USDA Animal and Plant Health Inspection Service
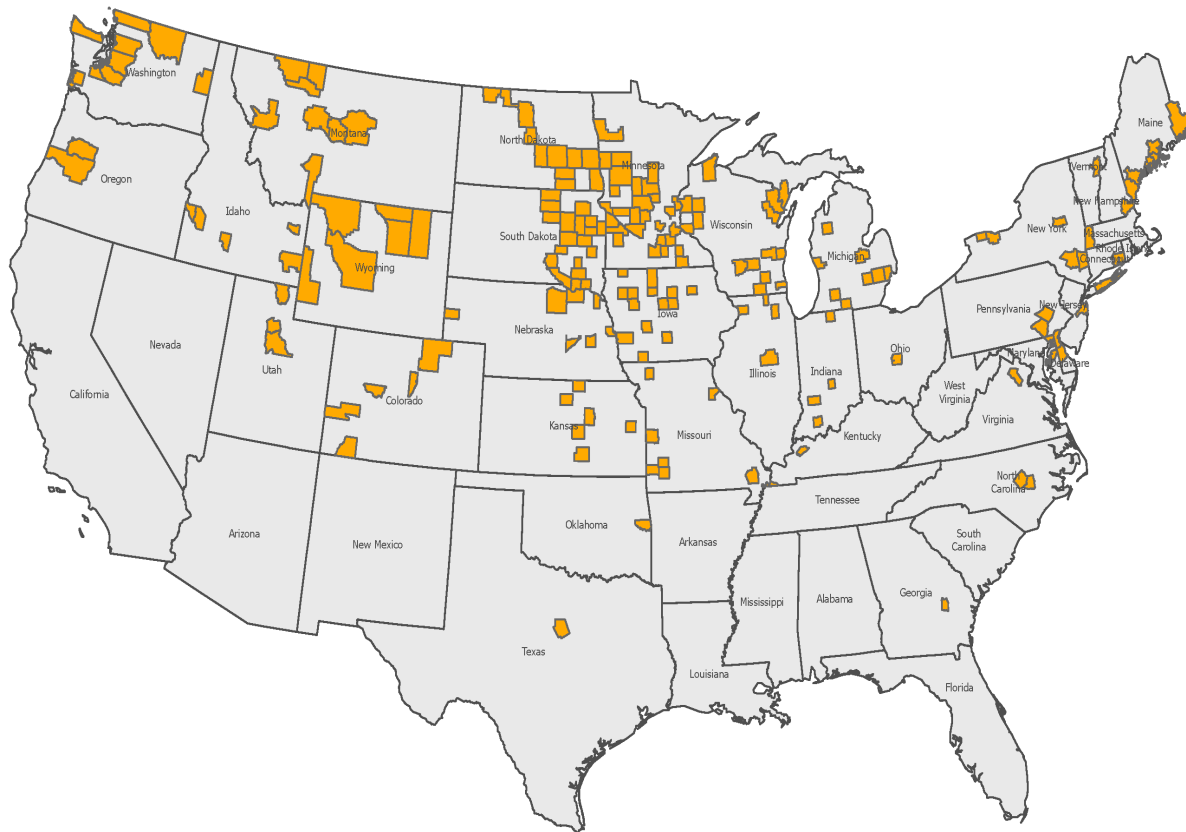U.S. DEPARTMENT OF AGRICULTURE

Epidemiologic and Other Analyses of HPAI Affected Poultry Flocks
July 2022 Interim Report

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Version Control

This document was first released in February 2023. The March 2023 update includes the following changes:

• Update to page numbers in the Table of Contents.

• Update to page numbers in the List of Figures and Tables.

• Footnote references revised on pages 15, 20, 23, and 44.

• Revisions and additions to the Reference section.

• Revisions and clarifications to the Acknowledgments section.

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EXECUTIVE SUMMARY

In January 2022, the clade 2.3.4.4b H5N1 highly pathogenic avian influenza (HPAI) was reported in a wild bird sample from Colleton County, South Carolina, and heralded what has become one of the largest avian influenza outbreaks in United States (U.S.) history, second only to the clade H5 2.3.4.4c outbreak in 2015. By 31 May 2022, HPAI had been confirmed in 35 States, including 130 turkey, 55 chicken, 11 duck, 3 pheasant, 21 poultry, and 137 backyard (non-poultry/non-commercial poultry) premises. In comparison to the 2014–2015 outbreak, which shattered multiple records for outbreak size and cost, the 2022 HPAI outbreak has spread over a wider geographic area, creating a much larger demand for resources and personnel. As of 5 May 2022, over 500 USDA-APHIS personnel and contractors have been deployed in support of the response, with an additional 500 State personnel responding. Following the 2014–2015 outbreak, APHIS made numerous changes to response processes to improve efficiency in control activities, indemnity and virus elimination payments, and repopulation processes and timelines. Initial estimates from the 2022 outbreak suggest that significant improvements have been made in all these areas.

Phylogenetic analyses of viruses from this outbreak show one major introduction of the Eurasian H5 clade 2.3.4.4b virus into the U.S. that has spread all the way to the Pacific Flyway. This H5 2.3.4.4b virus is more infectious for poultry species without the need for poultry adaptation, as compared to the earlier H5 clade 2.3.4.4c virus of 2015, and rapidly causes illness and death in chickens and turkeys, though some waterfowl may be infected and show no clinical signs. Additionally, when compared to the 2015 incursion, this virus lineage has caused significant wild bird mortalities. Reassortment of the H5 clade 2.3.4.4 virus with North American viruses were first identified in February 2022 from wild bird samples, and several genotypes have since been identified; reassortments account for at least 74 percent of wild bird viruses with several genotypes spilling over into poultry. At least 84 percent of analyzed U.S. detections in poultry are consistent with independent wild bird introductions. Unique to this outbreak, there have been several mammalian detections across all four flyways and as far south as Utah with at least nine species affected. To date, there have been only two reports of the H5N1 HPAI 2022 virus detected in humans—one in the United Kingdom and one in the United States.

In collaboration with State Animal Health Officials, USDA-APHIS conducted a case-series study of H5N1 HPAI infected commercial and backyard operations in the U.S. Risk factors examined include the movement of live and dead birds, transportation of manure, equipment sharing, and contaminated feed trucks, vehicles, water, and people. Visitors to the farm and employee connections with other farms were the most common risk factors identified among respondents. To better identify risk factors, USDA will be conducting case-control studies in layer and turkey operations with results expected in early 2023.

USDA-APHIS used the HPAI National Model to support budget and resource planning, as well as evaluate alternative control strategies and options. As the outbreak continued, disease spread and control modeling was used to help inform data-driven response strategies and resource allocation.

Other modeling approaches were also used to inform the response and improve our understanding of disease transmission. Time of introduction models use diagnostic testing, daily mortality, and water consumption data to predict the time of virus entry into a flock. Analysis of 26 commercial premises found that time to first positive sample varied by production type, introduction route, and reason for testing. The average adequate contact rate across all premises was 3.8 contacts per day, and overall mean R0 value was 13.3 (range 2–47), which would ensure rapid spread through a barn. This work highlighted the value of closely monitoring mortality, water consumption, and egg production to quickly identify disease issues in the flock, while recognizing that these factors may vary, so understanding the trends within each production setting is important.

The U.S. National Surveillance Plan for Highly Pathogenic Avian Influenza in Wild Birds was developed to maximize our ability to detect IAV in wild waterfowl. Between 1 June 2021 and 1 June 2022, over 22,000 wild waterfowl were sampled and tested by rRT-PCR for influenza A viruses. Overall, targeted surveillance and morbidity/mortality investigations of sick or dead birds has detected 1,611 H5N1 HPAI in wild birds from 42 States across all four U.S. flyways, with over 66 different avian species affected.

To better understand the risk of virus spillover from wild to domestic birds, USDA-APHIS collaborated with the University of Maryland, and the U.S. Geological Survey, Eastern Ecological Science Center to model spatio-temporal trends in transmission between wild waterfowl and domestic poultry. Model outputs were validated using the current outbreak, and counties with a spillover event had 12 times greater predicted risk, on average, than non-outbreak counties. Of the 62 spillover counties, 54 were at above-average risk for a spillover event. There were almost no spillovers in counties designated as low risk by the interface model. Model results are now available online for poultry owners to use to understand their own risk context.

Other valuable tools for understanding disease risk are eBird and BirdCast migration data. BirdCast migration maps show real-time intensities of nocturnal bird migration between local sunset to sunrise, as detected by the U.S. weather surveillance radar network. eBird is a database of species-specific, crowd-sourced observational data by scientists and birding enthusiasts. Intense periods of bird migration, as seen by BirdCast maps were correlated with outbreaks in domestic poultry, suggesting that this tool can be used to increase awareness of increased HPAI risk due to wild bird movements. Using eBird data, we estimated that HPAI-positive premises were more likely to be detected within the first seven days of heavy wild bird observation within a 50km spatial window.

Further information on the epidemiologic features of this outbreak and additional analyses will be provided in subsequent reports.

INTRODUCTION

In response to the H5N1 highly pathogenic avian influenza (HPAI) outbreaks in commercial and backyard poultry across a large portion of the United States, the United States Department of Agriculture (USDA) Animal and Plant Health Inspection Service (APHIS) Veterinary Services, APHIS Wildlife Services, and the affected States have initiated epidemiologic, genetic, and wildlife investigations. Due to the unprecedented size of this outbreak, we have chosen to issue an interim report looking at data from the start of the outbreak, until 31 May 2022 in the case of epidemiologic investigations, and through 29 June 2022 for phylogenetic analyses. Updates to this report will be made in the future. These studies aim to provide a better understanding of factors associated with avian influenza virus transmission and its introduction into poultry flocks.

These investigations include the following:

- Phylogenetic analyses of viral genomes;
- A case series evaluating the data collected through site visits and interviews with farm personnel;
- Application of the National HPAI Disease-Spread Model to inform the response;
- Analysis of mortality records, diagnostics, and in some cases, water consumption and egg production to understand virus transmission in barns and time to detection;
- Analysis of wild bird surveillance;
- Analysis of avian influenza transmission risk at the wild bird domestic poultry interface; and
- Analysis of correlation between migratory wild bird numbers captured by open-source tools eBird and BirdCast on HPAI transmission risk and timing.

This interim report includes the results from these investigations to provide producers, industry, and other stakeholders with current epidemiologic information. Infected domestic poultry premises were classified by species and production type. Species designations included chickens, turkeys, ducks, pheasants, and other poultry. In this report, backyard premises that met the World Organisation for Animal Health (WOAH, formerly known as OIE) reporting requirements for poultry are designated as "backyard/non-commercial" premises. Backyard premises that did not meet reporting requirements, because they only reared birds for household use and did not sell any animal products, are referred to as "backyard/non-poultry" premises.[1] Production types included multiple commercial poultry premises types, backyard producers, a wild game farm, and an animal rescue.

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[1] This terminology reflects premises designations used at the time of this report, which had a data cut-off of June 2022. Due to the evolving nature of terminology during an outbreak, the designations and numbers reported in this document may not match the data available online. For the most accurate case designations and numbers, see the APHIS HPAI website.

A. Description of Outbreak

USDA APHIS identified the Eurasian clade 2.3.4.4b H5N1 HPAI on 13 January 2022 in a wild bird in Colleton County, South Carolina.[2] This detection was the first Eurasian H5 HPAI detected in the United States since December 2016, and followed ongoing reports of clade 2.3.4.4b H5N1 HPAI in Europe[3] (starting 27 October 2021 for the migration season; note that ancestors of clade 2.3.4.4b have been circulating along Eurasian flyways since 2017) and in Canada[4] starting on 4 November 2021. For Europe, Canada, and the United States, wild bird detections have preceded detections in domestic poultry. Figure 1 describes the temporospatial detections of clade 2.3.4.4b H5N1 HPAI virus in poultry in the U.S.; refer to the phylogenetics section for further details.

MISSISSIPPI FLYWAY February – March 2022

The first poultry case in the U.S. was along the Mississippi Flyway in Indiana. On 7 February 2022, a commercial meat bird turkey operation in Dubois County, Indiana, submitted diagnostic test samples to the Indiana Animal Disease Diagnostic Laboratory (a member of the National Animal Health Laboratory Network [NAHLN]) after observing signs of lethargy, increased mortality, and decreased water consumption in one tom turkey production house. The samples tested non-negative for H5 and were forwarded to the National Veterinary Services Laboratories (NVSL). On 8 February 2022, the NVSL received samples from the affected premises and confirmed clade 2.3.4.4b H5N1 HPAI.

Continuing in the Mississippi Flyway, the next States affected were Kentucky and Virginia. On 11 February 2022, a commercial broiler production operation in Fulton County, Kentucky, submitted samples to the Murray State University Breathitt Veterinary Center laboratory (a member of the NAHLN network) after observing decreased water consumption and increasing mortality in one house. The NAHLN laboratory detected H5 and forwarded the samples; NVSL confirmed H5N1 HPAI on 12 February 2022. Also on 11 February 2022, oropharyngeal swabs from dead chickens and turkeys belonging to a mixed-species backyard flock in Fauquier County, Virginia, tested non-negative for H5 at the Virginia Department of Agriculture and Consumer Services Harrisonburg diagnostic laboratory (a member of the NAHLN network). The samples were transported to NVSL on 12 February 2022, where H5 HPAI was confirmed. Subsequently, between 8 February 2022 and 2 March 2022, H5N1 HPAI was confirmed in seven commercial meat bird turkey premises and one commercial broiler production premises in two counties in southern Indiana and two counties in western Kentucky (Figure 1).

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[2] https://www.aphis.usda.gov/aphis/newsroom/stakeholder-info/sa_by_date/sa-2022/hpai-sc
[3] https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1070246/Highly_pathogenic_avian_influenza__HPAI__in_the_UK_and_Europe__outbreak_update_23.pdf
[4] https://wahis.woah.org/#/in-event/4191/dashboard
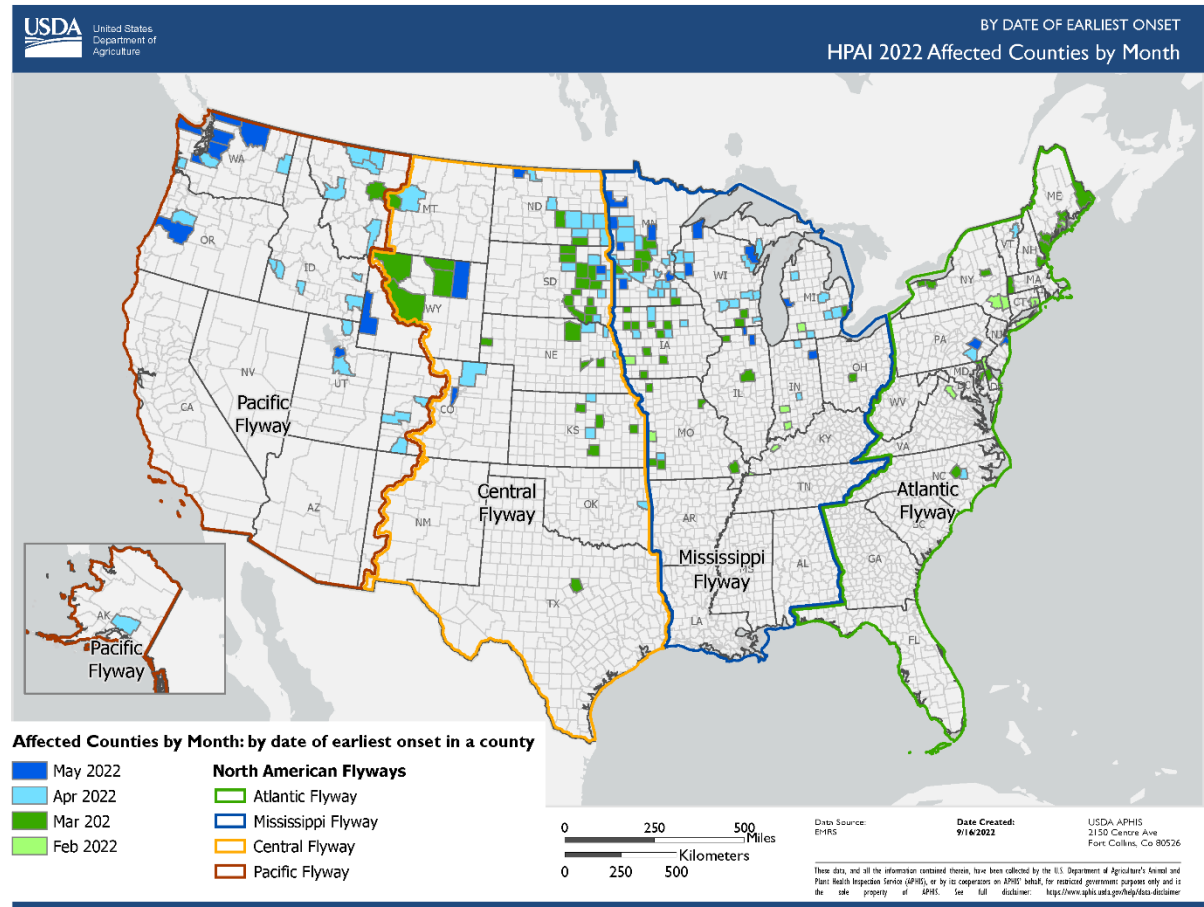
Figure 1. Counties with Highly Pathogenic Avian Influenza Detections in Poultry by Month and by Flyway.

ATLANTIC FLYWAY February – March 2022

Moving to the Atlantic Flyway, on 18 February 2022, the NVSL confirmed clade 2.3.4.4b H5N1 HPAI in a non-poultry premises in Suffolk County, New York. This detection was the first of a series of detections among backyard premises in Atlantic Flyway States along the Northeastern Atlantic coastline (Figure 1); impacted States included Maine, Connecticut, and Massachusetts (Table 1). On 20 February 2022, a commercial laying hen facility in New Castle County, Delaware, observed increased mortality in a single house. Samples were collected and submitted from the affected house to the Allen Laboratory at the University of Delaware (a member of the NAHLN network) on 21 February 2022 and H5 was detected the same day. NVSL confirmed HPAI on 22 February 2022. On 3 March 2022, a table egg layer premises located in Cecil County, Maryland, and within the established New Castle Control Area, observed increased mortality. This premises was already conducting daily continuity of business testing for permitted movement. Diagnostic samples were submitted, and the

NAHLN Laboratory detected H5 the same day. The NVSL confirmed H5N1 HPAI the following day. Subsequently, six more premises on the Delmarva Peninsula were confirmed between 8 March 2022 and 18 March 2022. Affected premises types included table egg layer, table egg processing, table egg pullet, and broiler production facilities.

