abell, L. Grogan, A. Wayne, L. F. Skerratt, P. Van Oosterzee, A. L. Shima, P. Daszak, H. Field, A. Reiss, and L. Berger. 2017. A guide for ecologists: detecting the role of disease in faunal declines and managing population recovery. *Biological Conservation* 214:136–146.
- Pyankova, O. G., I. M. Susloparov, A. A. Moiseeva, N. P. Kolosova, G. S. Onkhonova, A. V. Danilenko, E. V., Vakalova, G. L. Shendo, N. N. Nekeshina, L. N. Noskova, and J. V. Demina. 2021. Isolation of clade 2.3. 4.4 b A (H5N8), a highly pathogenic avian influenza virus, from a worker during an outbreak on a poultry farm, Russia, December 2020. *Eurosurveillance* 26:2100439.
- Ramey, A. M., T. J. DeLiberto, Y. Berhane, D. E. Swayne, and D. E. Stallknecht. 2018a. Lessons learned from research and surveillance directed at highly pathogenic influenza A viruses in wild birds inhabiting North America. *Virology* 518: 55–63.
- Ramey, A. M., N. J. Hill, T. Cline, M. Plancarte, S. De La Cruz, M. L. Casazza, J. T. Ackerman, J. P. Fleskes, T. W. Vickers, A. B. Reeves, and F. Gulland. 2017. Surveillance for highly pathogenic influenza A viruses in California during 2014–2015 provides insights into viral evolutionary pathways and the spatiotemporal extent of viruses in the Pacific Americas Flyway: Influenza A viruses in California during 2014–2015. *Emerging Microbes & Infections* 6:e80.
- Ramey, A. M., A. B. Reeves, T. Donnelly, R. L. Poulson, and D. E. Stallknecht. 2018b. Introduction of Eurasian-origin influenza A (H8N4) virus into North America by migratory birds. *Emerging Infectious Diseases* 24:1950.



- Ramey, A. M., A. B. Reeves, J. Z. Drexler, J. T. Ackerman, S. De La Cruz, A. S. Lang, C. Leyson, P. Link, D. J. Prosser, G. J. Robertson, and J. Wight. 2020. Influenza A viruses remain infectious for more than seven months in northern wetlands of North America. *Proceedings of the Royal Society B* 287:20201680.
- Ramey, A. M., A. B. Reeves, B. J. Lagassé, V. Patil, L. E. Hubbard, D. W. Kolpin, R. B. McCleskey, D. A. Repert, D. E. Stallknecht, and R. L. Poulson. 2021. Evidence for interannual persistence of infectious influenza A viruses in Alaska wetlands. *Science of the Total Environment* 803:150078.
- Ramey, A. M., A. B. Reeves, S. A. Sonsthagen, J. L. TeSlaa, S. Nashold, T. Donnelly, B. Casler, and J. S. Hall. 2015. Dispersal of H9N2 influenza A viruses between East Asia and North America by wild birds. *Virology* 482:79–83.
- Ramey, A. M., A. B. Reeves, J. L. TeSlaa, S. Nashold, T. Donnelly, J. Bahl, and J. S. Hall. 2016. Evidence for common ancestry among viruses isolated from wild birds in Beringia and highly pathogenic intercontinental reassortant H5N1 and H5N2 influenza A viruses. *Infection, Genetics and Evolution* 40:176–185.
- Ramey, A. M., B. D. Uher-Koch, A. B. Reeves, J. A. Schmutz, R. L. Poulson, and D. E. Stallknecht. 2019. Emperor geese (*Anser canagicus*) are exposed to a diversity of influenza A viruses, are infected during the non-breeding period and contribute to intercontinental viral dispersal. *Transboundary and Emerging Diseases* 66:1958–1970.
- Ramos, S., M. MacLachlan, and A. Melton. 2017. Impacts of the 2014–2015 highly pathogenic avian influenza outbreak on the US Poultry Sector. <https://www.ers.usda.gov/webdocs/outlooks/86282/ldpm-282-02.pdf?v=9749.2>. Accessed 24 Mar 2021.
