

Risk-based Targeted Surveillance: Identifying Areas and Populations of Importance for Surveillance of High-Path Avian Influenza in the United States

Ryan S. Miller¹, Matt L. Farnsworth², William L. Kendall³, Paul F. Doherty, Jr.⁴, James D. Nichols³, Gary C. White⁴, Kenneth P. Burnham⁵, Alan B. Franklin², Jerry E. Freier¹

¹USDA-APHIS-VS- Centers for Epidemiology and Animal Health, Fort Collins, Colorado; ²USDA-APHIS-WS- National Wildlife Research Center, Fort Collins, Colorado; ³USGS Patuxent Wildlife Research Center, Laurel, Maryland; ⁴Department of Fish, Wildlife, and Conservation Biology, Colorado State University, Fort Collins, Colorado; ⁵USGS Colorado Cooperative Fish & Wildlife Research Unit, Colorado State University, Fort Collins, Colorado.

Summary

The recent emergence of highly pathogenic avian influenza subtype Asian H5N1 and its rapid spread throughout Asia, Europe and Africa has focused attention on the need for enhanced avian influenza (AI) surveillance in domestic poultry and migratory waterfowl within the United States. However, geographic overlap and subsequent potential for virus exchange between wild bird populations and domestic poultry are poorly understood. Using a GIS and knowledge about the biology and ecology of migratory waterfowl, type-A influenzas, and considering the complications of data collection at a national scale, we identified areas of importance for surveillance of wild waterfowl and domestic poultry.

Introduction

The recent emergence of highly pathogenic Asian H5N1 and its rapid spread throughout Asia, Europe and Africa has focused attention on the need for enhanced avian influenza (AI) surveillance in domestic poultry and migratory waterfowl within the United States. Nationally, avian influenza surveillance programs have been established to detect the H5 and H7 subtypes of AI in domestic poultry and wild waterfowl.⁽⁶⁾ However, early detection of highly pathogenic Asian H5N1 will require targeted surveillance of populations at highest risk for emergence of the virus.

With certain limitations, continental movements of waterfowl can be estimated using data from bird-band recoveries. This analysis focused on avian functional groups [dabbling ducks (*Anas* spp.), light geese (*Chen* spp.), dark geese (*Branta* spp.), and swans (*Cygnus* spp.)] thought to be responsible for large-scale movements of high path Asian H5N1.^(1,2,3,4,5,9) Bird banding data from 1991 – 2006 were used to identify areas within the conterminous United States where higher proportions of migrant waterfowl originating from northeastern Asia, Alaska, and Canada stop over or overwinter.

Materials and Methods

To identify areas of importance for dabbling ducks, light geese, dark geese, and swans, we used bird banding data from the United States Geologic Survey Bird Banding Laboratory were used.⁷ Bird banding and subsequent encounters are used for studying the movement, survival, and behavior of birds, and these banding data are available at the continental scale. One attribute of critical interest for this analysis is that bird-banding data provide both the origin of the banded bird and the encounter location. Most encounter data are from hunter-harvested birds, which are often referred to as recoveries. In North America, waterfowl are typically banded on their breeding grounds in northern latitudes, and then bands are recovered during the fall migration and hunting season. Encounter data are reported to the Bird Banding Laboratory by hunters (or other people) and these

data are summarized in 10-minute blocks of degrees longitude and latitude (approximately 100 mi² blocks). Estimates of bird distribution patterns derived from hunter-gathered data can be inherently biased, or depend on untested assumptions. Our primary assumption is that hunter effort is uniform and selection of harvest locations directly corresponds to the presence of large aggregations of waterfowl. Despite this and other required assumptions, banding data are the best source of information on the spatial and temporal distribution of waterfowl species in North America.

We used, and summarized banding and recovery data from dabbling ducks, light geese, dark geese, and swans from 1991 through 2006 ($n = 241,619$ recoveries). These data represented 32 species with mallards (*Anas platyrhynchos*) accounting for 36.5% of recoveries and Canada geese (*Branta canadensis*) accounting for 41.8% of recoveries. These data were plotted and incorporated into a GIS to identify areas within the mainland United States where higher proportions of migrant waterfowl originating from northeastern Asia, Alaska, and Canada stop or overwinter and are subsequently harvested. This resulted in a national spatial database that identified the number of band recoveries by 10-minute degrees of latitude and longitude for the entire United States. We assumed that the number of band recoveries within a 10-minute block is representative of the relative concentration of migrant waterfowl in the block.

