

# **An Early Detection System for Highly Pathogenic H5N1 Avian Influenza in Wild Migratory Birds U.S. Interagency Strategic Plan**

## ***Introduction***

Avian influenza (AI) is a type A influenza virus that is naturally found in certain species of waterfowl and shorebirds. However, the occurrence of highly pathogenic avian influenza (HPAI) subtype highly pathogenic H5N1 avian influenza has raised concern regarding the potential impact on wild birds, domestic poultry, and human health should it be introduced into the United States (U.S.). Numerous potential routes for introduction of the virus into the U.S. exist including illegal movement of domestic or wild birds, contaminated products, via an infected traveler, as a bioterrorism event, and the migration of infected wild birds. This plan focuses primarily on the detection of a potential introduction of highly pathogenic H5N1 avian influenza virus by migratory birds.

Avian influenza viruses are classified on the basis of two proteins, hemagglutinin (H) and neuraminidase (N), found on the surface of the virus. Specific viral subtypes have one of 16 different H proteins and one of 9 different N proteins, resulting in 144 possible combinations or subtypes based on this classification scheme. Within each subtype, there are numerous combinations of genetic sequences that determine the pathogenicity of the subtype to an infected host.

Wild birds, in particular certain species of waterfowl and shorebirds, are considered to be the natural reservoirs for all 144 subtypes. These subtypes are adapted to survive in these wild species and usually cause little or no disease. However, gradual genetic drift (i.e., mutation) can occur and a particular subtype can become adapted to infect other species of wild birds and domestic birds. Although this slight genetic change in the virus allows it to infect new species, it usually does not cause disease in the new host. The virus can also change if a host is simultaneously infected with another type A influenza virus. In such situations, mixing of the genetic material from the two virus strains (genetic shift) can occur, resulting in the formation of a new strain. The combination of gradual drifts and rapid shifts results in the production of a strain that now causes morbidity and mortality in susceptible hosts. If the morbidity and mortality is significant, the virus is classified as a highly pathogenic avian influenza (HPAI) virus.

During 1995-96, it is thought that antigenic drift occurred in an AI virus of wild birds, allowing the virus to infect chickens in China. This was followed by reassortment into the HPAI virus subtype highly pathogenic H5N1 avian influenza. Since that time, this highly pathogenic H5N1 has been circulating in Asian poultry and domestic fowl resulting in significant mortality to these species. Highly pathogenic H5N1 avian influenza likely underwent further antigenic drift and

shift allowing infection in additional species of birds, mammals, and humans. More recently, this virus moved back into wild birds resulting in significant mortality of species such as bar-headed geese, brown-headed gulls, black-headed gulls, ruddy shelducks, and great cormorants in China during April 2005.

Although the spread of H5N1 in Asia has been primarily due to movement of domestic birds, the movement of this virus into wild birds raised the possibility that these species may also spread the virus. This was thought to be the case in August 2005, when bar-headed geese and whooper swans died on Erkhel Lake, Mongolia, in an area not known to have domestic poultry or fowl nearby.

Given the adaptation of highly pathogenic H5N1 avian influenza to wild birds, increasing concern has developed over the potential for migrating species to introduce the virus into new regions of the world such as North America. Therefore, at the request of the Homeland Security Council's Policy Coordinating Committee for Pandemic Influenza Preparedness, the U.S. Departments of Agriculture (USDA) and Interior (DOI) were asked to develop a coordinated National Strategic Plan for early detection of HPAI introduction into North America by wild birds. Dr. Tom DeLiberto (USDA-APHIS Wildlife Services) and Rick Kearney (USGS Biological Resources Division) convened an interagency Working Group, which consists of representatives from USDA, DOI, U.S. Department of Health and Human Services (HHS), the International Association of Fish and Wildlife Agencies (IAFWA), and the state of Alaska (Attachment 1).

