Guidelines on Wild Bird Surveillance for Highly Pathogenic Avian Influenza H5N1 Virus

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ABSTRACT: The recent spread of highly pathogenic avian influenza (HPAI) H5N1 from Southeast Asia into Europe and Africa emphasizes the need to better understand the mechanisms by which the disease is spread. Current wildlife surveillance has been limited to a combination of targeted sampling, opportunistic sampling, and recovery of dead wildlife. Recent interest in avian influenzas provides an opportunity to develop a global surveillance program for diseases in wild birds. This program should be based on specific principles with clearly defined aims, sound epidemiological sampling justifications, and sufficient technical skills and capabilities for appropriate field and laboratory activities. At present, although detection of H5N1 in healthy wild birds is sporadic, surveillance programs should be focused on: 1) determining the role wildlife plays in the epidemiology of HPAI H5N1 virus, and 2) guiding strategies to prevent disease exposure to humans and poultry. Surveillance should incorporate active and passive components using available natural history information such as intra- or interspecies mingling, population size, migratory patterns, and seasonal large-scale aggregations. Passive surveillance can include samples from bird banders/ringers, other wild bird research efforts, oil-spill response efforts, rehabilitation centers, zoological collections, beach-ad-bird surveys, and mortality events. A valuable wildlife surveillance program based on ecological and epidemiological information will require large-scale collaboration among national governments and ministries, multilateral agencies, nongovernment organizations, academicians, veterinarians, virologists, ornithologists, and many others.

Key words: Avian influenza, guidelines, HPAI, H5N1, surveillance, waterfowl, wild birds.

Over the past 5–10 yr, increasing numbers of infectious diseases in humans, wildlife, and domestic animals have emerged, and diseases such as mad cow disease, Lyme disease, monkey pox, nipah virus, and severe acute respiratory syndrome (SARS) have become common household terms. Most recently, with the emergence of highly pathogenic avian influenza (HPAI), subtype H5N1, global attention increased as people were informed that the virus could potentially represent the source of the next human influenza pandemic (de Jong et al., 1997).

While the scientific community acknowledges that this is primarily a poultry disease, and that prevention and control measures should be addressed at the level of agricultural production and farming practices, concern has been raised about the role that wild birds may play in harboring, perpetuating, and transmitting avian influenzas to new geographic locations internationally or intercontinentally. Wildlife species were not implicated as reservoirs or carriers of HPAI H5N1 during the initial outbreaks in poultry in Southeast Asia. From 2003 to 2005, however, large-scale mortality events in wild birds in China, Russia, Mongolia, and Eastern Europe clearly indicated that wild birds were susceptible to HPAI H5N1 (EMPRES Watch, 2005, 2006a; OIE, 2005–2006). Although suggestive, these initial events did not provide compelling evidence that infected wild birds could move these viruses over long distances during migration.

As of August 2006, wild bird mortality related to HPAI H5N1 had been documented in Azerbaijan, Hungary, Romania, Serbia, Turkey, and Ukraine, where concurrent poultry outbreaks were occurring. In other countries, such as Bosnia-Herzegovina, Bulgaria, Croatia, Czech Republic,
Georgia, Greece, Poland, Slovakia, and Slovenia, wild bird mortality occurred independent of known concurrent poultry outbreaks. This suggested that wild birds were infected elsewhere and flew into these countries before dying (EMPRES Watch, 2006b; Gilbert et al., 2006). This possibility was reinforced from fall 2005 through winter 2006 when HPAI H5N1 mortality in wild birds was documented across Western Europe. This mortality was mainly observed in mute swans (Cygnus olor), but other species were involved including mallard (Anas platyrhynchos) and common pochard (Aythya ferina) in France, great crested grebe (Podiceps cristatus) in Spain, little grebe (Tachybaptus ruficollis), tufted duck (Aythya fuligula), and common pochard in Switzerland, and whooper swan (Cygnus cygnus) in the United Kingdom (OIE, 2005–2006; USGS, 2006).

Although it had not yet been demonstrated that wild birds shed the virus during long-distance movements, a potentially important mechanism of disease spread via wildlife movements needed to be examined more carefully. To address the role of wild birds in the possible spread of HPAI H5N1, wildlife surveillance programs in 2005–2006 included sampling in the European Community in the framework of a European Commission (EC) activity; Eastern Europe, Asia, and Africa by the Food and Agriculture Organization (FAO) of the United Nations, Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), and Wetlands International; Canada by the Canadian Wildlife Service (CWS); United States by the US Fish & Wildlife Service (USFWS) and US Geological Survey (USGS); South and Central America, Africa, Eastern Europe, and Asia by the Wildlife Conservation Society’s Global Avian Influenza Network for Surveillance (GAINS); and many national programs, including, but not limited to, China, Russia, Mongolia, Switzerland, Germany, Vietnam, Indonesia, and Iran. These surveillance programs were specifically focused on surveillance for HPAI H5N1.