These summarized banding data were used in conjunction with U.S. Census of Agriculture data to rank counties with both a high prevalence of domestic poultry production and high numbers of migrant waterfowl recoveries. To identify areas of critical concern and overlap between commercial poultry production and concentrations of migratory waterfowl each dataset (commercial poultry and band recoveries) was stratified into quartiles (1-25%, 25-50%, 50-75%, and 75-100%) in terms of number of individual band recoveries or poultry farms occurring within a county. These quartiles were assigned an ordinal ranking from one ($\leq 25^{\text{th}}$ percentile) to four ($> 75^{\text{th}}$ percentile). Counties that did not have any band recoveries or poultry production were given a rank of 0. Both datasets were then spatially merged assuming an additive relationship between each dataset-quartile combination resulting in a subjective ranking for each county ranging from 0 to 8. The rankings were then assigned a subjective relative risk rank of very high (8), high (7), medium high (5, 6), medium low (3, 4), or low (0, 1, 2). This resulted in the identification of areas having relatively high levels of poultry production and high levels of migrating waterfowl. Ranking was done for both migrant waterfowl originating from northeast Asia and Alaska and also for waterfowl originating from Asia, Alaska and Canada. These ranks assume that counties with a higher rank have a greater risk of contact between domestic poultry and migrating waterfowl and are therefore identified as high importance for surveillance of Asian HPAI H5N1 in domestic poultry.

Federal and state wildlife refuges and management areas have historically been located to benefit waterfowl. These refuges and areas were ranked using two methods, first using the summarized band-recovery data and second using the county risk-based rank incorporating poultry production. To accomplish this, the 10-minute block band recoveries were intersected with geographic data of the National Wildlife Refuge system ($n = 512$) and State wildlife management areas ($n = 9,630$) for the conterminous United States. The total number of band recoveries by origin was then calculated for each refuge and state wildlife area. The refuges and wildlife management areas were then ordinaly ranked by the number of band recoveries originating from Alaska, northeast Asia and Canada. In some cases refuges or wildlife management areas did not intersect with a 10-minute block possessing band recoveries; these refuges were not ranked. However, the possibility exists that waterfowl harvested in 10-minute blocks adjacent to refuges may have originated from these

refuges. Each refuge was assigned the risk-based rank of the county containing the majority of the refuge's acreage.

Results

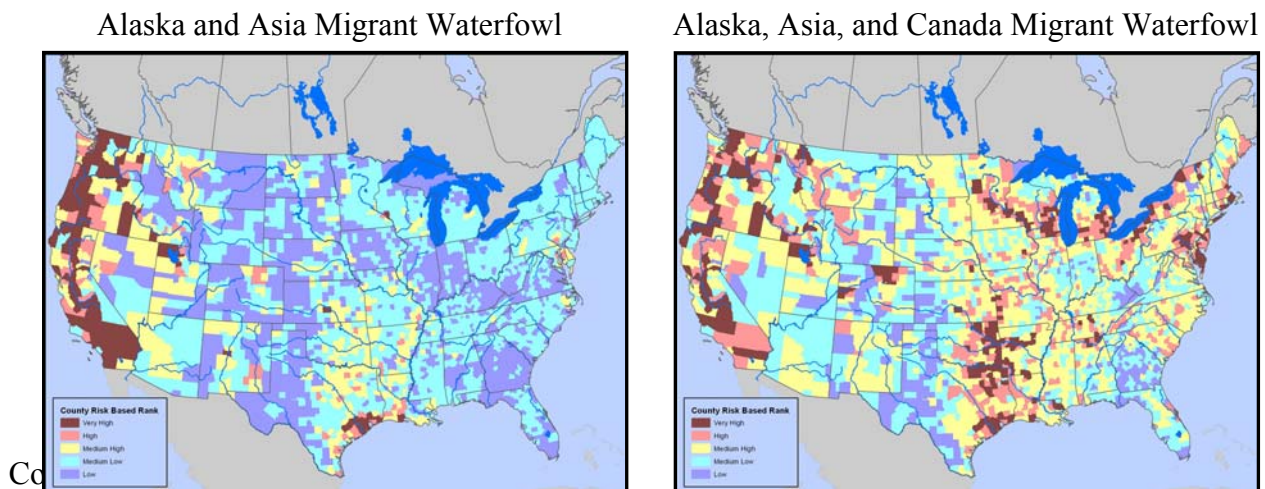
The spatial analysis identified 483 counties (15% of total) as very high, high and medium high priority for domestic poultry surveillance when analysis was restricted to migrant waterfowl originating from Alaska and northeastern Asia (Table 1). These 483 counties account for 29% of poultry farms and 26% of domestic poultry production in the United States and are primarily located along the Pacific flyway and critical overwintering areas along the Gulf Coast of Texas and Louisiana (Figure 1). Counties with critical migration stopover points in Utah, New Mexico, Kansas and other Midwestern States also ranked highly.

Ranking of National Wildlife Refuge system lands and State Wildlife Areas identified 9% (918) of all National Refuge system lands and State Wildlife area lands as important to sample. These 918 management areas represented 72% of band recoveries occurring on National Refuge system and State Wildlife area lands for birds originating from Alaska and northeastern Asia. Two National Refuges, Willow Creek and North Central Valley in California, accounted for 23% of band recoveries from Alaska and Northeastern Asia on National Wildlife Refuge system lands. County risk-based ranking identified 202 (40% of total) National Wildlife Refuge system lands that ranked very high, high, and medium high priority for surveillance when analysis was restricted to migrant waterfowl originating from Alaska and northeastern Asia (Table 1).

