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Surveillance of Wild Birds for Avian Influenza Virus

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Recent demand for increased understanding of avian influenza virus in its natural hosts, together with the development of high-throughput diagnostics, has heralded a new era in wildlife disease surveillance. However, survey design, sampling, and interpretation in the context of host populations still present major challenges. We critically reviewed current surveillance to distill a series of considerations pertinent to avian influenza virus surveillance in wild birds, including consideration of what, when, where, and how many to sample in the context of survey objectives. Recognizing that wildlife disease surveillance is logistically and financially constrained, we discuss pragmatic alternatives for achieving probability-based sampling schemes that capture this host–pathogen system. We recommend hypothesis-driven surveillance through standardized, local surveys that are, in turn, strategically compiled over broad geographic areas. Rethinking the use of existing surveillance infrastructure can thereby greatly enhance our global understanding of avian influenza and other zoonotic diseases.

Avian influenza virus (AIV) gained a high profile after the unprecedented bird-to-human transmission of highly pathogenic AIV (HPAIV) subtype H5N1 in 1997. Originating in Asia, HPAIV (H5N1) subsequently caused widespread deaths among wild and domestic birds in Southeast Asia and westward throughout Europe and Africa in 2005 and 2006. After ≈50 years of research in wild birds, a wide range of low-pathogenicity AIV (LPAIV) subtypes is known to circulate in numerous species (*1,2–5*), and LPAIVs are believed to perpetuate in aquatic bird populations (*6*). In contrast, outbreaks of HPAIV are extremely rare in wild birds (*7*). Although the role of wild birds in HPAIV maintenance remains controversial (*8*), the magnitude of the subtype H5N1 epidemics increased the demand for early recognition of potential threats to humans and poultry and an understanding of the natural history of AIV in wild birds. Consequently, surveillance of aquatic bird populations surged (*9*).

Although surveillance for AIV often uses state-of-the-art storage, transport and diagnostics, these must be underpinned by appropriate survey design, sampling, and interpretation in the context of the host population. In the wake of such rapid growth in surveillance, we reviewed the literature to determine a scientifically and statistically sound approach to the design, conduct, and interpretation of surveillance for AIV and other wildlife diseases.

Current Surveillance

We reviewed 191 published reports of surveillance in wild birds (online Technical Appendix, http://www.cdc.gov/EID/content/16/12/pdfs/10-0589-Techapp.pdf). The number of studies initiated per year rapidly increased after the first reports of HPAIV (H5N1) in Asia (Figure 1). All studies addressed 4 major lines of investigation: 1) early detection of HPAIVs; 2) ecology and epidemiology of LPAIV in host populations; 3) diversity and evolution of viral strains within wild birds; and 4) identification of the pathogens that infect individual birds or populations, often as part of multipathogen surveillance. Multiple aims can, and often are, addressed within the same surveillance program, albeit in a post hoc manner. However, identifying the aims in advance is vital, because what, when, and where to sample will critically depend on the purpose of the survey (*10,11*).

Early Detection of HPAIV

More than half of the studies reviewed, and all but a handful initiated since the mass bird deaths in 2005–2006, cited early detection of HPAIV as one of the main goals of conducting the research (Figure 1). Such early warning systems question whether HPAIV exists in a population at a given location and point in time. The global rarity of HPAIV in wild birds and apparent clustering of such cases (*7*) present additional challenges to addressing this aim.

Ecology and Epidemiology

Greater understanding of transmission cycles, reservoirs, and the role of wildlife in the dynamics of AIV invoke questions related to the epidemiology and ecology of the virus, including host range and spatial and temporal variation in infection (*12*,*13*). Elucidating such questions requires investigating not just presence or absence of infection in a specific host, but also prevalence over space and time.

Viral Diversity

Influenza viruses are highly diverse and capable of rapid genetic alteration. Understanding the pathogenic and antigenic properties of AIVs circulating in the host population and the rate and direction of genetic alterations could become a powerful tool for identifying transmission parameters, reservoir populations (*14*), viral maintenance in the face of host immunity (*12*,*15*), and factors promoting disease emergence (*10*). Such information also facilitates compilation of comprehensive diagnostic reference panels and generation of potential vaccines (*13*). Investigation of variation in the viral population requires isolates that represent the entire circulating virus pool.

Host Health

Almost 15% of the studies reviewed aimed to ascertain whether certain individuals or populations had been infected with AIV as part of broader health surveys within the context of conservation programs, or in an attempt to understand causes of death. Although these studies often have a predefined host population of interest, they are likely to be sensitive to the underlying spatial and temporal patterns of disease.

Critical Assessment

To characterize the specific features required for rigorous wildlife disease surveillance, it is critical to highlight methods that encumber our current approach. Our assessment therefore aims to foster the development of more objective and scientifically sound disease surveillance networks.

Maximizing Viral Yield

A successful surveillance program is often perceived as one that identifies a high number of positive samples. Moreover, exploitation of spatial, temporal, phylogenetic, and demographic differences in viral prevalence have been advocated to maximize the proportion of positive samples collected (*12,16*). Minimizing the number of negative samples is expedient from a laboratory perspective, particularly when labor-intensive virus isolation techniques are being used. However, a key tenet of surveillance is that the sampling scheme is representative: infection characteristics of the host population and genetic diversity of the viral population are sufficiently captured, and results can be interpreted on the basis of statistical probability (*11,17*). A study designed to maximize the number of positive samples by sampling historically high cohorts, populations, times, and locations can confirm the presence of the disease in the sampled cohort. However, such samples cannot be used to conclude the absence of AIV in the population or to estimate prevalence or diversity of circulating viral strains (*17*).

Host Range

Although AIVs have been isolated from >100 species, several species from the orders Anseriformes (ducks, geese, and swans) and Charadriiformes (shorebirds) are thought to act as the reservoir community for AIV (*6*), primarily because AIVs have been most frequently isolated from these groups (*9*). Yet, surveillance is rarely representative of the diversity of wild birds or their relative abundance at the time and location of sampling. Considerable bias exists toward species that are easily caught or are present in accessible areas at high concentrations (*9,13*). Surveys that have included a wide range of species often obtained samples in a highly opportunistic manner, resulting in few species being sampled in reasonable numbers (*12–13*). For instance, despite sampling >56,000 birds in the Netherlands from 1998 to 2009, only 20 of the 174 species were sampled >300 times. Moreover, prevalence in a given species may vary over space and time. Although passerines have often been found negative for AIV, recent evidence suggests that, when sampled in or near waterfowl-rich bodies of water, a high proportion of individuals from 8 different passerine families show infection (*18,19*). Current surveillance may, therefore, overlook many potential reservoir or transient host species and their role in the introduction, transmission, maintenance and diversity of AIV.

Temporal and Spatial Patterns

The prevalence of AIV infection has long been recognized to vary over time and space. Viruses have been most frequently isolated from duck populations in North America and Europe in late summer and early autumn (*5,15,20*), a pattern attributed to high concentrations of susceptible juvenile birds on premigratory staging grounds (*4,6*). Less frequent isolations from wintering populations have prompted suggestions that prevalence rapidly decreases over the course of autumn migration (*21*,*22*); thus, premigratory staging grounds in late summer and early autumn are considered the optimal time and location for conducting surveillance among waterfowl (*16*,*23*.*)* Yet when samples have been collected elsewhere, high numbers of AIVs have been isolated in winter (*21*,*24*), spring (*20*), and summer (*25*). Several positive samples from birds in the tropics (*26*) have also been found, including unexpectedly high numbers in tropical Africa (*27*). The temporal and spatial bias in existing surveillance may therefore result in delayed detection of novel strains or an incomplete understanding of AIV transmission, maintenance, diversity, and evolution.

Age-dependent Patterns

Pioneering work by Hinshaw et al. (*4*) found significantly higher prevalence of AIV infection among juvenile birds than among contemporaneously sampled adult birds, leading to the suggestion that immunological naivety may make juvenile birds a high-risk group within waterfowl populations. Emphasis has subsequently been placed on sampling juvenile birds; accounting for ≈80% in some recent surveys. However, wild bird populations are rarely composed of ≥80% juvenile birds, and numerous infected adults have also been found (*4*,*24*). Given that recent experimental results indicate that age at the time of infection might also affect the extent of viral shedding (*28*), different age cohorts may play different roles in the introduction, transmission, maintenance, and diversity of AIVs.

Site of Infection

AIVs replicate in the gastrointestinal tract (sampled by swabbing the cloaca or collecting droppings) and in the respiratory tract (sampled by swabbing the oropharynx) (*16*). Individual mallards (*Anas platyrhynchos*) have historically shown higher detection probability from cloacal c.f. oropharyngeal swabs (*29*; Figure 2). Accordingly, 61% of studies investigating contemporary infection sampled the gastrointestinal tract alone. However, the site of infection may differ between species. As part of ongoing surveillance (*21*,*29*), free-living Eurasian wigeons (*Anas penelope*) showed no difference in detection probability between the cloacal and oropharyngeal swabs ($p>0.05$, McNemar test; Figure 2). In contrast, white-fronted geese (*Anser albifrons*) were roughly 2× as likely to have infection detected in the oropharynx (6.58%; 95% confidence interval 6.57–6.59) than in the cloaca (3.13%; 95% confidence interval 3.13–3.14; $p<0.001$);

≈60% of the infected birds were positive by oropharynx sample alone (Figure 2). Together with the apparent oropharynx affinity of HPAIV (H5N1) in experimental and natural infections (*30*), these findings have ramifications for the quantification of viral diversity, prevalence of infection, or absence of AIV.

Disease-free Populations and Prevalence Estimates

In general, survey sample sizes must be sufficiently large to draw appropriate inferences, and interpretations of AIV in wild birds based on many current sampling schemes may be hampered due to the limited number of samples collected (*9*). Studies have often concluded that AIV, particularly HPAIV (H5N1), was absent from a certain population or location. Infected birds may indeed have been present, but at a prevalence below the level of detection of the study (*17*). Only 3 of the studies that reported negative findings acknowledged a detection limit, yet such information is crucial to screening for HPAIV incursion. Similarly, 81 (42%) of the articles reviewed explicitly reported prevalence or seroprevalence; however, just 3 of these accounted for the uncertainty of their estimates (i.e., confidence limits). Such reports have fostered an impression that prevalence is a fixed property of a given host population, rather than a dynamic quantity, potentially influenced by many temporal, geographic, and biological interactions.

Utility of Birds Found Dead

Many surveillance programs aimed at the early detection of HPAIV (H5N1) focus on collections from sick or dead birds, often without surveillance of the living avian population (*31*). Although finding an HPAIV (H5N1) infection is statistically more likely in birds found dead (*31*), the absence of dead birds (or infection in dead birds) does not indicate freedom from disease. Dead birds fail to provide information on any animals that survived the infection, any animals that were not infected, or any viruses that were not lethal (*30*). Moreover, large numbers of carcasses may go undetected or unreported (*10*).