On 10 August 2005, the Working Group met by teleconference to initiate development of a "Plan For the Detection of HPAI Virus in Migratory Birds in the United States". After some discussion among the participants it was decided that while the immediate concern was the introduction of highly pathogenic H5N1 avian influenza virus via migratory birds into Alaska and the Pacific Flyway (including Hawaii and other Pacific Islands), the group would also begin to address detection of the virus in all the North American flyways.

### ***Goal of the Strategic Plan***

The goal of this plan is to describe the essential components of a unified national system for the early detection of HPAI, specifically highly pathogenic H5N1 avian influenza, in migratory birds. While the immediate concern is a potential introduction of highly pathogenic H5N1 avian influenza into the U.S., the development of a system that is capable of detecting the introduction of all HPAI viruses through migratory birds would significantly improve the biosecurity of the Nation. This document provides guidance to Federal, State, university, and non-governmental organizations for conducting HPAI monitoring and surveillance of migratory birds in the U.S. It is expected that this document will be used by agencies and organizations to develop regional and/or state-specific implementation plans for HPAI surveillance.

Data collected in accordance with the guidelines presented in this document will be assimilated into a National database for use by all agencies, organizations, and policy makers. Furthermore, although the original charge of the Working Group was to monitor migratory birds as a potential route of entry into the U.S., the standardized methodologies and procedures identified in this

document are applicable to other wild birds as well. Agencies and organizations conducting monitoring and surveillance in non-migratory birds are encouraged to follow these guidelines so that their data can be incorporated into and tracked via the National Early Detection System. This system for highly pathogenic H5N1 avian influenza detection will provide early warning for potentially catastrophic mortality events in North American wild birds and poultry, and minimize the potential for human exposures. Agencies and organizations are encouraged to participate in this system by following the guidelines presented in this document when conducting AI sampling in wild birds.

While this plan focuses on detection of highly pathogenic H5N1 avian influenza virus, the Working Group fully supports efforts to characterize all AI viruses in wild birds. Such information is critical to our understanding of the ecology of AI viruses and their transmission among wildlife, livestock, and humans. Birds will be sampled in conjunction with existing studies when possible, and additional bird captures will be initiated as necessary to provide a broad species and geographic surveillance effort.

### ***A National Early Detection System for Highly pathogenic H5N1 avian influenza in Migratory Birds***

The ability to efficiently control the spread of a highly infectious, exotic disease such as highly pathogenic H5N1 avian influenza, is dependent upon the capacity to rapidly detect the pathogen if introduced. For this reason, a National Early Detection System for Highly pathogenic H5N1 avian influenza in Wild Migratory Birds is not only prudent, it is necessary. Effective implementation of this National Detection System will require decentralized planning and execution at regional and state levels, combined with centralized coordination to ensure national level analysis of surveillance data for risk assessment. It also must involve a partnership between public and private interests and include efforts by Federal, State, and local governments as well as nongovernmental organizations, universities, and other interest groups. Lastly, it requires flexibility and commitment by all groups for successful implementation.

#### **Decentralized Planning and Execution**

Wild migratory birds, by their very nature, are not subject to disease containment controls as are domestic birds and people. While their movements are generally uncontrollable, these movements are largely predictable on both a daily and seasonal basis. Local movements within or between breeding, feeding, and roosting areas are frequently well known by State and local wildlife management authorities and others familiar with local bird populations. Long range movements associated with seasonal migration are also well known for many species, especially those waterfowl and shorebird species of particular interest in highly pathogenic H5N1 avian influenza detection and surveillance.

Coordinating groups such as the four Flyway Councils already exist to deal with issues related to migratory bird management on a broad geographic scale. These Councils include representation from each of the States in their respective bird flyways as well as the U.S. Fish and Wildlife Service. Therefore, the planning and execution of local and regional highly pathogenic H5N1

avian influenza early detection efforts will best be accomplished by the States in collaboration with Federal agencies.

