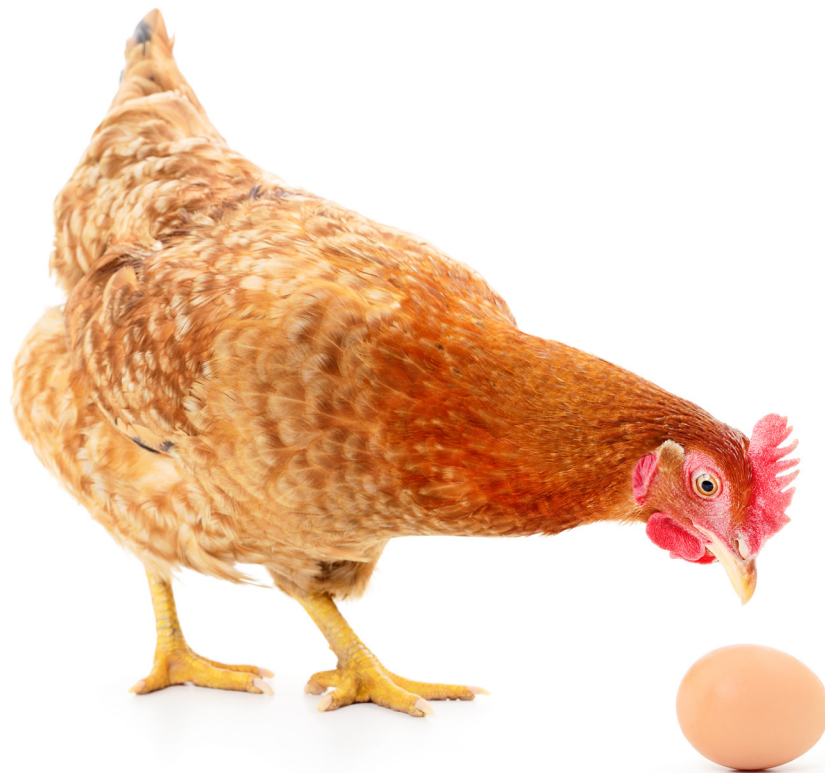




The surveillance programme for avian influenza (AI) in wild birds in Norway 2020



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Summary

Active surveillance in 2020 detected 47 cases of avian influenza infection in wild birds in Norway. Four of the cases were highly pathogenic avian influenza (HPAI), all belonging to the subtype H5N8.

On November 27th 2020, the Veterinary Institute detected the highly pathogenic avian influenza virus on a short-billed goose (*Anser brachyrhynchus*). The goose was observed sick in Sandnes municipality, Rogaland county, and died shortly afterwards. This bird, sampled in connection with passive surveillance for HPAI, was the first time that highly pathogenic avian influenza virus (HPAI) was detected in Norway (1).

Four samples from the active surveillance programme of avian influenza (AI) in wild birds collected from hunted Eurasian wigeon (*Anas penelope*) in Rogaland on November 14th and 15th 2020, were subsequently analysed for HPAI and came out with a positive diagnosis for HPAI H5N8. The first case of HPAI in Norway is therefore from Rogaland from mid-November 2020.

Introduction

The Norwegian Food Safety Authority is responsible for the active surveillance programme of avian influenza (AI) in wild birds. The programme consists of virological investigations in presumably healthy, live or hunted birds. The Norwegian Veterinary Institute (NVI), planned and conducted the laboratory investigations, and presents the findings for 2020 in this annual report. Introduced 15 years ago, the programme ran intermittently from 2005-2007, from 2009-2010, and onwards from 2016. In addition to this active surveillance, the NVI conducts analysis for AI in wild birds found sick or dead, constituting the passive surveillance for AI in Norway.

Being widespread in birds, AI viruses are highly contagious and can mutate rapidly to new strains. Wild waterfowl species, such as ducks, geese, swans, waders and gulls are natural host reservoirs for all low pathogenic influenza A viruses. These birds do not usually develop clinical disease, but could shed large amounts of virus in their faeces (2).

The high and low virulent influenza A viruses causes two main forms of disease. Although most low pathogenic AI (LPAI) viruses cause only mild disease in poultry, LPAI strains can potentially mutate into HPAI viruses when introduced into poultry populations. HPAI is a serious, highly contagious disease in poultry and other species of captive birds. All HPAI epidemics recorded so far have been of the hemagglutinin subtypes H5 or H7.

Wild migratory birds potentially have a major role in the dissemination and spread of HPAI viruses over long distances (3, 4). Prior to 2020, the surveillance did not detect HPAI in wild birds in Norway.