Screening for Only the Current Strain of Interest

Recently, some studies have only screened for H5 strains. Yet, none of the known genotypes can be ruled out as potential candidates for future pandemics. Additional information on all circulating gene segments is preferable as a novel-incursion warning system and in the broader context of AIV ecology, epidemiology, and evolution, particularly because no additional sample collection is necessary.

A Way Forward?

Although ≈50 years have passed since AIVs were first detected in wild birds, research is still in the exploratory phase, primarily because sampling wild animals is logistically challenging and expensive and techniques for high-throughput molecular surveillance have only recently become available. Wildlife disease surveillance regularly involves limited samples obtained in various ways that are already readily available, such as ornithologist-captured and hunter-collected birds. Although these methods of convenience sampling are often assumed to be representative of a population, sampling biases (most notably selection bias) do occur, making it difficult to develop statistically valid estimates of disease absence or prevalence, regardless of how many birds are sampled.

Our critique illustrates that to build on the findings of existing surveillance a scientifically sound approach is required. A study's aims need to be clearly identified at the outset, and appropriately designed sampling regimes and diagnostic techniques must be used. The global distribution of AIV and its avian hosts presents a major hurdle for such hypothesis-based research, making it difficult for individual research groups to tackle these questions in isolation. Our review highlights the need for global collation of existing wild bird AIV data and infrastructure, as well as the pooling of expertise and resources between epidemiologists, ornithologists, geneticists, and conservation organizations to unravel the complex interactions among diverse host and viral populations and the environments they utilize. Many such international initiatives exist in principle; however, there are currently several challenges in terms of data coverage, compatibility, management, and ownership. The following section outlines key considerations pertaining to the design, implementation, and interpretation of local surveys that could ameliorate data coverage and compatibility problems, paving the way for increasingly integrated studies of AIV and other wildlife diseases.

Sampling Unit

Target Virus

Particular strains, especially those with a history of HPAIV potential (H5 and H7), are of greatest interest when screening for HPAIV (*16*). However, screening for other virus subtypes by virus isolation, or targeting the matrix gene segment in molecular-based diagnostics, will simultaneously enhance our ecologic, epidemiologic, and virologic understanding of AIV.

Dead or Alive

Birds found dead may indicate rapid changes in host range, geographic range, viral pathogenicity, or disease emergence, and as such warrant swift investigation. However, to clarify the presence or absence of HPAIV, as well as trends in LPAIV presence, prevalence, and circulating strains, such surveys should be paired with active surveillance of the living wild bird population.

Sampling Site within the Bird

Viral strains of different host origin may differ in their affinity for either the digestive or respiratory tract and may also differ between different host species. Sampling the cloaca/feces and oropharynx is therefore desirable when screening wild birds. Such differences also exemplify the need for experimental clarification of tract affinity and how this may influence interpretations based on a single sample type (e.g., droppings).

Which Populations Should Be Sampled?

Target Population

With >10,000 species of birds worldwide, careful selection of a local target population is critical to the design of any surveillance program. Because the prevalence of infection is generally low (requiring large sample sizes) and can vary over time and between locations within a species, it is difficult to make an initial assessment of the most important species to target on the basis of virus detection alone. Each of the surveillance aims outlined above may be most appropriately addressed by considering 1) populations with evidence of previous infection, or ecologic potential for infection (*33*), on the basis of not only existing literature and conventional monitoring but also serosurveillance in a large number of locally and regionally abundant species; and 2) Evidence of contemporary AIV infection in populations that were identified in step 1, and species in which AIV has historically been detected (for comparative purposes). Surveillance for emergent HPAIV may also benefit from targeting species displaying natural histories of interest, including species that link wild and human/agricultural populations or disparate locations.

Serologic studies have great potential for enhancing wildlife disease surveillance and understanding. However, in isolation, cross-sectional observations of seroprevalence provide insufficient information to interpret the degree to which a population has been infected with AIV. Without age specificity, high seroprevalence may indicate a recent outbreak of infection or long-term antibody maintenance rather than persistence of AIV infection in the population (*14,16*). Moreover, low seroprevalence may result from a high mortality rate among infected birds, a long time interval between infection and sampling, or species-specific differences in the sensitivity or specificity of the antibody diagnostics. Explicit interpretation of seroprevalence calls for age-specific sampling, longitudinal observations, understanding of the underlying epidemiologic dynamics, and experimental validation of antibody diagnostics.

Individual Birds within Populations

Within each species, infection may depend on multiple factors, including age and prior exposure to AIV (*4*), gender (*33*), and even nutrition or social status (*8*). Given that most capture methods inherently result in biases within these cohorts, a population should ideally be sampled to account for these differences. Experimental validation of such interindividual differences in infection could greatly enhance the design and interpretation of surveillance.

When, Where, and How Often to Sample?

When and where sampling is conducted will critically depend on the question at hand and should be representative of the biology of the hosts of interest. Single time or location studies may be sufficient to inform of novel incursions of HPAIV (Table) and may therefore be best matched to times/locations with a high risk for wild bird–poultry interaction. Changes in climatic conditions, host population dynamics, and host population immunity are likely relevant to understanding the ecology, epidemiology, and evolution of AIV in its natural host(s) (*34*). Enhancing our knowledge in these areas will require information from before, during, and after infection from ecologically connected populations (*35*), often over longer periods and across large spatial scales when studying migratory birds (*36*). Coordinated local surveys, both along flyways and over time, will greatly enhance these efforts.

How Many Individual Birds Should Be Sampled?

As prevalence decreases, an increasingly large number of birds need to be sampled to detect contemporary infection (Figures 3, 4). Deciding just how many is critically dependent on the study aim, with a clear distinction between surveys that aim to substantiate freedom from infection (presence or absence), and those that are designed to provide an estimate of disease prevalence.

Presence/Absence

In practice, it is not possible to confirm disease freedom in a large population by any direct observational method. Instead, appropriate sampling and analysis can demonstrate that at that time and location, prevalence was below a nominal detection threshold (online Technical Appendix) (*17*). Although this nominal minimum detectable prevalence assumes binomial sampling, it can also be used for gaining a rough quantitative estimate of the minimum number of samples required before embarking on a surveillance program (Figure 3; online Technical Appendix). Given that information on the absence of pathogens is crucial to understanding disease dynamics (*10*), postsurveillance reporting of such maximum undetected prevalence is highly desirable for all studies with negative findings.

Prevalence

The proportion of positive findings among a given number of samples is rarely sufficiently precise to inform population prevalence. Thus, the confidence intervals of any observed proportion should be calculated and reported alongside any prevalence estimates when reporting surveillance results. Such confidence limits depend on the number of samples taken and the underlying true (unbiased) prevalence of infection (Figure 4).

Achieving Effective Surveillance

Each of the points above highlight the need for surveillance that captures the underlying temporal, spatial, demographic, and phylogenetic variation in the wild bird population, often requiring detailed information on host population size, density, demographic structure, rates of recruitment and attrition, habitat utilization, and species composition. However, wildlife surveillance is also faced with substantial logistical and financial constraints. Effective surveillance, therefore, requires a compromise between sampling that is based on probability and the constraints of sample collection, transport and analysis, the details of which will depend on the specific objectives of the survey. To this end, it is critical to have active, investigator-defined surveillance designs based on probability on a larger scale while using convenience sampling within these units (*11*). For instance, probability methods could be used to plan the species, locations, and months of the year to sample, and a certain number of individual birds within these units could be sampled by ornithologists and hunters, with additional top-up sampling where necessary. Such convenience-within-probability surveillance could provide statistically valid estimates of disease absence and prevalence by reducing the effect of bias generated by sampling on a first-come-first-served basis. It facilitates stipulation of an upper limit to the use of convenience samples, allowing targeted allocation of limited sampling, diagnostic, and financial resources.

To employ such convenience-within-probability surveillance, samples will often need to be collected from times, places, and species that are not currently covered by ornithologists and hunters. Preferably, individual birds should be sampled to confirm species, gender, age, and body mass, and sampling of digestive and respiratory tracts. However, when it is logistically and/or financially difficult to capture live birds several alternatives exist. Swabbing of fresh, species-specific feces is 1 method for collecting a regulated number of samples (*16*). Species should be identified through careful presampling observation of flocks, or, when sampling mixed-species flocks, through DNA barcoding of the fecal samples (*37*). Given that AIV can be detected from the same nucleic acid extract used in species identification (*37*), and substantially more samples can be collected at a much higher frequency than traditional trapping methods, dropping samples may greatly enhance our capacity to detect AIV in the population. Other, more proximate surveillance methods include sampling surface water that is, has been, or is about to be inhabited by wild birds (*16*), as well as regular sampling of sentinel species (*38*). Both methods are likely to yield insight into infection in the broader host population (*16*), although their usefulness for understanding infection in specific populations must be carefully assessed.

Conclusions

Surveillance for wildlife diseases is an inherently arduous task. However, as the vanguard of our understanding of these diseases, surveillance warrants a scientific approach. To make major inroads into the broader understanding of AIV ecology, epidemiology, and evolution, as well as risks associated with HPAIV, an integrated sampling strategy with clearly defined aims and appropriate methods is required. The financial and logistical constraints of covering vast spatial and temporal scales call for concerted efforts among our combined virologic, ecologic, and genetic expertise.

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References

1. Easterday BC, Trainer DO, Tumova B, Pereira HG. Evidence of infection with influenza viruses in migratory waterfowl. Nature. 1968;219:523–4. PubMed DOI: 10.1038/219523a0

2. Slemons RD, Johnson DC, Osborn JS, Hayes F. Type-A influenza viruses isolated from wild free-flying ducks in California. Avian Dis. 1974;18:119–24. PubMed DOI: 10.2307/1589250

3. Webster RG, Morita M, Pridgen C, Tumova B. Ortho- and paramyxoviruses from migrating feral ducks: characterization of a new group of influenza A viruses. J Gen Virol. 1976;32:217–25. PubMed DOI: 10.1099/0022-1317-32-2-217

4. Hinshaw VS, Webster RG, Turner B. The perpetuation of orthomyxoviruses and paramyxoviruses in Canadian waterfowl. Can J Microbiol. 1980;26:622–9. PubMed DOI: 10.1139/m80-108

5. Süss J, Schafer J, Sinnecker H, Webster RG. Influenza virus subtypes in aquatic birds of eastern Germany. Arch Virol. 1994;135:101–14. PubMed DOI: 10.1007/BF01309768

6. Webster RG, Bean WJ, Gorman OT, Chambers TM, Kawaoka Y. Evolution and ecology of influenza A viruses. Microbiol Rev. 1992;56:152–79. PubMed

7. Alexander DJ. An overview of the epidemiology of avian influenza. Vaccine. 2007;25:5637–44. PubMed DOI: 10.1016/j.vaccine.2006.10.051

8. Feare CJ, Yasué M. Asymptomatic infection with highly pathogenic avian influenza H5N1 in wild birds: how sound is the evidence? Virol J. 2006;3:96. PubMed

9. Spackman E. The ecology of avian influenza virus in wild birds: what does this mean for poultry? Poult Sci. 2009;88:847–50. PubMed DOI: 10.3382/ps.2008-00336

10. Stallknecht DE. Impediments to wildlife disease surveillance, research, and diagnostics. Curr Top Microbiol Immunol. 2007;315:445–61. PubMed DOI: 10.1007/978-3-540-70962-6_17

11. Nusser SM, Clark WR, Otis DL, Huang L. Sampling considerations for disease surveillance in wildlife populations. J Wildl Manage. 2008;72:52–60. DOI: 10.2193/2007-317

12. Stallknecht DE, Brown JD. Ecology of avian influenza in wild birds. In: Swayne DE, editor. Avian influenza. Ames (IA): Blackwell Publishing; 2008. p. 43–58.