### Centralized Coordination

States and flyways are exposed to varying degrees of threat from highly pathogenic H5N1 avian influenza. Each has unique circumstances that will shape the direction and intensity of its early detection efforts. Consequently, gaps among regional programs may emerge over time. Centralized coordination will evaluate the effectiveness of state and regional efforts, allowing for prioritization of available federal resources.

Integration of this National Early Detection System with similar influenza surveillance systems in other species (e.g., domestic, feral, zoo) as well as humans will also require centralized coordination. Surveillance data from all of these systems will be incorporated into national risk assessments, and preparedness and response planning efforts.

### ***Geographic Prioritization of Sampling Efforts***

This Strategic Plan targets bird species in North America that have the highest risk of being exposed to or infected with the highly pathogenic H5N1 avian influenza subtype because of their migratory movement patterns. Currently, these include birds that migrate directly between Asia and North America, birds that may be in contact with species from areas in Asia with reported outbreaks, or birds that are known to be reservoirs of AI. However, should highly pathogenic H5N1 avian influenza virus be detected in domestic birds in the U.S., sampling of wild birds within the affected flyway may become a high priority as well.

In general, bird flyways represent migration corridors within continental landmasses. However, Alaska and areas in Eastern Siberia represent a unique situation where major flyway systems cross continental boundaries (Attachment 2, fig. 2-1). Two major Asian flyways (the East Asian-Australasian and East Asian) include both Southeast Asia and the Arctic regions of Siberia, the Russian Far East, and Alaska. The East Asian-Australasian Flyway, defined primarily in the context of shorebird use, extends across 20 countries from the Siberian and Alaskan Arctic through North and Southeast Asia including U.S. trust territories in the Pacific to Australia and New Zealand.

Similarly, in North America, the Pacific Flyway extends from Arctic Canada, Alaska, and Eastern Siberia through coastal and western regions of Canada, the United States and Mexico, and on to Central and South America (Attachment 2, Fig. 2-2). Many migratory species that nest in Arctic Siberia, Alaska, and Canada follow the Pacific Flyway to wintering areas. Although not considered a major pathway, birds from both Eastern Siberia and Alaska intermingle in both the Pacific and Central Flyways. The overlap at the northern ends of these flyways and in Hawaii and Oceania establishes a path for potential disease transmission across continents and for mixing, re-assortment, and exchange of genetic material among strains from Eurasia and North America.

If highly pathogenic H5N1 avian influenza virus spreads to North America via migratory birds, the above analysis of the major flyways suggests that the virus would most likely arrive first in Alaska. Such a scenario is reasonable, as the contribution of Eurasian AI viruses to the genetic composition of viruses in North American migratory birds has already been demonstrated. Given the current knowledge on highly pathogenic H5N1 avian influenza distribution, the Working Group developed a prioritized sampling approach based on Alaska and the major North American flyways.

This approach prioritized the following regions in decreasing order of importance:

1. Alaska, the Pacific Flyway, and Oceania
2. Central Flyway
3. Mississippi Flyway
4. Atlantic Flyway

Agencies participating in the development of this plan are committed to efforts that ensure adequate sampling based on the above prioritization. However experiences with previous introductions of exotic diseases into North America (e.g., West Nile Virus) have demonstrated that detection and surveillance systems must be adaptable to changes in pathogens and risk factors associated with their potential introduction. If changes in the relative risks of highly pathogenic H5N1 avian influenza introduction into the US result in regional reprioritization, agencies must be prepared to redistribute resources accordingly.