MISSISSPPI FLYWAY February – May 2022

Back in the Mississippi Flyway, on 23 February 2022, the NVSL confirmed clade 2.3.4.4b H5N1 HPAI in a mixed species non-poultry flock in Kalamazoo County, Michigan. Subsequently, from 24 March 2022 to 10 May 2022, 12 additional premises in Michigan were confirmed; these included 9 backyard/non-poultry, 2 non-commercial poultry chicken flocks, and 1 commercial turkey meat bird premises. From 1 March 2022 to 18 May 2022, HPAI was confirmed in additional Midwest States located in the Mississippi Flyway, including Iowa, Missouri, Illinois, Wisconsin, Minnesota, and Ohio (Table 1; Figure 1). HPAI detections in Iowa and Missouri occurred predominately among commercial premises. In Iowa, affected premises included nine commercial turkey, six commercial table egg layers, and four non-poultry premises. In Missouri, detections included four commercial turkey, one commercial broiler, and three non-poultry premises. In Wisconsin, confirmed premises included 7 commercial turkey, 1 commercial table egg layer, 1 backyard/non-commercial, and 13 backyard/non-poultry premises. As of 31 May 2022, a total of 80 detections occurred in Minnesota, accounting for 22.4 percent of the total cases. Confirmed premises included 57 commercial turkey, 1 commercial table egg layer, 1 commercial broiler, and 21 backyard/non-poultry producers. Backyard premises in Minnesota included 19 non-poultry and 2 non-commercial poultry premises. HPAI detections in Illinois and Ohio were limited to backyard/non-poultry premises. From 8 April 2022 to 19 May 2022, additional confirmations in Indiana were reported for three commercial duck premises and two backyard/non-poultry premises.

CENTRAL FLYWAY March 2022

The first of several poultry premises were affected in the Central Flyway, and on 5 March 2022, the NVSL confirmed HPAI on a commercial meat-type turkey premises in Charles Mix County, South Dakota. From 12 March 2022 to 20 May 2022, additional detections in South Dakota were confirmed for 33 commercial turkey, 1 commercial table egg layer, 1 commercial gamebird, 2 backyard/non-commercial chicken, and 2 backyard/non-poultry premises. Detections in South Dakota accounted for 11.2 percent of all detections in domestic poultry as of 31 May 2022, and predominately occurred in the eastern side of the State. Following initial detections in South Dakota, subsequent detections were confirmed in Kansas starting 11 March 2022, in Nebraska starting 15 March 2022, and in North Dakota starting 29 March 2022. Confirmed detections in Kansas included two backyard/non-poultry, two backyard/non-commercial poultry, one backyard/non-commercial chicken, and one commercial turkey premises. In Nebraska, the detections included four backyard/non-

poultry, two commercial broiler, and two commercial table egg layer premises. In North Dakota, HPAI affected predominately backyard premises but was also found in four commercial turkey premises.

ATLANTIC FLYWAY March – May 2022

While HPAI detections were increasing within the Mississippi and Central Flyways, reports were received from previously unaffected States along the east coast in the Atlantic Flyway. These States included North Carolina, Pennsylvania, Vermont, and New Jersey. On 29 March 2022, the NVSL confirmed H5 HPAI in a commercial turkey premises in Johnston County, North Carolina. Active surveillance testing for the infection zone identified two additional commercial turkey premises. Between 1 April 2022 and 11 April 2022, HPAI was confirmed in three commercial turkey and three commercial broiler bird premises in Wayne County, North Carolina. A few days later in Pennsylvania, on 15 April 2022, HPAI was confirmed in a commercial table egg layer premises in Lancaster County. The NVSL later confirmed HPAI in four additional table egg layer and two commercial broiler premises in Lancaster County. On 29 April 2022, the NVSL confirmed HPAI infection in a commercial duck facility, which was the first detection in what would become a total of eight commercial duck premises in Lancaster and Berks Counties. Infections were also confirmed for two commercial table egg layer premises in Berks County. The confirmed detections in Vermont on 28 April 2022 and in New Jersey on 17 May 2022 occurred in backyard/non-poultry premises.

CENTRAL / PACIFIC FLYWAYS March – May 2022

Continuing in the Central Flyway and moving into the Pacific Flyway, on 28 March 2022, the NVSL confirmed the detection of H5N1 HPAI in a backyard/non-poultry premises in Johnson County, Wyoming. This detection represented movement of the outbreak into the Mountain West, which is split by the Central and Pacific Flyways (Figure 1). States with confirmed detections included Texas, Montana, Colorado, Idaho, Utah, and Oklahoma (Table 1). All confirmations in Wyoming, Montana, and Idaho occurred among backyard premises. In Wyoming, all eight detections were backyard/non-poultry premises. In Montana, the detections were among seven non-poultry and two non-commercial poultry premises. The 25 detections in Idaho included 15 backyard/non-poultry, 5 backyard/non-commercial chicken, 4 backyard/non-commercial poultry, and 1 backyard/non-commercial duck premises. NVSL-confirmed detections in Colorado and Utah included both backyard and commercial premises. In Colorado, one backyard/non-commercial chicken, one backyard/non-commercial poultry, one commercial broiler, one commercial table egg layer, and one non-poultry premises were detected. The four detections in Utah included three backyard/non-poultry and one commercial table egg layer premises. Detection of HPAI in Texas and Oklahoma was limited to one commercial upland game bird and one commercial broiler breeder premises, respectively.

Moving to the west coast, on 29 April 2022, the NVSL confirmed the detection of H5N1 HPAI in a backyard/non-poultry premises in Matanuska Susitna, Alaska. This detection represented the first detection along the coastline of the Pacific Flyway. On 5 May 2022, HPAI was confirmed in a backyard/non-poultry premises in Linn County, Oregon, and a backyard/non-commercial chicken premises in Pacific County, Washington. As of 31 May 2022, additional detections occurred in one backyard/non-commercial poultry premises in Oregon.

As of 31 May 2022, HPAI was confirmed in 35 States (Table 1), including 130 turkey, 55 chicken, 11 duck, 3 pheasant, 21 backyard/poultry, and 137 backyard/non-poultry premises (Table 2). An additional three premises were identified as dangerous contacts and underwent depopulation, disposal, and virus elimination. Figure 2 shows a map of all HPAI-affected counties, including both poultry and wild bird detections by flyway as of May 31, 2022. Figure 3 depicts the number of detections by week and species. Following all detections of HPAI, remaining birds on infected premises were depopulated, and active surveillance was conducted as outlined within the USDA HPAI Response Plan Red Book.[5] For commercial premises detections and backyard/poultry detections, 10km Control Areas, consisting of a 3km Infected Zone and a 7km Buffer Zone, surrounded by a 10km Surveillance Zone were established; for detections within backyard/non-poultry flock premises, 10km Surveillance Zones were established.

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[5] https://www.aphis.usda.gov/animal_health/emergency_management/downloads/hpai_response_plan.pdf
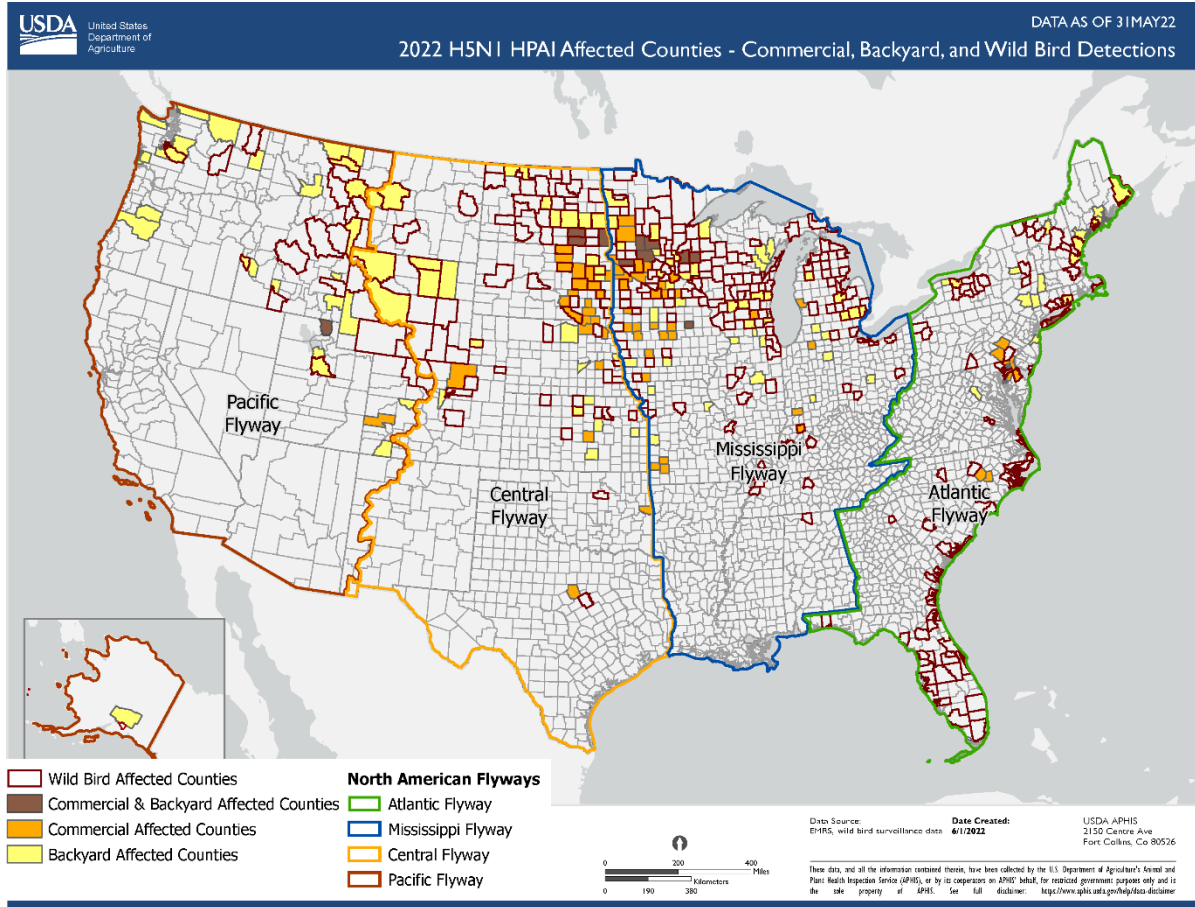
Figure 2. Bird Map of HPAI-Affected Counties by North American Flyway and Poultry Type or Wild Detection.

Table 1. Confirmed Detections of Highly Pathogenic Avian Influenza by State as of 31 May 2022.

State	Total Detections	First Detection	Last Detection	Chicken	Turkey	Duck	Upland Gamebird	Backyard Poultry	NP[a]
Indiana	11	2/8/2022	5/19/2022		6	3			2
Kentucky	2	2/12/2022	2/15/2022	1	1				
Virginia	1	2/12/2022	2/12/2022						1
New York	8	2/18/2022	4/6/2022	1			1	2	4
Maine	12	2/19/2022	4/5/2022					1	11
Delaware	3	2/22/2022	3/17/2022	3					
Michigan	13	2/23/2022	5/10/2022	2	1				10
Connecticut	1	3/1/2022	3/1/2022						1
Iowa	19	3/1/2022	5/4/2022	6	9				4
Maryland	4	3/4/2022	3/18/2022	4					
Missouri	9	3/4/2022	4/6/2022	1	5				3
South Dakota	40	3/5/2022	5/19/2022	3	33		1	1	2
Illinois	4	3/11/2022	5/17/2022						4
Kansas	6	3/11/2022	4/27/2022	1	1			2	2
Wisconsin	22	3/14/2022	5/23/2022	1	7			1	13
Nebraska	8	3/15/2022	4/29/2022	4					4
New	1	3/16/2022	3/16/2022						1
Minnesota	80	3/26/2022	5/31/2022	2	57			2	19
Massachusetts	1	3/29/2022	3/29/2022						1
North Carolina	9	3/29/2022	4/12/2022	3	6				
North Dakota	15	3/29/2022	5/17/2022	3	4			3	5
Ohio	1	3/29/2022	3/29/2022						1
Wyoming	8	3/29/2022	5/20/2022						8
Texas	1	4/3/2022	4/3/2022				1		
Montana	9	4/7/2022	5/6/2022					2	7
Colorado	5	4/8/2022	5/19/2022	3				1	1
Idaho	25	4/14/2022	5/24/2022	5		1		4	15
Pennsylvania	16	4/15/2022	5/23/2022	9	7				
Utah	4	4/15/2022	5/17/2022	1					3
Vermont	1	4/28/2022	4/28/2022						1
Alaska	1	4/29/2022	4/29/2022						1
Oklahoma	1	4/30/2022	4/30/2022	1					
Oregon	2	5/5/2022	5/17/2022					1	1
Washington	13	5/5/2022	5/27/2022	1					12
New Jersey	1	5/17/2022	5/17/2022					1	
Total	357			55	130	11	3	21	137

[a] Non-Poultry (NP) as defined by the World Organisation for Animal Health (WOAH)

Table 2. Confirmed Detections of Highly Pathogenic Avian Influenza by Production Type and World Organisation for Animal Health (WOAH) Reportable Species as of 31 May 2022.

Production Type	Chicken	Turkey	Duck	Upland Gamebird	Backyard Poultry	Non-Poultry
Commercial Broiler Production	11					
Commercial Broiler Breeder Pullets	1					
Commercial Broiler Breeder	2					
Commercial Table Egg Layer	20					
Commercial Table Egg Pullets	3					
Commercial Table Egg Breeder	2					
Commercial Turkey Meat Bird		118			1	
Commercial Turkey Breeder Hens		8				
Commercial Turkey Replacement Hens		2				
Commercial Turkey Poult Supplier		1				
Commercial Turkey Breeder Toms		1				
Commercial Duck Meat Bird			4			
Commercial Duck Breeder			6			
Commercial Upland Gamebird Producer				3		
Backyard Producer	16		1		20	135
Wild Game Farm						1
Animal Rescue / Rehabilitation						1
Total	55	130	11	3	21	137
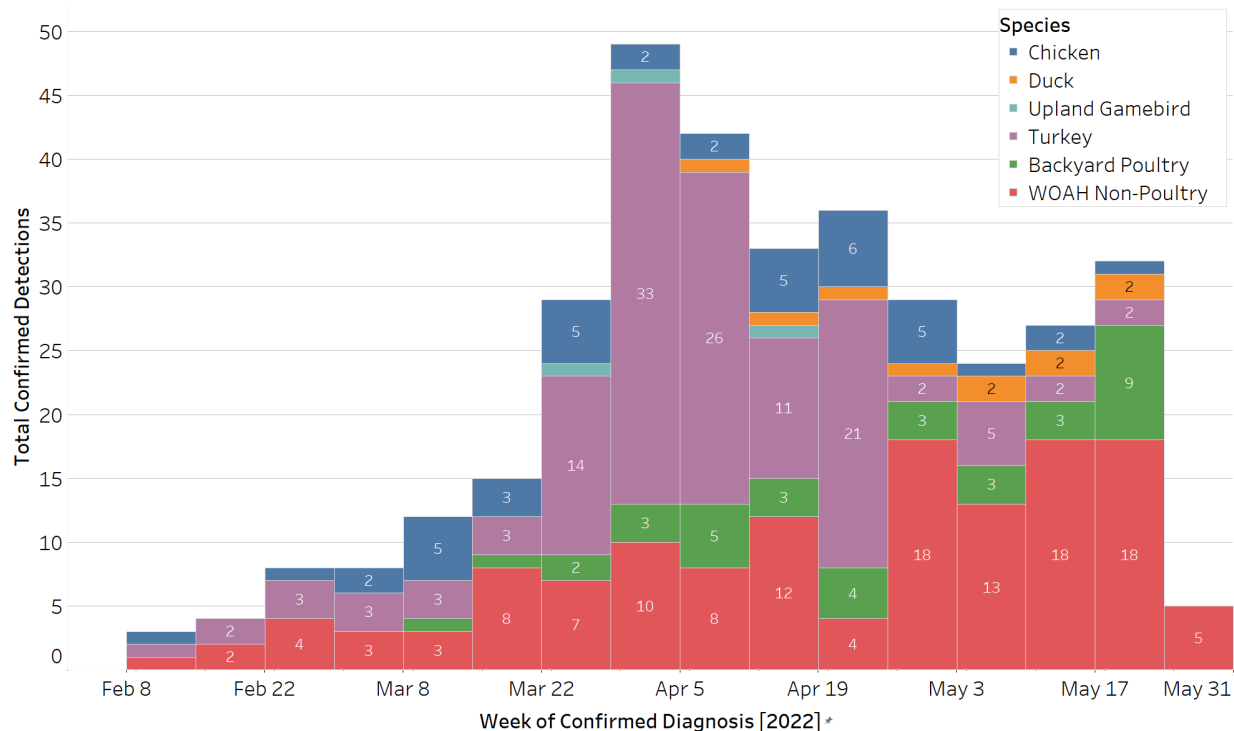
Figure 3. Weekly Highly Pathogenic Avian Influenza Detections by Species Type as of 31 May 2022.

B.   Comparison of 2022 HPAI Outbreak to 2015 HPAI Outbreak

2014–2015 HPAI Outbreak Final Report Highlights[6]

From December 2014 through June 2015, the U.S. endured what was at the time the largest animal health emergency in its history, with more than 200 cases of highly pathogenic avian influenza (HPAI) found in commercial and backyard poultry, as well as wild birds, across the country. In December 2014, HPAI was detected in the United States for the first time since 2004. From 11 December 2014 to 16 January 2015, the USDA received a total of seven reports of HPAI H5N2 or H5N8 in captive wild birds and backyard flocks from the Northwestern United States. Additional detections occurred in wild birds. The first infected commercial flock was identified on 23 January 2015 in California. From January to March, the disease spread slowly to multiple States, including Minnesota, Missouri, Arkansas, and Kansas. A significant increase in HPAI H5N2 in turkey flocks occurred through early April in Minnesota, followed by a rapid increase in Iowa in late April and throughout May, where large numbers of chicken layer flocks were affected. The last case of HPAI was confirmed in a commercial flock on 16 June 2015. In total, during the 2014–2015 outbreak, there were 211 detections on commercial operations and 21 detections on backyard premises

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[6] https://www.aphis.usda.gov/animal_health/emergency_management/downloads/hpai/2015-hpai-final-report.pdf.

