Surveillance of Wild Birds for Avian Influenza Virus

Technical Appendix

Source References

The articles reporting avian influenza surveillance in wild birds included in this review were obtained by searching for [influenza OR ortho*] AND [virus*] AND [surve* OR monitor* OR sampl*] AND [wild* OR free-living OR “free living” OR feral OR migratory OR resident] AND [avian OR bird* OR waterfowl] on both Pubmed and Web of Knowledge on March 18, 2010. All studies were initiated between 1961 and 2007. We refined our list by including only peer-reviewed articles, and by excluding studies on captive individuals, domesticated species, or duplicate reports from the same study, resulting in the following 191 articles:


Dasen CA, Laver WG. Antibodies to influenza viruses (including human A2/Asian/57 strain) in sera from

Davidson WR, Yoder HW, Brugh M, Nettles VF. Serological monitoring of eastern wild turkeys for
Apr;24(2):348–51.

De Marco MA, Campitelli L, Delogu M, Raffini E, Foni E, di Trani L, et al. Serological evidences
showing the involvement of free-living pheasants in the influenza ecology. Italian Journal of

De Marco MA, Foni E, Campitelli L, Delogu M, Raffini E, Chiapponi C, et al. Influenza virus circulation
in wild aquatic birds in Italy during H5N2 and H7N1 poultry epidemic periods (1998 to 2000).

De Marco MA, Foni E, Campitelli L, Raffini E, Delogu M, Donatelli I. Long-term monitoring for avian
influenza viruses in wild bird species in Italy. Veterinary Research Communications. 2003

Viruses in Wild Waterfowl Wintering in Italy During the 1993–99 Period: Evidence of Virus

influenza surveillance in wild birds, game birds, domestic ducks and geese in North Eastern Italy.

Deem SL, Noss AJ, Cuellar RL, Karesh WB. Health evaluation of free-ranging and captive blue-fronted
Amazon parrots (Amazona aestiva) in the Gran Chaco, Bolivia. Journal of Zoo and Wildlife

Deibel R, Emord DE, Dukelow W, Hinshaw VS, Wood JM. Influenza Viruses and Paramyxoviruses in
Ducks in the Atlantic Flyway, 1977-1983, including an H5N2 Isolate Related to the Virulent

Dormitorio TV, Giambrone JJ, Guo K, Hepp GR. Detection and characterization of avian influenza and
other avian paramyxoviruses from wild waterfowl in parts of the southeastern United States.


Iashkulov KB, Shchelkanov MI, L’Vov SS, Dzhambinov SD, Galkina IV, Fediakina IT, et al. [Isolation of influenza virus A (Orthomyxoviridae, Influenza A virus), Dhori virus (Orthomyxoviridae, Thogotovirus), and Newcastle’s disease virus (Paromyxoviridae, Avulavirus) on the Malyi Zhemchuzhnii Island in the north-western area of the Caspian Sea] [in Russian]. Voprosy Virusologii. 2008;53(3):34–8.


Sharp GB, Kawaoka Y, Wright SM, Turner B, Hinshaw V, Webster RG. Wild ducks are the reservoir for only a limited number of influenza A subtypes. Epidemiology and Infection. 1993;110:161–76.


Estimating Minimum Detectable Prevalence

To determine probability of detecting at least one infected individual, let \( p \) be the prevalence of infection in a very large population (in which infected individuals are homogenously distributed). A randomly chosen individual from this population therefore has a probability of \( p \) of being infected, but also a probability equal to \( (1-p) \) of not being infected. If we sample \( n \) individuals from this population at random, the probability that none of them are infected is \( (1-p)^n \). Thus the probability of finding at least one infected individual \( (P_{x>0}) \) is then:

\[
P_{x>0} = 1 - (1 - p)^n
\]  

(1)

Rearranging equation 1, we can calculate how many individuals to sample \( n \) to be \( (P_{x>0}) \) confident of detecting at least one infected individual when prevalence is above some pre-defined threshold \( (p_{max}) \):

\[
n = \frac{\log(1-P_{x>0})}{\log(1-p_{max})}
\]  

(2)

While prevalence is rarely known before initiating a survey, a conservative limit of detection should be used; a nominal prevalence of 0.5% (i.e. \( n=597 \)) has been suggested, indicating that at least 600 samples are required to achieve 95% confidence of disease freedom.

The maximum prevalence \( (p_{max}) \) of infection that could have been in the population is also calculable if all \( n \) individuals were negative:

\[
p_{max} = 1 - (1 - P_{x>0})^{\frac{1}{n}}
\]  

(3)

For example, if 300 individual birds were tested but no infection was detected, the study can be 95% confident that prevalence is less than 1%.