To date, over 80 species from 14 orders of birds have been found positive for HPAI H5N1 (USGS, 2006); almost all positive samples were from moribund, sick, or dead birds. These birds generally fell into three categories: migratory waterfowl, bridge species (most likely nonmigratory) which may transport disease from poultry to wildlife or vice versa, and predatory birds which likely scavenged dead birds (poultry or wild birds) or predated sick birds.

Information from healthy migratory birds includes more than 100,000 samples from EC, over 5,000 samples from Eastern Europe, Asia, and Africa, over 20,000 samples from the Americas, and hundreds of national program samples. Only one study thus far has demonstrated apparently healthy waterfowl positive for HPAI H5N1. The six positive birds (ducks) were not identified specifically in over 4,000 birds sampled in China from an area also used to raise domestic ducks (Chen et al., 2005).

In general, surveillance programs are difficult, complicated, and require a large, coordinated planning team(s). Most importantly, surveillance programs must be targeted and focused in order to obtain valuable information about disease ecology. Successful programs require biologists/ornithologists trained in proper monitoring and sample-collection techniques, year-round monitoring at wildlife habitat where species of concern are known to aggregate, and collaboration among biologists/ornithologists, veterinary services, and chief veterinary officers so coordinated disease sampling and testing activities can take place.

Broadly defined, surveillance includes the systematic collection of data referring to a particular disease in a population, the evaluation of such data, and the dissemination of the derived information to all who need to know. The classical definition encompasses two approaches and when applied specifically to HPAI H5N1 in-
cludes passive surveillance (opportunistic sampling from multiple sources especially related to wild bird morbidity and mortality events) and active surveillance (targeted samples to detect the targeted disease or agent).

Passive sampling takes advantage of pre-existing programs or sources of wild birds, such as rehabilitation or zoological exhibit animals, beached-bird monitoring programs, or birds collected through properly managed hunting programs. Samples cannot be guaranteed from a predetermined number of individuals, nor a specific species or group of species. In contrast, active surveillance programs can guarantee a certain level of detection and predetermined level of accuracy.

The most important goal of an HPAI H5N1 wildlife surveillance program is early detection of the virus, usually from a species or group of species that serve as a potential epidemiological reservoir. In the case of HPAI H5N1, a wildlife reservoir has not been identified or confirmed, and this limits the classical sampling approach according to a bimodal distribution (positive and negative individuals) in an infected population. Because an expected prevalence is not known, sampling intensity should conservatively focus on finding at least one positive animal assuming a very low prevalence (i.e., 0.5%). This often requires very large sample sizes.

The number of samples taken is a function of the population size combined with the expected number of positive animals. For infectious diseases, the population can be defined as the group of animals that has the same probability of being positive (or negative) during the surveillance period. Also, the geographical scope is of paramount importance: should surveillance occur at every lake or wetland in each country or at selected wetlands that have certain characteristics? The critical community size (CCS), defined as the number of individuals able to maintain an infection in the environment for a certain period of time, should guide this decision when possible. Although not known for HPAI H5N1, the CCS for low pathogenic avian influenza (LPAI) in wintering dabbling ducks indicates that wetlands containing 1,200–1,500 waterfowl should be included in a surveillance program (Guberti et al., 2007). The number of wetlands might be reduced by combining population size with other risk factors, such as presence or number of backyard poultry, commercial farms, rice fields, or integrated farms.

Considering the mortality associated with HPAI H5N1 in some wild species (Hulse-Post et al., 2005; Sturm-Ramirez et al., 2005; Brown et al., 2006), the CCS for the virus must be higher than that required for LPAI viruses.

Finally, surveillance strategies for HPAI H5N1 should consider the potential temporal and spatial factors that affect prevalence as it exists with LPAI in wild bird populations. In ducks in the Northern Hemisphere, prevalence is highest during late summer and early fall (premigration staging) and declines rapidly during winter (Hinshaw et al., 1980; Webster et al., 1992). If HPAI H5N1 virus prevalence trends are similar to LPAI viruses, the probability of finding the virus in northern latitudes would be highest during the premigration staging and molt period at the end of summer; likewise, the virus may be more difficult to detect as these birds migrate south (e.g., sub-Saharan Africa or Mediterranean Basin), especially at overwintering sites.

Bearing in mind that relevant information (CCS, expected prevalence, metapopulation sizes, species susceptibility and lethality) is still lacking for the establishment of an HPAI H5N1 surveillance program, and that logistical and financial limitations exist, we recommend a combined passive and active surveillance scheme. This will provide the best approach to detect HPAI H5N1 early and to assess viral presence in potentially endemic areas. The combination of active and passive surveillance will provide answers to the following important questions: do
HPAI H5N1 viruses exist and persist in wild bird populations, and if so, where, when, and in what species do they occur? To answer these questions, the following recommendations are offered.

