Norwegian Veterinary Institute

Report 54 – 2025

The surveillance programme for avian influenza (AI) in Norwegian wildlife 2024

REPORT 54/2025

The surveillance programme for avian influenza (AI) in Norwegian wildlife 2024

Authors

Silje Granstad, Bjørnar Ytrehus, Britt Gjerset, Ragnhild Tønnessen, Johan Åkerstedt

Suggested citation

Granstad, Silje, Ytrehus, Bjørnar, Gjerset, Britt, Tønnessen, Ragnhild, Åkerstedt, Johan. The surveillance programme for avian influenza (AI) in Norwegian wildlife 2024. Surveillance program report. Veterinærinstituttet 2025. © Norwegian Veterinary Institute, copy permitted with citation

Quality controlled by

Merete Hofshagen, Director of Animal Health, Animal Welfare and Food Safety, Norwegian Veterinary Institute

Commissioned by

Norwegian Food Safety Authority

Mattilsynet

Published

2025 on www.vetinst.no
ISSN 1890-3290 (electronic edition)

Colophon

Cover photo: Colourbox
www.vetinst.no

Content

Summary

Influenza A virus was detected in 64 of 723 wild birds examined in the surveillance programme for avian influenza in Norway in 2024. Passive surveillance detected influenza A virus in 20 wild birds, of which 16 were identified as highly pathogenic avian influenza (HPAI) H5. Three of the HPAI detections in wild birds in 2024 were H5N1, twelve were H5N5, and one were H5Nx. Of 29 wild mammals tested as part of passive surveillance, one lynx, one otter, and two red foxes tested positive for HPAI H5N5. Active surveillance detected influenza A virus in 44 wild birds, of which one was characterised as H5Nx, and none were confirmed as HPAI.

Introduction

Norway implements a surveillance programme for avian influenza (AI) in wild birds in accordance with Commission Delegated Regulation (EU) 2020/689 (1). The Norwegian Food Safety Authority (NFSA) is responsible for the surveillance programme, while the Norwegian Veterinary Institute (NVI) manages the planning, laboratory analyses, and reporting components. The programme is based on virological investigations of samples from live or hunted wild birds of target species (active surveillance) and dead or moribund wild birds and mammals (passive surveillance). Active surveillance of AI in wild birds has been running in the years 2005-2007, 2009-2010, and from 2016 and onwards. Passive surveillance in wild birds has been ongoing without interruption. Results of AI testing in wild mammals are also included in this report.

In addition to the above-mentioned surveillance program, NVI participates in the project “Setting up a coordinated surveillance under the One Health approach (OH4Surveillance)” funded by the European Union (Grant Agreement No. 101131473) under the EU4Health Programme. The aim of the project is to protect public health through early detection of emerging and re-emerging zoonotic pathogens in animals and the environment. OH4Surveillance is a consortium of eleven participating countries and is led by Statens Serum Institut (SSI) in Denmark. In Norway, the Norwegian Institute of Public Health (NIPH, Folkehelseinstituttet) is the beneficiary institution and leads the work, while NVI is an affiliated institution and performs the surveillance activities, including laboratory analyses. The project period is from 2024 to 2026. In Norway, a substantial part of OH4Surveillance focus on strengthening the passive surveillance of HPAI. This has been pursued by implementing a range of measures to increase engagement and facilitate participation among scientific and amateur ornithologists, rangers from the Norwegian Nature Inspectorate (SNO), personnel from the Norwegian Institute for Nature Research (NINA) and the Norwegian Polar Institute (NPI), taxidermists, and others who through their occupations or hobbies visit remote areas and/or are in frequent contact with wild birds. In other parts of the project, NVI has initiated collaborations to enhance active surveillance.

Avian influenza viruses (AIVs) are influenza A viruses that evolve rapidly by genetic drift and reassortment. Wild waterfowls, such as ducks, geese, swans, waders and gulls, are natural reservoir hosts for low pathogenic avian influenza (LPAI) viruses. These birds rarely develop clinical disease when infected with LPAI viruses but shed large amounts of virus in their faeces (2). Some LPAI viruses can infect poultry and typically cause only mild disease. However, LPAI viruses of the H5 and H7 subtypes can mutate into highly pathogenic avian influenza (HPAI) viruses when introduced into poultry flocks (3). HPAI is a severe and highly contagious disease causing high mortality in poultry. Migratory birds play a major role in the global spread of HPAI viruses (4, 5). Since 2021-2022, H5Nx belonging to the H5 clade 2.3.4.4.b have established in wild birds, and this has also led to increased detections in wild mammals (6). Since 2021, H5N1 has been the predominating HPAI subtype in Europe, causing severe illness and high mortality in birds and mammals. H5N5 has also circulated in Norway with sporadic detections in northern parts of Europe.