13. Olsen B, Munster VJ, Wallensten A, Waldenstrom J, Osterhaus A, Fouchier R. Global patterns of influenza A virus in wild birds. Science. 2006;312:385–8. PubMed DOI: 10.1126/science.1122438

14. Haydon DT, Cleaveland S, Taylor LH, Laurenson MK. Identifying reservoirs of infection: a conceptual and practical challenge. Emerg Infect Dis. 2002;8:1468–73. PubMed

15. Krauss S, Walker D, Pryor SP, Niles L, Li CH, Hinshaw VS, et al. Influenza A viruses of migrating wild aquatic birds in North America. Vector-Borne and Zoonotic Diseases. 2004;4:177–89.

16. Brown JD, Stallknecht DE. Wild bird surveillance for the avian influenza virus. In: Spackman E, editor. Methods in molecular biology, Vol 436. Totowa (NJ): Humana Press; 2008. p. 85–97.

17. Venette RC, Moon RD, Hutchison WD. Strategies and statistics of sampling for rare individuals. Annu Rev Entomol. 2002;47:143–74. PubMed DOI: 10.1146/annurev.ento.47.091201.145147

18. Peterson AT, Bush SE, Spackman E, Swayne DE, Ip HS. Influenza A virus infections in land birds, People's Republic of China. Emerg Infect Dis. 2008;14:1644–6. PubMed DOI: 10.3201/eid1410.080169

19. Gronesova P, Kabat P, Trnka A, Betakova T. Using nested RT-PCR analyses to determine the prevalence of avian influenza viruses in passerines in western Slovakia, during summer 2007. Scand J Infect Dis. 2008;40:954–7. PubMed DOI: 10.1080/00365540802400576

20. Wallensten A, Munster VJ, Latorre-Margalef N, Brytting M, Elmberg J, Fouchier RAM, et al. Surveillance of influenza A virus in migratory watefowl in northern Europe. Emerg Infect Dis. 2007;13:404–11. PubMed DOI: 10.3201/eid1303.061130

21. Munster VJ, Baas C, Lexmond P, Waldenström J, Wallensten A, Fransson T, et al. Spatial, temporal, and species variation in prevalence of influenza A viruses in wild migratory birds. PLoS Pathog. 2007;3:e61. PubMed DOI: 10.1371/journal.ppat.0030061

22. Stallknecht DE, Shane SM, Zwank PJ, Senne DA, Kearney MT. Avian influenza-viruses from migratory and resident ducks of coastal Louisiana. Avian Dis. 1990;34:398–405. PubMed DOI: 10.2307/1591427

23. Hanson BA, Luttrell MP, Goekjian VH, Niles L, Swayne DE, Senne DA, et al. Is the occurrence of avian influenza virus in Charadriiformes species and location dependent? J Wildl Dis. 2008;44:351–61. PubMed

24. Kleijn D, Munster VJ, Ebbinge BS, Jonkers DA, Muskens G, Van Randen Y, et al. Dynamics and ecological consequences of avian influenza virus infection in greater white-fronted geese in their winter staging areas. Proc R Soc Lond B Biol Sci 2010 Jul;277:2041–8.

25. Okazaki K, Takada A, Ito T, Imai M, Takakuwa H, Hatta M, et al. Precursor genes of future pandemic influenza viruses are perpetuated in ducks nesting in Siberia. Arch Virol. 2000;145:885–93. PubMed DOI: 10.1007/s007050050681

26. Haynes L, Arzey E, Bell C, Bucanan N, Burgess G, Cronan V, et al. Australian surveillance for avian influenza viruses in wild birds between July 2005 and June 2007. Aust Vet J. 2009;87:266–72. PubMed DOI: 10.1111/j.1751-0813.2009.00446.x

27. Gaidet N, Dodman T, Caron A, Balança G, Desvaux S, Goutard F, et al. Avian influenza viruses in water birds, Africa. Emerg Infect Dis. 2007;13:626–9. PubMed DOI: 10.3201/eid1304.061011

28. Costa TP, Brown JD, Howerth EW, Stallknecht DE. The effect of age on avian influenza viral shedding in Mallards (*Anas platyrhynchos*). Avian Dis. 2010;54:581–5. PubMed DOI: 10.1637/8692-031309-ResNote.1

29. Munster VJ, Baas C, Lexmond P, Bestebroer TM, Guldemeester J, Beyer WEP, et al. Practical considerations for high-throughput influenza A virus surveillance studies of wild birds by use of

molecular diagnostic tests. J Clin Microbiol. 2009;47:666–73. PubMed DOI: 10.1128/JCM.01625-08

30. Sturm-Ramirez KM, Hulse-Post DJ, Govorkova EA, Humberd J, Seiler P, Puthavathana P, et al. Are ducks contributing to the endemicity of highly pathogenic H5N1 influenza virus in Asia? J Virol. 2005;79:11269–79. PubMed DOI: 10.1128/JVI.79.17.11269-11279.2005

31. Komar N, Olsen B. Avian influenza virus (H5N1) mortality surveillance. Emerg Infect Dis. 2008;14:1176–8. PubMed DOI: 10.3201/eid1407.080161

32. Garamszegi LZ, Møller AP. Prevalence of avian influenza and host ecology. Proc R Soc B Biol Sci. 2007;274:2003–12.

33. Ip HS, Flint PL, Franson JC, Dusek RJ, Derksen DV, Gill RE, et al. Prevalence of influenza A viruses in wild migratory birds in Alaska: patterns of variation in detection at a crossroads of intercontinental flyways. Virol J. 2008;5:71. PubMed DOI: 10.1186/1743-422X-5-71

34. Reperant LA, Fuckar NS, Osterhaus A, Dobson AP, Kuiken T. Spatial and temporal association of outbreaks of H5N1 influenza virus infection in wild birds with the 0 degrees C isotherm. PLoS Pathog. 2010;6:e1000854. PubMed DOI: 10.1371/journal.ppat.1000854

35. Langstaff IG, McKenzie JS, Stanislawek WL, Reed CEM, Poland R, Cork SC. Surveillance for highly pathogenic avian influenza in migratory shorebirds at the terminus of the east Asian–Australasian Flyway. N Z Vet J. 2009;57:160–5. PubMed

36. Pearce JM, Ramey AM, Flint PL, Koehler AV, Fleskes JP, Franson JC, et al. Avian influenza at both ends of a migratory flyway: characterizing viral genomic diversity to optimize surveillance plans for North America. Evolutionary Applications. 2009;2:457–68. DOI: 10.1111/j.1752-4571.2009.00071.x

37. Cheung PP, Leung YHC, Chow CK, Ng CF, Tsang CL, Wu YO, et al. Identifying the species-origin of faecal droppings used for avian influenza virus surveillance in wild-birds. J Clin Virol. 2009;46:90–3. PubMed DOI: 10.1016/j.jcv.2009.06.016

38. Globig A, Baumer A, Revilla-Fernandez S, Beer M, Wodak E, Fink M, et al. Ducks as sentinels for avian influenza in wild birds. Emerg Infect Dis. 2009;15:1633–6. PubMed

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Table. Data requirements for assessment of major questions regarding avian influenza in wild birds*

Aim	Type of question	Geographic range	Temporal range	Frequency
Early detection of HPAIV	Presence/absence	Local/regional	Period when birds present	Approximately weekly (average infection duration)
Ecology and epidemiology	Comparative prevalence	Local to flyway, depending on the process in question	1 to many epidemic seasons (multiple times/year)	Weekly to monthly (multiple times before, during, and after an epidemic)
Diversity and evolution	Comparative prevalence (of viral strains)	Flyway to global	Decades (multiple times/year repeated for multiple years)	Monthly to seasonally

*Larger-scale studies can be compiled over large geographic areas from relevant local surveys that are methodologically comparable and over long periods from relevant annual surveys that are likewise methodologically comparable. HPAIV, highly pathogenic avian influenza virus.

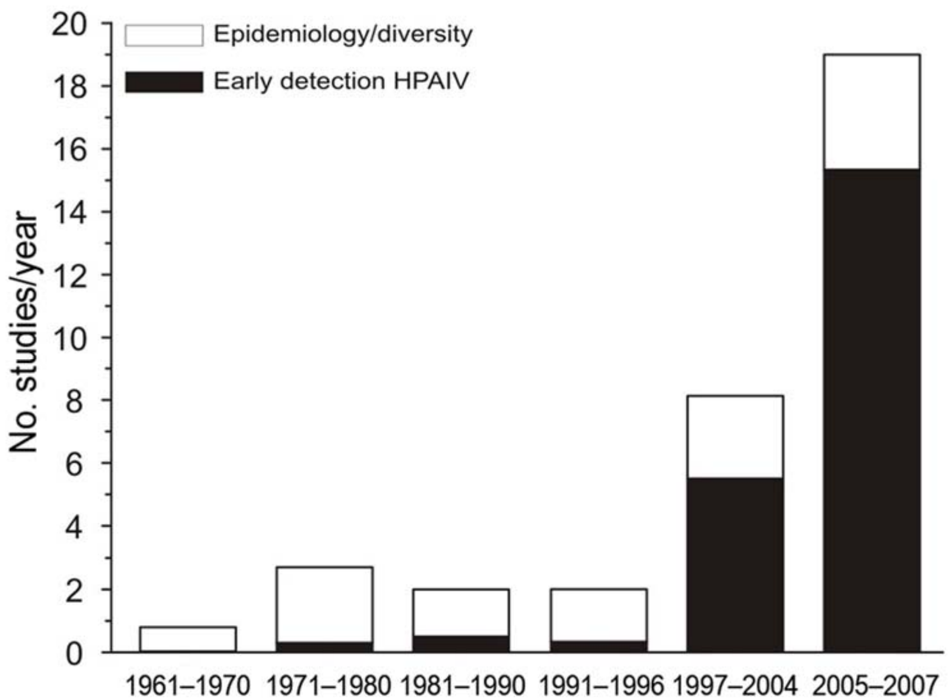

Figure 1. Average number of surveys of avian influenza in wild birds initiated per year in different awareness periods: each decade from the first discovery in 1961 until the outbreak of highly pathogenic avian influenza virus (HPAIV) (H5N1) in Asia in 1997; the period after the first outbreak, 1997–2004; and the period after mass deaths of wild birds from HPAIV (H5N1) (2005–2007). Black bar sections indicate studies citing the detection of contemporary HPAIV strains as one of the main aims of their survey are indicated in black; white bar sections indicate studies investigating other aspects of the wild bird–avian influenza system without mention of monitoring HPAIV.

