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Summary of surveillance for influenza A viruses of swine in the United States – Results and strategies

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Influenza A virus (influenza) infections of pigs are of high prevalence but cause low mortality and are considered endemic infections in swine. For these reasons, and perhaps others, the United States Department of Agriculture has not classified influenza as a reportable or regulated disease. Nevertheless, a number of collaborators at university, state, and private diagnostic laboratories have maintained conducted informal surveillance efforts of US veterinary diagnostic laboratories for several years. These syndromic surveillance effort have identified numerous, reassortant, recently circulating influenza viruses in swine. This informal surveillance system has been supported primarily by client-user fees or by influenza researchers willing to study influenza associated with endemic respiratory disease in pigs. A critical factor to its success has been the assurance of anonymity and the prevention of penalties to clients submitting specimens. Through these informal, syndromic surveillance efforts, influenza is detected in pig respiratory tissues submitted to diagnostic laboratories throughout the year, but with seasonal peaks in late fall and early spring. Five antigenically and genetically diverse HA clusters of H1 and 1 dominant H3 cluster of triple reassortant influenza have been identified in pigs in the US and Canada in the last decade. The H1 diversity is apparent in both antigenic and genetic evaluations of the viruses.

To supplement these informal, syndromic surveillance efforts, active influenza surveillance in pigs throughout the Midwestern United States began in June 2009 through multi-CEIRS collaborations. Thirty-two conveniently selected commercial pig farms were chosen to participate in this study. Farms were located in swine dense areas in Illinois, Indiana, Iowa and Minnesota. Thirty nasal swabs were collected every month for 12 consecutive months from growing pigs. Swabs were tested for influenza A viral RNA using a RRT-PCR targeting the matrix gene. During collection, the age of the pigs, group clinical signs and influenza vaccination history were recorded. A total of 6540 nasal swabs have been collected since Jun 2009 to May 2010 through this active surveillance program. From the total number of swabs collected, 3677 have been tested. Out of those swabs tested, 140(4.74%) were influenza A virus RRT-PCR positive. Fifty-three percent of all positive swabs were from pigs between 12 and 17 weeks of age. Influenza was detected in pigs as young as six weeks of age. The mean number of positive swabs in the positive groups was 5.4 with a minimum of 1 and a maximum of 29. Twenty-one (68%) out of the 32 initially enrolled farms have had at least one influenza positive group. Since the beginning of this project, at least one positive swab among participating farms has been identified every month with the exception of November 2009. As of January 2010, a total of 124 groups of pigs have been monitored. Twenty-six (21%) have had at least one positive swab. Interestingly, only five of those 26 positive groups had clinical signs on the day of the visit. Additionally, from the 26 positive groups, 12 groups had a history of influenza vaccination at the sow source farm. No statistical difference was seen when farm type, influenza vaccination history, and age were compared between positive and negative groups. Four groups of pigs have been diagnosed to be infected with the pandemic H1N1 strain, four with H3 and three with H1. Subtyping is still being conducted on the other positive groups. According to the preliminary results of the active surveillance work, influenza A virus is present in pigs regardless of the farm type, age, month of the year, and vaccination history. It is important to mention that even though the detection rate is low, the virus is being detected in populations in which there are no clinical signs at the moment of the visit highlighting the importance of an active surveillance system.

To address the role that swine may play in the ecology of influenza in wild birds, surveillance activities are ongoing in Minnesota to detect, isolate, and analyze novel avian-swine reassortant influenza A viruses in pigs by identifying AIV–positive turkey flocks or wild birds and monitoring nearby commercial swine for evidence of infection with similar influenza viruses. In addition to identify infected flocks or herds, we also analyze spatial-temporal relationships and identify risk factors for influenza infections in turkeys, wild birds, and swine. In the fall of 2009, 84 flu PCR positive wild bird samples collected from MN sites by USDA/APHIS/Wildlife Services in Fall 2009 were prepared for virus isolation and HA subtyping. All 84 samples were collected from sites that have pig locations within 10 miles. The first 15 samples, chosen because they

are from locations near confirmed swine farms within 3 miles, were subjected to 3 passages of egg inoculation. Of these 15, five samples have been isolated and confirmed positive for flu by matrix gene RRT-PCR and 10 were negative for influenza A virus by egg inoculation. The following HA subtypes were identified by sequencing of the HA2 portion of the hemagglutinin gene: H11, H6, H3, H4, and H4. These viruses are available as diagnostic reagents or for further characterization.