HPAI was confirmed for the first time in Norway in 2020, when HPAI H5N8 was detected in wild and captive birds (7). In 2022, HPAI H5N1 was diagnosed in red foxes (*Vulpes vulpes*), marking the first detections of this disease in terrestrial mammals in Norway (8).

Aims

The aim of the national surveillance programme is to monitor the prevalence of AIVs in wildlife, emphasising H5 and H7 subtype viruses. The surveillance is conducted in accordance with Commission Delegated Regulation (EU) 2020/689 (1).

Materials and methods

Sampling

Cloacal/rectal and tracheal/oropharyngeal swabs for virological testing were collected from live or hunted wild birds (active surveillance), and moribund or dead wild birds and mammals (passive surveillance). Tissue samples, particularly from brain and lungs, were occasionally collected from mammals.

For regular active surveillance, sampling equipment was sent to designated ornithologists and hunters. The recruitment of samplers was based on their geographical location and estimated access to hunted or live birds within *Anseriformes* and *Laridae*, respectively. Geographical regions were mainly targeted for active surveillance by a risk-based approach considering the relative density of poultry farms in a given area and their overlap with the flyways and rest areas of many species of waterfowl (9, 10). Active surveillance was ongoing year-round, but with a focus primarily in the autumn during hunting season.

For the active surveillance conducted under the OH4Surveillance project, bird populations considered to have a high likelihood of HPAIV presence were selected either due to recent outbreaks affecting these populations or because their migration patterns may facilitate the introduction of new HPAIV strains. In this work, NVI cooperates with, or receives samples from, field personnel at NINA and the NPI.

Passive surveillance was conducted by collecting swabs from dead or moribund wild birds and mammals across the entire country. Inspectors from the NFSA were responsible for the regular passive surveillance sampling. The wild bird species sampled were generally in accordance with, but not limited to, the EFSA list of target wild bird species for passive surveillance activities (11). Samples, mainly swabs, were taken from wild mammals in cases where HPAI was suspected based on clinical signs or when found dead in affected areas. Passive surveillance continued throughout the year. The passive surveillance carried out under the OH4Surveillance project enabled field ornithologists at NINA and NPI, rangers from SNO, and other contributors to submit samples from birds found dead or moribund and subsequently euthanised, without relying on the availability of local NFSA inspectors. Sample kits with pre-paid postage were distributed free of charge and could be ordered through a dedicated webpage.

Staff involved in sampling activities received written instructions on sampling procedure and were requested to fill in registration forms for individual cases. Swabs were placed in transport medium immediately after sampling and shipped directly to the NVI. Upon arrival, samples were registered and processed immediately or stored for a few days at 4°C until testing.

Analyses

Samples were tested for AIVs using a real-time reverse transcriptase polymerase chain reaction (rRT-PCR). The rRT-PCR used was an influenza A virus matrix (M) gene method recommended by the European Union Reference Laboratory (EURL) for Avian Influenza (12). The M gene rRT-PCR can detect all influenza A viruses, but cannot be used to determine the hemagglutinin (HA) or neuraminidase (NA) subtypes. Therefore, the influenza A virus positive samples were further analysed using H5- and H7-specific PCRs (12). If samples were H5- or H7-positive, the HA cleavage site was sequenced in order to determine pathogenicity and confirm HPAI or LPAI virus infection.

From June 2022, pathotyping by sequencing was replaced by a more rapid HPAI H5-detection rRT-PCR assay for 2.3.4.4b viruses recommended by the EURL (13). Additional NA subtyping rRT-PCR was performed on positive samples by methods recommended by EURL (14). Representative AIV-positive samples from the surveillance programme are further characterized by genome sequencing, but these results are not included in this report.

Results and discussion

In total, samples from 723 wild birds were analysed for the presence of influenza A virus (Table 1). Of these birds, 96 were sampled in the OH4Surveillance activities; 65 as a part of active and 31 as a part of passive surveillance. The majority of samples were collected between late summer and late autumn. A total of 64 wild birds (8.9%) tested positive for influenza A virus. Of these, none were H7-positive, while 17 (2.4%) were H5-positive. HPAI virus was detected in 16 wild birds (2.2%) in 2024.

