

# The surveillance programme for avian influenza (AI) in wild birds in Norway in 2017



**Veterinærinstituttet**  
Norwegian Veterinary Institute



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## Summary

Surveillance in 2017 did not detect highly pathogenic avian influenza infection in wild birds.

## Introduction

The Norwegian Food Safety Authority is responsible for implementing the active surveillance programme for avian influenza (AI) in wild birds. The programme started in 2005 and is based on virological investigations in presumably healthy, live or hunted birds. The Norwegian Veterinary Institute planned, conducted the laboratory investigations and composed this annual report. The programme has been running from 2005-2007, from 2009-2010, and in 2016 and onwards.

Being widespread in birds, AI viruses are highly contagious and can evolve rapidly by mutations. Wild waterfowl such as ducks, geese, swans, waders and gulls are the natural reservoirs for all low pathogenic influenza A viruses. These birds do not usually develop clinical disease, but do shed large amounts of virus in their faeces (1). The highly pathogenic avian influenza virus H5N1, on the other hand, is primarily shed via the airways, especially in poultry (2).

In domestic poultry, infection with influenza A viruses causes two main forms of disease distinguished by high and low virulence. Although most low pathogenic AI (LPAI) viruses cause only mild disease in poultry, LPAI strains have the potential to mutate to highly pathogenic AI (HPAI) viruses following introduction to poultry populations. HPAI viruses, on the other hand, induce a serious, highly contagious disease in poultry and other captive birds. All HPAI epidemics recorded so far have been of the hemagglutinin subtypes H5 or H7.

Wild migratory birds have been suggested to play a major role in the dissemination and spread of HPAI viruses over long distances (3, 4). Virus detections in wild birds mainly occur in migratory duck species, swans, sea gulls and birds of prey. HPAI has never been discovered in the wild birds surveillance in 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 on H5 and H7 viruses.

## Materials and methods

In 2017, the programme for wild birds consisted of molecular (PCR) screening of cloacal and tracheal swabs from healthy birds shot during the 2017 hunting season, and from live birds sampled during ringing. Sampling equipment consisted of flocked swabs and tubes containing virus transport medium for viral sampling, and was sent to hunters in the county of Rogaland, Østfold, Hedmark and Trøndelag. Choice of regions was based on relative density of poultry farms in the area, and their overlap with the flyways and resting areas of many species of waterfowl (5). Choice of hunters was based on their proficiency during previous hunting seasons. Sampling equipment was also sent to a hobby ornithologist in the Oslo area, who performed sampling during the process of ringing birds. All samplers were given written instructions on how to collect samples, and were requested to fill in registration forms for individual birds. Directly after sampling, swabs were placed in transport medium and mailed overnight to the Norwegian Veterinary Institute in Oslo. All samples were frozen at  $-70^{\circ}\text{C}$  upon arrival. In addition to samples taken by hunters and ornithologists, 124 samples from live birds were taken by scientists from the Norwegian Veterinary Institute in connection with a Danish research project on pink-footed geese (*Anser brachyrhynchus*). These geese were captured in large numbers in Skogn in Trøndelag county using cannon-nets. Altogether, eight species of wild birds were sampled in 2017 as shown in Table 1.

## Avian influenza analyses

Upon arrival in the laboratory, samples were registered and screened using a real-time reverse transcriptase polymerase chain reaction (rRT-PCR). The screening rRT-PCR used was a pan-influenza A virus rRT-PCR (6) recommended by the European Union reference laboratory for AI (Animal Plant and Health Agency, Weybridge; United Kingdom), that can reveal the presence of all subtypes of influenza type A viruses. However, the method does not distinguish which hemagglutinin (HA) or neuraminidase (NA) subtype is present in influenza positive samples. Therefore, the samples found positive in the initial pan-influenza A virus rRT-PCR were further tested, using H5, H7 and N1 specific PCRs (6). Hemagglutinin (HA) and neuraminidase (NA) sequence analysis was then performed on some of the positive samples (7, 8).

## Results and discussion

In total, samples from 512 birds were analysed (Table 1, Figure 1) for the presence of influenza A virus. Results showed that 29 (5.7 %) animals were positive for influenza A virus.