- Reynolds, B., M. Seeger, M. Palenchar, L. Gable, R. Holsinger, B. Neuberger, and T. Christoffel. Crisis and Emergency Risk Communication, 2014 edition. U.S. Department of Health and Human Services Centers for Disease Control and Prevention. [https://emergency.cdc.gov/cerc/ppt/cerc\\_2014edition\\_Copy.pdf](https://emergency.cdc.gov/cerc/ppt/cerc_2014edition_Copy.pdf). Accessed 4 Jun 2021.
- Rijks, J. M., H. Hesselink, P. Lollinga, R. Wesselman, P. Prins, E. Weesendorp, M. Engelsma, R. Heutink, F. Harders, M. Kik, and H. Rozendaal. 2021. Highly pathogenic avian influenza A (H5N1) virus in wild red foxes, the Netherlands, 2021. *Emerging Infectious Diseases* 27:2960–2962.
- Rowan, M. K. 1962. Mass mortality among European common terns in South Africa in April–May 1961. *British Birds* 55: 103–114.
- Runge, M. C., E. H. Grant, J. T. Coleman, J. D. Reichard, S. E. Gibbs, P. M. Cryan, K. J. Olival, D. P. Walsh, D. S. Blehert, M. C. Hopkins, and J. M. Sleeman. 2020. Assessing the risks posed by SARS-CoV-2 in and via North American bats—decision framing and rapid risk assessment. U.S. Geological Survey Open-File Report 2020-1060, Reston, Virginia, USA.
- Sagripanti, J. L., and C. D. Lytle. 2007. Inactivation of influenza virus by solar radiation. *Photochemistry and Photobiology* 83:1278–1282.
- Sakoda, Y., H. Ito, Y. Uchida, M. Okamatsu, N. Yamamoto, K. Soda, N. Nomura, S. Kuribayashi, S. Shichinohe, Y. Sunden, and T. Umemura. 2012. Reintroduction of H5N1 highly pathogenic avian influenza virus by migratory water birds, causing poultry outbreaks in the 2010–2011 winter season in Japan. *Journal of General Virology* 93:541–550.
- Seekings, A. H., C. J. Warren, S. S. Thomas, S. Mahmood, J. James, A. M. Byrne, S. Watson, C. Bianco, A. Nunez, I. H. Brown, and S. M. Brookes. 2021. Highly pathogenic avian influenza virus H5N6 (clade 2.3.4.4 b) has a preferable host tropism for waterfowl reflected in its inefficient transmission to terrestrial poultry. *Virology* 559:74–85.
- Segovia, K. M., M. S. França, C. L. Leyson, D. R. Kapczynski, K. Chrzastek, C. S. Bahnson, and D. E. Stallknecht. 2018. Heterosubtypic immunity increases infectious dose required to infect Mallard ducks with Influenza A virus. *PLoS One* 13:e0196394.
- Shearn-Bochsler, V. I., S. Knowles, and H. Ip. 2019. Lethal infection of wild raptors with highly pathogenic avian influenza H5N8 and H5N2 viruses in the USA, 2014–15. *Journal of Wildlife Diseases* 55:164–168.
- Shin, D. L., U. Siebert, J. Lakemeyer, M. Grilo, I. Pawliczka, N. H. Wu, P. Valentin-Weigand, L. Haas, and G. Herrler. 2019. Highly pathogenic avian influenza A (H5N8) virus in gray seals, Baltic Sea. *Emerging Infectious Diseases* 25:2295.
- Sims, L. D., J. Domenech, C. Benigno, S. Kahn, A. Kamata, J. Lubroth, V. Martin, and P. Roeder. 2005. Origin and evolution of highly pathogenic H5N1 avian influenza in Asia. *Veterinary Record* 157:159–164.
- Sims, L. D., T. M. Ellis, K. K. Liu, K. Dyrting, H. Wong, M. Peiris, Y. Guan, and K. F. Shortridge. 2003. Avian influenza in Hong Kong 1997–2002. *Avian Diseases* 47:832.