Active surveillance in 2024 detected influenza A virus in 44 (9.5%) out of 464 wild birds sampled (Table 1). One Eurasian teal (*Anas crecca*) from Klepp in Rogaland sampled under regular active surveillance tested positive for H5, but NA subtyping and pathotyping was not successful due to low viral load in the sample. Active surveillance under OH4S in 2024 focused on sampling black-legged kittiwake (Rissa tridactyla) populations in the northernmost part of Norway that experienced large HPAI outbreaks in 2023. None of the 65 kittiwakes tested positive for influenza A virus.

Passive surveillance in 2024 detected influenza A virus in 20 (7.7%) of 259 wild birds sampled. Among these, HPAI viruses was detected in 16 birds. Three of the HPAI detections from dead or moribund wild birds in 2024 were H5N1, twelve were H5N5 and one were H5Nx, i.e. NA subtyping was not successful due to low viral load in the sample. The number of wild birds sampled from each county or territory are shown in Figure 1.

Table 1. Number of wild birds sampled in the surveillance programme for avian influenza in Norway in 2024.

	Total 2024	Jan	Feb	Mar	Apr	May	June	July	Aug	Sept	Oct	Nov	Dec
Active surveillance													
H5Nx	1											1	
Other influenza A*	43								1	10	21	8	3
Influenza A negative	420				17	43	10	84	28	68	93	46	31
Total	**464**				17	43	10	84	29	78	114	55	34
Passive surveillance													
HPAI H5N1	3	1	1		1								
HPAI H5N5	12	1									5	5	1
HPAI H5Nx	1										1		
Other influenza A*	4	1									1	2	
Influenza A negative	239	39	21	24	20	11	25	22	21	5	11	27	13
Total	**259**	42	22	24	21	11	25	22	21	5	18	34	14
Active and passive surveillance													
Total	**723**	42	22	24	38	54	35	106	50	83	132	89	48

