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 samp*] 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:


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:

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

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 \( (p_{max}) \):

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

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:

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

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%.