- Sivay, M. V., S. G. Sayfutdinova, K. A. Sharshov, A. Y. Alekseev, A. K. Yurlov, J. Runstadler, and A. M. Shestopalov. 2012. Surveillance of influenza A virus in wild birds in the Asian portion of Russia in 2008. *Avian Diseases* 56:456–463.
- Sleeman, J. M., T. DeLiberto, and N. Nguyen. 2017. Optimization of human, animal, and environmental health by using the One Health approach. *Journal of Veterinary Science* 18:263–268.
- Smith, G. J., R. O. Donis, World Health Organization/World Organisation for Animal Health/Food and Agriculture Organization (WHO/OIE/FAO) H5 Evolution Working Group. 2015. Nomenclature updates resulting from the evolution of avian influenza A (H5) virus clades 2.1.3.2a, 2.2.1, and 2.3.4 during 2013–2014. *Influenza and Other Respiratory Viruses* 9:271–276.





- Soos, C., E. J. Parmley, K. McAloney, B. Pollard, E. Jenkins, F. Kibenge, and F. A. Leighton. 2012. Bait trapping linked to higher avian influenza virus detection in wild ducks. *Journal of Wildlife Diseases* 48:444–448.
- Spackman, E., D. J. Prosser, M. J. Pantin-Jackwood, A. M. Berlin, and C. B. Stephens. 2017. The pathogenesis of clade 2.3.4.4 H5 highly pathogenic avian influenza viruses in ruddy duck (*Oxyura jamaicensis*) and lesser scaup (*Aythya affinis*). *Journal of Wildlife Diseases* 53:832–842.
- Stallknecht, D. E. 2003. Ecology and epidemiology of avian influenza viruses in wild bird populations: waterfowl, shorebirds, pelicans, cormorants, etc. *Avian Diseases* 47:61–69.
- Suetens, C., R. Snacken, G. Hanquet, B. Brochier, S. Maes, I. Thomas, F. Yane, T. Van den Berg, S. Van Borm, and B. Lambrecht. 2004. Eagles testing positive for H5N1 imported illegally into Europe from Thailand. *Eurosurveillance* 8: 2575.
- Swayne, D. E. 2008. Epidemiology of avian influenza in agricultural and other man-made systems. Pages 59–85 in D. Swayne, editor. *Avian influenza*. Blackwell Publishing, Ames, Iowa, USA.
- Swayne, D. E., and D. L. Suarez. 2000. Highly pathogenic avian influenza. *Revue Scientifique et Technique—Office International des Épizooties* 19:463–482.
- van den Brand, J. M., J. H. Verhagen, E. J. Veldhuis Kroeze, M. W. Van de Bildt, R. Bodewes, S. Herfst, M. Richard, P. Lexmond, T. M. Bestebroer, R. A. Fouchier, and T. Kuiken. 2018. Wild ducks excrete highly pathogenic avian influenza virus H5N8 (2014–2015) without clinical or pathological evidence of disease. *Emerging Microbes & Infections* 7:67.
- Van Kerkhove, M. D., E. Mumford, A. W. Mounts, J. Bresee, S. Ly, C. B. Bridges, J. Otte. 2011. Highly pathogenic avian influenza (H5N1): pathways of exposure at the animal-human interface, a systematic review. *PloS ONE* 6:14582.
- Verhagen, J. H., R. A. Fouchier, N. Lewis. 2021. Highly pathogenic avian influenza viruses at the wild-domestic bird interface in Europe: future directions for research and surveillance. *Viruses* 13:212.
- Verhagen, J. H., H. P. Van Der Jeugd, B. A. Nolet, R. Slaterus, S. P. Kharitonov, P. De Vries, O. Vuong, F. Majoer, T. Kuiken, and R. A. Fouchier. 2015. Wild bird surveillance around outbreaks of highly pathogenic avian influenza A (H5N8) virus in the Netherlands, 2014, within the context of global flyways. *Eurosurveillance* 20:21069.