Table 1. Summary of risk-based rank with Alaska and Northeastern Asia migrant waterfowl.

Risk Rank	Number of Refuges		Number of Counties		Number of Poultry Farms		Estimated Poultry Population	
		%		%		%		%
Very High & High	90	18	147	5	17,155	12	113,941,098	7
Medium High	112	22	336	11	24,729	17	308,497,272	19
Medium Low	196	38	1,377	44	86,227	59	1,124,351,378	68
Low	114	22	1,281	38	18,016	12	95,681,294	6
TOTAL	512		3,141		146,127		1,642,471,042	

Figure 1. County risk-based rank for critical overlap of domestic poultry industry with migrant waterfowl.



Discussion

In summary, these analyses are a good foundation for understanding the geographic distribution and overlap between high-risk waterfowl and the commercial poultry industry. Based on this overlap, we provide initial guidance for geographic allocation of surveillance and sampling efforts related to high risk poultry flocks and commercial poultry producers. However, our analyses do not provide information on the connectivity of wild birds and domestic poultry and the subsequent potential for virus exchange between these two populations. Further analysis is needed to better quantify the potential for interactions and virus exchange between these populations. In addition, analysis is needed to better define the temporal aspects of migration and the effect on surveillance, and to better define the geographic location and densities of backyard poultry. Analysis is currently being conducted to identify areas of importance to migrant waterfowl that may intermix with birds originating from Europe and also migrant waterfowl populations that overwinter in South and Central America.

References

1. Brown JD, Stallknecht DE, Beck JR, Suarez DL, Swayne DE. 2006. Susceptibility of North American ducks and gulls to H5N1 highly pathogenic avian influenza viruses. *Emerging Infectious Diseases* 12:1663-1670.
2. Chen, H., Smith, G. J., Li, K. S., Wang, J., Fan, X. H., Rayner, J. M., Vijaykrishna, D., Zhang, J. X., Zhang, L. J., Guo, C. T., Cheung, C. L., Xu, K. M., Duan, L., Huang, K., Qin, K., Leung, Y. H., Wu, W. L., Lu, H. R., Chen, Y., Xia, N. S., Naipospos, T. S., Yuen, K. Y., Hassan, S. S., Bahri, S., Nguyen, T. D., Webster, R. G., Peiris, J. S., and Guan, Y. (2006). Establishment of multiple sublineages of H5N1 influenza virus in Asia: implications for pandemic control. *Proc Natl Acad Sci USA* 103, 2845-50.
3. Olsen, B., V. J. Munster, A. Wallensten, J. Waldenstrom, A. D. M. E. Osterhaus, and R. A. M. Fouchier. 2006. Global patterns of influenza A virus in wild birds. *Science* 312:384-388.
4. Sturm-Ramirez, K. M., Hulse-Post, D. J., Govorkova, E. A., Humberd, J., Seiler, P., Puthavathana, P., Buranathai, C., Nguyen, T. D., Chaisingh, A., Long, H. T., Naipospos, T. S., Chen, H., Ellis, T. M., Guan, Y., Peiris, J. S., and Webster, R. G. (2005). Are ducks contributing to the endemicity of highly pathogenic H5N1 influenza virus in Asia? *J Virol* 79, 11269-79.
5. Tumpey, T. M., C. F. Basler, P. V. Aguilar, H. Zeng, A. Solorzano, D. E. Swayne, N. J. Cox, J. M. Katz, J. K. Taubenberger, P. Palese, and A. Garcia-Sastre. 2005. Characterization of the reconstructed 1918 Spanish influenza pandemic virus. *Science* 310:77-80.
6. United States Department of Agriculture. An Early Detection System for Asian H5N1 Highly Pathogenic Avian Influenza in Wild Migratory Birds, U.S. Interagency Strategic Plan. 2006. (No. 0094.06). United States of America: Author. www.usda.gov/documents/wildbirdstrategicplanpdf.pdf
7. United States Department of Interior, U.S. Geological Survey, Bird Banding Laboratory, North American Banding Program Data Base. Data as of November 2006.
8. United States Department of Agriculture, National Agricultural Statistics Survey. 2002 Census of Agriculture.
9. Woolcock, P. R., Suarez, D. L., and Kuney, D. 2003. Low-pathogenicity avian influenza virus (H6N2) in chickens in California, 2000-02. *Avian Dis* 47, 872-81.

Suggested Citation:

Ryan S. Miller, Matthew Farnsworth, William Kendall, Paul Doherty, James Nichols, Gary White, Kenneth Burnham, Alan Franklin, Jerome Freier. Risk-based Targeted Surveillance: Identifying Areas and Populations of Importance for Surveillance of High Path Avian Influenza in the United States. *GIS Vet. Copenhagen, Denmark. 2007.*