

# **USGS Highly Pathogenic Avian Influenza Research Strategy**

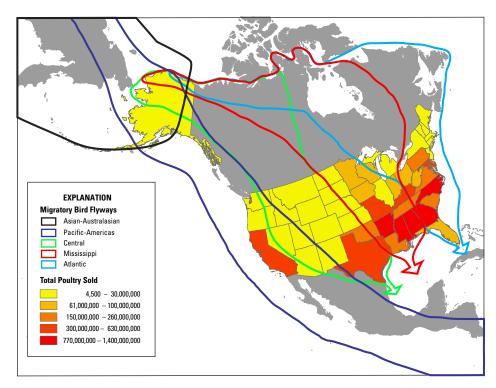
### Background

Avian influenza viruses are naturally occurring in wild birds such as ducks, geese, swans, and gulls. These viruses generally do not cause illness in wild birds, however, when spread to poultry they can be highly pathogenic and cause illness and death in backyard and commercial farms. Outbreaks may cause devastating agricultural economic losses and some viral strains have the potential to infect people directly. Furthermore, the combination of avian influenza viruses with mammalian viruses can result in strains with the ability to transmit from person to person, possibly leading to viruses with

pandemic potential. All known pandemic influenza viruses have had some genetic material of avian origin. Since 1996, a strain of highly pathogenic avian influenza (HPAI) virus, H5N1, has caused infection in wild birds, losses to poultry farms in Eurasia and North Africa, and led to the deaths of several hundred people. Spread of the H5N1 virus and other influenza strains from China was likely facilitated by migratory birds. In December 2014, HPAI was detected in poultry in Canada and migratory birds in the United States. Since then, HPAI viruses have spread to large parts of the United States and will likely continue to spread through migratory bird flyways



Migratory waterfowl, such as this Northern Pintail (*Anas acuta*), are common carriers of avian influenza throughout North America and Asia. USGS research demonstrated that these birds are involved in the dispersal of avian influenza between Asia and North America. Photograph by B. Guzetti, U.S. Geological Survey.



Migratory bird flyways in North America in relation to total number of poultry sold in 2012 by State. The map depicts three important concepts: (1) Asian and North American wild bird migratory flyways overlap in Alaska; (2) this overlap creates routes of introduction and virus spread into North America; and (3) shows the potential for impacts to the U.S. poultry industry depending on the flyway where highly pathogenic avian influenza is detected. Poultry data from the 2012 Census of Agriculture (agcensus.USDA.gov).

and other mechanisms throughout North America. In the United States, HPAI viruses have severely affected the poultry industry with millions of domestic birds dead or culled. These strains of HPAI are not known to cause disease in humans; however, the Centers for Disease Control and Prevention (CDC) advise caution when in close contact with infected birds. Experts agree that HPAI strains currently circulating in wild birds of North America will likely persist for the next few years. This unprecedented situation presents risks to the poultry industry, natural resource management, and potentially human health. Scientific knowledge and decision support tools are urgently needed to understand factors affecting the persistence of HPAI in wild birds, to forecast future spread of HPAI by wild birds, and to detect novel strains of HPAI that may emerge.



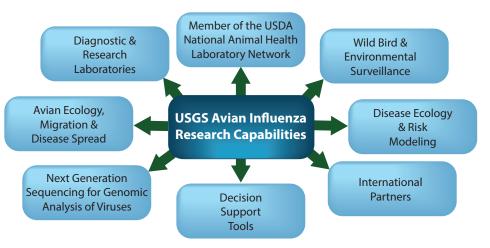
The USGS tests thousands of avian influenza samples annually from across the United States and adjacent countries to determine virus distribution, strain type, molecular evolution, and pathogenicity.

## Why the USGS Is Involved

As the science agency of the U.S. Department of the Interior (DOI), the U.S. Geological Survey (USGS) has been conducting research on avian influenza since 2006. USGS is part of the State and Federal interagency team for the detection and response to HPAI viruses in North America. The U.S. Department of Agriculture and DOI actively coordinate with other State and Federal wildlife, agricultural and human

#### Key USGS Avian Influenza Research Findings since 2006

- Genetic evidence of intercontinental dispersal of avian influenza by wild birds.
- Rates and ranges of virus dispersal in Eurasia and North America determined from satellite telemetry, genetics, and band-recovery data.
- Risk assessment of HPAI to wild birds through experimental infection.
- Use of genetics to optimize earlywarning surveillance for introduction of Asian, European, and South Americanorigin viruses to North America.
- Risk maps of virus transmission at the interface of domestic poultry and wild birds.
- Dynamics of avian influenza viruses in wetland environments.



The USGS has considerable scientific capabilities nationwide to investigate avian influenza.

health agencies to understand avian influenza distribution and dynamics to aid natural resource managers, agricultural officials and the poultry industry with this disease.

## The USGS Role and Response to Highly Pathogenic Avian Influenza in North America

The USGS conducts research on avian influenza at multiple science centers across the nation and has amassed substantial national and international expertise investigating this disease. Scientists are defining the role of migratory birds in viral spread, characterizing genetics of viruses in wild birds, determining



The USGS was instrumental in the initial response to the detection of highly pathogenic avian influenza in wild birds of North America by conducting live bird sampling and avian mortality investigations.