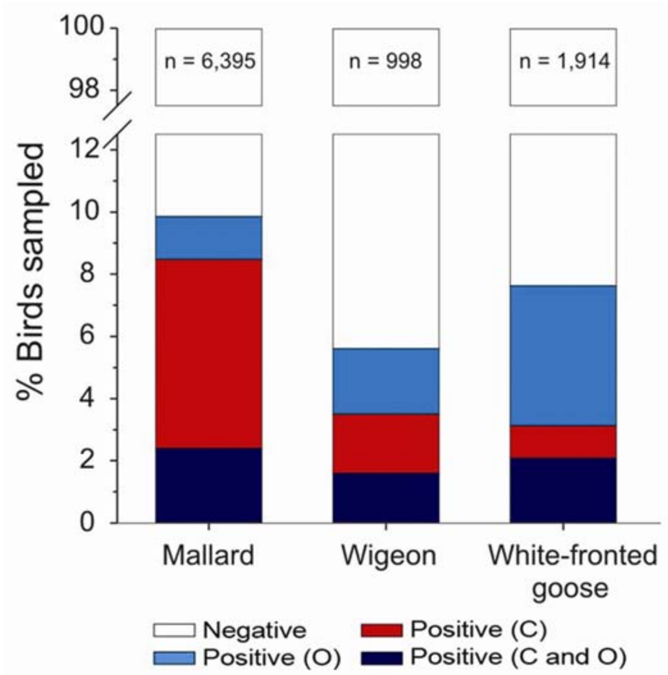

Figure 2. Proportion of wild mallards (*Anas platyrhynchos*), Eurasian wigeons (*Anas penelope*), and white-fronted geese (*Anser albifrons*) positive for low-pathogenicity avian influenza virus when sampled in the cloaca (C) and the oropharynx (O), the Netherlands, September 2006–March 2009.

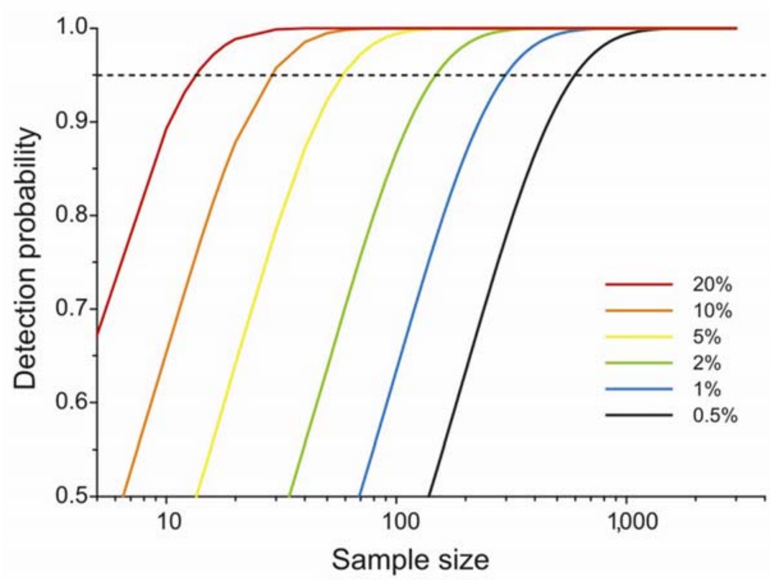

Figure 3. Probability of detecting ≥1 individual bird infected with avian influenza virus from a given number of samples selected at random from an extremely large population in which individual birds are infected at random at different prevalence levels. Although this nominal minimum detectable prevalence assumes binomial sampling, it can also be used for gaining a rough quantitative estimate of the minimum number of samples required before embarking on a surveillance program.

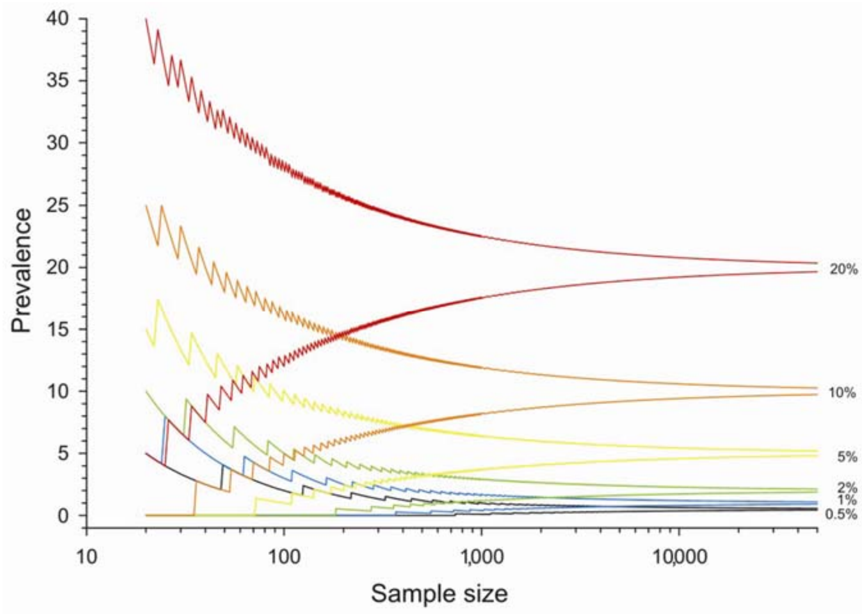

Figure 4. The 95% confidence intervals for prevalence in an independent population for a given number of samples, derived from the binomial distribution. Confidence intervals depend on the number of samples taken and unbiased prevalence of infection; they should be calculated and reported along with prevalence estimates when reporting surveillance results.

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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:

Abolnik C, Cornelius E, Bisschop SPR, Romito M, Verwoerd D. Phylogenetic analyses of genes from South African LPAI viruses isolated in 2004 from wild aquatic birds suggests introduction by Eurasian migrants. In: Schudel A, Lombard M, editors. OIE/FAO International Scientific Conference on Avian Influenza. Basel: Karger; 2006. p. 189–99.

Al-Attar MY, Danial FA, Al-Baroodi SY. Detection of Antibodies Against Avian Influenza Virus in Wild Pigeons and Starlings. Journal of Animal and Veterinary Advances. 2008;7(4):448–9.

Alekseev AY, Sharshov KA, Zolotykh SI, Drozdov IG, Shestopalov AM. Monitoring of influenza A viruses in synanthropic birds in South of Western Siberia in H5N1 epizootic and postepizootic period. Infection Genetics and Evolution. 2008 Jul;8(4):S32.

Alfonso CP, Cowen BS, Vancampen H. Influenza-a Viruses Isolated from Waterfowl in 2 Wildlife Management Areas of Pennsylvania. Journal of Wildlife Diseases. 1995 Apr;31(2):179–85.

Anraku MM, de Godoy F, Oscar MG, de Fario WC. Avian influenza in wild Brazilian birds. I. Serological survey by means of immunodiffusion [in Portuguese]. Revista do Instituto de Medicina Tropical de São Paulo. 1977;19(4):237–40.

Arenas A, Carranza J, Perea A, Miranda A, Maldonado A, Hermoso M. Type-A influenza-viruses in birds in southern spain - serological survey by enzyme-linked-immunosorbent-assay and hemagglutination inhibitin tests. Avian Pathology. 1990;19(3):539–46.

Artois M, Manvell R, Fromont E, Schweyer JB. Serosurvey for Newcastle disease and avian influenza A virus antibodies in great cormorants from France. Journal of Wildlife Diseases. 2002;38(1):169–71.

Astorga RJ, Leon L, Cubero MJ, Arenas A, Maldonado A, Tarradas MC, et al. Avian Influenza in Wild Waterfowl and Shorebirds in the Donana-National-Park - Serological Survey Using the Enzyme-Linked-Immunosorbent-Assay. Avian Pathology. 1994;23(2):339–44.

Austin FJ, Hinshaw VS. The isolation of Influenza-A viruses and paramyxoviruses from feral ducks in New Zealand. Australian Journal of Experimental Biology and Medical Science. 1984;62:355–60.

Bahl AK, Pomeroy BS, Easterday BC, Mangundimedjo S. Isolation of type A influenza viruses from migrating waterfowl along the Mississippi flyway. Journal of Wildlife Diseases. 1975;11:360–3.

Barbic L, Turk N, Zupancic Z, Kovac S, Stojevic Z, Drazenovic V, et al. Antibodies against human influenza viruses in sentinel duck flocks in the ornithological reserve Kopacki rit in Croatia. Veterinarski Arhiv. 2009 Nov-Dec;79(6):573–82.

Barral M, Alvarez V, Juste RA, Agirre I, Inchausti I. First case of highly pathogenic H5N1 avian influenza virus in Spain. BMC Vet Res. 2008 Dec;4:5.

Baumeister E, Leotta G, Pontoriero A, Campos A, Monalti D. Serological evidence of influenza A virus infection in Antarctica migratory birds. International Congress Series. 2004;1263:737–40.

Becker WB. Isolation and classification of tern virus - Influenza virus A/Tern/South Africa/1961. Journal of Hygiene. 1966;64(3):309–20.

Betakova T, Marcin J, Kollerova E, Molcany T, Dravecky M, Nemeth J, et al. Detection of an influenza virus in wild waterbirds migrating through Slovakia in autumn 2004. Acta Virologica. 2005;49(4):287–9.

Bolte AL, Lutz W, Kaleta EF. [Investigations on the occurrence of ortho- and paramyxovirus infections among free living greylag geese (*Anser anser* Linne, 1758)] [in German]. Zeitschrift Fur Jagdwissenschaft. 1997;43(1):48–55.

Bonner BM, Lutz W, Jager S, Redmann T, Reinhardt B, Reichel U, et al. Do Canada geese (*Branta canadensis* Linnaeus, 1758) carry infectious agents for birds and man? European Journal of Wildlife Research. 2004 Jul;50(2):78–84.