Aims

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

Materials and methods

Sampling

In 2020, the AI surveillance in wild birds was by molecular (PCR) screening of cloacal and oropharyngeal swabs from healthy birds shot during the 2020 hunting season, and from live birds sampled during ringing. Sampling equipment sent to hunters in the counties of Rogaland, Østfold, Hedmark and Trøndelag, consisted of flocked swabs and tubes containing virus transport medium for viral sampling. Geographical regions targeted for surveillance was by a risk-based approach, by considering relative density of poultry farms in the area, and their overlap with the flyways and resting areas of many species of waterfowl (5). Recruitment criterion of hunters for the programme was their proficiency performance during previous hunting seasons. Two ornithologists in the Oslo area also received sampling equipment and participated in the program by sampling birds in conjunction with ringing. Both hunters and ornithologists received written instructions on how to collect samples, and were requested to fill in registration forms for individual birds. Swabs, placed in transport medium immediately after sampling, were mailed overnight to the NVI. Upon arrival, processing of samples was either done immediately or the samples were frozen at -70°C for future processing. Altogether, 15 species of wild birds were sampled in 2020, as shown in Table 1.

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 method (6) as recommended by the European Union reference laboratory for AI (Istituto Zooprofilattico Sperimentale delle Venezie (IZSVE), Legnaro, Italy), that can detect all subtypes of influenza type A viruses. However, the method does not distinguish the specific hemagglutinin (HA) or neuraminidase (NA) subtype in influenza positive samples. Therefore, the samples found positive in the initial pan-influenza A virus rRT-PCR underwent further testing, using H5 and H7 specific PCRs (6).

Results and discussion

In total, samples from 498 wild birds were analysed (Table 1, Figure 1) for the presence of influenza A virus. Results showed that 47 (9.4 %) birds were positive for influenza A virus.

Proportions of influenza A virus detected in different species of waterfowl during active surveillance were Green-winged Teal (*Anas crecca*) 20.8 % (10/48), Eurasian wigeon (*Anas penelope*) 18.1% (23/127) and mallard (*Anas platyrhynchos*) 8.8 % (14/160).

All influenza A positive samples were further tested for the presence of subtype H5 and H7. Seven out of the 47 influenza A positive samples were H5 positive, while none of the samples were H7 positive.

Table 1: Number of birds analysed in the Surveillance Programme for Avian influenza in Norway in 2020.

Species (Nor.)	Species (Eng.)	Species (Lat.)	No. tested	Infl. A positive	H5 positive	H7 positive	N8 positive	HPAI H5N8
Brunnakke	Eurasian Wigeon	<i>Mareca penelope</i>	127	23	6		6	4
Fiskemåke	Mew Gull	<i>Larus canus</i>	13					
Fugl, art ukjent	Bird (species unknown)	<i>Aves</i>	3					
Grågås	Graylag Goose	<i>Anser anser</i>	26					
Gråmåke	Herring Gull	<i>Larus argentatus</i>	23					
Hettemåke	Black-headed Gull	<i>Larus ridibundus</i>	34					
Hvitkinngås	Barnacle Goose	<i>Branta leucopsis</i>	6					
Kortnebbgås	Pink-footed Goose	<i>Anser brachyrhynchus</i>	25					
Krikkand	Green-winged Teal	<i>Anas crecca</i>	48	10				
Kvinand	Common Goldeneye	<i>Bucephala clangula</i>	8					
Mandarinand	Mandarin Duck	<i>Aix galericulata</i>	1					
Siland	Red-breasted Merganser	<i>Mergus serrator</i>	3					
Sildemåke	Lesser Black-backed Gull	<i>Larus fuscus</i>	12					
Stokkand	Mallard	<i>Anas platyrhynchos</i>	160	14	1			
Svartbak	Great Black-backed Gull	<i>Larus marinus</i>	7					
Toppand	Tufted Duck	<i>Aythya fuligula</i>	2					
Total			498	47	7	0	6	4

Since 2009, the total number of samples collected in the surveillance programme for avian influenza in wild birds decreased greatly. In addition, suspension of the programme from 2010 to 2015 impeded the study of temporal trends in AI prevalence in wild birds at annual intervals. The prevalence of AI infection amongst wild birds in Norway have been relatively stable low compared to results from 2009 and 2010 (Figure 2) (7, 8, 9).

