

Analysis identifies areas, populations for Asian H5N1 HPAI surveillance

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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. Waterfowl and shorebirds appear to be the primary natural reservoirs for type A influenzas and have been implicated as the progenitors of previous human flu pandemics^{1,2}.

Nationally, AI surveillance programs have been established to detect the H5 and H7 subtypes of AI in domestic poultry and wild waterfowl. However, early detection of highly pathogenic Asian H5N1 will require targeted surveillance of populations at highest risk for emergence of the virus. Using knowledge about the ecology of migratory waterfowl and type A influenzas, while considering the complications of national scale data collection, an interagency analysis identified areas of importance for surveillance of wild waterfowl. Agencies involved were APHIS VS CEAH Center for Emerging Issues; APHIS VS CEAH National Surveillance Unit; APHIS Wildlife Services; the U.S. Geological Survey (USGS) Patuxent Wildlife Research Center; Colorado State University (CSU) Department of Fish, Wildlife and Conservation Biology; and USGS Colorado Cooperative Fish and Wildlife Research Unit, CSU. The working group's analysis also identified areas of concern for surveillance in domestic poultry.

Analysis focused on primary avian functional groups (dabbling ducks, light geese, dark geese, and swans) thought to be responsible for large-scale movements of Asian H5N1. Recoveries of banded birds from 1991 through 2006 ($n = 241,619$) were used to identify areas within the mainland United States where higher proportions of migrant waterfowl originating from Asia, Alaska, and Canada stop or overwinter. Bird banding data were used in conjunction with U.S. Census of Agriculture data to rank counties with a high prevalence of domestic poultry production and relatively high numbers of migrant waterfowl.

To identify areas of critical concern and overlap between commercial poultry production and concentrations of migratory waterfowl, each stratified data set (commercial poultry and band recoveries), was ordinally ranked from low, 25th percentile to high, 75th percentile (Figure 1). The spatial analysis identified 483 counties (15 percent of total) at very high, high and medium high priority for domestic poultry surveillance when analysis was restricted to migrants originating from Alaska and Asia. These 483 counties account for 29 percent of poultry farms and 26 percent of domestic poultry production (2002 NASS data) and are primarily located along the Pacific flyway and critical overwintering areas along the Gulf Coast of Texas and Louisiana. Counties with critical

migration stopover points in Utah, New Mexico, Kansas and other Midwestern States also rank high. Table 1 presents the number of counties in each risk category and the number of commercial poultry farms represented by those counties.

Table 1. Summary of counties by risk-based rank with Alaska, Asia, and Canadian migrant waterfowl.

Risk Rank	Number of Counties		Number of Farms		Estimated Poultry Population	
		%		%		%
Very High	210	7	26,887	18	342,437,349	21
High	428	14	35,282	24	285,690,255	17
Medium High	1,208	38	62,173	43	858,185,648	52
Medium Low	895	28	19,465	13	138,389,285	8
Low	400	13	2,320	2	17,768,505	1
TOTAL	3,141		146,127		1,642,471,042	

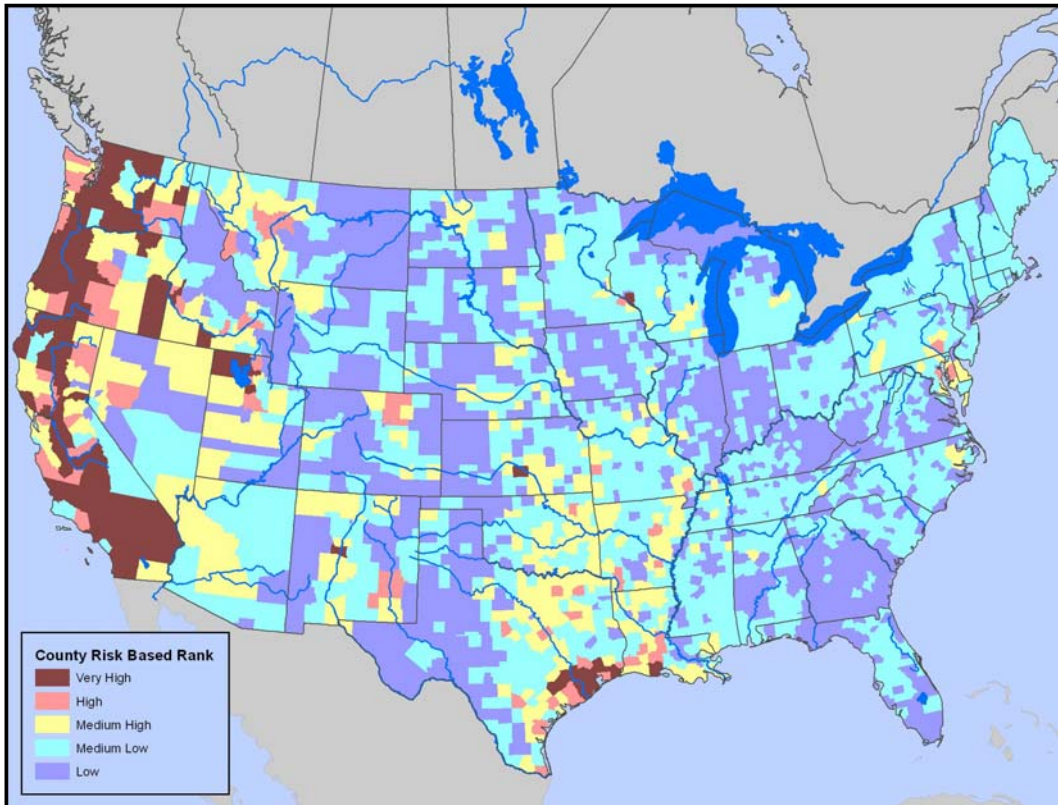
In summary, these analyses are a good foundation for understanding geographic distribution of waterfowl and the relationship to the commercial poultry industry. They also provide sound guidance for geographic allocation of surveillance and sampling efforts related to backyard poultry flocks and commercial poultry producers. However, further analysis is needed to better classify the risk-based rank of counties with a predominance of small poultry producers. In addition, analysis is needed to further define the temporal aspects of migration and their effects on surveillance, and to better define the geographic location and densities of backyard poultry. Further analysis is ongoing to identify areas of importance for migrant waterfowl originating in Europe and Greenland and also migrant waterfowl populations that overwinter in South and Central America. *For more information about this analysis, contact Ryan Miller at ryan.s.miller@aphis.usda.gov.*