1) Implement bird observation and monitoring programs at key wildlife habitats to enable daily to weekly monitoring of bird deaths and facilitate collection and testing of fresh carcasses. This monitoring requires minimally trained staff, a reporting mechanism and information repository, and coordination with veterinary services to provide diagnostic support. This level of surveillance can be applied easily to any important bird habitat. Supplemental training of personnel involved in monitoring programs could provide insight into conservation issues such as species presence and absence during the year, numbers of individuals, behavioral ecology, changing environmental conditions, and presence of other avian diseases. If financial resources are limited, effort should be focused on sick or dead birds to facilitate finding HPAI H5N1 at a few select habitats where additional risk factors exist.

2) Based on the international epidemiological situation of HPAI H5N1, a prompt investigation of wild bird morbidity or mortality events should be considered at local areas when at risk. In areas that are ecologically linked with recent outbreaks or ongoing poultry outbreaks, single cases of mortality in high-risk species (mainly Anseriformes and Charadriiformes) must be investigated. In low-risk species and when concurrent poultry outbreaks are not occurring, unusual mortality events involving 10 or more individuals in less than a week within a 10 km radius from a wetland, lake, or pond should be investigated. The costs associated with this type of response are relatively minor, and information gained about other infectious diseases will be inherently valuable. If funding is limited, diagnostic work should be restricted to check for HPAI H5N1 virus only. Finally, full understanding of the disease ecology of HPAI in endemic or outbreak areas needs to include potential transmission between agricultural production and wetland habitats by “bridge species” such as doves (Columbidae), starlings (Sturnidae), sparrows (Passeridae), swallows (Hirundinidae), and other primary synanthropic bird species. An effective communication network to report any epidemiological event linked to the possible spread of the virus needs to be developed.

3) If expertise in bird capture and handling exists, and financial support is available, bird surveillance should be conducted on healthy, live birds using the principles outlined in the previous section, including: a viral prevalence less than 1%; tracheal swabs (or oropharyngeal swabs in smaller species) together with cloacal swabs collected on all birds; sample collection during seasons when viral detection is most likely; if waterfowl are to be sampled, wetlands containing more than 1,200–1,500 waterfowl should be targeted; and if possible, habitats adjacent to poultry farms, or species visiting these farms, should be sampled.

If capture of live healthy birds is not an option, then samples should be collected from nationally sanctioned hunted birds; however, prevalence may be affected if hunting seasons occur in late fall or winter. Note that this strategy lacks knowledge about the CCS and the populations investigated. Also, financial limitations and small sample sizes often associated with live bird captures may dictate sampling and laboratory testing efforts.

Sampling efficacy can be significantly improved if a wild reservoir of HPAI H5N1 virus exists and is identified and when global coordination and information exchange can address macroareas and species to be sampled in light of the
ongoing spatial distribution and epidemiological situation of HPAI H5N1 virus. Such information will improve surveillance at the local scale, especially in selecting species at risk, appropriate sample sizes, and appropriate season. Current HPAI H5N1 virus surveillance strategies using many locations, each with a relatively small sampling intensity, may not reveal infected birds because the prevalence (as of 1 April 2007) appears to be very low, and sampled individuals may not belong to the same population.

Only regular and repeated surveillance of appropriate habitats will have the sensitivity to detect mortality and provide opportunities to sample moribund or fresh carcasses where HPAI H5N1 is most likely to be found. Other ongoing programs, such as beached-bird monitoring, wildlife rehabilitation, or bird banding/ringing, also may provide inexpensive samples as long as the species are appropriate for HPAI H5N1 testing. These “passive surveillance” samples are opportunistic and capitalize on previously established programs.

Active targeted sampling programs developed by the EC, FAO, CWS, USGS, USFWS, and GAINS are only possible with significant financial backing. However, no active surveillance programs can guarantee early detection of the HPAI H5N1 virus if infection is sporadic and prevalence is low in wild birds. Surveillance programs can detect diseases only when a detectable level of disease is present, and even then, success depends on a combination of factors including viral epidemiological parameters, host population size, and sampling intensity.

Understanding whether a wild reservoir species exists, and then identifying possible drivers of HPAI emergence, such as anthropogenic changes to the environment, intensified agricultural practices, or selection pressure for dominance of viral strains adapted to survive in a modified environment (Morse, 1993; Schragg and Wiener, 1995), are important next steps in the control and management of HPAI H5N1 virus. Environmental, agricultural, and ecological conditions also affect disease infection rates, likelihood of transmission, and maintenance or persistence of disease. Once risk factors are clearly identified, resource management decisions, including those specific for improved biosecurity, can minimize disease spread among domestic poultry, wildlife, and humans.

LITERATURE CITED


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