Busquets N, Alba A, Napp S, Sánchez A, Serrano E, Rivas R, et al. Influenza A virus subtypes in wild birds in North-Eastern Spain (Catalonia). Virus Research. 2010;[Epub ahead of print].

Campitelli L, Mogavero E, De Marco MA, Delogu M, Puzelli S, Freeza F. Influenza surveillance in birds in Italy (1999-2002): first evidence in the wild avian reservoir of direct virus precursor of strains circulating in commercial poultry. International Congress Series. 2004;1263:766–70.

Cattoli G, Terregino C, Guberti V, De Nardi R, Drago A, Salviato A, et al. Influenza virus surveillance in wild birds in Italy: Results of laboratory investigations in 2003-2005. Avian Diseases. 2007;51(1):414–6.

Chang CM, Lebarbenchon C, Gauthier-Clerc M, Le Bohec C, Beaune D, Le Maho Y, et al. Molecular surveillance for avian influenza A virus in king penguins (*Aptenodytes patagonicus*). Polar Biol. 2009 Apr;32(4):663–5.

Charlton KG. Antibodies to selected disease agents in translocated wild turkeys in California. Journal of Wildlife Diseases. 2000 Jan;36(1):161–4.

Chen HX, Shen HG, Li XL, Zhou JY, Hou YQ, Guo JQ, et al. Seroprevalance and identification of influenza A virus infection from migratory wild waterfowl in China (2004-2005). Journal of Veterinary Medicine Series B-Infectious Diseases and Veterinary Public Health. 2006 May;53(4):166–70.

Cheng MC, Wang CH, Kida H. Influenza A virological surveillance in feral waterfowl in Taiwan from 1998 to 2002. International Congress Series. 2004;1263:745–8.

Chernetsov I, Slepushkin AN, L'vov DK, Braude NA, Gavrilov AE. [Isolation of influenza virus from Chlidonias nigra and serologic examination of the birds for antibodies to influenza virus] [in Russian]. Voprosy Virusologii. 1980(1):35–40.

Dalessi S, Hoop R, Engels M. The 2005/2006 avian influenza monitoring of wild birds and commercial poultry in Switzerland. Avian Diseases. 2007;51(1):355–8.

D'Amico VL, Bertellotti M, Baker AJ, Diaz LA. Exposure of Red Knots (*Calidris canutus rufa*) to select avian pathogens; Patagonia Argentina. Journal of Wildlife Diseases. 2007;43(4):794–7.

Dasen CA, Laver WG. Antibodies to influenza viruses (including human A2/Asian/57 strain) in sera from Australian shearwaters (*Puffinus pacificus*). Bulletin of the World Health Organization. 1970;42(6):885–9.

Davidson WR, Yoder HW, Brugh M, Nettles VF. Serological monitoring of eastern wild turkeys for antibodies to Mycoplasma spp and avian influenza-viruses. Journal of Wildlife Diseases. 1988 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 Animal Science. 2005;4(3):287–91.

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). Avian Pathology. 2005 Dec;34(6):480–5.

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 Sep;27:107–14.

De Marco MA, Foni GE, Campitelli L, Raffini E, Trani LD, Delogu M, et al. Circulation of Influenza Viruses in Wild Waterfowl Wintering in Italy During the 1993–99 Period: Evidence of Virus Shedding and Seroconversion in Wild Ducks. Avian Diseases. 2003;47:861–6.

De Nardi R, Terregino C, Cattoli G, Toffan A, Beato MS, Guberti V, et al. Preliminary results of an influenza surveillance in wild birds, game birds, domestic ducks and geese in North Eastern Italy. Italian Journal of Animal Science. 2005 Jul-Sep;4(3):292–5.

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 Medicine. 2005 Dec;36(4):598–605.

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 Chicken Virus. Avian Diseases. 1985;29(4):970–85.

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. Poultry Science. 2009;88(4):851–5.

Douglas KO, Lavoie MC, Kim LM, Afonso CL, Suarez DL. Isolation and Genetic Characterization of Avian Influenza Viruses and a Newcastle Disease Virus from Wild Birds in Barbados: 2003-2004. Avian Diseases. 2007;51(3):781–7.

Downie JC, Hinshaw V, Laver WG. The ecology of influenza: Isolation of type ‘A’ influenza viruses from Australian pelagic birds. Australian Journal of Experimental Biology and Medical Science. 1977;55(DEC):635–43.

Downie JC, Laver WG. Isolation of a Type a Influenza-Virus from an Australian Pelagic Bird. Virology. 1973;51(2):259–69.

Ducatez MF, Tarnagda Z, Tahita MC, Sow A, de Landtsheer S, Londt BZ, et al. Genetic characterisation of HPAI (H5N1) viruses from poultry and wild vultures, Burkina Faso. Emerging Infectious Diseases. 2007;13(4):611–3.

Dusek RJ, Bortner JB, DeLiberto TJ, Hoskins J, Franson JC, Bales BD, et al. Surveillance for High Pathogenicity Avian Influenza Virus in Wild Birds in the Pacific Flyway of the United States, 2006–2007. Avian Diseases. 2009;53:222–30.

Easterday BC, Trainer DO, Tumova B, Pereira HG. Evidence of Infection with Influenza Viruses in Migratory Waterfowl. Nature. 1968;219(5153):523–4.

Ellström P, Latorre-Margalef N, Griekspoor P, Waldenstrom J, Olofsson J, Wahlgren J, et al. Sampling for low-pathogenic avian influenza A virus in wild Mallard ducks: Oropharyngeal versus cloacal swabbing. Vaccine. 2008 Aug;26(35):4414–6.

Fereidouni SR, H. BM, Starick E, Werner O, Amini H, Modirrousta H, et al. Serological Monitoring of Avian Influenza in Migratory Birds of Iran. Archives of Razi Institute. 2005;60:11–9.

Fereidouni SR, Werner O, Starick E, Beer M, C. HT, Aghakhan M, et al. Avian influenza virus monitoring in wintering waterbirds in Iran, 2003-2007. Virology Journal. 2010;[Epub ahead of print].

Ferrazzi V, Martin AM, Lelli D, Gallazzi D, Grilli G. Microbiological and serological monitoring in hooded crow (*Corvus corone cornix*) in the Region Lombardia, Italy. Italian Journal of Animal Science. 2007;6(3):309–12.

Ferro PJ, El-Attrache J, Fang XW, Rollo SN, Jester A, Merendino T, et al. Avian influenza surveillance in hunter-harvested waterfowl from the Gulf Coast of Texas (November 2005-January 2006). Journal of Wildlife Diseases. 2008 Apr;44(2):434–9.

Fujimoto Y, Ito H, Shivakoti S, Nakamori J, Tsunekuni R, Otsuki K, et al. Avian Influenza Virus and Paramyxovirus Isolation from Migratory Waterfowl and Shorebirds in San-In District of Western Japan from 2001 to 2008. Journal of Veterinary Medical Science. 2010;[Epub ahead of print].

Gaidet N, Dodman T, Caron A, Balança G, Desvaux S, Goutard F, et al. Avian influenza viruses in water birds, Africa. Emerging Infectious Diseases. 2007;13(4):626–9.

Gaidet N, Dodman T, Caron A, Balança G, Desvaux S, Goutard F, et al. Influenza Surveillance in Wild Birds in Eastern Europe, the Middle East, and Africa: Preliminary Results from an Ongoing FAO-led Survey. Journal of Wildlife Diseases. 2007;43(3):S22–S28.

Ghersi BM, Blazes D, Icochea E, Gonzalez RI, Kochel T, Tinoco Y, et al. Avian Influenza in wild birds from the central coast of Peru. Emerging Infectious Diseases. 2009;15(6):935.

Gilbert M. Disease Surveillance: Avian Influenza in Migratory Birds in Mongolia - Results of Extensive Surveys – 2006. Ulaanbaatar, Mongolia.: Wildlife Conservation Society; 2007.

Globig A, Baumer A, Revilla-Fernandez S, Beer M, Wodak E, Fink M, et al. Ducks as Sentinels for Avian Influenza in Wild Birds. Emerging Infectious Diseases. 2009;15(10):1633–6.

Globig A, Starick E, Werner O. Isolation of avian influenza from migratory waterfowl in Germany. Results of a two year study [in German]. Berliner Und Munchener Tierarztliche Wochenschrift. 2006 Mar-Apr;119(3-4):132–9.

Goujgoulova G, Oreshkova N. Surveillance on avian influenza in Bulgaria. Avian Diseases. 2007;51:382–6.

Graham DA, German A, Abernethy D, McCullough SJ, Manvell RJ, Alexander DJ. Isolation of ortho- and paramyxoviruses from wild birds in Northern Ireland during the 1997 Newcastle disease epizootic. Veterinary Record. 1999;145(1):20–1.

Graves IL. Influenza-viruses in birds of the Atlantic Flyway. Avian Diseases. 1992 Jan-Mar;36(1):1–10.

Gronesova P, Ficova M, Mizakova A, Kabat P, Trnka A, Betakova T. Prevalence of avian influenza viruses, *Borrelia garinii*, *Mycobacterium avium*, and *Mycobacterium avium* subsp paratuberculosis in waterfowl and terrestrial birds in Slovakia, 2006. Avian Pathology. 2008;37(5):537–43.

Gronesova P, Kabat P, Trnka A, Betakova T. Using nested RT-PCR analyses to determine the prevalence of avian influenza viruses in passerines in western Slovakia, during summer 2007. Scandinavian Journal of Infectious Diseases. 2008;40(11-12):954–7.

Halvorson DA, Kelleher CJ, Senne DA. Epizootiology of Avian Influenza - Effect of Season on Incidence in Sentinel Ducks and Domestic Turkeys in Minnesota. Applied and Environmental Microbiology. 1985;49(4):914–9.

Hanson BA, Luttrell MP, Goekjian VH, Niles L, Swayne DE, Senne DA, et al. Is the occurrence of avian influenza virus in Charadriformes species and location dependent? Journal of Wildlife Diseases. 2008;44(2):351–61.

Hanson BA, Stallknecht DE, Swayne DE, Lewis LA, Senne DA. Avian Influenza Viruses in Minnesota Ducks During 1998–2000. Avian Diseases. 2003;47:867–71.

Hanson BA, Swayne DE, Senne DA, Lobpries DS, Hurst J, Stallknecht DE. Avian influenza viruses and paramyxoviruses in wintering and resident ducks in Texas. Journal of Wildlife Diseases. 2005 Jul;41(3):624–8.

Happold JR, Brunhart I, Schwermer H, Stärk KDC. Surveillance of H5 Avian Influenza Virus in Wild Birds Found Dead. Avian Diseases. 2008;52:100–5.