### ***Sampling Strategies***

This strategic plan recommends decentralized planning and execution of highly pathogenic H5N1 avian influenza early detection efforts. To provide a uniform structure for the development of local plans, it recommends the consideration of five strategies for collecting monitoring and surveillance data on highly pathogenic H5N1 avian influenza virus in wild birds. Agencies and organizations are encouraged to use one or more of these strategies when designing AI surveys in wild birds. These strategies are:

#### **Investigation of Morbidity/Mortality Events (Attachment 3):**

Over 40 species of wild birds have been shown to be susceptible to infection with highly pathogenic H5N1 avian influenza virus. While not all species infected necessarily exhibit disease, the current strain(s) of H5N1 circulating in Asia have been shown to cause morbidity and mortality in a wide variety of these species. The systematic investigation of morbidity and mortality events in wild birds to determine if highly pathogenic H5N1 avian influenza is playing a role in causing illness and death offers the highest and earliest probability of detecting the virus if it is introduced by migratory birds into the United States. State natural resource agencies and Federal refuges and parks, primarily within the DOI's U.S. Fish and Wildlife Service National Wildlife Refuge System and the National Park Service, are the principal authorities in a position to detect and respond to mortality events involving wild birds. Morbidity and mortality events

involving wildlife are often detected by, or reported to, these agencies and entities. This strategy capitalizes on an existing morbidity/mortality program being conducted by DOI and its partners.

#### Surveillance in Live Wild Birds (Attachment 4):

This strategy incorporates sampling of live-captured, apparently healthy wild birds to detect the presence of highly pathogenic H5N1 avian influenza virus. This effort will select bird species in North America that represent the highest risk of being exposed to, or infected with, Highly pathogenic H5N1 avian influenza virus because of their migratory movement patterns, which include birds that migrate directly between Asia and North America, or birds that may be in contact with species from areas in Asia with reported outbreaks. Should highly pathogenic H5N1 avian influenza virus be detected in domestic birds in the U.S., sampling of wild birds in the flyway in the affected area may become a high priority as well. Data collected by organizations currently conducting research and monitoring for avian influenza in Alaska will be incorporated with additional bird captures as necessary to provide a broad species and geographic surveillance effort. This strategy capitalizes on research activities currently being conducted by DOI, USDA and their partners.

#### Surveillance in Hunter-killed Birds (Attachment 5)

Check stations for waterfowl hunting are operated by the US Fish and Wildlife Service and state natural resource agencies. Hunter check stations provide an opportunity to collect additional samples to determine the presence of HPAI and other subtypes of avian influenza viruses and supplement data collected during surveillance of live wild birds. As with surveillance of live wild birds, sampling of hunter-killed birds will focus on hunted species that are most likely to be exposed to HPAI in Asia; have relatively direct migratory pathways from those areas to the U.S. via Alaska or directly to the Pacific Coast; mix in Alaska staging areas with species that could bring the virus from Asia; or should HPAI be detected in domestic birds in the U.S., may mix with wild birds in the flyway of the affected area. Collection of samples from these species will occur at hunter check stations in the lower 48 states during hunting seasons in areas where these birds stage during migration or over-wintering.

#### Sentinel Species (Attachment 6):

Waterfowl, exhibition gamefowl, and poultry flocks reared on backyard premises have been used as sentinels for active surveillance for avian diseases of interest to the commercial poultry industry and regulatory agencies. Currently in Alaska, the State veterinarian uses targeted surveillance of domestic flocks at concentration points due to remote location of villages and lack of resources; enthusiasts travel to poultry exhibitions with birds from distant locations; and surveillance effectively covers a large geographic area. Enhancement of this approach would be valuable. However, placement of sentinel ducks in strategic locations may also prove useful. Placement of sentinel ducks has been used successfully for surveillance of diseases of importance to the poultry industry, including influenza A. Also, sentinel ducks in wild pelagic bird colonies improved virus detection rates fivefold, suggesting that this approach is advantageous in ecological studies.

## Environmental Sampling (Attachment 7):

Avian influenza viruses are generally released by waterfowl through the intestinal tract and viable virus can be detected in both feces and the water in which the birds swim, defecate and feed. This is the principal means of virus spread to new avian hosts and potentially to poultry, and other susceptible livestock. Analysis of both water and fecal material from waterfowl habitat can provide evidence of AI virus circulating in wild bird populations, the specific AI subtypes, levels of pathogenicity, and possible risks to poultry and susceptible livestock. Monitoring of water and/or fecal samples gathered from waterfowl habitat is a reasonably cost effective, technologically achievable means to assess risks to poultry.

