

Novel Eurasian Highly Pathogenic Influenza A H5 Viruses in Wild Birds, Washington, USA, 2014

[Announcer] This program is presented by the Centers for Disease Control and Prevention.

The novel Eurasian highly pathogenic avian influenza HPAI A (H5N8) virus spread rapidly and globally during 2014, substantially affecting poultry populations. The first outbreaks were reported during January 2014 in chickens and domestic ducks in South Korea and subsequently in China and Japan, reaching Germany, the Netherlands, and the United Kingdom by November and Italy in early December 2014. Also in November 2014, a novel H5N2 virus was reported in outbreaks on chicken and turkey farms in Fraser Valley, British Columbia, Canada. This H5N2 influenza virus is a reassortant. Taiwan also recently reported more novel reassortants.

The appearance of highly similar Eurasian H5N8 viruses in Europe, Asia, and now the United States suggests that this novel reassortant may be well adapted to certain waterfowl species, enabling it to survive long migrations. These appearances also represent a major change in Eurasian H5 virus circulation. After the reported spread of HPAI H5N1 virus in Asia, a large, interagency avian influenza virus, or AIV, surveillance effort was implemented throughout the United States during April 2006 to March of 2011. Of nearly 500,000 wild bird samples tested, none harbored Eurasian subtype H5 AIV. The overall prevalence of AIV was about 11 percent. 86 percent were detected in dabbling ducks. Although H5N8 subtype viruses have been detected previously in the United States, all have been low pathogenicity AIV of North American wild bird lineage.

After the November 2014 report of H5N2 HPAI outbreaks among poultry in British Columbia, the US Departments of Agriculture and Interior, together with state agency personnel, increased surveillance of poultry flocks, hunter-harvested wild birds, and wild bird die-offs along the US–Canada border. A wild bird die-off was reported on December 1, 2014 at Wiser Lake in Whatcom County, Washington, USA. The lake, which has a history of waterfowl deaths caused by lead poisoning and aspergillosis, is located about 32 kilometers from the location of the index cases in Fraser Valley. Up to 10,000 waterfowl were on the lake when the deaths began. The dead birds consisted primarily of mallards, American wigeon, and northern pintail, along with smaller numbers of other waterfowl species.

Nine carcasses were submitted to the National Wildlife Health Center; 6 were examined in detail. *Aspergillus fumigatus* was isolated from 5 birds with characteristic lesions of airsacculitis. In addition, cloacal and/or oral swab samples from 5 birds had molecular assay results positive for influenza A and H5. A Eurasian lineage H5 was isolated from a lung specimen. Whole-genome sequencing indicated the virus was highly similar to the H5N2 reassortant virus from Canada. Both viruses have 3 RNA segments of North American wild bird lineage and 5 RNA segments that showed more than 99 percent similarity to the 2014 Eurasian H5N8 viruses. According to World Organisation for Animal Health guidelines, the virus was consistent with HPAI.

In a related event, on December 6, 2014, an American wigeon was captured and partially consumed by a captive-reared falcon in Whatcom County, about 8 kilometers from Wiser Lake. The wigeon remains were also fed to 3 other falcons and falcon–peregrine hybrids at a farm with another 25 raptors and 40 pigeons. The first falcon died on December 8 and was submitted to the National Wildlife Health Center. The second falcon also died on December 8 and the third on December 11; the fourth was euthanized on December 11. Carcasses of these last 3 falcons were submitted to the Washington Animal Disease Diagnostic Laboratory. No further deaths or illnesses have been reported among other raptors at the facility. Histologic and pathologic findings for the 3 raptors were consistent with those described in previous reports of H5N8 infections, and the severity of the lesions correspond to virus concentrations detected in the tissues by molecular assays. Molecular assay results for oral and cloacal swab samples and major organ and brain samples from one falcon were positive for influenza A and H5 viruses. For two falcons, partial HA and NA genes were directly sequenced from brain and oral swab samples. And a Eurasian AIV, H5N8, was isolated from the brain of another falcon. All 8 RNA segments for the strain were more than 99 percent similar to those for 2014 Group A H5N8 strains from South Korea.

Phylogenetic analysis of the H5 viruses detected in the United States resulted in 3 major findings. First, the Eurasian lineage avian H5N8 virus survived introduction into North America in its entirety. Second, introduction of Eurasian H5N8 virus into North America appears to be independent from introductions of the virus into Europe. Third, the duration of circulation of H5N8 virus in the Pacific flyway—California, Idaho, Nevada, Oregon, Utah, and Washington—is unknown, but it was sufficient for reassortment with low pathogenicity North American lineage wild bird AIV.

The ongoing circulation of these Eurasian HPAI H5 viruses in wild birds considerably alters the potential risks and subsequent consequences for US poultry and wildlife rehabilitation centers. Detection of HPAI H5N8 virus in apparently healthy common teal, Eurasian wigeon, mallard, spot-billed duck, and tundra swans suggests that wild birds may contribute to further spread of this HPAI H5 lineage in North America. However, culling and otherwise disturbing wild birds or their habitats has not been shown to be beneficial in the control of avian flu. The scientifically supported management action, however, is to enhance biosecurity to minimize contacts between poultry, wild birds, and their formites. In addition, hunters should be cognizant of risks from handling potentially infected carcasses.

Examination of wild bird surveillance samples collected before December 2014 may provide further insight into the timing and route of introduction of the Eurasian H5N8 virus into North America. In addition, enhanced and ongoing influenza surveillance in wild birds and poultry will contribute to a better understanding of the geographic distribution and species involved in the spread of these HPAI H5 viruses. Together, these data may enable waterfowl managers and poultry producers to better assess and manage disease risks. Human infections have not been associated with either virus; however, H5N1 virus has caused human death, so caution is warranted. During preparation of this article, H5N8 was reported in wild birds and poultry along

the Pacific flyway; novel H5N2 virus was detected in Idaho, Oregon, and Washington; and another novel reassortant H5N1 was detected in Washington and British Columbia. These detections have had major effects on US poultry trade.

I'm Sarah Gregory for *Emerging Infectious Diseases*. You can read the entire May 2015 article, Novel Eurasian Highly Pathogenic Influenza A H5 Viruses in Wild Birds, Washington, USA, 2014, online at cdc.gov/eid.

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