Hars J, Ruette S, Benmergui M, Fouque C, Fournier JY, Legouge A, et al. The epidemiology of the highly pathogenic H5N1 avian influenza in mute swan (*Cygnus olor*) and other Anatidae in the Dombres Region (France), 2006. Journal of Wildlife Diseases. 2008;44(4):811–23.

Haynes L, Arzey E, Bell C, Bucanan N, Burgess G, Cronan V, et al. Australian surveillance for avian influenza viruses in wild birds between July 2005 and June 2007. Australian Veterinary Journal. 2009;87:266–72.

Heard DJ, Mulcahy DM, Iverson SA, Rizzolo DJ, Greiner EC, Hall J, et al. A blood survey of elements, viral antibodies, and hemoparasites in wintering Harlequin Ducks (*Histrionicus histrionicus*) and Barrow's Goldeneyes (*Bucephala islandica*). Journal of Wildlife Diseases. 2008 Apr;44(2):486–93.

Hesterberg U, Harris K, Stroud D, Guberti V, Busani L, Pittman M, et al. Avian Influenza surveillance in wild birds in the European Union in 2006. Influenza and Other Respiratory Viruses. 2009;3(1):1–14.

Hinshaw VS, Nettles VF, Schorr LF, Wood JM, Webster RG. Influenza virus surveillance in waterfowl in Pennsylvania after the H5N2 avian outbreak. Avian Diseases. 1986 Jan-Mar;30(1):207–12.

Hinshaw VS, Webster RG, Turner B. The perpetuation of orthomyxoviruses and paramyxoviruses in Canadian waterfowl. Canadian Journal of Microbiology. 1980;26:622–9.

Hinshaw VS, Wood JM, Webster RG, Deibel R, Turner B. Circulation of Influenza-Viruses and Paramyxoviruses in Waterfowl Originating from two Different Areas of North-America. Bulletin of the World Health Organization. 1985;63(4):711–9.

Hlinak A, Muhle RU, Werner O, Globig A, Starick E, Schirrmeier H, et al. A virological survey in migrating waders and other waterfowl in one of the most important resting sites of Germany. Journal of Veterinary Medicine Series B-Infectious Diseases and Veterinary Public Health. 2006 Apr;53(3):105–10.

Honda E, Kida H, Yanagawa R, Matsuura Y, Yagyu K, Tsuji M, et al. Survey of influenza viruses in feral birds in 1979 and isolation of a strain possessing Hav6Nav5 from cloaca of an eastern dunlin. Japanese Journal of Veterinary Research. 1981;29(3-4):83–7.

Hopkins BA, Skeeles JK, Houghten GE, Slagle D, Gardner K. A survey of infectious-diseases in wild turkeys (*Meleagridis gallopavo silvestris*) from Arkansas. Journal of Wildlife Diseases. 1990;26(4):468–72.

Hua Y-P, Chai H-L, Yang S-Y, Zeng X-W, Sun Y. Primary survey of avian influenza virus and Newcastle disease virus infection in wild birds in some areas of Heilongjiang Province, China. Journal of Veterinary Science. 2005;6(4):311–5.

Hurt AC, Hansbro PM, Selleck P, Olsen B, Minton C, Hampson AW, et al. Isolation of avian influenza viruses from two different transhemispheric migratory shorebird species in Australia. Archives of Virology. 2006 Nov;151(11):2301–9.

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 Zhemchuzhnyi Island in the north-western area of the Caspian Sea] [in Russian]. Voprosy Virusologii. 2008;53(3):34–8.

Ip HS, Flint PL, Franson JC, Dusek RJ, Derksen DV, Gill RE, et al. Prevalence of Influenza A viruses in wild migratory birds in Alaska: Patterns of variation in detection at a crossroads of intercontinental flyways. Virology Journal. 2008 Jun;5:71.

Ito T, Okazaki K, Kawaoka Y, Takada A, Webster RG, Kida H. Perpetuation of Influenza-a Viruses in Alaskan Waterfowl Reservoirs. Archives of Virology. 1995;140(7):1163–72.

Iverson SA, Takekawa JY, Schwarzbach S, Cardona CJ, Warnock N, Bishop MA, et al. Low Prevalence of Avian Influenza Virus in Shorebirds on the Pacific Coast of North America. Waterbirds. 2008 Dec;31(4):602–10.

Jahangir A, Ruenphet S, Ueda S, Ueno Y, Shoham D, Shindo J, et al. Avian influenza and Newcastle disease viruses from northern pintail in Japan: Isolation, characterization and inter-annual comparisons during 2006–2008. Virus Research. 2009;143(1):44–52.

Jahangir A, Watanabe Y, Chinen O, Yamazaki S, Sakai K, Okamura M, et al. Surveillance of avian influenza viruses in Northern Pintails (*Anas acuta*) Tohoku District, Japan. Avian Diseases. 2008;52:49–53.

Jonassen CM, Handeland K. Avian influenza virus screening in wild waterfowl in Norway, 2005. Avian Diseases. 2007;51(1):425–8.

Karesh WB, Uhart MM, Frere E, Gandini P, Braselton WE, Puche H, et al. Health evaluation of free-ranging rockhopper penguins (*Eudyptes chrysocomes*) in Argentina. Journal of Zoo and Wildlife Medicine. 1999 Mar;30(1):25–31.

Karunakaran D, Hinshaw V, Poss P, Newman J, Halvorson D. Influenza-A outbreaks in minnesote Turkeys due to subtype-H10N7 and possible transmission by waterfowl. Avian Diseases. 1983;27(2):357–66.

Kawamoto AHN, Mancini DAP, Pereira LE, Cianciarullo AM, Cruz AS, Dias ALF, et al. Investigation of influenza in migrating birds, the primordial reservoir and transmitters of influenza in Brazil. Braz J Microbiol. 2005 Jan-Mar;36(1):88–93.

Kawaoka Y, Chambers T, Sladen W, Webster RG. Is the gene pool of Influenza Viruses in shorebirds and gulls different from that in wild ducks. Virology. 1988;163:247–50.

Kishida N, Sakoda Y, Shiromoto M, Bai GR, Isoda N, Takada A, et al. H2N5 influenza virus isolates from terns in Australia: genetic reassortants between those of the Eurasian and American lineages. Virus Genes. 2008 Aug;37(1):16–21.

Kocan AA, Hinshaw VS, Daubney GA. Influenza a Viruses Isolated from Migrating Ducks in Oklahoma. Journal of Wildlife Diseases. 1980;16(2):281–5.

Kocan AA, Snelling J, Greiner EC. Some infectious and parasitic diseases in Oklahoma raptors. Journal of Wildlife Diseases. 1977;13(3):304–6.

Komar N, Olsen B. Avian influenza virus (H5N1) mortality surveillance. Emerging Infectious Diseases. 2008 Jul;14(7):1176–8.

Kou Z, Li YD, Yin ZH, Guo S, Wang ML, Gao XB, et al. The Survey of H5N1 Flu Virus in Wild Birds in 14 Provinces of China from 2004 to 2007. PLoS One. 2009 Sep;4(9):e6926.

Krauss S, Obert CA, Franks J, Walker D, Jones K, Seiler P, et al. Influenza in migratory birds and evidence of limited intercontinental virus exchange. PLoS Pathogens. 2007;3(11):e167.

Krauss S, Walker D, Pryor SP, Niles L, Li CH, Hinshaw VS, et al. Influenza A viruses of migrating wild aquatic birds in North America. Vector-Borne and Zoonotic Diseases. 2004 Fal;4(3):177–89.

Lai AC, McPhillips AM. Isolation of avian influenza viruses in central Oklahoma. Journal Oklahoma State Medical Association. 1999;92(12):565–7.

Langstaff IG, McKenzie JS, Stanislawek WL, Reed CEM, Poland R, Cork SC. Surveillance for highly pathogenic avian influenza in migratory shorebirds at the terminus of the East Asian-Australasian Flyway. New Zealand Veterinary Journal. 2009;57(3):160–5.

Laver WG, Webster RG. Antibodies to Human Influenza-Virus Neuraminidase (a/Asian/57 H2n2 Strain) in Sera from Australian Pelagic Birds. Bulletin of the World Health Organization. 1972;47(4):535–41.

Lebarbenchon C, Chang C-M, van der Werf S, Aubin J-T, Kayser Y, Ballesteros M, et al. Influenza A Virus in Birds during Spring Migration in the Camargue, France. Journal of Wildlife Diseases. 2007 October 1, 2007;43(4):789–93.

Lebarbenchon C, van der Werf S, Thomas F, Aubin JT, Azebi S, Cuvelier F, et al. Absence of detection of highly pathogenic H5N1 in migratory waterfowl in southern France in 2005-2006. Infection Genetics and Evolution. 2007 Sep;7(5):604–8.

Lillehaug A, Jonassen CM, Bergsjo B, Hofshagen A, Tharaldsen J, Nesse LL, et al. Screening of feral pigeon (*Colomba livia*), mallard (*Anas platyrhynchos*) and graylag goose (*Anser anser*) populations for Campylobacter spp., Salmonella spp., avian influenza virus and avian paramyxovirus. Acta Veterinaria Scandinavica. 2005;46(4):193–202.

Lindh E, Huovilainen A, Ratti O, Ek-Kommonen C, Sironen T, Huhtamo E, et al. Orthomyxo-, paramyxo- and flavivirus infections in wild waterfowl in Finland. Virology Journal. 2008 Feb;5:35.

Lipkind M, Weisman Y, Shihmanter E, Shoham D. Review of the Three-Year Studies on the Ecology of Avian Influenza Viruses in Israel. Avian Diseases. 2003;47:69–78.

L'vov DK, Easterday BC, Webster RG, Sazonov AA, Zhilina NN. [Virological and serological examination of wild birds during the spring migrations in the region of the Manych Reservoir, Rostov Province] [in Russian]. Voprosy Virusologii. 1977;Jul-Aug(4):409–14.

L'vov DK, Shchelkanov MI, Deriabin PG, Burtseva EI, Galkina IV, Grebennikova TV, et al. Highly pathogenic influenza A/H5N1 virus-caused epizooty among mute swans (*Cygnus olor*) in the lower estuary of the Volga River (November 2005) [in Russian]. Voprosy Virusologii. 2006;51(3):10–6.

L'vov DK, Shchelkanov MY, Deryabin PG, Grebennikova TV, Prilipov AG, Nepoklonov YA, et al. [Isolation of influenza A/H5N1 virus strains from poultry and wild birds in West Siberia during epizooty (July 2005) and their depositing to the state collection of viruses (August 8, 2005)] [in Russian]. Voprosy Virusologii. 2006;51(1):11–4.

L'vov DK, Yamnikova SS, Gambaryan AS, Fedyakina IT, Matrosovich MN. Isolation of influenza viruses from wild birds in the Volga River basin and in the North Caspian Region. International Congress Series. 2001;1219:251–8.