(including those premises designated as a Dangerous Contact Premises). HPAI was detected in commercial premises, backyard flocks, wild captive birds, and/or wild birds in 21 States (Arkansas, California, Iowa, Idaho, Indiana, Kansas, Kentucky, Michigan, Minnesota, Missouri, Montana, North Dakota, Nebraska, New Mexico, Nevada, Oregon, South Dakota, Utah, Washington, Wisconsin, and Wyoming). Approximately 7.4 million turkeys and 43 million egg layers/pullet chickens, as well as a limited number of mixed poultry flocks, were affected by HPAI and died from the disease or were depopulated as part of the response. These birds accounted for about 12 percent of the U.S. table-egg laying population and 8 percent of the estimated inventory of turkeys grown for meat. In response to this historic animal-disease event, many destination markets for U.S. poultry commodities levied trade restrictions on U.S. poultry exports, distorting markets and exacerbating economic losses. Broiler export losses accounted for the overwhelming majority of lost poultry export income. In 2015, broiler exports were $1.1 billion lower than in 2014, a 26-percent decrease; egg export income declined $41 million, a loss of 13 percent; and turkey export income was $177 million lower, a 23-percent decline.[7]

APHIS personnel deployed to the first HPAI cases in December 2014 and continued deploying throughout the response effort. The number of APHIS responders and contractors dedicated to the response continued to increase as the outbreak grew in scale. At the height of response operations, more than 3,400 personnel were deployed: approximately 250 APHIS personnel, 180 State responders, and over 3,000 support contractors. Over the course of the outbreak, there were over 1,200 total deployments by APHIS personnel. Approximately 300 additional employees were deployed or worked at an APHIS headquarters location to support the outbreak as part of the Incident Coordination Group.

While HPAI detections ended in mid-June 2015, many response operations—including virus elimination, environmental sampling, and restocking—continued throughout the fall. On 18 November 2015, the United States sent a final report to the World Organisation for Animal Health (WOAH); at that time, the 2014–2015 outbreak in the United States was considered closed. For the 2014–2015 outbreak, nearly $850 million was obligated for response activities (including personnel support) and indemnity payments. Another $100 million was made available for further preparedness activities. At the time, it was the most expensive animal health incident recorded in U.S. history.

2022 Outbreak Comparison

The primary driver for the spatial extent of spread of the 2022 HPAI event has been migratory wild bird movements. The first poultry detection was in the Mississippi Flyway, which followed earlier detections in wild birds along the Atlantic Flyway. The virus then moved through the migration patterns in and out of Canada through the Atlantic, Central,

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[7] U.S. Department of Agriculture, Foreign Agricultural Service (FAS). 2016. "Global Agricultural Trading System (GATS)."

and Pacific Flyways. In contrast, the 2015 HPAI event, while initially preceded by migratory movements, was more heavily influenced by spread through lateral transmission after introduction to the Midwest, with farm-to-farm spread potentially associated with movement of people, equipment, and materials between farms. Figure 4 shows the overlap in affected States between the 2015 and 2022 outbreaks, while Figure 5 shows the same information at the county scale.

During the 2014–2015 outbreak, the virus was introduced into the Pacific Flyway and moved eastward as far as Indiana; there were no detections in the Atlantic Flyway. During 2022, virus was initially introduced via the Atlantic Flyway, with that virus moving westward across all four flyways all the way to Alaska. Despite this expanded geographic range and reach of the virus in wild birds, at least 85 percent of the premises affected during the 2022 outbreak have been consistent with independent introductions of wild bird-origin virus, and shaping the spatial distribution of cases, as seen at the county level. Although more counties have been impacted in 2022, many of these counties represent a very small number of cases with no further spread. This shift may suggest that improvements in biosecurity on farms and increased messaging around the importance of proactive measures to reduce the spread between locations have had an impact on limiting lateral spread.
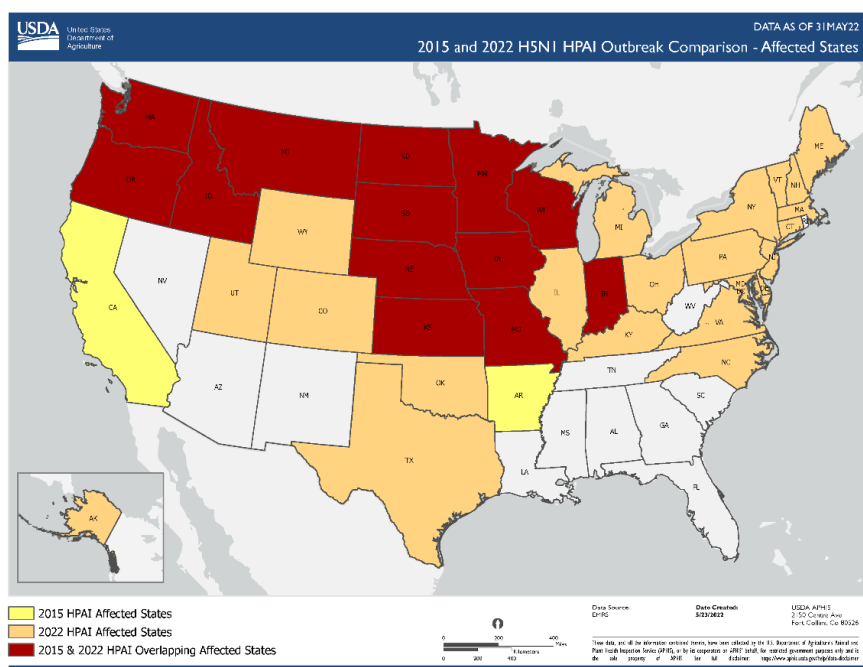
Figure 4. Map Showing a Comparison of States Affected by the 2014–2015 Outbreak of HPAI and Those Affected by the 2022 Outbreak of HPAI as of 31 May 2022.
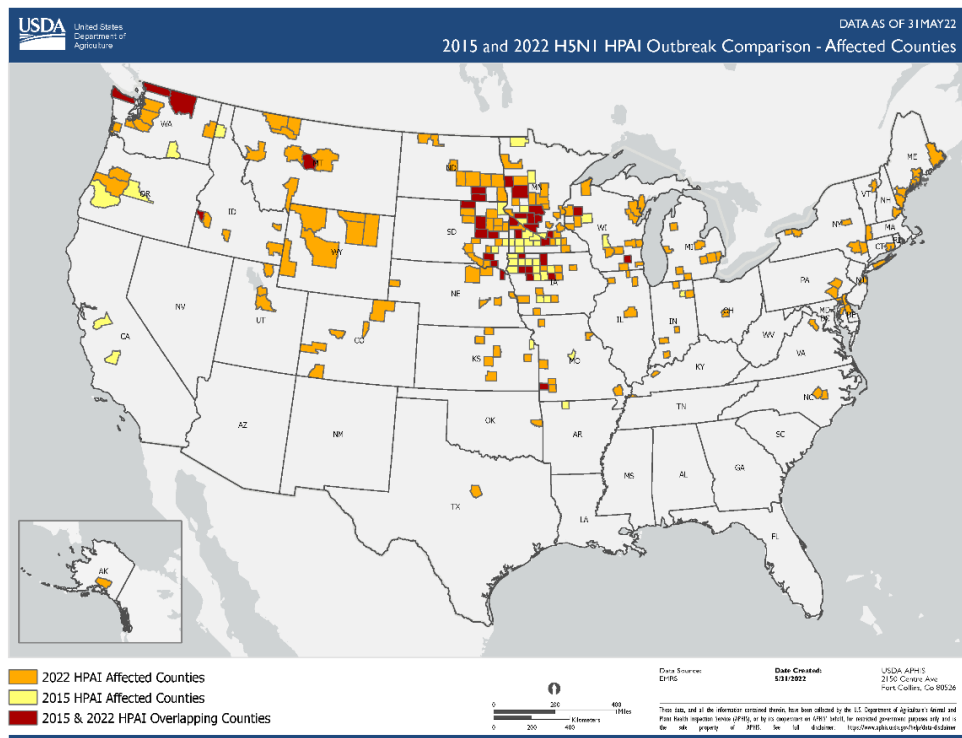
Figure 5. Comparison of Counties With Confirmed Detections of Highly Pathogenic Avian Influenza by Outbreak Year as of 31 May 2022.

The greater geographic extent of this outbreak has had serious impacts on resource requirements for response. APHIS personnel began deploying to the first detection in February 2022 and have continued to deploy through the time of drafting this report. More than 500 USDA-APHIS personnel and contractors have been deployed in support of the response, with an additional 500 State personnel responding.

The distribution of farm types impacted over the course of these outbreaks also differed. In comparison to the 2015 outbreak, which only had 21 backyard flocks impacted in total, the 2022 outbreak has confirmed 172 backyard flocks as of 31 May 2022. This likely reflects the increased prevalence of the virus in wild birds across all flyways and requires appropriate messaging to promote the importance of reporting HPAI in backyard flocks by government and industry partners, increased social media information sharing, and an increased number of backyard birds overall. Additionally, during the 2020 COVID-19 event, the number of people engaged in backyard chickens being reared as a hobby and egg source increased

exponentially.[8] To date, infections of backyard flocks help to alert the presence of virus among wild birds, but as with the outbreak in 2014–2015, there has been no evidence to support backyard flocks as a driver for virus spread to commercial poultry based on epidemiologic and phylogenetic analyses. Figure 6 shows a comparison of the epidemiologic curves and number of birds lost or depopulated due to disease between the two outbreaks. The larger number of cases but smaller number of birds seen during the 2022 outbreak is reflective of the increased detections of HPAI in backyard flocks seen during this outbreak.
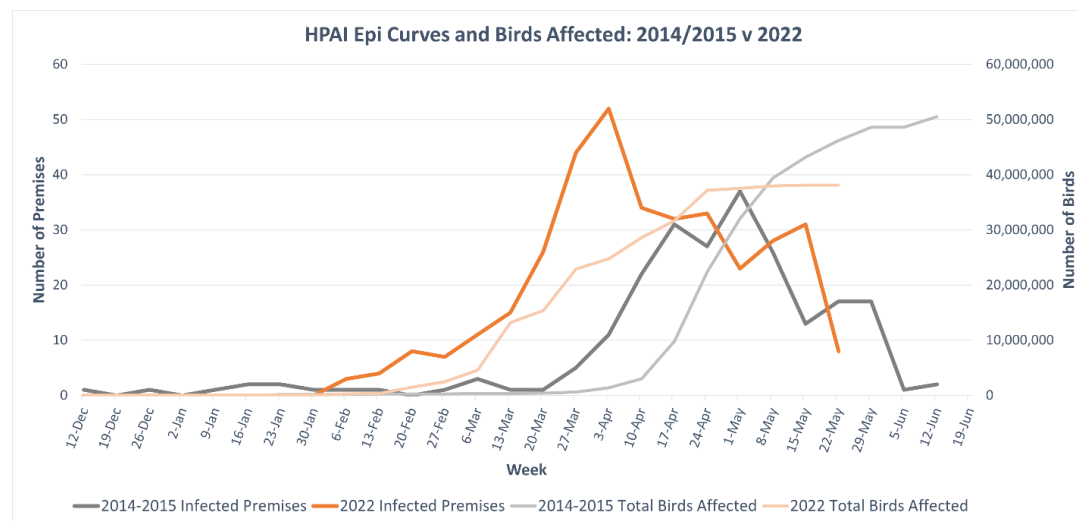
Figure 6. Comparison of Weekly Confirmed Detections of Highly Pathogenic Avian Influenza and Total Birds Affected by Outbreak Year.

As the outbreak continues to evolve, additional comparisons and lessons learned between the two outbreaks are underway. Following the 2014–2015 outbreak, APHIS made numerous changes to response processes to improve efficiency in control activities, indemnity and virus elimination payments, and repopulation processes and timelines. Initial estimates from the 2022 outbreak suggest that significant improvements have been made in all these areas, and more detailed information will be provided in the final report for this outbreak.

Trade impacts associated with the 2022 outbreak have been lower than those experienced during the 2014–2015 outbreak. As of 31 May 2022, the U.S.A. Poultry and Egg Export Council estimates that total losses associated with domestic drops in poultry value (broiler, turkey, egg) and export losses combined are over $800 million USD, significantly lower than the 2014–2015 outbreak losses. Supply impacts associated with the 2022 outbreak have

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[8] [5 ways 2020 changed the backyard chicken industry | The Poultry Site](#)

also been lower.[9] The realized effects of HPAI are the reduced number of layers on hand and the resulting effect on table and processed egg production. In the broiler industry, after cleaning, disinfection, and quarantine, replenishment can be addressed more rapidly than in the egg industry. The egg industry must wait for hatched eggs to reach sexual maturity before egg production begins (approximately 20 weeks); the broiler industry can start a new cycle after incubation (approximately 21 days). In response to increased demand for layers, the number of egg-type hatched eggs set increased early in 2022. In 2015, replenishment was delayed until near the end of the event through setbacks and general uncertainty. The lessons from that event led to a better understanding of replenishment in the face of a disease event and how to maintain business continuity during HPAI. For the 2022 event, the number of hatching eggs increased at the beginning of the event in preparation for restocking of layers. While pullets and layers were both affected, this forethought allowed for replenishment, reallocation of replacement stocks, and increased lay time to help support egg buyers and allied industry partners during the event. Forced molting in June 2022 aimed to ease some of the logistic concerns of the replenishment process. Overall, the response from 2022 applied the recommendations identified during the 2015 outbreak's areas for improvement.

Looking specifically at egg market impacts, the Bureau of Labor Statistics reports average retail prices (Figure 9), and the differences when prices spiked can be compared between the 2015 and 2022 events. Production supply will ultimately affect consumer prices for either table or processed eggs. These prices reflect the shortened supply and distributional challenges faced during HPAI. For the 2015 event, prices did not spike until May. This was related to the movement of eggs in the supply chain, the massive reduction in layer numbers, and from the previous section, the limited number of replacement layers on hand. These prices remained high for much of 2015 before easing into 2016. The impact of HPAI in 2022 had a different timeline and was more geographically dispersed. This helps in replenishment efforts, where a farm can complete the entire response process in a timely manner without being placed in another control area due to additional detections in neighboring farms. The easing in prices from May 2022 to June 2022 may indicate the price changes will not be as long term as those seen in 2014–2015.

This current outbreak is still on-going at the time of this report, and as the situation continues to evolve, comparisons with the 2014–2015 outbreak will evolve as well. To date, while the outbreaks share some similarities in terms of severity, there remain numerous differences in scale and complexity between the outbreaks. These differences suggest that the response costs and total economic impact of the two outbreaks may be influenced by different factors, ultimately yielding two very different outbreaks in terms of impact.

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[9] Economic analysis of supply impacts conducted and summarized by Dr. Jada Thompson, University of Arkansas, August 12, 2022, personal communication; unreferenced.

State Level Retail Egg Prices Grade A Table Eggs
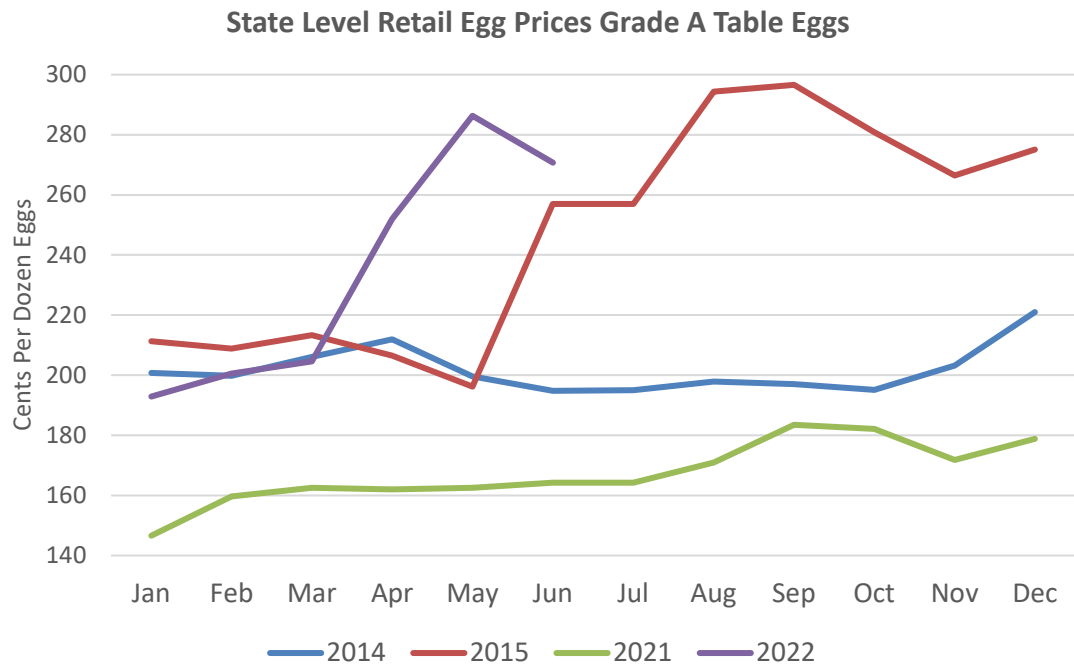
Figure 7. Example of State Level (New York) Egg Prices Delivered to Retailers 2014–2015 and 2021–2022, US BLS/LMIC.

PHYLOGENETIC ANALYSIS AND DIAGNOSTICS

A. Phylogenetic Analyses

The overarching phylogenetic and biologic analysis has been conducted in collaboration with USDA Wildlife Services and the Southeast Poultry Research Laboratory. Phylogenetic analyses up to 31 May 2022 show one major introduction of the Eurasian H5 clade 2.3.4.4b virus into the U.S. that has spread westward all the way to the Pacific Flyway. This H5 2.3.4.4b virus is more infectious for poultry species without the need for poultry adaptation, as compared to the earlier H5 clade 2.3.4.4c virus of 2015, and rapidly causes illness and death in chickens and turkeys, though some waterfowl may be infected and show no clinical signs. Additionally, this lineage has caused significant wild bird mortalities as compared to the 2015 incursion.

As shown in Figure 8, the initial introduction (Group 1) was followed by a second, smaller introduction (Group 2) identified in mid-February among a small number of wild birds and backyard flocks in the Northeastern U.S. (Connecticut, Maine, Massachusetts, New York, and North Carolina); a third introduction into the Pacific Flyway (Group 3) was identified from a wild bird in Alaska collected on 26 April 2022, with no detections in poultry as of 31 May 2022. Reassortment of the H5 clade 2.3.4.4 virus with North American viruses were first identified in February 2022 from wild bird samples, and several genotypes have since been identified; reassortments account for at least 74 percent of wild bird viruses (refer to the section on Avian Influenza Surveillance in Wild Birds for more details) with several genotypes spilling over into poultry. Unique to this outbreak, as compared to 2015, have been several mammalian detections across all four flyways with at least nine species affected. Mammals are typically dead-end hosts for this virus, but if predated or scavenged, could contribute to onward transmission.