- Wan, X. F. 2012. Lessons from emergence of A/Goose/Guangdong/1996-like H5N1 highly pathogenic avian influenza viruses and recent influenza surveillance efforts in southern China. *Zoonoses and Public Health* 59:32–42.
- Wan, X. F., L. Dong, Y. Lan, L. P. Long, C. Xu, S. Zou, Z. Li, L. Wen, Z. Cai, W. Wang, and X. Li. 2011. Indications that live poultry markets are a major source of human H5N1 influenza virus infection in China. *Journal of Virology* 85: 13432–13438.
- Ward, M. P., D. Maftai, C. Apostu, and A. Suru. 2008. Environmental and anthropogenic risk factors for highly pathogenic avian influenza subtype H5N1 outbreaks in Romania, 2005–2006. *Veterinary Research Communications* 32:627–634.
- Ward, M. P., D. N. Maftai, C. L. Apostu, and A. R. Suru. 2009. Association between outbreaks of highly pathogenic avian influenza subtype H5N1 and migratory waterfowl (family Anatidae) populations. *Zoonoses and Public Health* 56:1–9.
- Weber, T. P., and N. I. Stilianakis. 2008. Inactivation of influenza A viruses in the environment and modes of transmission: a critical review. *Journal of Infection* 57:361–373.
- WHO/OIE/FAO H5N1 Evolution Working Group. 2012. Continued evolution of highly pathogenic avian influenza A (H5N1): updated nomenclature. *Influenza and Other Respiratory Viruses* 6:1–5.
- Wille, M., G. J. Robertson, H. Whitney, D. Ojic, and A. S. Lang. 2011. Reassortment of American and Eurasian genes in an influenza A virus isolated from a great black-backed gull (*Larus marinus*), a species demonstrated to move between these regions. *Archives of Virology* 156:107–115.
- Winker, K., and D. D. Gibson. 2010. The Asia-to-America influx of avian influenza wild bird hosts is large. *Avian Diseases* 54:477–482.
- World Organisation for Animal Health [OIE]. 2021a. Immediate notification of infection of non-poultry including wild birds with highly pathogenic influenza A viruses, United Kingdom. <https://wahis.oie.int/#/home>. Accessed 29 Mar 2021.
- World Organisation for Animal Health [OIE]. 2021b. Immediate notification of infection of non-poultry including wild birds with highly pathogenic influenza A viruses, United Kingdom. <https://wahis.oie.int/#/report-info?reportId=30629>. Accessed 24 Mar 2021.
- World Organisation for Animal Health [OIE]. 2021c. Immediate notification of infection of non-poultry including wild birds with highly pathogenic influenza A viruses, China. <https://wahis.oie.int/#/report-info?reportId=34710>. Accessed 16 Jun 2021.
- Xu, X., K. Subbarao, N. J. Cox, and Y. Guo. 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.
- Yang, Z. F., C. K. Mok, J. S. Peiris, and N. S. Zhong. 2015. Human infection with a novel avian influenza A (H5N6) virus. *New England Journal of Medicine* 373:487–489.





Zohari, S., A. Neimanis, T. Härkönen, C. Moraeus, and J. F. Valarcher. 2014. Avian influenza A (H10N7) virus involvement in mass mortality of harbour seals (*Phoca vitulina*) in Sweden, March through October 2014. *Eurosurveillance* 19:20967.

*Associate Editor: Bill Block.*

**How to cite this article:** Ramey, A. M., N. J. Hill, T. J. DeLiberto, S. E. J. Gibbs, M. Camille Hopkins, A. S. Lang, R. L. Poulson, D. J. Prosser, J. M. Sleeman, D. E. Stallknecht, and X.-F. Wan. 2022. Highly pathogenic avian influenza is an emerging disease threat to wild birds in North America. *Journal of Wildlife Management* 1–21. <https://doi.org/10.1002/jwmg.22171>