### **Sample Collection**

Samples collected for AI surveillance may include carcasses, tracheal and cloacal swabs, feces, and environmental samples (e.g., water). Prior to initiating a surveillance activity, it is important to identify the laboratory in which the samples will be submitted. Sample handling and transportation procedures may differ among laboratories. It is recommended that samples collected for inclusion into the National Early Detection System be submitted to a laboratory that uses standardized procedures identified in the Laboratory Diagnosis section of this document or by using the attached detailed descriptions of sampling methodologies.

If birds are found morbid or dead, it is important to use proper personal protection techniques ([http://www.nwhc.usgs.gov/publications/wildlife\\_health\\_bulletins/WHB\\_05\\_03.jsp](http://www.nwhc.usgs.gov/publications/wildlife_health_bulletins/WHB_05_03.jsp), <http://www.cdc.gov/flu/avian/professional/protect-guid.htm>) and to submit the entire carcass to a veterinary diagnostic laboratory for necropsy (Attachment 8). Field biologists should contact the specific laboratory that they will be working with well in advance of any specimen collection and shipping to receive specific instructions for specimen submissions to that laboratory. Laboratories should always be notified ahead of time when a shipment is being made to their facility.

When collecting samples from live or hunter-killed birds, tracheal and cloacal swabs are preferred. Most AI strains tend to replicate more efficiently in the intestinal tract than in the respiratory tract of natural host species (i.e., waterfowl and shorebirds). Consequently, cloacal swabs are generally preferred. However, recent isolations of highly pathogenic H5N1 avian influenza virus in wild birds have documented higher levels of virus in tracheal samples. Therefore, it is recommended that both samples be collected from birds when possible. While the collection of cloacal swabs is a relatively easy procedure, obtaining proper tracheal swabs can be problematic and requires personnel trained in the sampling technique. Examples of tracheal/cloacal swab collection protocols can be found in Attachment 9. Tracheal and cloacal swabs should be placed in separate tubes, and swabs should not be pooled across individuals.

Monitoring of water and/or fecal samples gathered from waterfowl habitat is a reasonably cost effective, technologically achievable means to detect the presence of HPAI and alert decision makers to the risks to poultry in the Western Hemisphere from new, potentially highly pathogenic subtypes of AI (Attachment 7). A surveillance system based on water sampling is not ready to implement at the present. However, the validation of this method could come on-

line in a short period of time and would represent considerable cost savings without loss of sensitivity. Fecal sampling is an established technique and is ready for use in surveillance with the establishment of sampling guidelines. Both approaches yield advantages where individual bird sampling is too costly or logistically impractical. Either approach could yield a spatial and habitat risk assessment for site contamination with highly pathogenic H5N1 avian influenza virus. The main considerations are where and when to get the samples, ensuring proper storage and transport, and the capacities and capabilities of the laboratories doing the analyses. Real-time reporting and the infrastructure to support such reporting is a serious constraint on any surveillance system. The ability to integrate, analyze, and responsibly disseminate these data is critical and needs to be addressed.

### ***Sample Size Determination***

Prior to initiating a surveillance program, it is important to determine the sample size necessary to make statistically valid inferences concerning the presence of highly pathogenic H5N1 avian influenza virus in a sample population. In the context of this plan, the population of interest is not defined because this definition will vary by geographic location, time of year, species of interest, and sampling method employed. For example, sampling a breeding population versus a wintering population, for a single species, may result in very different interpretations of the geographic distribution of the population of interest. If water samples are being collected, then the population may consist of several water bodies. Therefore, it is crucial that prior to collections beginning, statistically valid sample size estimations be incorporated into regional and state implementation plans.