Proportions of influenza A virus detected in different species of waterfowl during surveillance were common teal (*Anas crecca*) 7.8 % (4/51), mallard (*Anas platyrhynchos*) 10 % (19/190) and Eurasian wigeon (*Anas penelope*) 9.7 % (6/62).

All influenza A positive samples were further tested for the presence of subtype H5 and H7. Out of the 29 influenza A positive samples, six samples were H5 positive, whereas no samples were H7 positive. Five of the H5 positive samples were from mallards, and one H5 positive sample was from a Eurasian wigeon. None of these were positive for neuraminidase subtype N1. Sequencing of the HA genes identified all six viruses as low pathogenic (LPAI).

Table 1. Number and species of birds tested in the surveillance programme for avian influenza in wild birds in 2017.

Species	No. tested	InfA negative	InfA positive	LPAI H5	HPAI H5	LPAI H7	HPAI H7
Common teal ( <i>Anas crecca</i> )	55	51	4	0	0	0	0
Eurasian wigeon ( <i>Anas penelope</i> )	68	62	6	1	0	0	0
Mallard ( <i>Anas platyrhynchos</i> )	209	190	19	5	0	0	0
Red-breasted merganser ( <i>Mergus serrator</i> )	7	7	0	-	-	-	-
Ducks (species unknown) ( <i>Anatidae</i> )	6	6	0	-	-	-	-
Barnacle goose ( <i>Branta leucopsis</i> )	10	10	0	-	-	-	-
Canada goose ( <i>Branta canadensis</i> )	10	10	0	-	-	-	-
Greylag goose ( <i>Anser anser</i> )	23	23	0	-	-	-	-
Pink-footed goose ( <i>Anser brachyrhynchys</i> )	124	124	0	-	-	-	-
Total	512	483	29				

Since 2009, the total number of samples collected in the surveillance programme for avian influenza in wild birds was greatly reduced. In addition, suspension of the programme from 2010 to 2015 impedes the study of temporal trends in AI prevalence in wild birds at annual intervals. However, the prevalence of AI infection amongst wild birds tested in 2017 was the lowest since the surveillance programme started in 2009 (Figure 2) (10, 11, 12).