* Other influenza A: H5/H7-negative

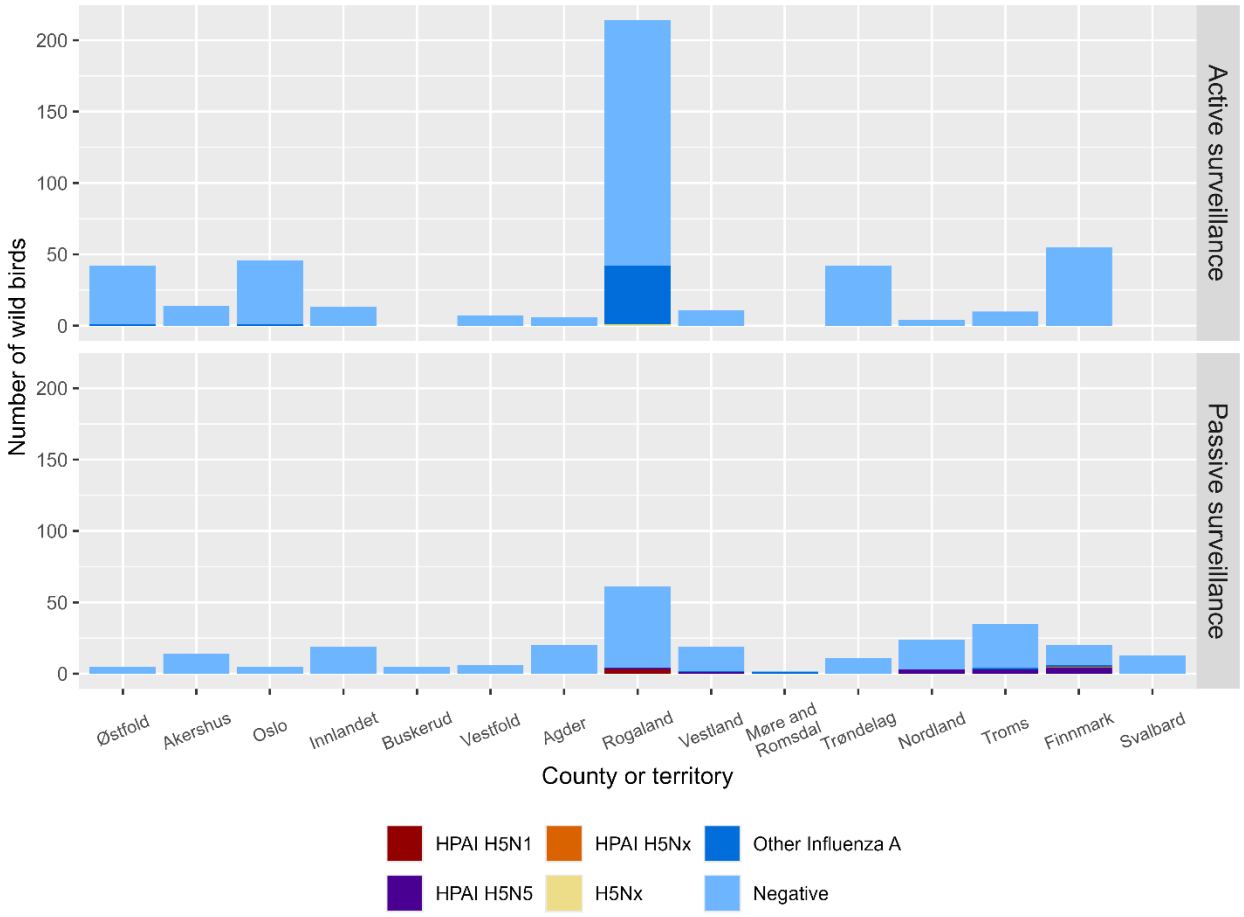

Figure 1. The number of wild birds from counties and territories included in the active and passive surveillance programmes for avian influenza in Norway in 2024.

Among all wild birds sampled through active or passive surveillance, HPAI H5 subtype virus was detected in samples from 16 birds. All confirmed HPAI-positive wild birds in 2024 were identified through passive surveillance, and most of these birds were found dead. HPAI cases were reported in seven wild bird species in 2024 (Table 2). The geographical distribution of HPAI-detections is shown in Figure 2. The detected subtypes and affected species, primarily raptors, colony-breeding seabirds and waterfowls, reflects detections across Europe.

Among wild birds sampled through active surveillance, influenza A virus was detected in 36.0% (31/86) of Eurasian teals (*Anas crecca*), 9.2% (9/98) of Mallards (*Anas platyrhynchos*), 7.1% (3/42) of Eurasian wigeons (*Mareca penelope*), and 4.2% (1/24) of Common gulls (*Larus canus*) (Table 3). All influenza A-positive samples were further analysed for the presence of subtype H5 or, if negative, for H7. One of the 44 influenza A-positive samples was H5-positive, while none was H7-positive. Pathotyping and NA subtyping was not successful due to low viral load. LPAI subtypes H13N6 and H1N1 were detected in a Common gull and a Mallard, respectively. However, characterization of LPAI viruses other than H5 and H7 falls outside the scope of the surveillance programme and is not performed on a routine basis.

Twenty-nine wild mammals, including both marine and terrestrial species, were sampled as part of passive surveillance for AI. Influenza A virus was detected in one Eurasian otter (*Lutra lutra*), three red foxes (*Vulpes vulpes*) and one Eurasian lynx (*Lynx lynx*) (Table 4). Notably, in some of the carnivore cases, such as the lynx, swab samples collected from the trachea and rectum tested negative, whereas samples collected from the brain during necropsy tested positive. This has prompted a revision of the written sampling instructions,

recommending routinely sampling of the brain in cases where wild mammals show clinical signs consistent with avian influenza virus infection.

In 2024, two outbreaks of HPAI were confirmed in poultry in Norway: one in a broiler parent flock in Rogaland, and another in a backyard poultry flock in Trøndelag. Increased mortality in both flocks triggered suspicion of HPAI, and birds were subsequently sampled for diagnostic testing. In both cases, spillover events from wild birds were suspected. Serological surveillance of AI in poultry is presented in a separate report (15).

Table 2. Species distribution of HPAIV-positive wild birds in Norway in 2024.