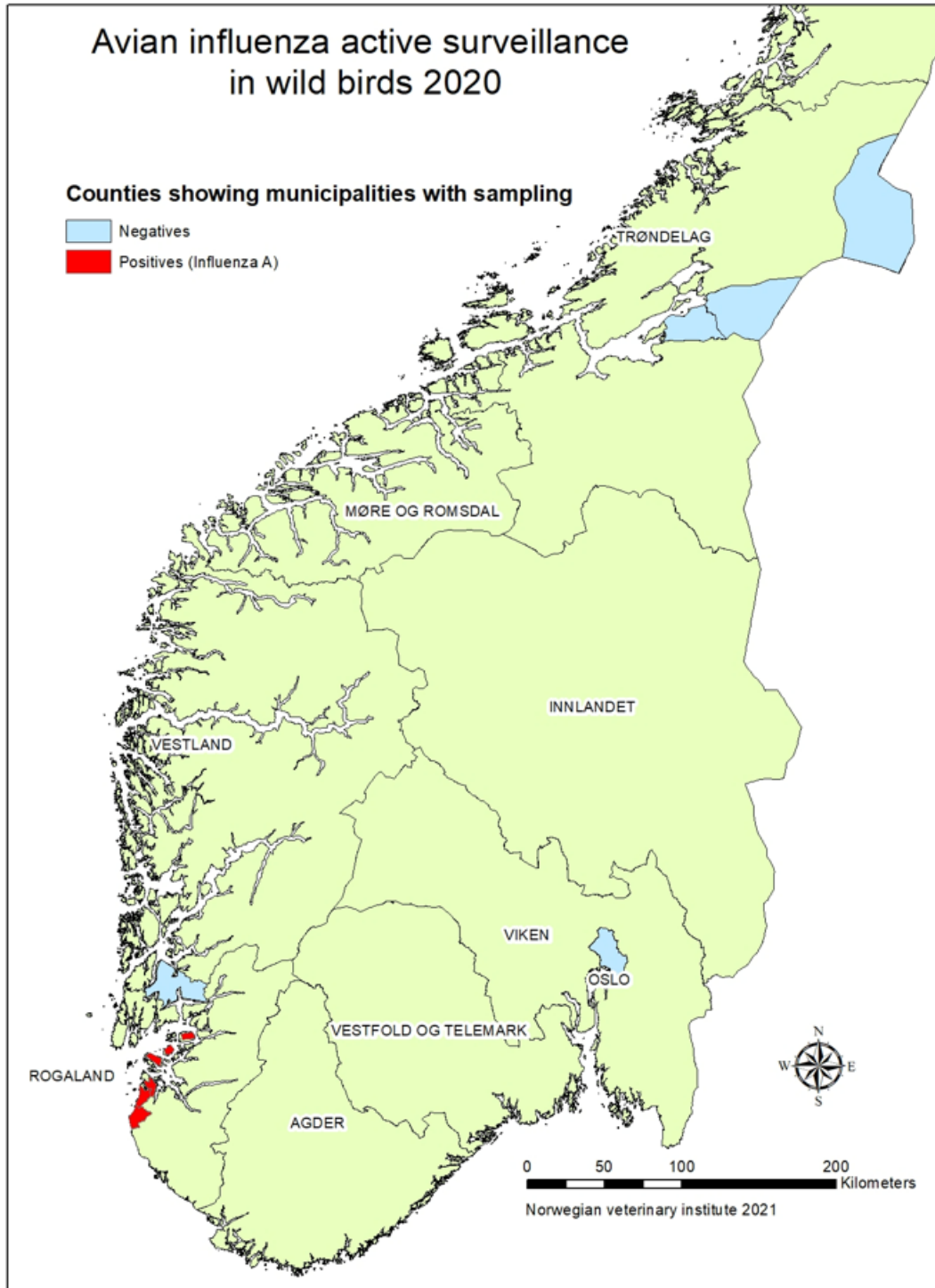


Figure 1: Map showing regions of wild bird sampling during the 2020 surveillance programme for avian influenza in wild birds. Red colour marks municipalities with positive samples for influenza A, whereas purple colour marks municipalities with only negative results.