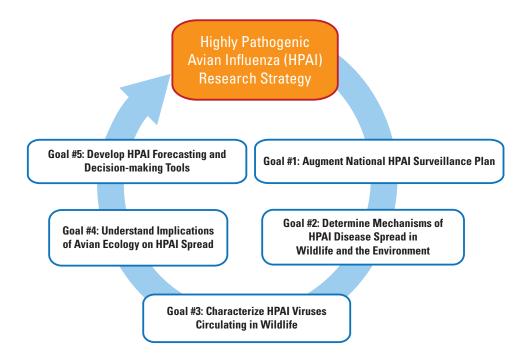
water conditions affecting survival of the virus in wetlands, and describing stages of infection in migratory birds. Additionally, USGS has capabilities in avian influenza diagnostics, surveillance and mathematical modeling to map potential risk factors for disease spread between wild and domestic bird species.

In December 2014, the USGS was instrumental in first detecting HPAI viruses in wild birds of North America through its wildlife health and diagnostic network. The USGS has contributed substantial resources to enhance surveillance for HPAI across North America and to provide scientific information about the type, distribution, and wildlife species that harbor HPAI through timely public alerts (Wildlife Health Bulletins), a new online Wildlife Health Information Sharing Partnership – Event Reporting System (WHISPers), and scientific publications.

In collaboration with partners, USGS developed a national science strategy for HPAI. This science plan will augment on-going research to allow forecasts of future disease spread by wild birds, detection of novel strains, characterization of factors that control survival of HPAI in the environment, and risk assessments to poultry, natural resources, and human health.

#### The USGS Avian Influenza Research Strategy

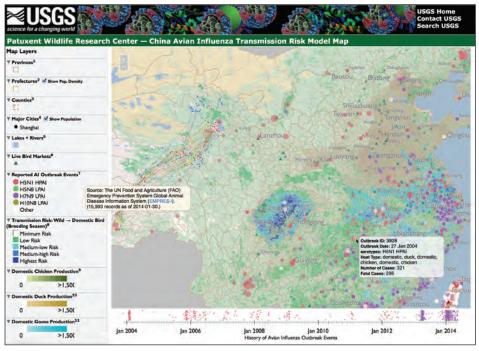
The USGS HPAI Research Strategy will build on existing USGS research and science capabilities to provide scientific information and risk assessment tools for decision-making by natural resource managers, poultry producers, and public health officials.



The USGS Highly Pathogenic Avian Influenza Research Strategy is composed of five main science goals. USGS will augment Federal Interagency Surveillance Plan (Goal #1), improve our understanding of HPAI dynamics in wildlife and the environment (Goals #2–4), and inform managers as we integrate out science into HPAI forecasting and decision-making tools (Goal #5).



An example of information from Goals #1 and #2. Bald Eagles are predators of fish and waterbirds. USGS research determined that some birds of prey are sensitive to HPAI. Surveillance found that HPAI-infected prey led to mortalities in raptors including a Bald Eagle. Photograph by B. Uher-Koch, U.S. Geological Survey.



An example of a decision-making tool from Goal #5. In collaboration with the Food and Agriculture Organization, the USGS has examined the risk of HPAI moving between wild birds and poultry in China. Similar risk models are being developed for the current outbreak in the United States http://www.pwrc.usgs.gov/ai/.

#### USGS Web Links and Selected Publications

USGS National Wildlife Health Center (http://www.nwhc.usgs.gov), USGS Alaska Science Center (http://alaska. usgs.gov), USGS Patuxent Wildlife Research Center (https://www.pwrc.usgs. gov/health), USGS Western Ecological Science Center (http://www.werc.usgs. gov), WHISPers (http://www.nwhc.usgs. gov/whispers).

- Dusek, R.J., Hallgrímsson, G.T., Ip, H.S., Jónsson, J.E., Sreevatsan, S., Nashold, S.W., TeSlaa, J.L., Enomoto, S., Halpin, R.A., Lin, X., Fedorova, N., Stockwell, T.B., Dugan, V., Wentworth, D.E., and Hall, J.S., 2014, North Atlantic migratory bird flyways provide routes for intercontinental movement of avian influenza viruses: PLoS ONE, v. 9, p. e92075, doi: 10.1371/journal. pone.0092075.
- Gaidet, N., Cappelle, J., Takekawa, J.Y., Prosser, D.J., Iverson, S.A., Douglas, D.C., Perry, W.M., Mundkur, T., and Newman, S., 2010, Potential spread of highly pathogenic avian influenza H5N1 by wildfowl—Dispersal ranges and rates determined from large-scale satellite telemetry: Journal of Applied Ecology, v. 47, p. 1147–1157, doi: 10.1111/j.1365-2664.2010.01845.x.
- Hall, J.S., Hallgrímsson, G.T.,
  Suwannanarn, K., Sreevatsen, S.,
  Ip, H.S., Magnusdottir, E., TeSlaa,
  J.L., Nashold, S.W., and Dusek, R.J.,
  2014, Avian influenza virus ecology
  in Iceland shorebirds: intercontinental
  reassortment and movement:
  Infection, Genetics and Evolution,
  v. 28, p. 130–136, doi: 10.1016/j.
  meegid.2014.09.013.
- Hall, J.S., Ip, H.S., Franson J.C., Meteyer, C., Nashold, S., TeSlaa, J.L., French, J., Redig, P., and Brand, C., 2009, Experimental infection of a North American raptor, American kestrel (Falco sparverius), with highly pathogenic avian influenza virus (H5N1): PLoS ONE, v. 4, p. e7555. doi:10.1371/journal.pone.0007555.
- Henaux, V., Samuel, M.D., Dusek,
  R.J., Fleskes, J.P., and Ip, H.S., 2012,
  Presence of avian influenza viruses in waterfowl and wetlands during summer 2010 in California: PLoS ONE,
  v. 7, p. e31471. doi:10.1371/journal.
  pone.0031471.