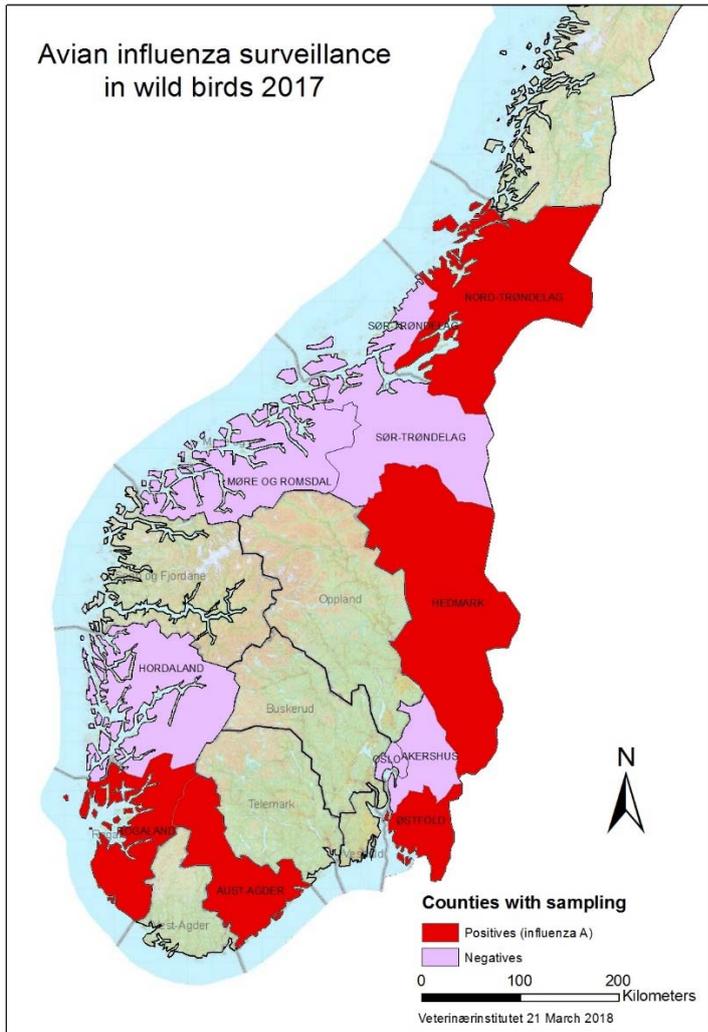


Figure 1. Map showing regions of wild bird sampling during the 2017 surveillance programme for avian influenza in wild birds. Red colour marks counties where birds positive for influenza A were sampled, whereas pink colour marks counties with only negative results.

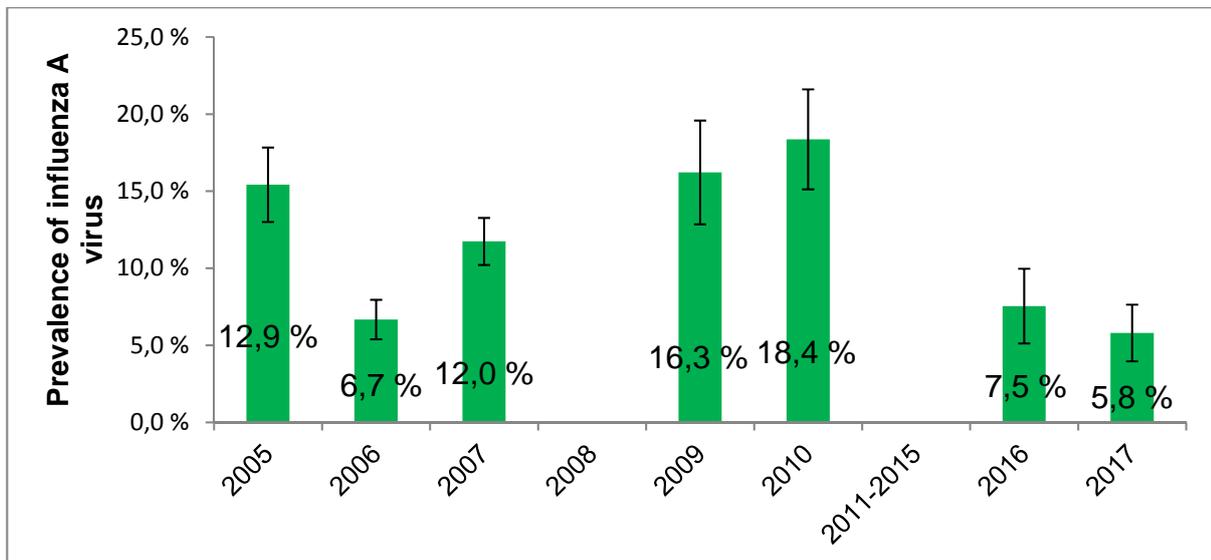


Figure 2. Prevalence of influenza A virus in ducks and gulls in the surveillance programme for avian influenza in wild birds from 2005-2017.

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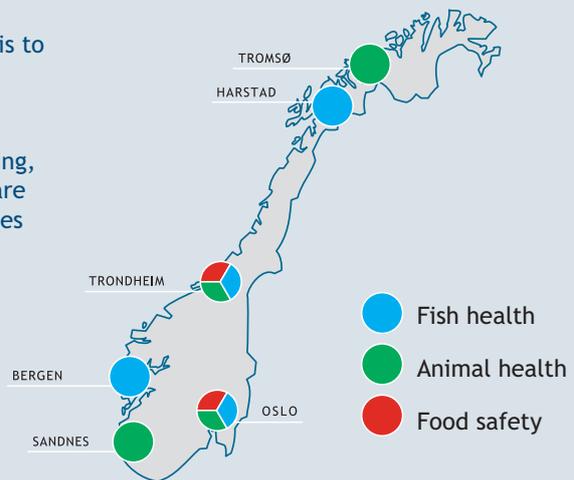
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