REFERENCES

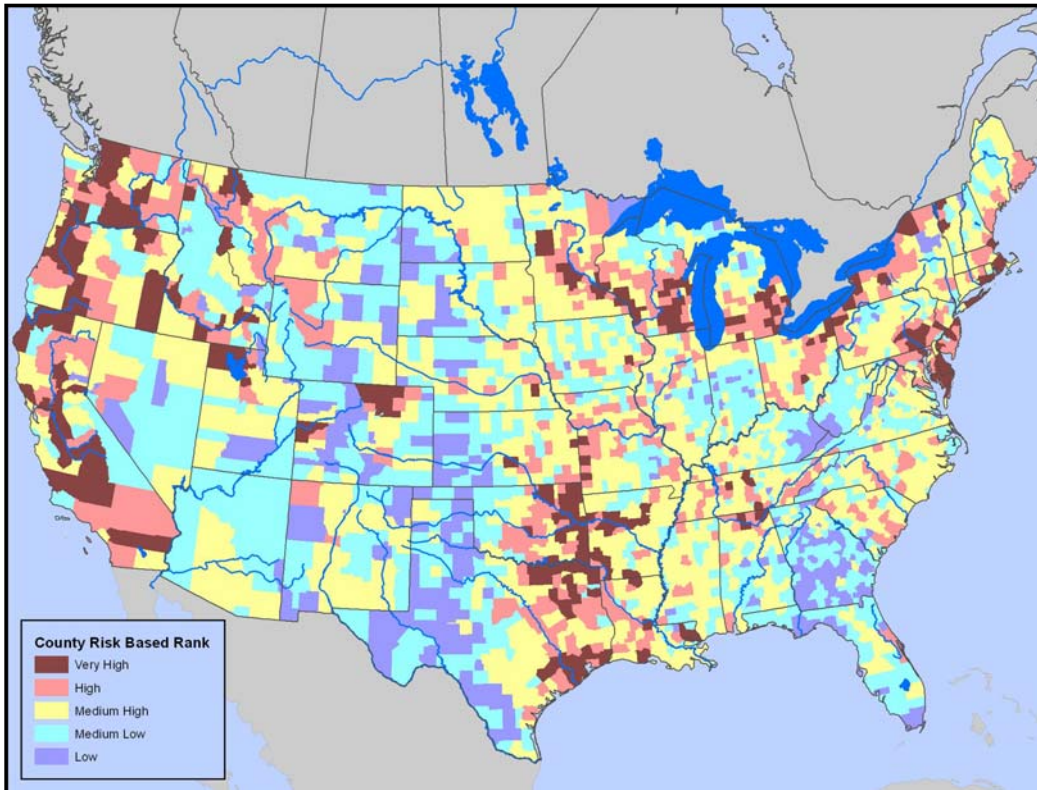
- Olsen, B., Munster, V. J.; A. Wallensten, J. Waldenstrom, A. D. M. E. Osterhaus, and R. A. M. Fouchier. 2006. Global patterns of influenza A virus in wild birds. *Science* 312:384-388.
- Tumpey, T. M., C. F. Basler, P. V. Aguilar, H. Zeng, A. Solorzano, D. E. Swayne, N. J. Cox, J. M. Katz, J. K. Taubenberger, P. Palese, and A. Garcia-Sastre. 2005. Characterization of the reconstructed 1918 Spanish influenza pandemic virus. *Science* **310**:77-80.

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

Alaska and Asia Migrant Waterfowl



Alaska, Asia, and Canada Migrant Waterfowl



Acknowledgements

This analysis was conducted with waterfowl band recoveries processed as part of the interagency working group. Future analysis, which will further identify areas of importance for domestic poultry surveillance, is being conducted in cooperation with an interagency National Risk Analysis Working Group being led by Dr. Paul Doherty of Colorado State University and Dr. Alan Franklin of the National Wildlife Research Center. The interagency working group includes Dr. Gary White, Dr. Jim Nichols, Dr. Matt Farnsworth, Dr. Ken Burnham, and Ryan Miller.