Mackenzie JS, Edwards EC, Holmes RM, Hinshaw VS. Isolation of Ortho- and Paramoxyviruses from wild birds in Western Australia, and the characterisation of novel Influenza A viruses. Australian Journal of Experimental Biology and Medical Science. 1984;62(1):89–99.

Mikami T, Izawa H, Kodama H, Onuma M, Sato A, Kobayashi S, et al. Isolation of Orthomyxovirus and paramyxovirus from migrating feral ducks in Hokkaido. Archives of Virology. 1982;74(2-3):211–7.

Mizakova A, Gronesova P, Betakova T. Monitoring of influenza viruses in waterfowl and terrestrial birds in eastern Slovakia. Acta Virologica. 2008;52(1):71–3.

Morishita TY, Aye PP, Ley EC, Harr BS. Survey of pathogens and blood parasites in free-living passerines. Avian Diseases. 1999;43(3):549–52.

Morishita TY, McFadzen ME, Mohan R, Aye PP, Brooks DL. Serologic survey of free-living nestling prairie falcons (*Falco mexicanus*) for selected pathogens. Journal of Zoo and Wildlife Medicine. 1998 Mar;29(1):18–20.

Motha J, Gibbons AM, Reed CEM. A survey for avian paramyxoviruses and influenza viruses in feral pigeons and native birds in New Zealand. New Zealand Veterinary Journal. 1997;45(5):215–6.

Müller T, Hlinak A, Freuling C, Muhle RU, Engelhardt A, Globig A, et al. Virological Monitoring of White Storks (*Ciconia ciconia*) for Avian Influenza. Avian Diseases. 2009 Dec;53(4):578–84.

Munster VJ, Baas C, Lexmond P, Waldenström J, Wallensten A, Fransson T, et al. Spatial, Temporal, and Species Variation in Prevalence of Influenza A Viruses in Wild Migratory Birds. PLoS Pathogens. 2007;3(5):e61.

Nagy A, Machova J, Hornickova J, Tomci M, Nagl I, Horyna B, et al. Highly pathogenic avian influenza virus subtype H5N1 in Mute swans in the Czech Republic. Veterinary Microbiology. 2007 Feb;120(1-2):9–16.

Nettles VF, Wood JM, Webster RG. Wildlife surveillance associated with an outbreak of lethal H5N2 avian influenza in domestic poultry. Avian Diseases. 1985;29(3):733–41.

Okazaki K, Takada A, Ito T, Imai M, Takakuwa H, Hatta M, et al. Precursor genes of future pandemic influenza viruses are perpetuated in ducks nesting in Siberia. Archives of Virology. 2000;145(5):885–93.

Oliveira JG, Belluci MSP, Vianna JSM, Mazur C, Andrade CM, Fedullo LPL, et al. [Serological survey on influenza virus in domestic and wild birds from Rio do Janeiro State, Brazil] [in Portuguese]. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia. 2001;53(3):299–302.

Otsuki K, Kariya H, Matsuo K, Sugiyama S, Hoshina K, Yoshikane T, et al. Isolation of influenza-A viruses from migratory waterfowls in San-in district, Western Japan in winters of 1984-1985. Japanese Journal of Veterinary Science. 1987 Aug;49(4):721–3.

Otsuki K, Takemoto O, Fujimoto R, Kawaoka Y, Tsubokura M. Isolation of influenza-A viruses from migratory waterfowls in San-in district, Western Japan in winters of 1980-1982. Zentralblatt Fur Bakteriologie Mikrobiologie Und Hygiene Series a-Medical Microbiology Infectious Diseases Virology Parasitology. 1987;265(1-2):235–42.

Otsuki K, Takemoto O, Fujimoto R, Yamazaki K, Kubota N, Hosaki H, et al. Isolation of influenza-A viruses from migratory waterfowls in San-in district, Western Japan in winters of 1982-1983. Acta Virologica. 1987;31(5):439–42.

Otsuki K, Takemoto O, Fujimoto R, Yamazaki K, Kubota N, Hosaki H, et al. Isolation of influenza-A viruses from migratory waterfowls in San-in district, Western Japan in winters of 1983-1984. Research in Veterinary Science. 1987;43(2):177–9.

Pannwitz G, Wolf C, Harder T. Active Surveillance for Avian Influenza Virus Infection in Wild Birds by Analysis of Avian Fecal Samples from the Environment. Journal of Wildlife Diseases. 2009 Apr;45(2):512–8.

Pant GR, Selleck PW. Surveillance for avian influenza in Nepal 2004-2005. Avian Diseases. 2007;51(1):352–4.

Papanikolaou J, Koumbati-Artopiou M. Epidemiological investigation of avian influenza in regions of Northern Greece. Journal of the Hellenic Veterinary Medical Society. 2002;53(2):132–7.

Parmley EJ, Bastien N, Booth TF, Bowes V, Buck PA, Breault A, et al. Wild bird influenza survey, Canada, 2005. Emerging Infectious Diseases. 2008 Jan;14(1):84–7.

Pasick J, Handel K, Robinson J, Bowes V, Li Y, Leighton T, et al. Relationship between H5N2 avian influenza viruses isolated from wild and domestic ducks in British Columbia, Canada. Avian Diseases. 2007;51:429–31.

Pawar S, Pande S, Jamgaonkar A, Koratkar S, Pal B, Raut S, et al. Avian influenza surveillance in wild migratory, resident, domestic birds and in poultry in Maharashtra and Manipur, India, during avian migratory season 2006-07. Current Science. 2009 Aug;97(4):550–4.

Pearce JM, Ramey AM, Flint PL, Koehler AV, Fleskes JP, Franson JC, et al. Avian influenza at both ends of a migratory flyway: characterizing viral genomic diversity to optimize surveillance plans for North America. Evolutionary Applications. 2009 Nov;2(4):457–68.

Pereda AJ, Uhart M, Perez AA, Zaccagnini ME, La Sala L, Decarre J, et al. Avian influenza virus isolated in wild waterfowl in Argentina: Evidence of a potentially unique phylogenetic lineage in South America. Virology. 2008 Sep;378(2):363–70.

Peroulis I, O'Riley K. Detection of avian paramyxoviruses and influenza viruses amongst wild bird populations in Victoria. Australian Veterinary Journal. 2004 Jan-Feb;82(1-2):79–82.

Peterson AT, Bush SE, Spackman E, Swayne DE, Ip HS. Influenza A virus infections in land birds, People's Republic of China. Emerging Infectious Diseases. 2008 Oct;14(10):1644–6.

Peterson MJ, Aguirre R, Ferro PJ, Jones DA, Lawyer TA, Peterson MN, et al. Infectious disease survey of Rio Grande wild turkeys in the Edwards Plateau of Texas. Journal of Wildlife Diseases. 2002;38(4):826–33.

Peterson MJ, Ferro PJ, Peterson MN, Sullivan RM, Toole BE, Silvy NJ. Infectious disease survey of lesser prairie chickens in north Texas. Journal of Wildlife Diseases. 2002;38(4):834–9.

Pfitzer S, Verwoerd DJ, Gerdes GH, Labuschagne AE, Erasmus A, Manvell RJ, et al. Newcastle disease and avian influenza A virus in wild waterfowl in South Africa. Avian Diseases. 2000 Jul-Sep;44(3):655–60.

Rabl S, Rinder M, Neubauer-Juric A, Bogner KH, Korbel R, Buttner M. [Surveillance of wild birds for Avian Influenza A Virus (AIV) in Bavaria in the years 2007 and 2008] [in German]. Berliner Und Munchener Tierarztliche Wochenschrift. 2009 Nov-Dec;122(11-12):486–93.

Račnik J, Slavec B, Trilar T, Zadravec M, Dovč A, Krapež U, et al. Evidence of avian influenza virus and paramyxovirus subtype 2 in wild-living passerine birds in Slovenia. European Journal of Wildlife Research. 2008;54:529–32.

Raleigh PJ, Flynn O, O'Connor M, O'Donovan T, Purcell B, De Burca M, et al. Avian influenza viruses detected by surveillance of waterfowl in Ireland during 2003-2007. Epidemiology and Infection. 2009 Apr;137(4):464–72.

Razumova IV, Shchelkanov MI, Zolotykh SI, Durymanova AA, Ternovoi VA, Beklemishev AB, et al. [The 2003 results of monitoring of influenza A virus in the populations of wild birds in the south of Western Siberia] [in Russian]. Voprosy Virusologii. 2006;51(3):32–7.

Romváry J, Mészáros J, Tanyi J, Rózsa J, Fábián L. Influenza infectedness of captured and shot wild birds on north-eastern and south-eastern parts of Hungary. Acta Veterinaria Academiae Scientiarum Hungaricae. 1976;26(3):363–8.

Rosenberger JK, Krauss WC, Slemons RD. Isolation of Newcastle-disease and Type-A Influenz a Viruses from migratory waterfowl in Atlantic Flyway. Avian Diseases. 1974;18(4):610–3.

Runstadler JA, Happ GM, Slemons RD, Sheng Z-M, Gundlach N, Petrula M, et al. Using RRT-PCR analysis and virus isolation to determine the prevalence of avian influenza virus infections in ducks at Minto Flats State Game Refuge, Alaska, during August 2005. Archives of Virology. 2007.

Rutz C, Dalessi S, Baumer A, Kestenholz M, Engels M, Hoop R. Avian influenza: Wildbird monitoring in Switzerland between 2003–2006 [in German]. Schweizer Archiv Fur Tierheilkunde. 2007 Nov;149(11):501–9.

Schnebel B, Dierschke V, Rautenschlein S, Ryll M, Neumann U. Investigations on infection status with H5 and H7 avian influenza virus in short-distance and long-distance migrant birds in 2001. Avian Diseases. 2007;51(1):432–3.

Sekler M, Ruzica A, Krnjaic D, Palic T, Milic N, Tanja J, et al. Examination of presence os specific antibodies against avian influenza virus in some species of wild birds. Acta Veterinaria-Beograd. 2009;59(4):381–402.

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.

Sharshov KA, Zolotykh SI, Fedorov EG, Ivanov IV, Druziaka AV, Shestopalov AM, et al. Surveillance for avian influenza virus in synanthropic birds during epizootic and postepizootic periods on the south of west Siberia [in Russian]. Zhurnal Mikrobiologii Epidemiologii i Immunobiologii. 2007(4):53–6.

Shchelkanov MY, Ananyev VY, Lvov DN, Kireyev DY, Guryev YL, Akanina DS, et al. Complex environmental and virological monitoring in the Primorye Territory in 2003–2006 [in Russian]. Voprosy Virusologii. 2007;52(5):37–48.

Shengqing Y, Shinya K, Otsuki K, Ito H, Ito T. Isolation of myxoviruses from migratory waterfowls in San-in district, western Japan in winters of 1997-2000. Journal of Veterinary Medical Science. 2002;64(11):1049–52.