Based on analysis of more than 2,700 full genome sequences as of 31 May 2022 and in consideration of available epidemiologic data, at least 84 percent of U.S. detections in poultry premises and non-poultry flocks are consistent with independent introductions of wild bird-origin viruses. Representative poultry and mammal sequences have been uploaded to a public database.[10]

In-depth epidemiologic investigations have been launched where possible to investigate those with potential for common source exposure and/or lateral transmission. The National Veterinary Services Laboratories will continue to sequence all newly detected premises, analyze those results, and report them to appropriate officials.

> **NOTE: The outcomes of phylogenetic analysis should be interpreted in context of all available virus and epidemiologic information and should not be used directly to infer transmission.**

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[10] https://gisaid.org/
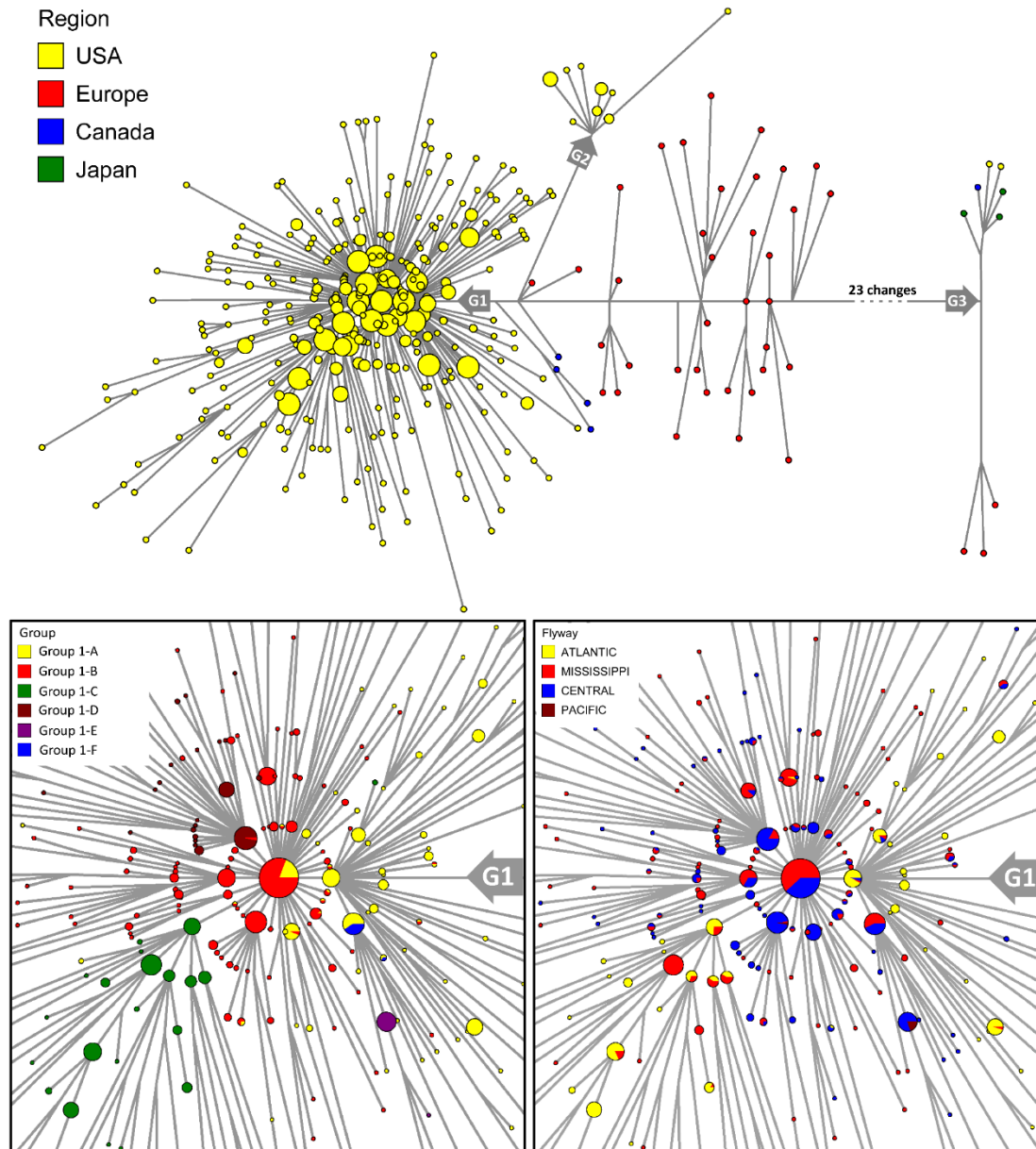
Figure 8. HA/NA Network Analysis of Analysis of Viruses Isolated During the 2022 Outbreak of HPAI.[11] **The initial introduction (G1) was followed by a second introduction (G2) identified in mid-February among a small number of wild birds and four backyard flocks in the Northeastern U.S. A third introduction (G3) into the Pacific Flyway has been found in wild bird mortalities and a wild fox in Alaska starting in April 2022 but has not been detected in poultry to date.**

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[11] Information presented at the United States Animal Health Association (USAHA) October Conference by Dr. Sungsu Youk, USDA ARS Southeast Poultry Research Laboratory; unreferenced.

B.   Public Health Aspects

The NVSL rapidly shares genetic and biological materials in collaboration with the Influenza Division of the Centers for Disease Control and Prevention, USDA-APHIS Wildlife Services, and USDA ARS Southeast Poultry Research Laboratory, as well as other key partners. Whole genome sequence data is used to monitor the virus evolution and assess the risk to veterinary and public health based upon the presence/absence of specific amino acid substitutions or protein motifs.

To date, there has only been one report of clade 2.3.4.4b H5N1 HPAI virus detection in humans in the U.S. and only two globally. The U.S. case was involved with bird depopulation at an affected site in Colorado and tested positive by PCR only on the day of depopulation; all other testing was negative. No human-to-human transmission of this subclade has been identified. CDC will continue to watch this situation closely for signs that the risk to human health has changed. The health of response workers and on-farm personnel was monitored at the State level in cooperation with APHIS and CDC.

C.   Diagnostics and Characterization

Avian influenza subtypes H5 and H7 are reportable worldwide because of their potential for mutation to high pathogenicity during replication in poultry. The presence of basic amino acids at the cleavage site contribute to the mutation from low to high pathogenicity. Mechanisms by which H5/H7 mutate from LPAI to HPAI include the gradual accumulation of basic amino acids (AA), insertion of repeated basic AA, and insertion of non-homologous genetic material (only reported for H7 viruses).

Molecular diagnostic tests for influenza A virus (IAV) are used across the U.S. National Animal Health Laboratory Network (NAHLN). The most sensitive and specific tool for influenza A detection is the Type A-specific rRT-PCR, which targets at least the matrix gene (IAV-M); this is the primary surveillance tool used and provides a semi-quantitative result. The NAHLN tests samples first by the IAV-M test and further by the NAHLN H5 and H7 tests where IAV is detected. Genetic data are also used to confirm that diagnostic assays are fit for purpose. *In silico* analysis confirmed high similarity between the H5N1 virus sequences and the relevant primers and probes used for the IAV and H5 diagnostic rRT-PCR tests.

All poultry samples with a non-negative test result for IAV (serology or PCR) are forwarded to NVSL for confirmatory testing. The NVSL uses Sanger sequencing protocols to generate partial HA/NA gene sequence directly from the sample for subtype and pathotype determination, when sufficient viral RNA is present. Whole genome sequencing is conducted on all isolated viruses, and select viruses are further characterized by pathotype assay in specific pathogen-free chickens.

NVSL confirms the virus HA and NA subtype through molecular sequencing and/or antibody subtyping, and the pathotype (LPAI vs HPAI). Where no virus can be recovered, nor sequence obtained directly from sample(s), the pathotype is determined by the clinical presentation of the flock compared to the USDA-APHIS HPAI case definition.

EPIDEMIOLOGIC STUDY TO INVESTIGATE THE H5N1 VIRUS IN COMMERCIAL AND BACKYARD POULTRY IN THE UNITED STATES

A. Case Series

In collaboration with State Animal Health Officials, USDA-APHIS conducted a case-series study of H5N1 HPAI infected commercial and backyard operations in the United States. A questionnaire was administered to the individual(s) on each farm most familiar with the farm's management and operations. Questions focused on the three-week period prior to detection of HPAI (Appendix A). The purpose of the study was to generate hypotheses for potential risk factors for infection with HPAI based on descriptive information about farm characteristics and management practices.

The outbreak was ongoing at the time of this study. A confirmed infection date of 5 April 2022 was used as a cutoff for inclusion. By that date, there were 146 farms confirmed infected with H5N1 HPAI; 94 (64%) of those provided questionnaires in time to be included in this study. The questionnaires represented farms in 18 of the 24 States that had confirmed infections by 5 April 2022 (Table 3). The largest number of questionnaires were from farms in South Dakota (n=30), followed by Iowa (n=15). Of the responding farms, 16 were backyard poultry operations, and the remaining 76 fell into 9 commercial poultry production types (Table 4). The most common commercial production type was turkey meat bird (n=53), followed by table egg layer (n=9).

Transmission of virus in previous outbreaks of avian influenza in the United States has been attributed to the movement of live and dead birds, transportation of manure, equipment sharing, and contaminated feed trucks, vehicles, water, and people (McQuiston et al., 2005, Halvorson, 2009, Garber et al., 2016). Results of the questionnaire, focusing on risk factors identified in previous outbreaks, are summarized below and in Table 5.

- Movements of bird and bird products – 18 farms moved birds off site in the three weeks prior to detection and 21 farms introduced new birds. 17 farms moved eggs off site and 2 received eggs in the three weeks prior to detection.
- Dead-bird disposal method – Only 12 farms (13%) reported using rendering as a dead-bird disposal method. Most farms (59%) reported using composting. Of the farms that use rendering, 11 were commercial turkey meat bird operations and 1 was a table egg layer operation. Six of the farms that reported using rendering were located in North Carolina, four were in South Dakota, one was in Minnesota, and one was in Iowa.
- Employees – 20 farms reported that employees visited other premises with poultry in the three weeks prior to detection and 21 farms reported having employees in a community living situation where they interact with employees from other poultry premises. Fourteen farms reported having occasional workers on the farm during the three weeks prior to detection.
- Visitors – 77 (82%) of the farms reported having visitors in the three weeks prior to detection. The most common categories of visitor were feed trucks (n=53), company service people

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       (n=29), crews (e.g., load-out crews or catch crews; n=24), garbage collectors (n=17), occasional workers (n=14), and private veterinarians (n=14).

- Shared equipment – Only 18 (19%) farms reported sharing equipment with other farms. The most common category of shared equipment was manure/litter handling equipment (n=7).
- Manure movement – Only eight premises reported moving manure off site and two farms reported receiving manure from another site in the three weeks prior to detection.

Results showed that some factors and management practices were shared across infected farms; however, the significance of these similarities is difficult to interpret given the study design and the lack of a non-infected farm group to use for comparison. When considered in conjunction with knowledge of practices and risk factors from previous outbreaks, this information may provide insights into trends of management practices over time and reveal opportunities to implement additional mitigations in the future.

Table 3. Numbers of Commercial and Backyard Farms Infected With H5N1 HPAI That Submitted Questionnaires for This Study by State Where the Farm is Located.

State	Total Number of Farms	Number of Commercial Farms	Number of Backyard Farms
Delaware	3	3	0
Illinois	1	0	1
Indiana	6	6	0
Iowa	15	14	1
Kentucky	2	2	0
Maine	5	0	5
Maryland	4	4	0
Michigan	1	0	1
Minnesota	3	3	0
Missouri	8	5	3
Nebraska	1	1	0
New York	3	0	3
North Carolina	6	6	0
North Dakota	3	2	1
South Dakota	30	30	0
Texas	1	1	0
Virginia	1	0	1
Wisconsin	1	1	0

Table 4. Production Types of H5N1 Infected Farms That Submitted Questionnaires for This Study.

Production Type	Number of Farms
Backyard	16
Broiler production	5
Table egg breeder	1
Table egg layer	9
Table egg pullets	3
Turkey breeder hens	3
Turkey breeder replacement hens	2
Turkey meat bird	53
Turkey poult supplier	1
Upland game bird	1
Total	94

Table 5. Characteristics of H5N1 HPAI Infected Farms in the 21 Days Prior to Detection.

Characteristic	Level or Response	Number/Responses
Movements of birds and bird products		
Birds introduced	Yes	21/88
Birds moved off site	Yes	18/88
Eggs moved on site last 21 days	Yes	2/87
Eggs moved off site	Yes	17/86
Dead bird disposal method	Compost	53/89
	Burial	11/89
	Incineration	11/89
	Rendering	12/89
	Landfill	3/86
	Disposal offsite	16/89
Manure		
Moved offsite	Yes	8/87
Moved onsite	Yes	3/86
Employees		
Visited other premises with poultry	Yes	20/88

Shared living situation with employees from other poultry premises	Yes	21/86
Visitors		
Crews (e.g., catch-crew, load out)	Yes	24/88
Federal/State animal health official	Yes	9/87
University extension	Yes	1/87
Private veterinarian	Yes	14/87
Company service person	Yes	29/86
Nutritionist/feed company consultant	Yes	10/87
Inspector/auditor	Yes	6/87
Feed delivery	Yes	53/88
Egg truck	Yes	9/87
Litter/bedding delivery	Yes	6/87
Litter/bedding removal	Yes	5/87
Renderer/dead bird pickup	Yes	9/87
Pest control	Yes	6/87
Manure truck	Yes	5/87
Garbage collection	Yes	17/87
Occasional worker	Yes	14/87
Wholesaler/buyer	Yes	1/87
Customer/private consumer	Yes	4/87
Other	Yes	19/87
Equipment shared with another premises		
ATV/4-wheeler	Yes	0/88
Tractor	Yes	4/88
Gates Panels	Yes	3/88
Skid steer loader	Yes	4/84
Egg flats	Yes	0/88
Egg racks	Yes	2/89
Pallets	Yes	1/89
Dead bird containers	Yes	0/87

Manure/litter handling equipment	Yes	7/88
Pressure sprayer/washer/foamer	Yes	1/88
Other cleaning equipment	Yes	1/88
Vaccination equipment	Yes	0/88
Bird Catching equipment	Yes	1/88
Live haul loader	Yes	5/88
Other	Yes	7/89

ESTIMATING DISEASE SPREAD WITH THE NATIONAL HPAI DISEASE-SPREAD MODEL

A.   Highly Pathogenic Avian Influenza (HPAI) National Model Overview

A series of epidemiologic scenarios were developed in InterSpread Plus® v. 6.01.44 (Stevenson et al., 2013) to model the introduction and spread of H5N1 HPAI from confirmed premises throughout the United States following the first detection. Chicken, turkey, and specialty bird (duck, geese, guinea fowl, and pheasant) flocks residing in commercial and backyard (less than 1,000 birds) farm units, hatcheries, and live bird markets were incorporated into the National HPAI Disease-Spread Model. The Model initiates disease spread and implements integrated control activities (Figure 9) across 28 operation types to generate a series of outcomes that characterize the severity (number of infected, detected, and depopulated premises; estimated number of depopulated birds), duration, and geographic spread of simulated HPAI outbreaks.

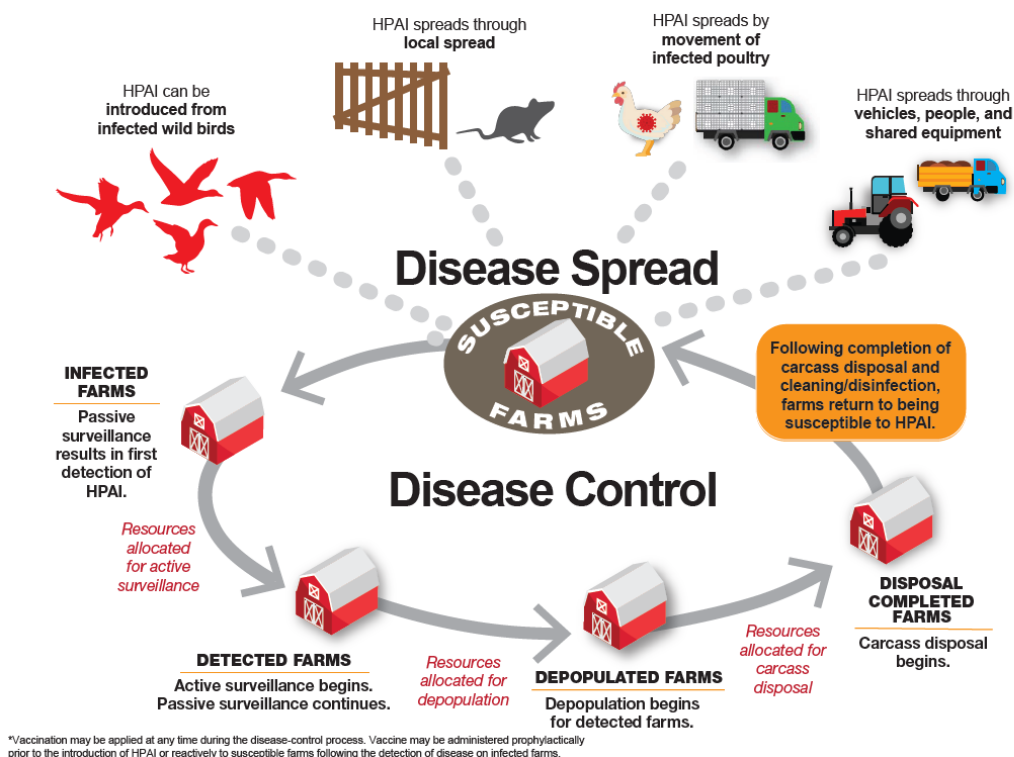**Figure 9. Highly Pathogenic Avian Influenza National Model Overview. [12]**

The Farm Location and Animal Population Simulator (Burdett et al., 2015) was used to generate likely farm locations based on geospatial characteristics with backyard farm locations adapted from

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[12] Note that restocking of farms is not explicitly included in the model, although this is a critical timestep in the actual response.

current and historic outbreak-related data. Model parameters were developed to reflect the impact of disease spread from wild migratory birds, variable levels of lateral spread, seasonal estimates of disease transmission, and alternative disease-response strategies.

B.   Applications for the HPAI National Model

Applications for the HPAI National Model for this outbreak included:

- Providing estimates of outbreak size for respective production classes to inform budget estimates for outbreak response costs;
- Assessing the impact of alternative levels of lateral spread, relative species susceptibilities, and seasonal and geographic influences on outbreak size and duration;
- Evaluating the effect of alternative levels of biosecurity and disease reporting;
- Comparing the modeled effectiveness of alternative active surveillance strategies;
- Identifying geographic areas of highest risk for future infection;
- Forecasting county-level disease introductions and spread for State-based disease response teams; and
- Estimating the contribution of additional placements of backyard birds to disease introductions onto backyard poultry farms.

