

The surveillance and control programme for avian influenza (AI) in wild birds in Norway

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Results were negative for the 2009 surveillance for highly pathogenic avian influenza virus in wild birds.

Introduction

The surveillance also revealed that Mallards, Wigeons, Gulls, and Teals are the most relevant reservoirs of influenza A virus in Norway.

The Norwegian Food Safety Authority is responsible for the implementation of the active surveillance programme for avian influenza (AI) in wild birds. The programme, which was started in 2005, is based on virological investigations in healthy, live or hunted birds. The National Veterinary Institute is responsible for planning, laboratory investigations and reporting components of the programme. The programme was suspended in 2008.

AI is a serious, highly contagious disease of poultry and other captive birds caused by many different subtypes of influenza type A viruses. The level of risks posed by the different subtypes to animal and public health is very variable, and are sometimes unpredictable. This is due to rapid virus mutation and possible re-assortment of the genetic material between different subtypes.

Wild waterfowls are the natural reservoirs for all influenza A virus subtypes. Infected birds do not usually develop clinical disease, but shed large amounts of virus in their faeces (1). The highly pathogenic avian influenza (HPAI) virus H5N1 is primarily shed via the airways (2).

HPAI has never been reported in wild birds of Norway.

Aims

The aim of the national surveillance programme for AI in wild birds is to study and understand the threats posed by wild birds in relation to influenza viruses of avian origin, with special emphasis to H5 and H7 viruses.

Materials and methods

In 2009 the programme for wild birds consisted of molecular screening of cloacal and tracheal swabs from healthy birds shot during the 2009 hunting season. Sampling equipment consisted of a sample tube containing a virus transport medium. Swabs were sent to hunters in the county of Rogaland (South-Western Norway). Choice of hunters was based on their proficiency during previous hunting seasons. The hunters were also given written instructions on how to sample the animals. They were requested to fill in registration forms for individual birds. The swabs were taken from shot birds, and then placed in the transport medium. The swabs were sent by overnight post to the National Veterinary Institute in Oslo. The samples were frozen at -70 °C upon arrival.

The sampling comprised the following species shown in Table 1.

H5/H7

The samples were registered upon arrival and screened using a reverse transcriptase polymerase chain reaction (RT-PCR). The screening RT-PCR used was a pan-influenza A virus RT-PCR that reveals the presence of all subtypes of influenza type A virus. The method does not, however, give information as to which hemagglutinin (HA) or neuraminidase (NA) subtype is present in influenza positive samples. Therefore, the samples found to be positive in the initial pan-influenza A virus RT-PCR were further subtyped, using RT-PCRs specific for H5 and H7 or RT-PCRs for amplification of the full-length HA and NA genes. Samples positive for the pan-influenza A virus RT-PCR were also inoculated in embryonated eggs for virus isolation following the procedures described in the OIE Manual (3), with some minor modifications.

Table 1. Birds examined in 2009 and the results of the examination for influenza virus.

Species	No. of examined	Negative	Influenza A	Low pathogenic H5	High pathogenic H5	Low pathogenic H7	High pathogenic H7
Duck family (Anatidae)	7	6	1	0	0	0	0
Mallard (<i>Anas platyrhynchos</i>)	231	189	41	11	0	0	0
Eurasian Wigeon (<i>A. penelope</i>)	22	20	2	0	0	0	0
Common Teal (<i>A. crecca</i>)	45	33	12	3	0	0	0
Tufted Duck (<i>Aythya fuligula</i>)	5	4	1	0	0	0	0
Common Eider (<i>Somateria mollissima</i>)	1	1	0	0	0	0	0
Common Merganser (<i>Mergus merganser</i>)	1	1	0	0	0	0	0
Common Goldeneye (<i>Bucephala clangula</i>)	13	13	0	0	0	0	0
Gull family (Laridae)	3	3	0	0	0	0	0
Herring Gull (<i>Larus argentatus</i>)	49	47	2	0	0	0	0
Great Black-Backed Gull (<i>L. marinus</i>)	1	1	0	0	0	0	0
Common Gull (<i>L. canus</i>)	27	20	7	0	0	0	0
Total	405	338	66	14	0	0	0

Results

In total, samples from 421 birds were received. Of these where 14 samples rejected from examination leaving 407 for analysis. Of these, 66 were positive for influenza A virus. None of the samples were positive for HPAI viruses.

The prevalence for influenza A virus in waterfowls in which the virus was isolated was: Common Teal 26.7 % (12/45), Tufted duck 20 % (1/5), Mallard 17.7 % (41/231) and Eurasian Widgeon 9.1 % (2/22), and. In addition, there was 1 positive sample of a total of 7 collected from unidentified birds defined as ducks (14.3 %).

And in other gulls; Common Gull 25.9 % (7/27) and Herring Gull 4.1 % (2/49).

Sub-typing of all the samples found positive for influenza A virus are not yet complete. All of these samples have been tested for the presence of subtype H5 and H7. None of the samples were H7 positive. Eleven Mallards and 1 Teal were found to carry H5 subtypes, one of the Teal samples has been further characterised and found to be H5N1. Sequencing of the HA gene has identified these viruses as low pathogenic avian influenza (LPAI) viruses.

The other subtypes identified thus far include H3N8, H4N2, H4, H6, H9, H9N2, and H13N2.

Table 2. Birds examined 2006 to 2007 in the program for avian influenza and the results of the examinations (The programme was suspended in 2008).

Year	No. of samples	Negative	Influenza A	Low pathogenic H5	High pathogenic H5	Low pathogenic H7	High pathogenic H7
2006	1274	1189	85	0	0	0	0
2007	1528	1344	183	12	0	0	0
2009	405	338	66	14	0	0	0

Discussion

Similar to previous years, amongst the waterfowl there were positive samples from Mallards, Wigeons and Teals this year. Unfortunately, the national surveillance programme for AI in wild birds was suspended in 2008, so comparisons must be made with previous years (Table 2). Also, the dramatic cut in the number of birds sampled resulted in all the samples being taken from one area in the country, Rogaland county. This area was chosen due to the relative density of poultry operations in the area and their overlap with the flyways and resting areas of many species of waterfowl (4). But in comparison with the national surveillance programme for AI in wild birds in 2006 and 2007, the general prevalence of AI infection amongst wild birds tested in 2009 was higher (5, 6, 7).

Only three species of gull were sampled in 2009. Two of these, the Common Gull and the Herring Gull, were positive for influenza A infection. The Great Black-backed Gull was negative, however, this was also the Gull species that was least sampled (n=1).

The findings of this study indicate that Mallards, Wigeons, Gulls, and Teals are the most relevant reservoirs of influenza A virus in Norway.

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The NFSA advises and reports to the Ministry of Agriculture and Food, the Ministry of Fisheries and Coastal Affairs and the Ministry of Health and Care Services.

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