Shestopalov AM, Solotych SI, Shchelkanov MY, Razumova YV, Alekseev AY, Durymanov AG, et al. [Results of two-year-old inspection of wild birds in territory of the Western Mongolia on the presence infuenza virus] [in Russian]. Zhurnal Mikrobiologii Epidemiologii i Immunobiologii. 2006(5):55–9.

Simulundu E, Mweene AS, Tomabechi D, Hang'ombe BM, Ishii A, Suzuki Y, et al. Characterization of H3N6 avian influenza virus isolated from a wild white pelican in Zambia. Archives of Virology. 2009 Sep;154(9):1517–22.

Sinnecker H, Sinnecker R, Zilske E, Koehler D. Detection of influenza A viruses and influenza epidemics in wild pelagic birds by sentinels and population studies. Zentralblatt Fur Bakteriologie Mikrobiologie Und Hygiene Series a-Medical Microbiology Infectious Diseases Virology Parasitology. 1982;253(3):297–304.

Sinnecker R, Sinnecker H, ZIlske E, Kohler D. Surveillance of pelagic birds for influenza A viruses. Acta Virologica. 1983;27:75–9.

Slemons RD, Hansen WR, Converse KA, Senne DA. Type A influenza virus surveillance in free-flying, nonmigratory ducks residing on the eastern shore of Maryland. Avian Diseases. 2003;47:1107–10.

Slemons RD, Johnson DC, Osborn JS, Hayes F. Type-A Influenza-Viruses Isolated from Wild Free-Flying Ducks in California. Avian Diseases. 1974;18(1):119–24.

Slemons RD, Shieldcastle MC, Heyman LD, Bednarik KE, Senne DA. Type-A Influenza-Viruses in Waterfowl in Ohio and Implications for Domestic Turkeys. Avian Diseases. 1991 Jan-Mar;35(1):165–73.

Slepuskin AN, Pysina TV, Gonsovsky FK, Sazonov AA, Isacenko VA, Sokolova NN, et al. Haemagglutination-inhibiting activity to type A influenza viruses in the sera of wild birds from the far east of the USSR. Bulletin of the World Health Organization. 1972;47(4):527–30.

Smietanka K, Minta Z, Domanska-Blicharz K, Tomczyk G, Wijaszka T. Avian influenza H5N1 outbreak in a flock of Mute swans in the city of Torun, Poland, in 2006. Bulletin of the Veterinary Institute in Pulawy. 2008;52(4):491–5.

Smietanka K, Minta Z, Tomczyk G, Domanska-Blicharz K, Bartnicka B, Szewczyk B, et al. Prevalence of avian influenza virus infections in poultry and wild birds. Medycyna Weterynaryjna. 2005 Jun;61(6):676–9.

Smith GJD, Vijaykrishna D, Ellis TM, Dyrting KC, Leung YHC, Bahl J, et al. Characterization of Avian Influenza Viruses A (H5N1) from Wild Birds, Hong Kong, 2004-2008. Emerging Infectious Diseases. 2009 Mar;15(3):402–7.

Smith KM, Karesh WB, Majluf P, Paredes R, Zavalaga C, Reul AH, et al. Health Evaluation of Free-Ranging Humboldt Penguins (*Spheniscus humboldti*) in Peru. Avian Diseases. 2008 Mar;52(1):130–5.

Smitka CW, Maassab HF. Ortho-myxoviruses and paramyxoviruses in the migratory waterfowl of Michigan. Journal of Wildlife Diseases. 1981;17(1):147–51.

Song MS, Oh TK, Moon HJ, Yoo DW, Lee EH, Lee JS, et al. Ecology of H3 avian influenza viruses in Korea and assessment of their pathogenic potentials. Journal of General Virology. 2008 Apr;89:949–57.

Spackman E, McCracken KG, Winker K, Swayne DE. An avian influenza virus from waterfowl in South America contains genes from North American avian and equine lineages. Avian Diseases. 2007;51(1):273–4.

Spackman E, Swayne DE, Gilbert M, Joly DO, Karesh WB, Suarez DL, et al. Characterization of low pathogenicity avian influenza viruses isolated from wild birds in Mongolia 2005 through 2007. Virology Journal. 2009 Nov;6:8.

Stallknecht DE, Shane SM, Zwank PJ, Senne DA, Kearney MT. Avian Influenza-Viruses from Migratory and Resident Ducks of Coastal Louisiana. Avian Diseases. 1990 Apr-Jun;34(2):398-405.

Stanislawek WL. Avian influenza survey of New Zealand wild ducks. Surveillance. 1990;17(2):13–4.

Stanislawek WL. Survey of wild ducks for evidence of avian influenza viruses, 1989 and 1990. Surveillance. 1992;19(1):21–2.

Stanislawek WL, Wilks CR, Meers J, Horner GW, Alexander DJ, Manvell RJ, et al. Avian paramyxoviruses and influenza viruses isolated from mallard ducks (*Anas platyrhynchos*) in New Zealand. Archives of Virology. 2002;147(7):1287–302.

Stone EG, Montiel-Parra G, Perez TM. A survey of selected parasitic and viral pathogens in four species of Mexican parrots, *Amazona autumnalis*, *Amazona oratrix*, *Amazona viridigenalis*, and *Rhynchopsitta pachyrhyncha*. Journal of Zoo and Wildlife Medicine. 2005;36(2):245–9.

Stoops AC, Barbara KA, Indrawan M, Ibrahim IN, Petrus WB, Wijaya S, et al. H5N1 Surveillance in Migratory Birds in Java, Indonesia. Vector-Borne and Zoonotic Diseases. 2009 Dec;9(6):695–702.

Süss J, Schafer J, Sinnecker H, Webster RG. Influenza virus subtypes in aquatic birds of eastern Germany. Archives of Virology. 1994;135:101–14.

Tanaka T, Tanoue G, Yamasaki M, Takashima I, Sakoda Y, Ochiai K, et al. Chemical deicer poisoning was suspected as a cause of the 2005-2006 wintertime mortality of small wild birds in Hokkaido. Journal of Veterinary Medical Science. 2008 Jun;70(6):607–10.

Terregino C, De Nardi R, Guberti V, Scremin M, Raffini E, Martin AM, et al. Active surveillance for avian influenza viruses in wild birds and backyard flocks in Northern Italy during 2004 to 2006. Avian Pathology. 2007;36(4):337–44.

Toro H, Pavez EF, Gough RE, Montes G, Kaleta EF. Serum chemistry and antibody status to some avian pathogens of free-living and captive condors (*Vultur gryphus*) of central Chile. Avian Pathology. 1997;26(2):339–45.

Travis EK, Vargas FH, Merkel J, Gottdenker N, Miller RE, Parker PG. Hematology, serum chemistry, and serology of Galapagos penguins (Spheniscus mendiculus) in the Galapagos Islands, Ecuador. Journal of Wildlife Diseases. 2006 Jul;42(3):625–32.

Travis EK, Vargas FH, Merkel J, Gottdenker N, Miller RE, Parker PG. Hematology, plasma chemistry, and serology of the flightless cormorant (*Phalacrocorax harrisi*) in the Galapagos Islands, Ecuador. Journal of Wildlife Diseases. 2006 Jan;42(1):133–41.

Tsubokura M, Otsuki K, Kawaoka Y, Yanagawa R. Isolation of influenza A viruses from migratory waterfowls in San-in District, Western Japan in 1979-1980. Zentralblatt Fur Bakteriologie

Mikrobiologie Und Hygiene Serie B-Umwelthygiene Krankenhaushygiene Arbeitshygiene Praventive Medizin. 1981;173(6):494–500.

Uhart M, Aprile G, Beldomenico R, Solis G, Marull C, Beade M, et al. Evaluation of the health of free-ranging greater rheas (*Rhea americana*) in Argentina. Veterinary Record. 2006 Mar;158(9):297–303.

Uhart MM, Quintana F, Karesh WB, Braselton WE. Hematology, plasma biochemistry, and serosurvey for selected infectious agents in southern giant petrels from Patagonia, Argentina. Journal of Wildlife Diseases. 2003 Apr;39(2):359–65.

Wahlgren J, Waldenstrom J, Sahlin S, Haemig PD, Fouchier RAM, Osterhaus A, et al. Gene Segment Reassortment Between American and Asian Lineages of Avian Influenza Virus from Waterfowl in the Beringia Area. Vector-Borne and Zoonotic Diseases. 2008 Dec;8(6):783–90.

Wallensten A, Munster VJ, Latorre-Margalef N, Brytting M, Elmberg J, Fouchier RAM, et al. Surveillance of influenza A virus in migratory watefowl in northern Europe. Emerging Infectious Diseases. 2007;13(3):404–11.

Wallensten A, Munster VJ, Osterhaus A, Waldenstrom J, Bonnedahl J. Mounting evidence for the presence of influenza A virus in the avifauna of the Antarctic region. Antarctic Science. 2006;18:353–6.

Webster RG, Morita M, Pridgen C, Tumova B. Ortho- and Paramyxoviruses from Migrating Feral Ducks: Characterization of a New Group of Influenza A Viruses. Journal of General Virology. 1976;32:217–25.

Winker K, McCracken KG, Gibson DD, Pruett CL, Meier R, Huettmann F, et al. Movements of birds and avian influenza from Asia into Alaska. Emerging Infectious Diseases. 2007;13(4):547–52.

Winkler WG, Trainer DO, Easterday BC. Influenza in Canada geese. Bulletin of the World Health Organization. 1972;47(4):507–13.

Yamane N, Odagiri T, Arikawa J, Ishida N. Isolation and characterization of influenza A viruses from wild ducks in northern Japan: appearance of HSW1 antigens in the Japanese duck population. Acta Virologica. 1979;23(5):375–84.

Zakstel'skaja LJ, Isacenko VA, Osidze NG, Timofeeva CC, Slepushkin AN, Sokolova NN. Some observations on the circulation of influenza viruses in domestic and wild birds. Bulletin of the World Health Organization. 1972;47(4):497–501.

Zarkov IS, Bochev I, Manvell R, Shell W. Isolation of avian influenza virus in Bulgaria. Veterinary Record. 2006 Jan;158(3):106–7.

Zeng X, Hua Y, Li X, Zhang Z. Monitoring Influenza A virus and Newcastle disease virus in migratory waterfowls in Sanjiang natural Reserve of Heilongjiang Province [in Chinese]. Weishengwu Xuebao. 2008;48(10):1403–7.

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:

$$P_{x>0} = 1 - (1 - p)^n \tag{1}$$

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}):

$$n = \frac{\log(1 - P_{x>0})}{\log(1 - p_{max})} \tag{2}$$

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:

$$p_{max} = 1 - (1 - P_{x>0})^{\frac{1}{n}} \tag{3}$$

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%.