C.   Configurations for the National HPAI Disease-Spread Model

To complete the listed modeling applications, several configurations of simulated HPAI outbreaks were developed to incorporate observed and evolving spread conditions and forecast outbreak size, duration, and geographic spread. Initially, parameters derived during previous HPAI outbreaks were used to generate preliminary outcomes. As the outbreak progressed, parameters specific to this outbreak, such as the potential for disease spread from wild birds, specific species susceptibilities, directionality of geographic spread, and alternative estimates for between-premises lateral spread, were added to subsequent disease-spread scenarios.

Disease-spread scenarios developed after the earliest detections in domestic poultry in the Atlantic and Mississippi Flyways suggested only a small likelihood of lateral spread between premises using baseline levels for seasonal influences on disease spread and baseline biosecurity. At this time, parameters describing disease introductions from exposure to wild birds and specific species susceptibilities were not included in the modeled scenarios.

After the potential impact of wild bird introductions was better understood, additional 100-iteration scenarios were developed to simulate the spread and control of HPAI. Expanding on configurations from the previous HPAI scenarios, these simulations integrated variable levels of disease introduction from exposure to wild birds, lateral spread from infectious premises to susceptible premises, and seasonal viral persistence (Table 6).

Table 6. Variable Parameters Used in Preliminary Modeling Configurations.

Potential for Wild Bird Introductions	Potential for Lateral Spread	Seasonal Viral Persistence
Static – High	Moderate	Moderate
Static – High	Moderate	Low
Static – High	Low	Moderate
Static – High	Low	Low
Progressive – High to Low	Moderate	Moderate
Progressive – High to Low	Low	Low

Outcomes from these modeled scenarios projected that greater numbers of commercial premises would be infected than backyard premises; turkey premises would be infected at higher rates than chicken premises; greater viral persistence led to longer outbreaks; and increased levels of lateral spread resulted in the largest simulated outbreaks. Additionally, four specific geographic regions experienced the greatest likelihood of future infections during the simulated outbreaks: central Minnesota, central North Carolina, Southeast Pennsylvania, and Northwest Arkansas/Southwest Missouri (Figure 10). In the period since these scenarios were completed, outbreaks among commercial premises were detected in areas forecasted by modeling in Minnesota, North Carolina, and Pennsylvania.
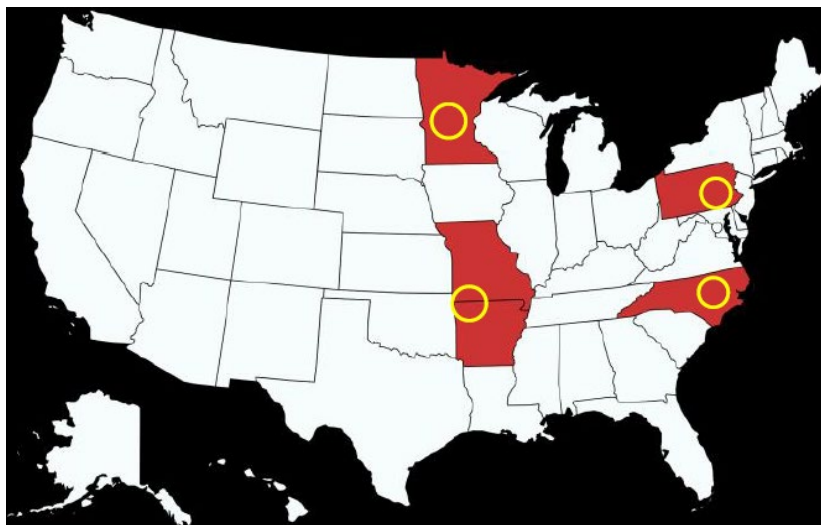
Figure 10. Geographic Areas With Greatest Potential for Disease Introductions in Preliminary Modeling Outcomes.

A subsequent series of 100-iteration disease-spread scenarios incorporated additional parameters to simulate the evolving outbreak. Differing from previous HPAI scenarios, these simulations

integrated wild bird H5N1 introductions, alternative probabilities for lateral spread, estimated seasonal viral persistence, and estimated relative species' susceptibilities to the H5N1 virus (Table 7). Compatible with previous disease-spread scenarios, the largest outbreaks tended to be associated with extended periods of lateral spread. Lowering the relative susceptibility for chicken and farm-raised specialty birds generated species-specific infection rates approximating the infection rates observed in the actual outbreak. Considering that very low to low levels of lateral spread had been estimated at this point in the outbreak, two scenarios with outcomes (highlighted in yellow) represented the best projection at that time for the potential severity of the outbreak. Outcomes associated with the number of infected premises, distribution of infected premises between commercial and backyard premises, and the estimated number of depopulated birds informed project cost estimates for outbreak response.

Table 7. Enhanced Parameters and Outcomes in Mid-Outbreak Modeling Configurations.

Potential for Wild Bird Introductions	Potential for Lateral Spread	Seasonal Viral Persistence	Relative Avian Class Susceptibility to H5N1v	Number of Infected Premises	Birds Depopulated (millions)
Static – High	Low	Moderate	Chicken – high Specialty – moderate Turkey – very high	238 – 367	40 – 49
Static – High	Low	Moderate	Chicken – high to very high Specialty – moderate Turkey – very high	250 – 394	41 – 47
Static – High	Moderate	Moderate	Chicken – high Specialty – moderate Turkey – very high	300 – 674	43 – 69
Static – High	Moderate	Moderate	Chicken – high to very high Specialty – moderate Turkey – very high	406 – 1,089	41 – 76

In addition to offering national-level projections, disease-spread modeling was used to forecast the progression of H5N1 HPAI within high-risk States. After seeding the model with county-level approximations of known detections, simulated outbreaks introduced disease from exposure to infectious wild birds and lateral spread between infectious and susceptible premises. The scenario was configured to generate low levels of lateral spread, a low to moderate seasonal influence on disease spread, and a progressive geographic/seasonal-based reduction in exposure to migratory birds. Focusing on simulated spread occurring after the end of the known disease-history period, these new infections defined the future extent of spread within counties in Minnesota and contributed to total disease spread within Minnesota.

At the time of scenario development, modeled outcomes identified central Minnesota as the area with the greatest likelihood of future infections, especially premises in Kandiyohi, Morrison, Otter Tail, Stearns, and Todd Counties (Figure 11). Deriving outcomes from 100 simulated outbreaks, the total number of infected premises in Minnesota ranged from a minimum projection of 68 to a maximum of 116. Currently, 80 premises have been detected in Minnesota during the 2022 H5N1 HPAI outbreak.
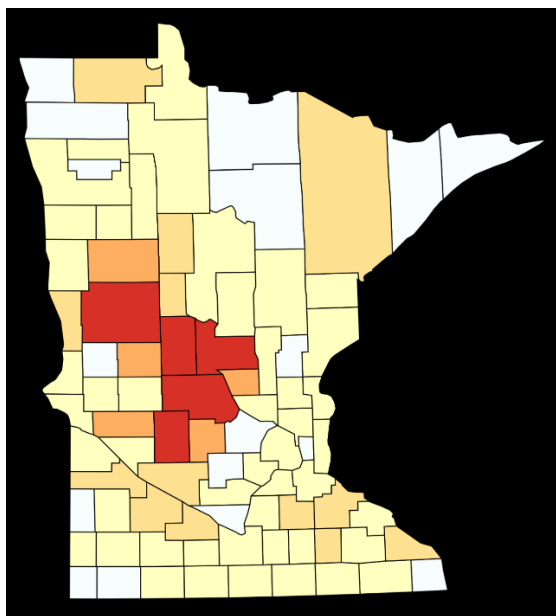
> Red to orange to yellow to white shading describes counties with the highest to lowest number of infected premises following the known disease-history period over 100 simulated outbreaks.

Figure 11. Geographic Projection of Areas with Highest Likelihood of Infected Premises in Minnesota Based on Modeling Results.

During the first three months of the outbreak in Minnesota and other States, disease was detected predominantly in commercial operations. Similarly, commercial operations represented 60 to 70 percent of infected premises in simulated outbreaks. More recently, larger numbers of backyard operations have been detected with H5N1 HPAI. Consequently, disease-spread scenarios developed in the last month have been enhanced to reflect the observed change in detections.

To generate plausible revisions to existing parameters, an assumption that seasonal bird placements on backyard premises in northern latitudes contributed to increased exposure to wild migratory birds guided scenario development. Two new scenarios were developed in mid-May 2022: one depicting a small increase in exposure/susceptibility for backyard operations to represent a minimal expansion in seasonal bird placements, and one with a larger increase in exposure/susceptibility for backyard operations to represent a moderate expansion of seasonal bird placements.

The scope of additional assumptions affecting disease introduction and spread for these scenarios included:

- Low levels of lateral spread from movements of infected domestic birds; contaminated equipment, people, or vehicles; or local spread from nearby infected premises;
- Greater numbers of migratory wild birds in northern latitudes than in southern latitudes as birds progressively migrate from the United States to Canada;
- Consistent northwesterly movement of migratory wild birds throughout each iteration;
- Species-specific relative susceptibilities to the H5N1 virus (turkeys higher than chickens and specialty birds);
- Low to moderate seasonal impact on probabilities of disease transmission; and
- Higher rates of infections/detections in backyard operations than in commercial operations.

As could be expected, the assumption of placement of additional backyard bird flocks in northern latitudes of the conterminous United States resulted in greater levels of exposure, susceptibility, and subsequent disease transmission between wild or migratory birds and backyard flocks in simulated outbreaks. Compatible with the frequency of recent detections on backyard and commercial premises in the 2022 H5N1 HPAI outbreak, greater than 80 percent of new infections in modeled scenarios occurred in backyard premises. For these scenarios, as shown in Table 8, values for the median and maximum number of detected premises and outbreak duration are related to the magnitude of additional backyard bird placements. Commercial premises are still becoming infected in simulated outbreaks, albeit at a much lower rate than backyard operations. The potential for oversummering of the outbreak was observed in a small percentage of iterations and was associated with prolonged periods of disease introductions onto backyard premises.

Table 8. Modeling Outcomes Assuming Alternative Levels of Backyard Bird Placements.

Scenario Description	Number of Detected Premises [median]	Number of Detected Premises [maximum]	Outbreak Duration* (days) [median] [June 1 = day 113]	Outbreak Duration (days) [maximum] [June 1 = day 113]
Small increase in backyard bird placements	360	399	141	184
Moderate increase in backyard bird placements	378	438	154	213

*Outbreak duration is defined as the number of days from first detection to last detection for each iteration. Post-outbreak surveillance to regain disease-free status is not included in these values.

In terms of the spatial distribution of future infections, the majority of disease introductions in simulated outbreaks occurred in States near the northern border of the United States. For outbreaks

assuming a small increase in backyard bird placements, Idaho, Minnesota, and Pennsylvania experienced the greatest number of new infections (Figure 12). As bird placements increased, New York, Oregon, Washington, and Wisconsin were added to the group of States with the highest likelihood of future infections (Figure 13).
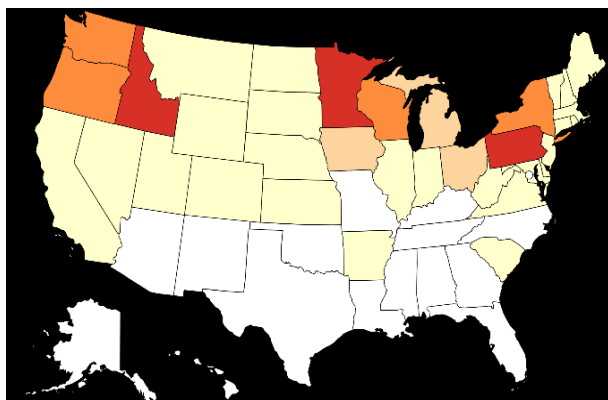
> Red to orange to yellow to white shading describes States with the highest to lowest number of future infections.

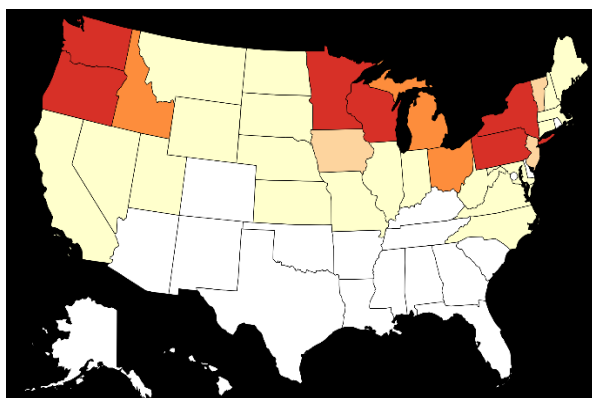**Figure 12. Potential Geographic Spread of HPAI Associated With a Small Increase in Backyard Bird Placements.**

Figure 13. Potential Geographic Spread of HPAI Associated With a Moderate Increase in Backyard Bird Placements.

D.   Limitations on Estimating Disease Spread

Any single disease-spread scenario offers only a snapshot view of an evolving outbreak. Although useful in estimating severity, duration, and geographic spread of an ongoing disease event and for comparing the effectiveness of alternative control strategies, modeling outcomes are sensitive to any biological, physical, or environmental change that impacts biosecurity, disease reporting, infectivity, environmental persistence, or other factors affecting disease transmission. Consequently, developing a series of scenarios throughout the outbreak and integrating data

generated from field and lab settings with scenario-specific assumptions evaluating alternative spread possibilities offers the greatest benefit to response planning.

ESTIMATING THE TIME OF H5N1 HPAI INTRODUCTION INTO COMMERCIAL POULTRY FLOCKS USING DIAGNOSTIC TEST RESULTS AND PRODUCTION DATA

A. Summary

Determining the time of HPAI virus introduction in a flock is an important part of outbreak investigations. By narrowing the time window of possible virus introduction, we can better identify the potential transmission routes and enhance our understanding of the pattern of disease spread. In this analysis, diagnostic testing, daily mortality, and water consumption data (where applicable) were used to estimate the time of introduction for 26 commercial poultry premises of interest. Premises included 13 commercial meat turkey flocks, 3 broiler chicken flocks, 7 table egg layer flocks, 1 table egg layer pullet flock, and 1 broiler breeder flock. Detailed modeling methodology can be found in Appendix B.

B. Results

The analyzed premises were grouped into geographic clusters and results are presented by a cluster-specific, relative timeline (i.e., Day 1 for each cluster is a different calendar date than Day 1 for the other clusters, Figure 14). For each premises analyzed, a most likely day of introduction was estimated, as well as a 95 percent confidence interval, which represents a window of virus introduction for each premises. The day of presumptive diagnosis is also noted in Figure 14 to provide an indication of the period of likely infectiousness for each premises. The source of introduction, also indicated in Figure 14, is based on phylogenetic analysis (see Phylogenetic Analysis and Diagnostics) that is supportive of either independent wild bird introduction or common source/lateral spread. Phylogenetic evidence is valuable in identifying and supporting potential sources of introduction but cannot be considered definitive proof and must be evaluated in conjunction with available epidemiological data. Among the premises included in this analysis, the phylogenetic data supported independent, wild-bird introductions on 15 premises and common source of infection or lateral spread on 11 premises.

Each geographic cluster presents a unique pattern that in combination with phylogenetic evidence, can be suggestive of the timing and routes of introduction that can help narrow the focus of epidemiologic investigations.

Cluster A is comprised of four premises. The phylogenetic evidence supported three independent wild bird introductions and one common source or lateral spread introduction (premises A4). The window of introduction for A4 overlapped with periods of likely infectiousness for Premises A2 and A3. Also of note is that A2 was detected a day later than A3, but A2's most likely day of introduction is earlier than A3's, highlighting that the timing of detection may not always line up perfectly with the timing of infection.

Cluster B is comprised of six premises. The phylogenetic evidence supported only one independent wild bird introduction and five common source or lateral spread introductions. The suggestive wild bird introduction (premises B1) was the first premises detected in the cluster and its period of

infectiousness overlapped with only B2; however, B2 had a very long period of infectiousness which overlapped with the other four premises. B2 was also detected three days later than B3 but was estimated to have been infected much earlier than B3. This pattern suggested that a closer look at the timing of potential contacts between B2 and the other premises would be valuable, and this information was relayed to the local response.

Cluster C includes only two premises, one with potential wild bird introduction and the other with a common source or lateral spread introduction. The windows of introduction for the two premises have tight overlap. Potential contacts between the two premises that occurred on days 3-8 were prioritized for epidemiologic investigation.

Cluster D is comprised of eight premises. The phylogenetic data supported independent wild bird introductions on five premises and common source or lateral spread on three premises. Interestingly, the windows of introduction for the three common source introduction premises occurred on or after the days of presumptive diagnosis for the five independent wild bird introductions, suggesting the possibility that another premises, not included in this analysis, may have served as an intermediary in the transmission chain.