- Hill, N.J., Takekawa, J.Y., Cardona, C.J., Ackerman, J.T., Schultz, A.K., Spragens, K.A., and Boyce, W.M., 2010, Waterfowl ecology and avian influenza in California: do host traits inform us about viral occurrence?: Avian Diseases, v. 54, s1,
  - p. 426-432.
- Ip, H.S., Torchetti, M.K., Crespo, R., Kohrs, P., DeBruyn, P., Mansfield, K.G., Baszler, T., Badcoe, L., Bodenstein, B., Shearn-Bochsler, V., Killian, M.L., Pedersen, J.C., Hines, N., Gidlewski, T., DeLiberto, T., and Sleeman, J.M., 2015, Novel Eurasian highly pathogenic avian influenza A H5 viruses in wild birds, Washington, USA, 2014: Emerging Infectious Diseases, v. 21, no. 5, p. 886–890, doi:10.3201/eid2105.142020.
- Keeler, S.P., Dalton, M.S., Cressler, A.M., Berghaus, R.D., and Stallknecht, D., 2014, Abiotic factors affecting persistence of avian influenza virus in surface water from waterfowl habitats: Applied and Environmental Microbiology, v. 80, p. 2910–2917, doi:10.1128/AEM.03790-13.
- Lee, D.H., Torchetti, M.K., Winker, K., Ip, H.S., Song, C.S., and Swayne, D.E., 2015, Intercontinental spread of Asianorigin H5N8 to North America through Beringia by migratory birds: Journal of Virology, v. 89, p. 6521–6524, doi:10.1128/JVI.00728-15.
- Meixell, B.W., Borchardt, J.S., and Spencer, S.K., 2013, Accumulation and inactivation of avian influenza virus by the filter-feeding invertebrate, Daphnia magna: Applied and Environmental Microbiology, v. 79, p. 7249–7255, doi:10.1128/AEM.02439–13.
- Palm, E., Newman, S., Prosser, D., Xiao, X., Ze, L., Batbayar, N., Balachandran, S., and Takekawa, J., 2015, Mapping migratory flyways in Asia using dynamic Brownian bridge movement models: Movement Ecology, v. 3, no. 1, p. 3.
- Pearce, J.M., Ramey, A.M., Flint, P.L., Koehler, A.V., Fleskes, J.P., Franson, J.C., Hall, J.S., Derksen, D.V., and Ip, H.S., 2009, Avian influenza at both ends of a migratory flyway— Characterizing viral genomic diversity to optimize surveillance plans for North America: Evolutionary Applications, v. 2, p. 457–468, doi:10.1111/j.1752-4571.2009.00071.x.

- Prosser, D.J., Hungerford, L.L., Erwin, R.M., Ottinger, M.A., Takekawa, J.Y., and Ellis, E.C., 2013, Mapping risk of avian influenza transmission at the interface of domestic poultry and wild birds: Frontiers in Public Health, v. 1, p. 1–11, doi:10.3389/ fpubh.2013.00028.
- Ramey, A.M., Walther, P., Link, P., Poulson, R.L., Wilcox, B.R., Newsome, G.M., Spackman, E., Brown, J.D., and Stallknecht, D.E., 2014, Optimizing surveillance for South American origin influenza A viruses along the United States Gulf Coast through genomic characterization of isolates from Blue-winged Teal (Anas discors): Transboundary and Emerging Diseases, doi: 10.1111/tbed.12244.
- Torchetti, M.K., Killian, M.L., Dusek, R.J., Pedersen, J.C., Hines, N., Bodenstein, B., White, C.L., and Ip, H., 2015, Novel H5 clade 2.3.4.4 reassortant (H5N1) virus from a Green-winged Teal in Washington, USA: Genome Announcements, v. 3, p. e00195-15, doi:10.1128/ genomeA.00195-15.
- Yamaguchi, N., Hupp, J.W., Higuchi, H., Flint, P.L., and Pearce, J.M., 2010, Satellite-tracking of Northern Pintail Anas acuta during outbreaks of the H5N1 virus in Japan: implications for virus spread: Ibis, v. 152, p. 262–271.

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