### ***Laboratory Diagnostics***

All samples collected for inclusion in the National Early Detection System should be analyzed in accordance with the standard procedures included in this document. A list of laboratories certified to conduct testing for highly pathogenic H5N1 avian influenza virus is included in Attachment 11. Samples will be analyzed as soon as possible after collection. Tracheal/cloacal swabs and fecal samples will be analyzed by real-time reverse transcriptase-polymerase chain reaction (RT-PCR) using the matrix gene RT-PCR assay (Attachment 12). The matrix gene RT-PCR assay is capable of detecting all 16 hemagglutinin and nine neuraminidase subtypes. Matrix gene RT-PCR-positive samples would indicate the presence of avian influenza and they should be further characterized by the H5- and H7-specific RT-PCR assays of Spackman et al. (2002) as modified in Attachment 11. The H5 RT-PCR test is known to detect the current Highly pathogenic H5N1 avian influenza viruses.

Positive H5 and H7 RT-PCR tests would indicate the presence of AI viruses with the potential of causing pathology in domestic poultry. Therefore, all samples positive for H5 and H7 by RT-PCR will be submitted for virus isolation for verification. Samples positive for live virus in virus isolation and positive for H5 or H7 by RT-PCR will be submitted to the USDA APHIS National Veterinary Services Laboratory (NVSL) for confirmation. The NVSL is capable of performing the intracranial chicken pathogenicity index (ICPI) test on the resultant virus to determine directly the pathogenicity of the virus in chickens. Identification of a highly pathogenic H5 or H7 virus is a reportable disease and immediate notification to the agency submitting the sample,



the state veterinarian, the area veterinarian in charge (AVIC), the state public health official and the CDC/USDA Select Agent program. Samples will be immediately secured as required by the Select Agent Programs.

All positive H5 and H7 samples will also be sent to the USDA Agriculture Research Service Southeastern Poultry Research Laboratory in Athens, GA, for complete molecular sequencing. This will provide for complete typing of the virus and allow for phylogenetic analysis.

### ***Data Management***

Real-time reporting and the infrastructure to support such reporting is a serious constraint on any surveillance system. The ability to integrate, analyze, and responsibly disseminate these data is critical. In addition, the data collected for this National Surveillance System will consist of samples submitted by many agencies and organizations. This will require a system to manage the input of animal and sample collection data through multiple routes, the ability to easily match, compare, and transfer laboratory data about these samples, and provide a platform in which all data is secure, accessible, and able to be mapped and used for spatial modeling.

The National Biological Information Infrastructure Wildlife Disease Information Node (WDIN) managed by the U.S. Geological Survey's National Wildlife Health Center has created a prototype web-enabled HPAI data management system, which will serve as a template for data collected from live and hunter-killed wild birds. (See <http://wildlifedisease.nbi.gov/ai>). The WDIN has developed comparable systems for the management of data from multiagency wildlife disease surveillance efforts such as Chronic Wasting Disease, and for USDA APHIS Wildlife Services Plague and Tularemia. General aspects of the proposed WDIN Interagency HPAI Data Management System are described in Appendix 13.

Sentinel bird data will be incorporated into a web-enabled, national data management system for backyard and small-flock poultry developed by the USDA APHIS Veterinary Services' Application Information Management Team at the Centers for Epidemiology and Animal Health. This database system was developed to reduce the number of data-collection problems experienced by field personnel and to generally improve the quality and efficiency of data collection. The initial testing of the design occurred in October 2005, with actual deployment scheduled for December 2005. If the project is successful in the pilot state of California, the system will likely be expanded for national implementation in 2006. This system will allow all necessary data collected in the field to be shared among all approved organizations without the need for manual data entry, and will provide greater chain-of-custody assurance from a legal and diagnostic perspective. Field personnel will be equipped with computer hardware and software which will facilitate the rapid and accurate collection of samples and data. These devices will share the collected information as needed with the diagnostic lab (National Veterinary Services Laboratories), and will send the data to primary information systems within USDA. To assist in data entry and to further improve data quality, bar-coding will be implemented as key identifiers for samples collected and for cases submitted.