Cluster E is comprised of six premises. The phylogenetic evidence suggests that the earliest infection was via an independent wild bird introduction, while the other five were common source or lateral spread introductions. The windows of introduction for the four earliest infections all closely overlap, while the two premises with later windows of infection (premises E5 & E6) overlap with the periods of infectivity for E2 and E4. Similar to premises A2 and A3, E2 had a later presumptive positive day than E3, but was estimated to have an earlier most likely introduction day. Assuming the order of infection matches the order of detection may lead to misinterpretation of contact tracing information. The infectious periods overlap for several premises in this cluster. The timing of contacts before and after the detection of these premises should be evaluated to identify potential epidemiological links and directionality of disease spread.
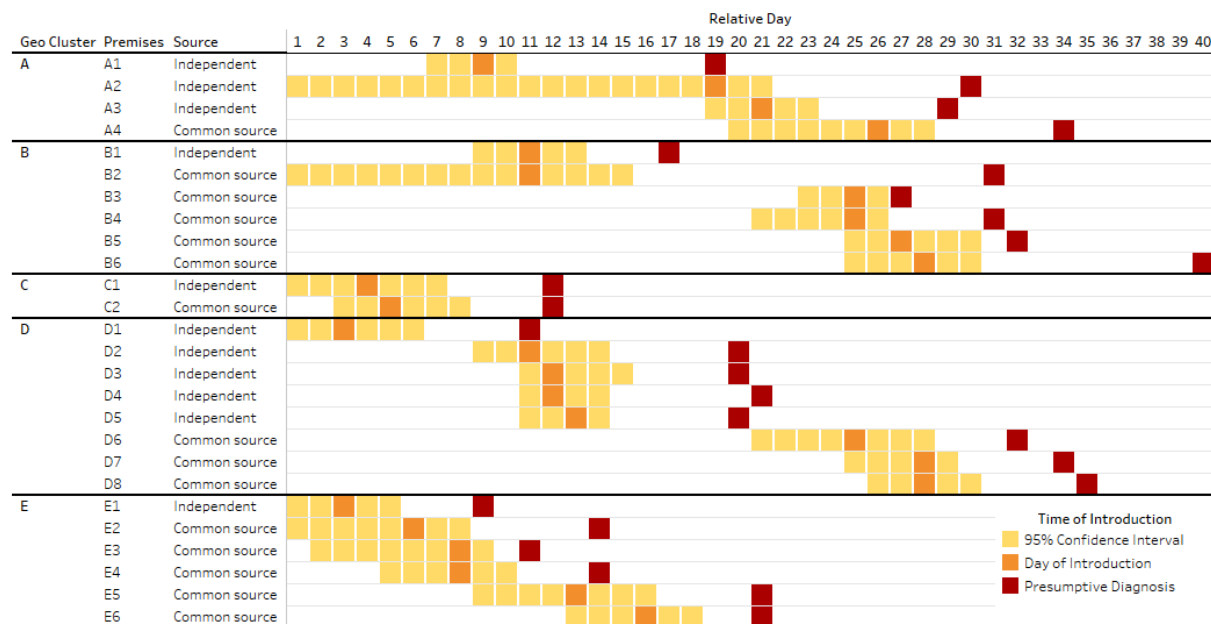
Figure 14. Relative Timeline for Time of Introduction Analysis by Geographic Cluster, Premises, and Likely Source of Introduction.

For this analysis, we defined time to first positive sample (TFPS) as the estimated time interval between flock exposure to when the first rRT-PCR positive samples were collected. We observed differences among the production types in TFPS (Figure 15). Table egg layers or pullet premises had the shortest TFPS with a range of two to six days. Broiler production premises had the longest TFPS with a range of 8 to 17 days. Turkey meat bird premises were in between with a range of 6 to 11 days.

A potential explanation for the shorter time to first positive sample for table egg layers may be due to most of the table egg layer premises included in the analysis (seven out of eight) being under active surveillance as part of Control Area or Surveillance Zone protocols. When grouped by reason for testing, the estimated mean TFPS was 6.4 days for premises under ongoing surveillance testing; e.g., testing within a Surveillance Zone or Control Area or for movement permits, and 9.1 days when testing was requested based on observing HPAI clinical signs in the flock. When grouped by the likely source of introduction, the estimated median TFPS was seven days for common source or lateral spread introductions and eight days for independent or wild bird source introductions. However, TFPS for common source introductions is likely skewed due to broiler premises having delayed detections. Within table egg layer and turkey premises, TFPS was shorter for common source introductions than for independent introductions.
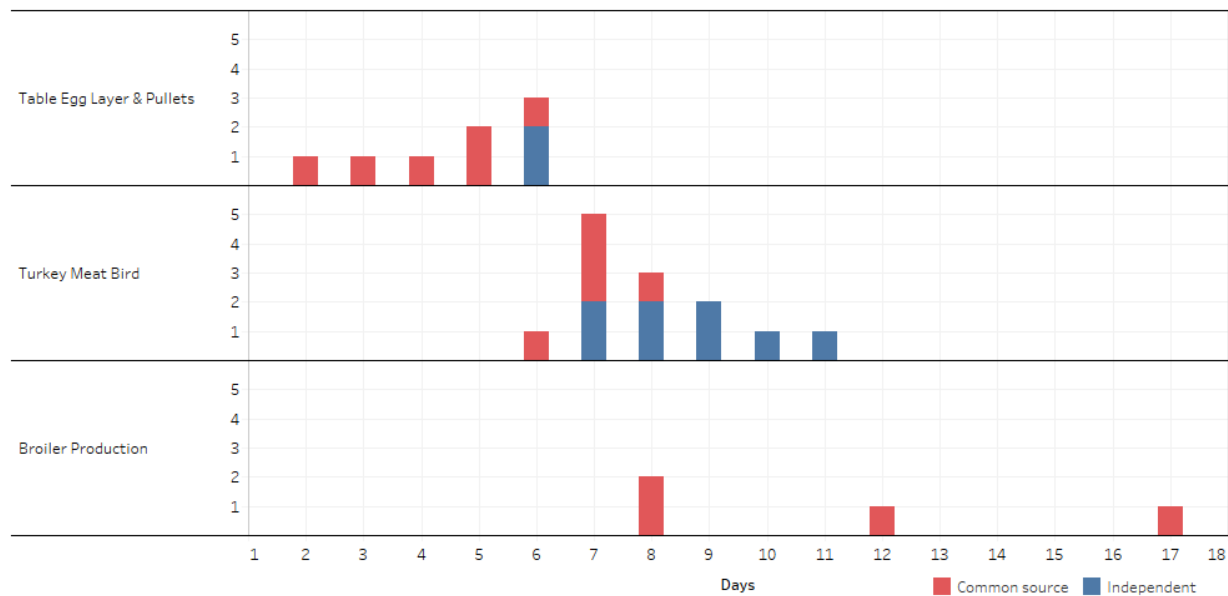
Figure 15. Time from Estimated HPAI Introduction to Detection by Production Type and Likely Source of Introduction.

The estimated adequate contact rate, or transmission parameter, is the number of contacts per day a bird has with other birds that would be sufficient to result in infection; it is the parameter that determines the rate of virus spread within the flock. The mean of the most likely value for the adequate contact rate from all premises was 3.8 contacts per day (range 0.5–9, Figure 16). Turkey and table egg layer/pullet premises had similar mean contact rates, while the mean contact rate for broiler production premises was lowest. For turkey premises, the mean contact rate was 4.2 (range 0.5–9) contacts per day. For table egg layer and pullet premises, the mean was also 4.2 (range 1.1–8.6) contacts per day. The mean contact rate in broiler production premises was 1.7 (range 0.6–2.7) contacts per day. The reason for the difference between broiler production premises and the other production types is unknown but may be a combination of factors related to species, housing, and other management practices. For example, turkey meat bird and broiler production premises are both floor-raised production types, where birds can interact with any other bird in the house; however, past studies have shown turkeys to be more susceptible to avian influenza viruses than chickens, which may result in a higher rate of spread in turkey houses (Pillai et al., 2010). The difference between broilers and table egg layers may be related to differences in housing type, ventilation, foot traffic, or other production practices that could increase the rate of spread in table egg layer houses compared to broilers. When grouped by the source of introduction, the estimated mean contact rate was 2.4 for common source or lateral spread introductions and 4.4 for independent wild bird introductions.
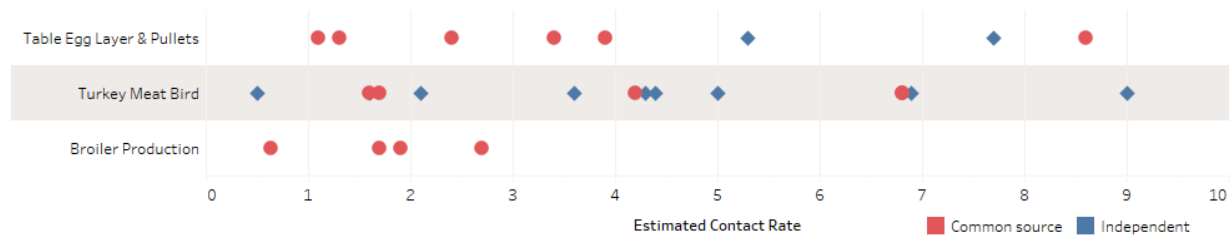
Figure 16. Contact Rate by Production Type and Likely Source of Introduction, Estimated by Time of Introduction Analysis.

The following is a similar breakdown by production type for the estimated basic reproduction number (R0), the number of secondary infections that result when one infectious individual is introduced into a completely susceptible population (R0, Figure 17). The overall mean R0 value was 13.3 (range 2–47). For turkeys, the mean R0 was 18.1 (range 3–47). For table egg layer and pullet premises, the mean R0 was 8.7 (range 2–22). For broilers, the mean R0 was 5.6 (range 2.4–-8). The basic reproduction number is a function of the rate of transmission and the duration of infectiousness; therefore, the difference in R0 between turkeys and table egg layers that wasn't observed in their contact rates is due to differences in the duration of infectiousness. As mentioned previously in relation to TFPS, the difference in duration of infectiousness may be related to faster detection in table egg layers than turkeys because of a greater intensity of active surveillance and/or premovement testing applied to the table egg layers in this analysis. Grouped by source of introduction, the median basic reproduction number was 6 for common source introductions and 18 for independent introductions, which may be indicative of a larger viral load initially introduced via independent wild bird introductions compared to common source or lateral spread introductions.
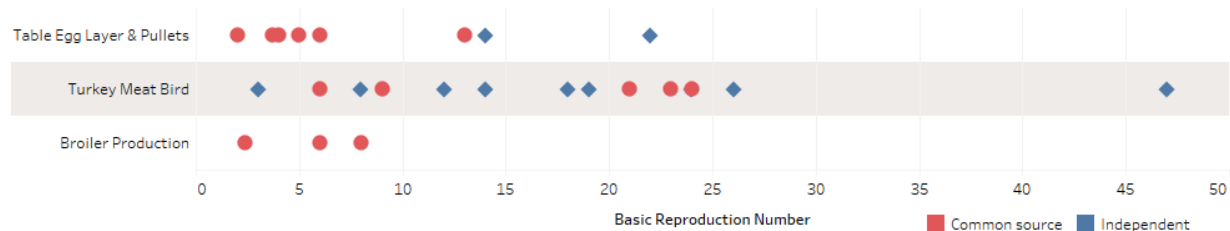
Figure 17. Basic Reproduction Number (R0) by Production Type and Likely Source of Introduction, Estimated by Time of Introduction Analysis.

C.   Discussion

Estimating the time of HPAI virus introduction provides a valuable piece of information for epidemiologic investigations and outbreak response. In this analysis, we estimated the time window for HPAI introduction and transmission model parameters for 26 infected barns using diagnostic test results and production data. The analysis was used to narrow the time window of possible virus introduction to help identify routes of transmission.

We observed that broiler production premises had lower estimated mean contact rates and R0 than turkey meat bird and table egg layer/pullet production types. Turkey meat bird premises and table egg layer/pullet premises had similar adequate contact rates, but turkey meat bird premises had a higher mean estimated R0 than table egg layer/pullet premises, indicating a longer duration of infectiousness in turkey production types. We also observed that premises where the phylogenetic evidence supported independent wild bird introductions tended to have higher contact rates and R0, suggesting that a larger initial viral load may have been introduced via that route compared to common source or lateral spread.

This work is dependent on information on the progression of disease mortality and clinical signs from production records and regular laboratory diagnostic testing. Access to different categories of detailed, high quality production data such as daily mortality, egg production, and water consumption helps to provide more robust estimates of the time of introduction (TOI) and reduce the uncertainty. For example, the estimated TOI 95 percent confidence interval was narrower where both daily mortality and water consumption data were incorporated into the analysis. Conversely, the estimated intervals for time of introduction were wider for premises without elevated mortality and with fewer days of diagnostic testing. This work also highlights the value of closely monitoring mortality, water consumption, and egg production to quickly identify disease issues in the flock. These factors may vary across flocks and between barns, so understanding the trends within each production setting is important.

AVIAN INFLUENZA SURVEILLANCE IN WILD BIRDS

Waterfowl are natural reservoir hosts for influenza A viruses (IAV; subtypes H1-H16), but not usually highly pathogenic avian influenza (HPAI). Influenza A viruses in wild birds tend to circulate seasonally within migratory flyways, and subtype prevalence can wax/wane in multiyear cycles. Areas where birds from different flyways congregate provide opportunities for viruses to mix across flyways.

Waterfowl migration in North America generally consists of north-south seasonal movements between breeding grounds and wintering areas. There are four major flyways in North America (Figure 18). These flyways are broadly defined corridors where the migratory paths of many species of interest tend to converge and are associated with major topographical features in North America, which also tend to be aligned along a north-south axis. The four North American flyways have areas of overlap and convergence, particularly at the north and south ends. Flyway boundaries are defined administratively and are not biologically fixed or sharply defined.
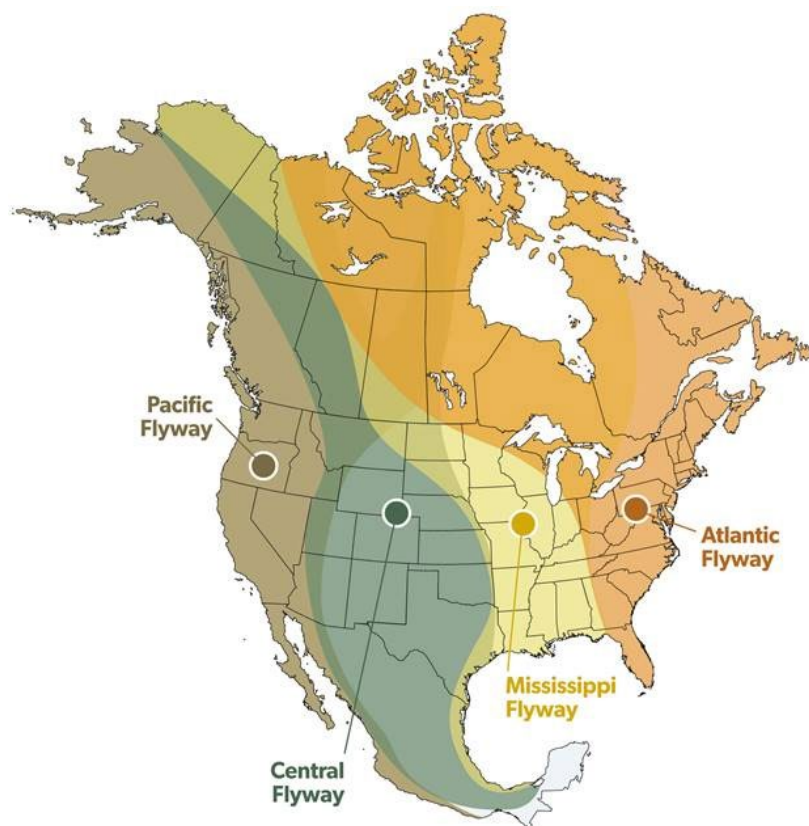

Figure 18. Map Depicting the Four Primary North American Waterfowl Flyways.[13]

North American flyways represent the predominant pathways of migratory bird movements within broad geographic areas. Many migratory bird species use specific flyways during spring and fall;

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[13] North American Flyways 2016, https://www.multivu.com/players/English/7804651-ducks-unlimited-migration/

however, many species migrate across flyways. The first detection of Eurasian strain (EA) H5N1 HPAI in North America occurred in a great black-backed gull in December 2021in Newfoundland and Labrador, Canada. The bird was showing neurologic signs and was part of a large mortality event. The first subsequent detection of H5N1 HPAI in the United States occurred in a dabbling duck in January 2022 in South Carolina. The bird was exhibiting no neurologic signs and was an apparently healthy bird collected during hunter harvest.

The U.S. National Surveillance Plan for Highly Pathogenic Avian Influenza in Wild Birds was developed to maximize our ability to detect IAV in wild waterfowl. Surveillance helps to: 1) understand how IAV is distributed in the United States, 2) detect the spread of IAV to new areas of concern, 3) monitor wild dabbling duck populations for introductions of novel viruses, and 4) estimate the apparent prevalence of IAVs of concern (e.g., Eurasian lineage H5 and H7). The surveillance plan targets areas with extensive mixing of wild bird populations and a history of IAV detection.

Between 1 June 2021 and 1 June 2022, over 22,000 wild waterfowl were sampled and tested by rRT-PCR for IAV. Table 9 and Table 10 break down sampling strategy by species and avian group, respectively, for all HPAI detections. Overall, targeted surveillance and morbidity/mortality investigations of sick or dead birds has resulted in the detection of 1,611 H5N1 HPAI lineage virus in 42 States (Figure 19) across all four Flyways: Atlantic – 557, Central – 422, Mississippi – 462, Pacific – 117. The virus has been detected in a total of 66 different avian species (Table 10).
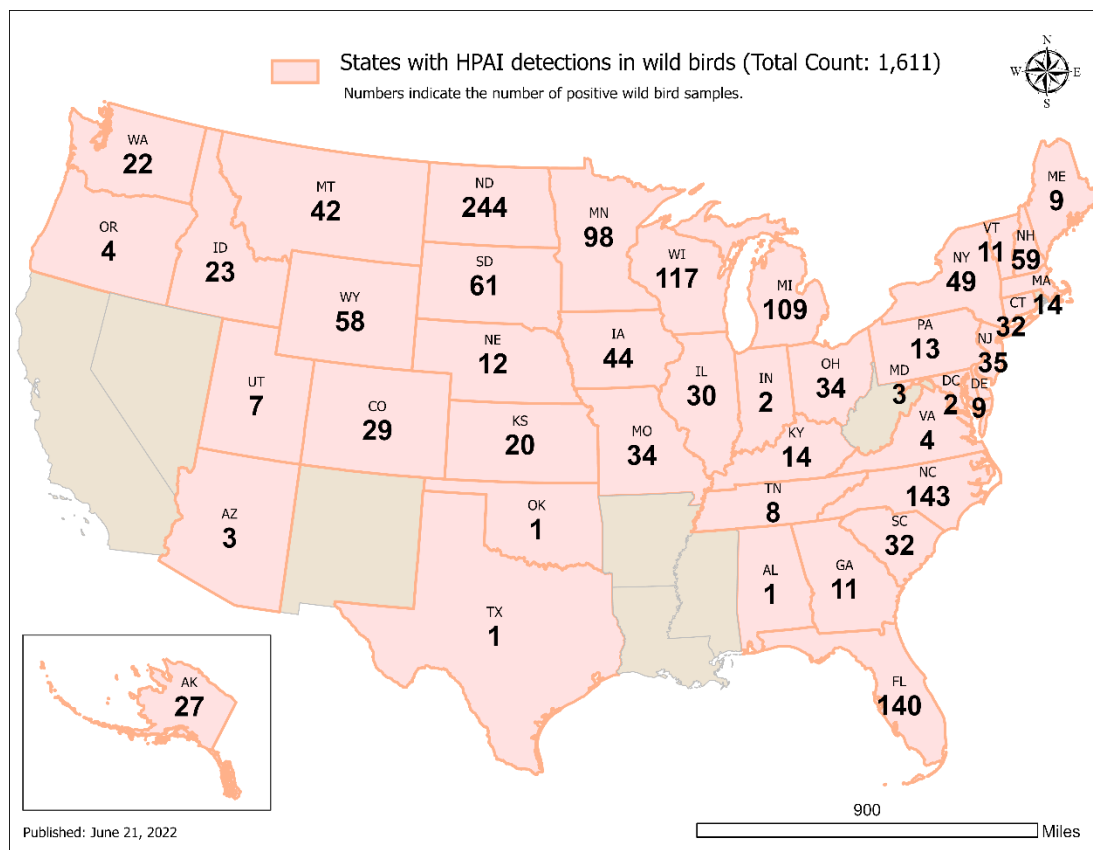
Figure 19. States With H5N1 Detections in Wild Bird Species as of 21 June 2022.