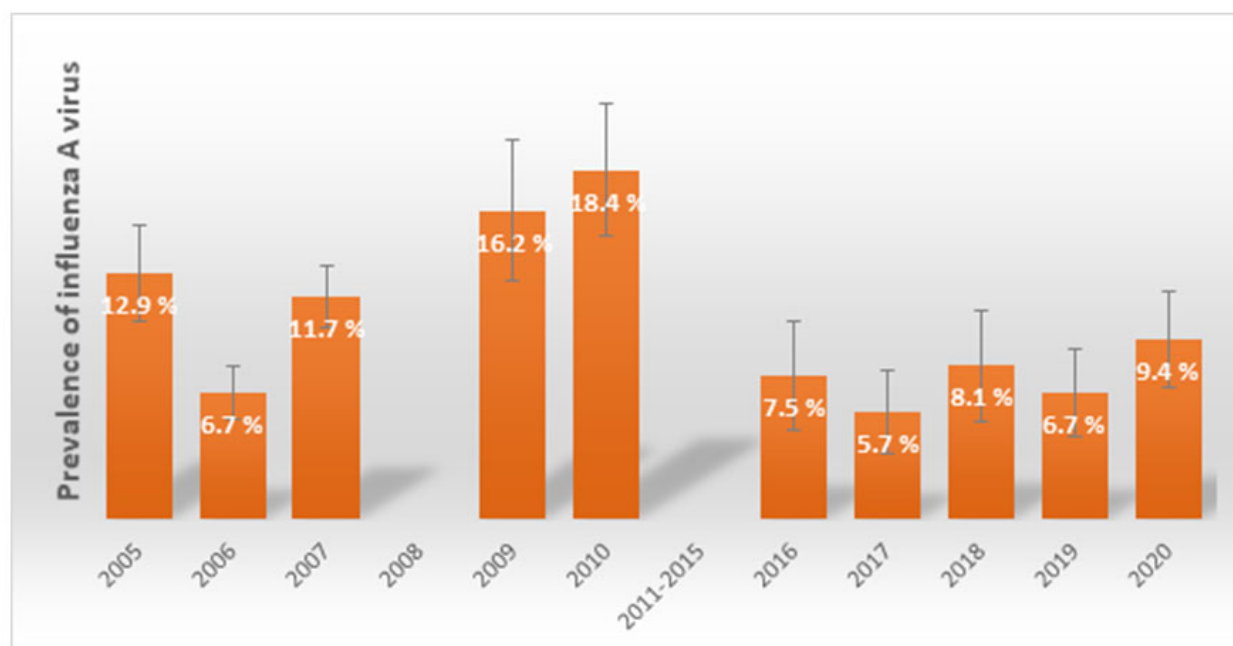
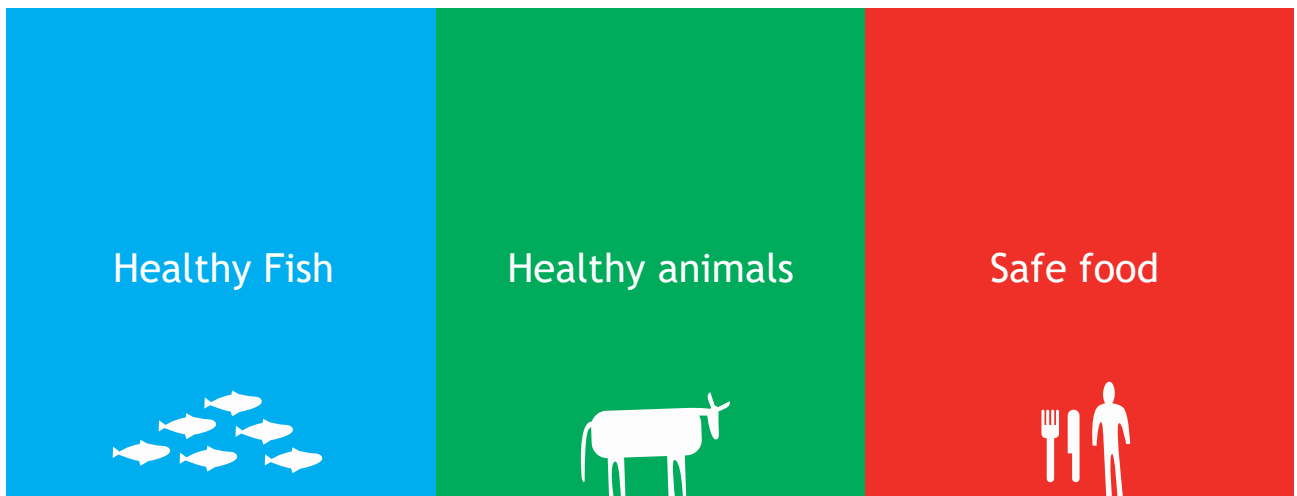


Figure 2: Prevalence of influenza A virus in ducks and gulls in the surveillance programme for avian influenza in wild birds from 2005-2020. Data bars show percentage (\pm 95 % confidence intervals) of influenza A positive birds for each sampling year.

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