### ***Recommendations***

Given the current state of knowledge of the epidemiology of highly pathogenic H5N1 avian influenza virus it is recommended that a coordinated interagency/organization early detection system be implemented in the U.S. An analysis of risk factors, including current worldwide distribution of the virus and the migratory patterns of wild birds, indicated that this system should primarily focus sampling efforts in Alaska, Oceania, and the Pacific and Central flyways. However, if adequate resources become available, the system should be expanded to include surveillance of migratory birds in the Mississippi and Atlantic Flyways as well.

State and Federal agencies should immediately begin developing implementation plans based on the guidance provided in this Strategic Plan. Development of these plans should be conducted with the participation of all relevant management agencies and organizations such that sampling designs are produced that allow for statistically sound inference of the presence or absence of highly pathogenic H5N1 avian influenza virus in wild birds. Furthermore, it is recommended that such coordination be conducted through the Flyway Councils, so that regionally based sampling designs can be implemented. Each Flyway (Atlantic, Mississippi, Central, and Pacific) has a Flyway Council, a formal organization generally composed of one member from each State and Province in that Flyway. The Flyway Councils, established through the International Association of Fish and Wildlife Agencies (IAFWA), also assist in researching and providing management techniques for Federal, State, and Provincial Governments, as well as private groups and the public.

State and Federal agencies also should develop communication plans in the event that a HPAI is detected in wild birds. For example, highly pathogenic H5N1 avian influenza virus is a reportable disease that requires notification of the State Veterinarian, and the Area Veterinarian in Charge (AVIC). Highly pathogenic H5N1 avian influenza is also a CDC/USDA Select Agent, requiring notification of the CDC/USDA Select Agent Programs and adherence to Select Agent guidelines is required.

Finally, it is recommended that a Steering Committee, consisting of one representative each from USGS, FWS, USDA APHIS, IAFWA, HHS, the National Flyway Council, and the State of Alaska be formed to coordinate wild bird AI surveillance in the United States. Specific roles of this Committee should include:

- Facilitate communication between state and federal agencies, and organizations involved in AI surveillance for wild birds.
- Coordinate implementation and data analysis of AI surveillance programs nationally.
- Provide periodic summaries of AI surveillance for wild birds in the United States.
- Provide periodic recommendations for AI surveillance in wild birds based on previous sampling efforts and changes in virus epidemiology.
- Facilitate communication and coordination among state and federal agencies for contingency planning and other preparations for the appearance of highly pathogenic H5N1 avian influenza virus in wild birds in North America.

Sampling strategies to detect highly pathogenic H5N1 avian influenza virus in wild bird populations will change depending upon the risk assessment and management goals and prevailing status of the pathogen in North America. For early detection of highly pathogenic

H5N1 avian influenza virus, efforts should focus on likely cross-over routes of birds from Asia to North America (e.g., Alaska). Efforts should focus on areas of high aggregations of waterfowl intersecting with logistical sampling support such as the National Wildlife Refuge System and state waterfowl management areas.

If highly pathogenic H5N1 avian influenza virus gains a foothold in North America, the surveillance network should be placed along known waterfowl movement paths from the point of origin (i.e., point of detection). These paths can be inferred from known migration routes of specific species. However, practically, and given the patterns emerging in Eurasia, if highly pathogenic H5N1 avian influenza virus becomes established in North America the likelihood of rapid and diffusive spread across the continent is high. At this point local waterfowl and environmental sampling should target areas of strategic value, e.g., human population centers and areas of high density of poultry production. In the former case, such areas would be represented by urban zoo-parks and lakes. These areas would represent the highest level of risk of human contact with contaminated water and/or waterfowl. In the latter case, ponds, lakes and waterfowl management areas around high density poultry production areas would provide the best ability to assess risk of transmission to humans and poultry. Surveillance efforts patterned on these areas are most amenable to local and state efforts for first detection and subsequent risk assessment if H5N1 subtype(s) achieve enzootic status in North America