Targeted surveillance focuses on sampling apparently healthy dabbling duck species. During morbidity and mortality events, sick or dead birds may be submitted for additional testing and cause of death determination, and a subset of birds may be sampled for avian influenza testing.

The number of H5N1 lineage virus detections is based on viruses recovered at NVSL from H5N1 presumptive samples forwarded by NAHLN laboratories.

- Wild bird surveillance testing follows the NAHLN testing algorithm: samples are first tested by a Type A-specific test (IAV-M) and further tested by the H5/H7 subtype tests in which viral RNA is detected. H5 and H7 samples are forwarded to NVSL, as genetic sequencing is the most reliable test for determining virus subtype(s) in wild birds.

Table 9. Number of Apparently Healthy and Sick/Dead Birds Sampled During the 2022 HPAI Outbreak. List Current as of 21 June 2022.

Avian Group	# Apparently Healthy Birds Sampled	# Sick/Dead Birds Sampled (Morbidity/Mortality Events)
Blackbird	0	3
Crow/Jay	0	33
Duck	455	457
Game bird	0	18
Gull/Tern	0	38
Hawk/Falcon	0	418
Heron	0	9
Loon	0	3
Owl	0	105
Seabird	1	58
Shorebird	0	11
Sparrow	0	1
Thrush	0	1
Total	456	1155

Table 10. Number of Apparently Healthy and Sick/Dead Birds Sampled During the 2022 HPAI Outbreak. List Current as of 21 June 2022.

Species	# Apparently Healthy Birds Sampled	# Sick/Dead Birds Sampled (Morbidity/Mortality Events)
American black duck	31	0
American crow	0	28
American green-winged teal	42	1
American kestrel	0	1
American robin	0	1
American white pelican	1	32
American wigeon	63	1
Bald eagle	0	164
Barred owl	0	7
Black vulture	0	114
Black-billed magpie	0	3
Blue-winged teal	11	0
Brant	0	1
Broad-winged hawk	0	1
Brown pelican	0	3
Canada goose	1	121
Caspian tern	0	9
Common goldeneye	0	2
Common grackle	0	1
Common loon	0	3
Common raven	0	2
Common tern	0	2
Cooper's hawk	0	6
Cormorant (not otherwise specified)	0	7
Dark-eyed junco	0	1
Double-crested cormorant	0	11
Duck (not otherwise specified)	0	2
Eared grebe	0	1
Fish crow	0	1
Gadwall	33	1

Goose (not otherwise specified)	0	2
Great blue heron	0	4
Great horned owl	0	84
Greater white-fronter goose	0	1
Gull (not otherwise specified)	0	1
Hawk (not otherwise specified)	0	1
Herring gull	0	20
Hooded merganser	1	19
Horned grebe	0	2
Laughing gull	0	1
Lesser scaup	3	22
Mallard	142	12
Merganser (not otherwise specified)	0	6
Muscovy duck	0	8
Mute swan	1	2
Neotropic cormorant	0	3
Northern harrier	0	2
Northern pintail	4	0
Northern shoveler	14	0
Owl (not otherwise specified)	0	4
Pelican (not otherwise specified)	0	2
Peregrine falcon	0	8
Pheasant (not otherwise specified)	0	3
Redhead duck	2	8
Red-shouldered hawk	0	2
Red-tailed hawk	0	76
Red-winged blackbird	0	1
Ring-billed gull	0	3
Ring-necked duck	0	5
Ross's goose	14	49

Rough-legged hawk	0	4
Royal tern	0	2
Ruddy duck	0	2
Sanderling	0	11
Sandhill crane	0	4
Sharp-shinned hawk	0	3
Snow goose	77	150
Snowy egret	0	1
Snowy owl	0	10
Swainson's hawk	0	1
Swan (not otherwise specified)	0	2
Trumpeter swan	0	6
Tundra swan	0	5
Turkey vulture	0	34
Vulture (not otherwise specified)	0	1
Wild turkey	0	15
Wood duck	16	26
Total	456	1155

MODELING AVIAN INFLUENZA TRANSMISSION AT THE INTERFACE OF WILD BIRDS AND DOMESTIC POULTRY

A. Summary

In collaboration with the University of Maryland, and the U.S. Geological Survey, Eastern Ecological Science Center, we have completed preliminary models that explore the spatio-temporal trends in avian influenza transmission from wild waterfowl to domestic poultry across the continental United States for the full annual cycle.

These models account for not only the number of waterfowl in an area but also species-specific prevalence rates to determine the effective waterfowl population or presented disease risk. When paired with information on the distribution of poultry farms, we can identify an area's risk of spillover. Upon completion, these models should provide critical insight into how to best prepare for potential spillover events.

B. Preliminary Results and Discussion

Figure 20 shows sample results from our model at a county level by week for several example weeks, and Figure 21 looks more closely at model results from the State of North Carolina. For North Carolina, there is a general trend of the winter months (November through January) showing concentrated areas of risk in the East. As the year progresses, this risk becomes more evenly distributed throughout the State as the concentrated waterfowl populations along the East Coast disperse and migrate northward.

Data from the current outbreak were used to evaluate model performance. Using data through spring 2022, we showed that the model performed well at predicting county-level avian influenza virus spillover risk (Figure 22). The model classified the average county that experienced a spillover event as being more at risk than random. Counties with a spillover event had 12 times greater predicted risk, on average, than non-outbreak counties, and 54 of the 62 spillover counties were at above-average risk for a spillover event. There were almost no spillovers in counties designated as low risk by the interface model.

These preliminary models have proven valuable in understanding spatial risk during the current outbreak. As more data from the current outbreak become available, we will update model parameters to further characterize and refine transmission at the wild bird domestic poultry interface across the continental United States. Model results and related information could be of use to mitigate on-farm risk, for response planning, and to support preparedness activities. The latest modeling results can be found online at: Visualizing Avian Influenza (usgs.gov).
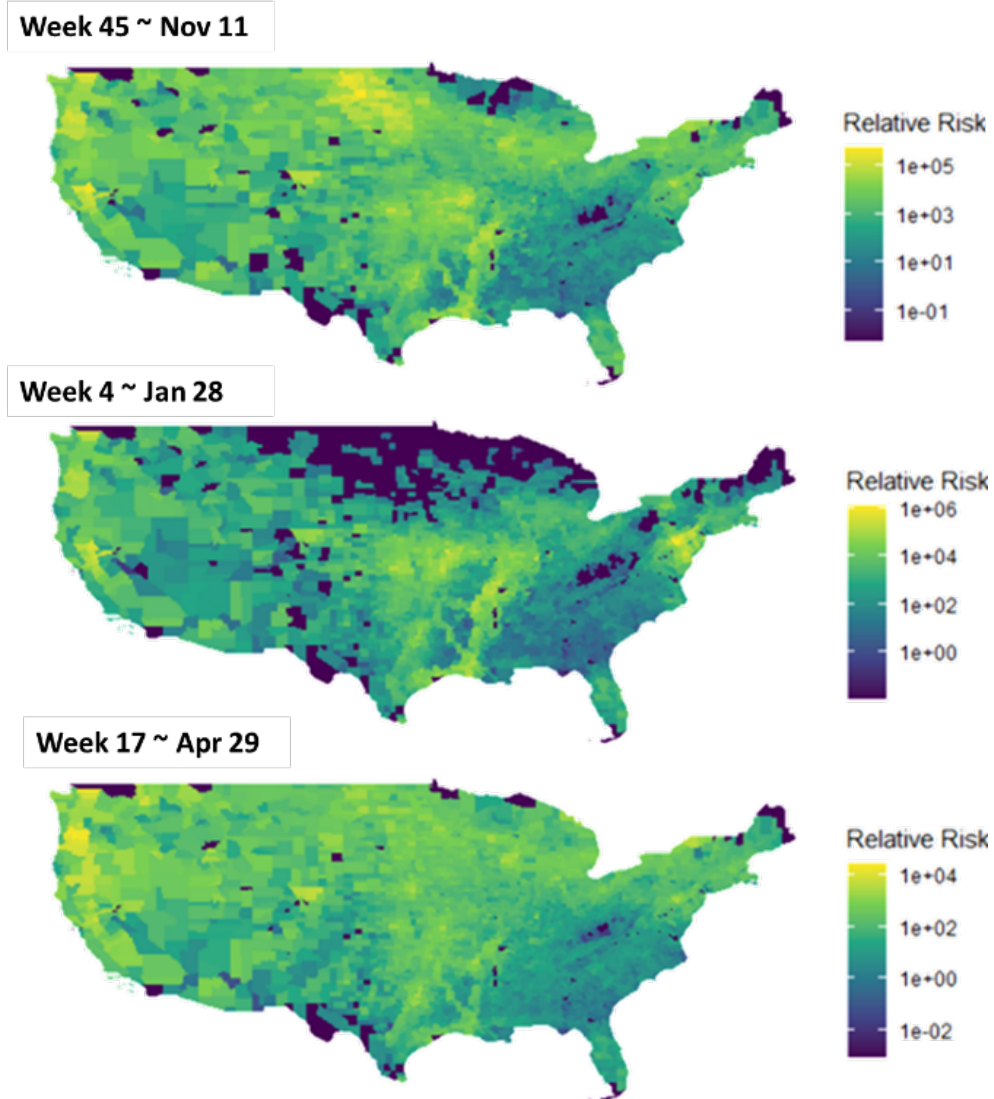
Figure 20. Weekly Relative Risk of Avian Influenza Spillover From Wild Birds to Domestic Poultry by County for Several Example Weeks.

Figure 21. Relative Risk of Avian Influenza Spillover From Wild Birds to Domestic Poultry for Several Example Weeks for the State of North Carolina. Counties With Initial Infected Premises Events Outlined in Red.
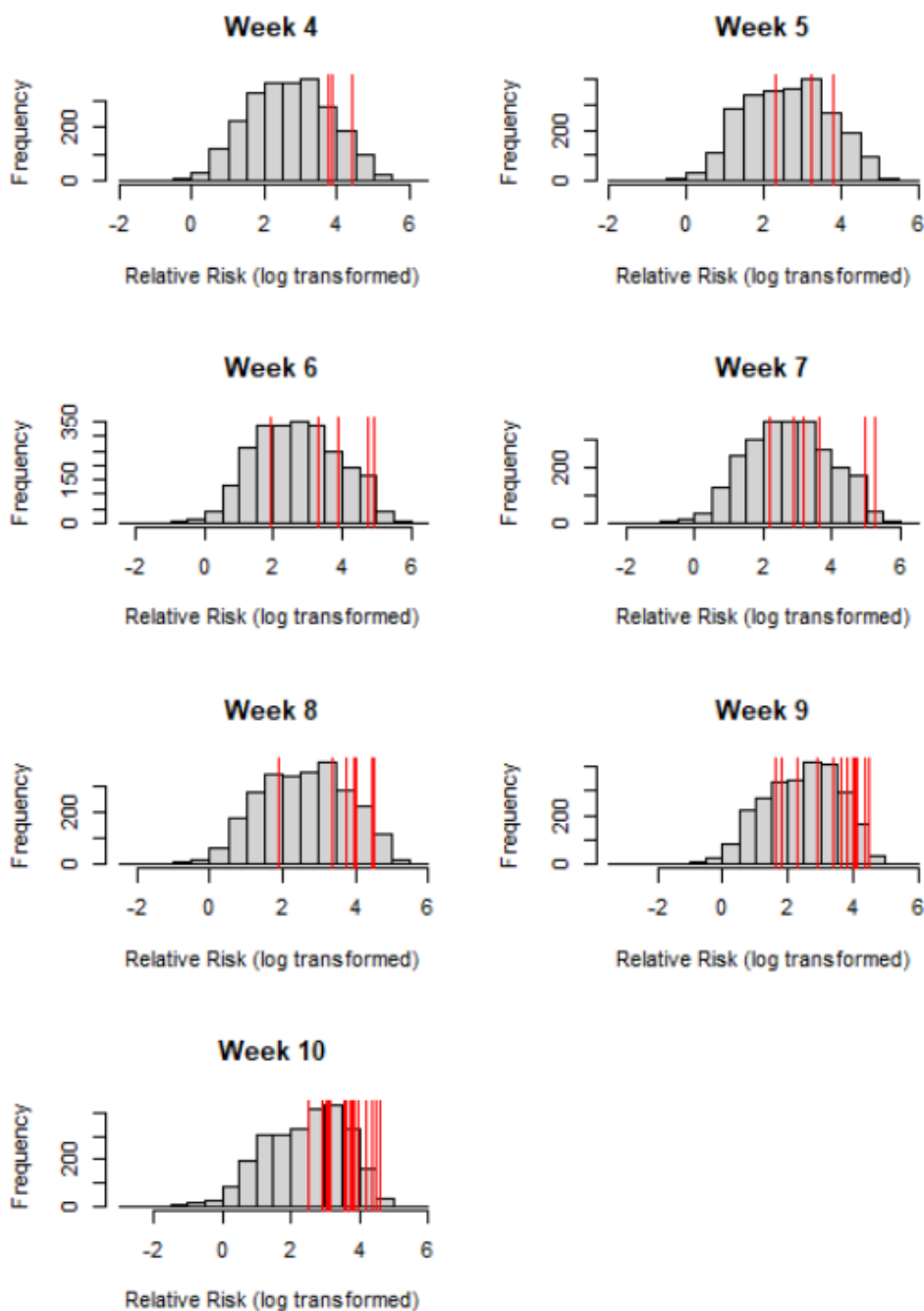
Figure 22. Validation of the Preliminary Interface Model Using Outbreak Data Through Spring 2022, With Counties With a Spillover Event Shown in Red.

ANALYSIS OF EBIRD AND BIRDCAST MIGRATION DATA: IMPLICATIONS FOR DISEASE INTRODUCTION, SPREAD, AND PREVENTION

A.   Potential Use of BirdCast Data for Awareness to Enhance Prevention Measures

The BirdCast live bird migration maps present real-time intensities of nocturnal bird migration as detected by the U.S. weather surveillance radar network, between local sunset to sunrise. All graphics are relative to the eastern time zone. When present, the red line moving east to west represents the timing of local sunset, with the yellow line representing the timing of local sunrise. Areas with lighter colors experienced more intense bird migration. Orange arrows show directions of bird movement. Green dots represent radar locations for which data are available, and red dots represent radar locations with no data available. Note that mountainous areas (e.g., the Rockies) have obstructions that restrict radar coverage, providing the appearance of no migration where migration may be occurring. Brighter colors indicate a higher migration traffic rate (MTR) expressed in units of birds/km/hour.

As another prevention tool following initial detections of HPAI in wild birds in the United States, BirdCast can be used to increase awareness of potential increased risk to poultry producers by noting areas of more intense bird migration. The following 1 February 2022 7:45 a.m. ET BirdCast live bird migration map depicts, with strong colors, areas of more intense bird migration over States, including Indiana and Kentucky, just five days prior to Indiana's first HPAI detection on 6 February 2022 on a commercial turkey farm, and eight to nine days prior to Kentucky's first two HPAI detections on 9 February 2022 and 10 February 2022 on a commercial chicken farm and a commercial turkey farm, respectively (Figure 23). These early H5N1 HPAI detections were preceded by HPAI detections in wild birds, which began on 13 January 2022.
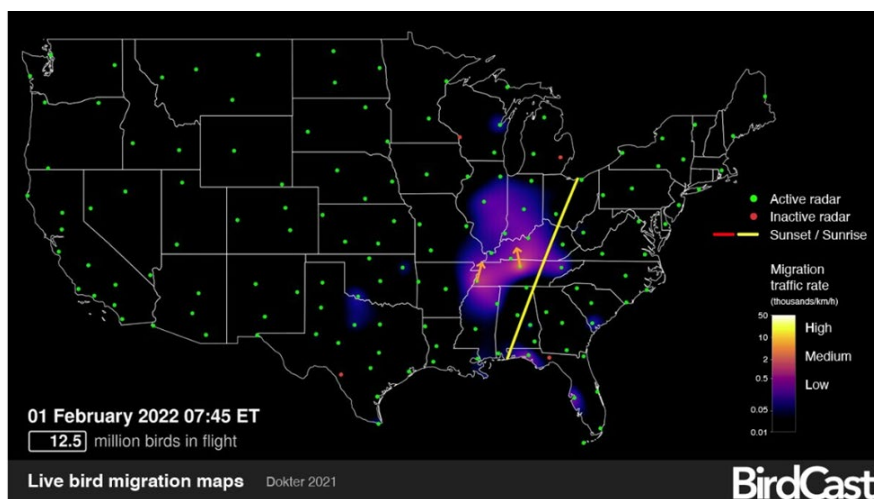

Figure 23. BirdCast's Live Bird Migration Map for 1 February 2022 at 7:45 a.m. Eastern Time.

Figure 24 depicts data from the BirdCast maps, noting the daily highest number of birds in flight, in the millions (royal blue line), reported over 24-hour stretches, through BirdCast's live bird migration maps. This line is drawn over stacked bars representing the 2022 United States HPAI H5 and H5N1 detections in wild birds (turquoise stacked bar), and the H5N1 HPAI detections in domestic birds on WOAH non-poultry and WOAH poultry premises (dark orange and light orange stacked bars, respectively).

The high migration numbers in October 2021 through December 2021 are a continued part of the fall migration season. Canada experienced their first HPAI detections in November 2021. The first wild bird detections in the United States were on 13 January 2022, followed by additional detections in wild birds in January and early February 2022. The increase in numbers of birds in flight, measured on the left axis, follows the initial increase in HPAI detections in domestic birds on WOAH non-poultry and WOAH poultry premises, likely influencing the continued HPAI detections through May, and decreasing as the United States-reported HPAI detections have decreased over that same timeframe.
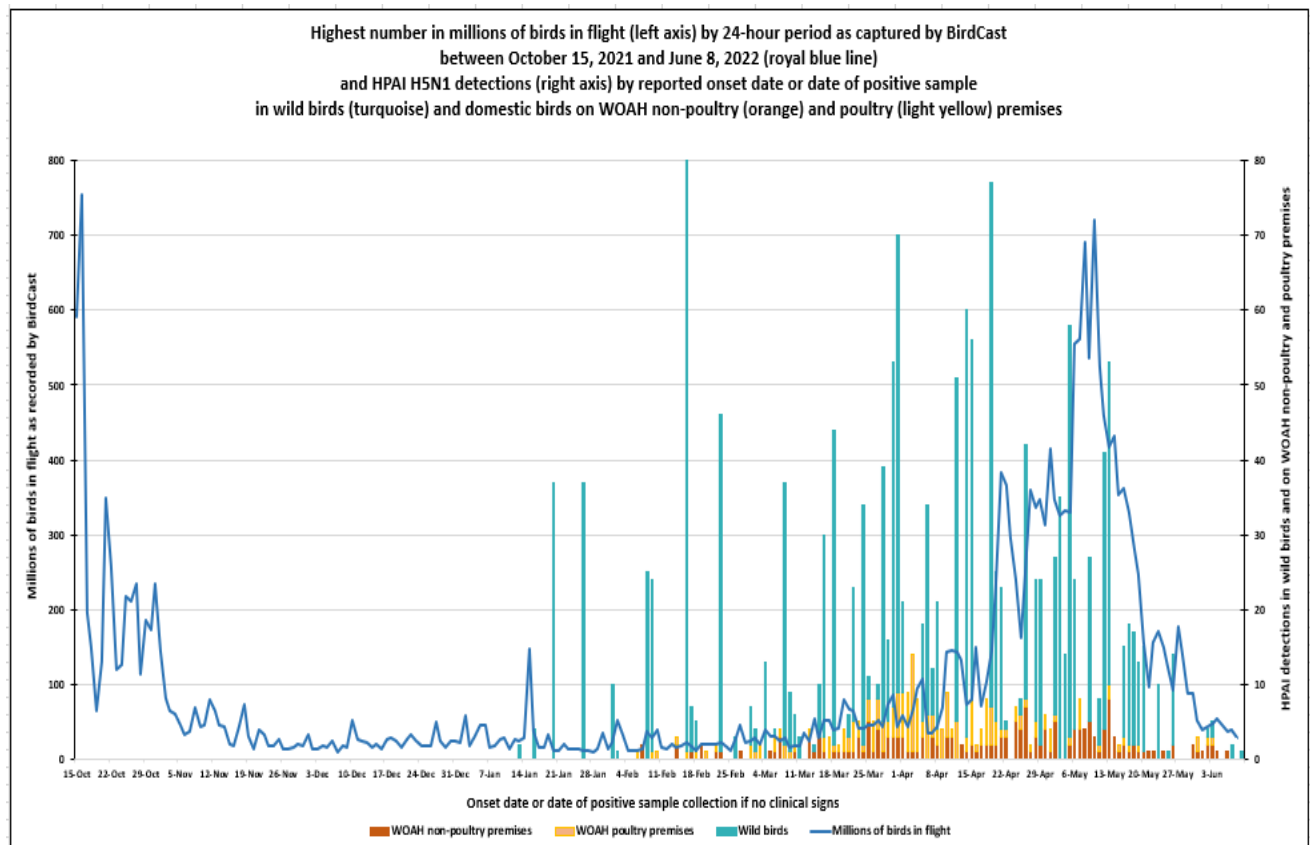

Figure 24. Graph Showing BirdCast's Highest Count of Millions of Birds in Flight by Day Overlayed With HPAI Detections in Wild Birds and on Non-Poultry and Poultry Premises.

B.   Space-time Cluster Analysis of eBird Observation Data

In the previous section, visual interpretation of BirdCast migration maps showed possible association of high densities of wild bird migration over areas where detections of HPAI occurred in commercial and backyard premises subsequently occurred. However, we did not have direct access to the spatial data layers behind BirdCast. To evaluate space-time associations between wild bird migration and HPAI-positive premises, we accessed eBird observational data.

eBird is a database of species-specific, crowd-sourced observational data by scientists and birding enthusiasts. While the data does not capture birds in flight, we assumed that high numbers of bird observations correlate with heavy migration over the area.

Using the "reBird" R-package, we pulled eBird observations between 1 February 2022 and 15 April 2022. For each HPAI-positive premise during that timeframe, we pulled all eBird observations within a 50km window and up to 14 days prior to the date that premises was positive. We used a wide spatial window, assuming that the highly mobile nature of birds could result in an infectious bird exposing domestic birds within a potentially large area. Within each spatial window for each date of observation, we calculated the density of wild birds and retrieved the date of highest bird density observed around the premise within the 14-day window. We calculated the time difference in days between observations of highest wild bird densities with the date of onset for the premises (Figure 25). HPAI-positive premises were more likely to be detected within the first seven days of heavy wild bird observation within a 50km spatial window.
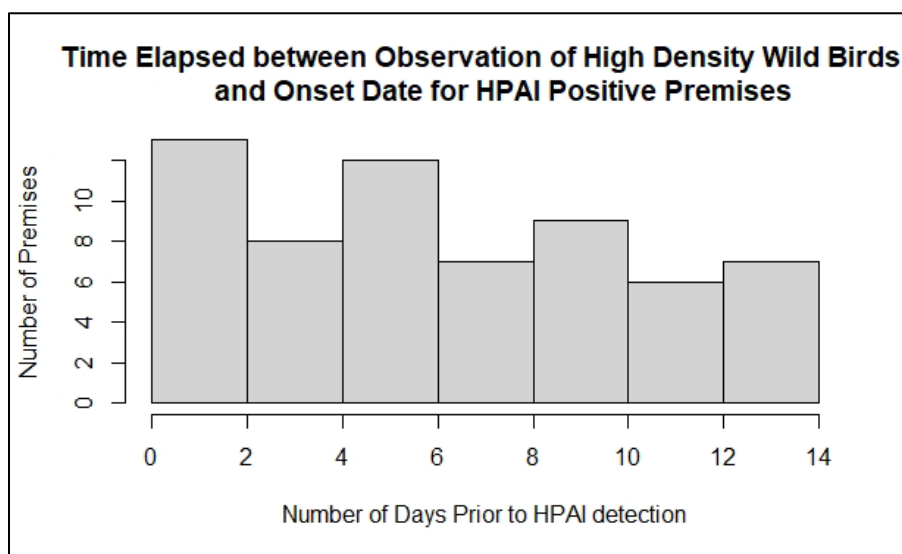
Figure 25. Frequency Histogram Depicting Elapsed Number of Days Between Observed Highest Density of Wild Birds Within a 50km Radius and Detection Date for an HPAI-Positive Premise.

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ACKNOWLEDGEMENTS

APPENDIX A: INITIAL CONTACT EPI REPORT FORM

USDA United States Department of Agriculture

HPAI Response

Initial Contact Epidemiological (Epi) Report

June 27, 2016

I. PREMISES INFORMATION

Premises Identification Number: _____

Name of Premises: _____

Owner of Premises: _____

Address of Premises: _____

County of Premises: _____

Premises Owner Phone: _____

Premises Owner Email: _____

Premises Entrance Latitude: _____

Premises Entrance Longitude: _____

II. OWNER INFORMATION

Owner of Animals: _____

Address of Animal Owner: _____

Animal Owner Phone: _____

Animal Owner Email: _____

III. INTERVIEW CONTACT INFORMATION

Name of person administering questionnaire: _____

Name of person answering questionnaire: _____

Phone: _____

Position (e.g., owner, manager, veterinarian, etc.): _____

Date of interview: _____

IV. FLOCK INFORMATION

Clinical signs (*brief* description)	
Baseline daily mortality rate: (insert rate from farm records)	
Daily mortality rate (# of dead birds/bird population on date of initial sampling)	
Date first clinical signs were noted	
Date initial samples were collected	
Laboratory to which initial samples were submitted	
Results of any AI tests in past 21 days	
Date premises quarantine or hold order was issued	

House ID	Type of Birds	Number of Birds	Age of Birds	House Dimensions	Ceiling Height	Ventilation Type	Date of Onset of Clinical Signs

Do you have a veterinarian who regularly advises you on disease prevention?

☐ Yes   ☐ No

If yes, name of veterinarian:

Do you have a pre-arranged depopulation plan for this flock? ☐ Yes   ☐ No

If yes, briefly describe the pre-arranged depopulation method: _____

_____

Have you exercised or used this method previously? ☐ Yes   ☐ No

V. TRACE-IN AND TRACE-OUT QUESTIONNAIRE

Name of person administering questionnaire: _____

Name of person answering questionnaire: _____

Phone: _____

Position (e.g., owner, manager, veterinarian, etc.): _____

1. How are dead birds (daily mortality) disposed of on this farm (please circle

   one or more)? Also specify if disposal occurs on or off this premises.

   a. Composting

   b. Burial

   c. Incineration

   d. Rendering

   e. Landfill

   Other (specify): _____

   If disposal occurs at another premises:

Name and Location (company name)	Transported by

2. List any locations that **accept manure/litter** from this premises during the last 21 days.

Name and location (company name)	Date (mm/dd/yy)	Intended use

3. Was manure or animal material from another premises brought **onto** this premises during the last 21 days?

☐ Yes   ☐ No   If yes:

Product	Source	Date (mm/dd/yy)

4. Have you or any of your employees (including any contractors or volunteers) visited any other premises with poultry or any processors of eggs or poultry products during the last 21 days (e.g., farm, slaughter, processing, market, residence with poultry)?

☐ Yes   ☐ No   If yes:

Premises/processor name	Person/title	Date (mm/dd/yy)

5. Is there a community living situation where farm workers from this premises interact with workers from other poultry facilities?

☐ Yes   ☐ No

If Yes, describe: _____

6. Did any crews (e.g., catch crews, load-out, vaccination, insemination) enter the premises during the last 21 days?

☐ Yes   ☐ No   If yes:

Date (mm/dd/yy)	Crew type	Name/company

7. Did any of the following visit the premises during the last 21 days? If Yes, give date and name or company information.

Visitor type	Date(s) of visit	Name/company
a. Federal/State veterinary or animal health worker		
b. Extension agent or university veterinarian		
c. Private or company veterinarian		
d. Company service person		
e. Nutritionist or feed company consultant		
f. Inspector (e.g., FDA, NOP, biosecurity auditor, etc.)		
g. Feed delivery		
h. Egg truck		
i. Litter/bedding delivery		
j. Litter removal		
k. Renderer/dead bird pick up		
l. Pest/rodent control		
m. Manure truck		
n. Trash pick up		
o. Occasional worker (e.g., family member, part-time help over holiday)		
p. Wholesaler, buyer, or dealer		

q. Customer/consumer (private individual)		
r. Other		

8. Specify if any equipment was shared with another premises during the last 21 days, whether you received or loaned the equipment, and the location and name of the companies or premises the equipment was shared with:

Vehicle	Received/loaned	Specify (name, company, location)
ATV/4-wheeler	☐ Rec'd ☐ Loaned	
Tractor	☐ Rec'd ☐ Loaned	
Gates/panels	☐ Rec'd ☐ Loaned	
Skid-steer loaders	☐ Rec'd ☐ Loaned	
Egg flats	☐ Rec'd ☐ Loaned	
Egg racks	☐ Rec'd ☐ Loaned	
Pallets	☐ Rec'd ☐ Loaned	
Dead bird containers	☐ Rec'd ☐ Loaned	
Manure/litter handling equipment	☐ Rec'd ☐ Loaned	
Pressure sprayers/ washers/foamers	☐ Rec'd ☐ Loaned	
Other cleaning equipment	☐ Rec'd ☐ Loaned	
Vaccination equipment	☐ Rec'd ☐ Loaned	
Bird catching equipment	☐ Rec'd ☐ Loaned	
Live haul loader	☐ Rec'd ☐ Loaned	
Other (specify: _____ _____)	☐ Rec'd ☐ Loaned	

9. Were any birds introduced onto the premises during the last 21 days?

☐ Yes ☐ No   If yes:

Date (mm/dd/yy)	Bird type (e.g., chicks, poults, spiking roosters, layers, breeders, etc.)	Source	Transported by

10. Have any birds moved off the premises during the last 21 days?

☐ Yes   ☐ No   If yes:

Date (mm/dd/yy)	Bird type (e.g., chicks, poults, spiking roosters, layers, breeders, etc.)	Destination	Transported by

11. Were any birds moved within the premises during the last 21 days? (e.g., from one barn to another on the same premises)

☐ Yes   ☐ No

If Yes,

   a. Was a contract crew used?

      ☐ Yes   ☐ No

      If Yes, specify company/crew name: _____

   b. Was farm specific equipment used?

      ☐ Yes   ☐ No

      If No, describe: _____

12. Were any eggs moved onto the premises during the last 21 days?

☐ Yes   ☐ No

If Yes,

   a. List source (name and location) for eggs **coming onto** this premises during the last 21 days, the dates eggs were received, and whether the eggs were intended for hatching, or were processed or unprocessed from source.

Source name and location (company name)	Date (mm/dd/yy)	Intended for hatching?	Processed?*
		☐ Yes ☐ No	☐ Yes ☐ No
		☐ Yes ☐ No	☐ Yes ☐ No
		☐ Yes ☐ No	☐ Yes ☐ No
		☐ Yes ☐ No	☐ Yes ☐ No
		☐ Yes ☐ No	☐ Yes ☐ No
*Method of processing: _____			

13. Were any eggs moved off the premises during the last 21 days?

☐ Yes ☐ No

If Yes,

    a. List source (name and location) for eggs **moving off** this premises during the last 21 days, the dates eggs left, and whether the eggs were intended for hatching, or were processed or unprocessed from source.

Source name and location (company name)	Date (mm/dd/yy)	Intended for hatching?	Processed?*
		☐ Yes ☐ No	☐ Yes ☐ No
		☐ Yes ☐ No	☐ Yes ☐ No
		☐ Yes ☐ No	☐ Yes ☐ No
		☐ Yes ☐ No	☐ Yes ☐ No
		☐ Yes ☐ No	☐ Yes ☐ No
*Method of processing: _____			

14. Is there any additional or important information that we need to know at this time regarding the disease on your farm?

☐ Yes ☐ No

If Yes, describe: _____

APPENDIX B: TIME OF INTRODUCTION MODELING METHODS

We used approximate Bayesian computation (ABC) to estimate the likely time of virus introduction and the key model parameters, such as the adequate contact rate (a parameter which regulates the rate of within-flock disease spread) from the available production and test data.

A stochastic individual-based simulation model was first used to simulate the disease mortality, infection prevalence over time, and water consumption (where applicable) over a wide range of values for model parameters, such as the adequate contact rate, times of disease introduction, and bird-level latent and infectious period distributions (i.e., prior distributions).

In the next step, the sum of the squared distance between the model-predicted daily mortality and water consumption (where applicable) and the observed data, and the difference between observed and simulated diagnostic test results was calculated as a measure of deviation between the model output and data (ψ). The parameters in model iterations where the metric ψ was sufficiently small, indicating a good fit to the data, were then accepted to estimate the distribution of the time of introduction and other model parameters.

We used wide priors for input variables based on published literature and estimates from previous SEPRL challenge studies. Preliminary data from SEPRL challenge studies in turkeys and chickens with a current outbreak isolate (A/American Widgeon/SC/22-000345-001/2022 (H5N1) HPAIV) were made available in May 2022. We estimated the disease state durations from the challenge study data using MCMC algorithms. The estimated disease state durations were then used to update the prior distributions for the latent and infectious periods. The updated prior distributions used in the analysis for commercial meat turkey and table egg layer flocks based on SEPRL data and other published studies are summarized in Table B and table B2. We also performed a sensitivity analysis for the impact of the mean infectious period prior for selected premises given the uncertainty in this parameter.

Table B1. Input Prior Distribution Parameters Used in the ABC Approach to Estimate the Adequate Contact Rate and Time of Virus Introduction for Commercial Meat Turkey Flocks.

| Parameter Name	Description	Distribution
Adequate Contact Rate	Daily average number of contacts a bird has with other birds that are sufficient to transmit infection	Uniform (min = 0.2, max = 7) per day
Latent Period Length Distribution	Length of the interval when a bird is latently infected and is not infectious	Gamma (shape = 4.037, scale = 0.1809); mean = 0.64 days; variance = 0.67
Mean infectious period	Prior distribution for the mean infectious period	Uniform (1.9–6.3 days)
Shape parameter for infectious period	Prior distribution for shape parameter of gamma distributed infectious period	Uniform (1–20)

Table B2. Input Prior Distribution Parameters Used in the ABC Approach to Estimate the Adequate Contact Rate and Time of Virus Introduction for Table Egg Layer Flocks.

Parameter Name	Description	Distribution
Adequate Contact Rate	Daily average number of contacts a bird has with other birds that are sufficient to transmit infection	Uniform (min = 0.5, max = 9) per day
Latent Period Length Distribution	Length of the interval when a bird is latently infected and is not infectious	Gamma (shape = 2.54, scale = 0.33); mean = 0.84 days
Mean infectious period	Prior distribution for the mean infectious period	Uniform (0.74–4)
Shape parameter for infectious period	Prior distribution for shape parameter of gamma distributed infectious period	Uniform (1–20)

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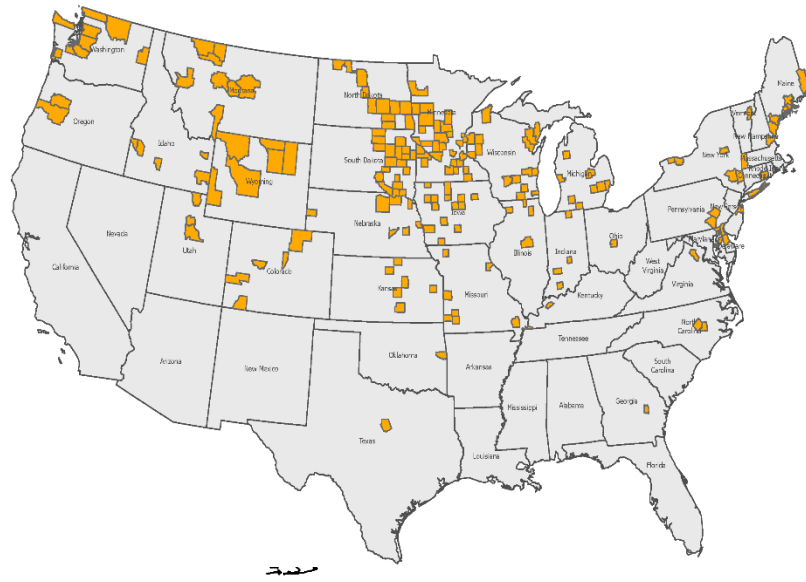
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