Species (Eng.)	Species (Nor.)	Species (Lat.)	HPAI H5N1	HPAI H5N5	HPAI H5Nx
Common Buzzard	Musvåk	*Buteo buteo*	1		
Eurasian Eagle-Owl	Hubro	*Bubo bubo*	1		
European Herring Gull	Gråmåke	*Larus argentatus*		3	1
Great Black-backed Gull	Svartbak	*Larus marinus*		3	
Gyrfalcon	Jaktfalk	*Falco rusticolus*	1		
Hooded Crow	Kråke	*Corvus cornix*		3	
White-tailed Eagle	Havørn	*Haliaeetus albicilla*		2	
Gulls, Terns, Skuas and Skimmers (species unknown)	Måkefugler (art ukjent)	*Lari* (suborder)		1	
Total			3	12	1

Figure 2. Geographical distribution of HPAI virus detections in wild birds in Norway in 2024. Colour marks municipalities with one or more detections of HPAI-positive wild birds: HPAI H5N1 (red) and HPAI H5N5 (purple). If more than one HPAI subtype was detected in a municipality in 2024, the colour representing the most recent detected subtype at the end of the year is shown.

Table 3. Number of wild birds sampled in the active surveillance programme for avian influenza in Norway in 2024.

Species (Eng.)	Species (Nor.)	Species (Lat.)	No. sampled	Positive		
				Inf. A	H5	H7
Barnacle Goose	Hvitkinngås	*Branta leucopsis*	5			
Black-headed Gull	Hettemåke	*Chroicocephalus ridibundus*	26			
Black-legged Kittiwake	Krykkje	*Rissa tridactyla*	65			
Canada Goose	Kanadagås	*Branta canadensis*	5			
Common Goldeneye	Kvinand	*Bucephala clangula*	6			
Common Gull	Fiskemåke	*Larus canus*	24	1		
Common Merganser	Laksand	*Mergus merganser*	2			
Eurasian Teal	Krikkand	*Anas crecca*	86	31	1	
Eurasian Wigeon	Brunnakke	*Mareca penelope*	42	3		
European Herring Gull	Gråmåke	*Larus argentatus*	4			
Great Black-backed Gull	Svartbak	*Larus marinus*	2			
Greylag Goose	Grågås	*Anser anser*	44			
Lesser Black-backed Gull	Sildemåke	*Larus fuscus*	14			
Mallard	Stokkand	*Anas platyrhynchos*	98	9		
Mute Swan	Knoppsvane	*Cygnus olor*	5			
Northern Raven	Ravn	*Corvus corax*	13			
Pink-footed Goose	Kortnebbgås	*Anser brachyrhynchus*	21			
Red-breasted Merganser	Siland	*Mergus serrator*	3			
Waterfowl (species unknown)	Andefugler (art ukjent)	*Anseriformes* (order)	3			
Total			464	44	1	

Table 4. Number of wild mammals sampled for surveillance of avian influenza in Norway in 2024.

Species (Eng.)	Species (Nor.)	Species (Lat.)	No. sampled	Positive		
				Inf. A	H5	HPAI H5N5
American mink	Amerikansk mink	*Neovison vison*	2			
Arctic fox	Fjellrev	*Vulpes lagopus*	1			
Beluga whale	Hvithval	*Delphinapterus leucas*	2			
Eurasian lynx	Gaupe	*Lynx lynx*	1	1	1	1
Eurasian otter	Oter	*Lutra lutra*	8	2	2	1
Harpoise porpoise	Nise	*Phocoena phocoena*	2			
Red fox	Rødrev	*Vulpes vulpes*	8	2	2	2
Walrus	Hvalross	*Odobenus rosmarus*	2			
Pinnipeds (species unknown)	Seler (art ukjent)	*Pinnipedia* (suborder)	2			
Total			28	5	5	4

Acknowledgements

The authors would like to thank the technical staff at the Norwegian Veterinary Institute for performing the analyses with excellence. Moreover, the authors would like to thank personnel from the Norwegian Food Safety Authority, the Norwegian Institute for Nature Research, the Norwegian Polar Institute, the Norwegian Nature Inspectorate, and others for collection and submission of samples.

References

1. Commission Delegated Regulation (EU) 2020/689 of 17 December 2019 supplementing Regulation (EU) 2016/429 of the European Parliament and of the Council as regards rules for surveillance, eradication programmes, and disease-free status for certain listed and emerging diseases Council Directive 2005/94/EC. OJ L 174, 3.6.2020, p. 211–340. https://eur-lex.europa.eu/eli/reg_del/2020/689/oj
2. Webster RG, Bean WJ, Gorman OT, Chambers TM, Kawaoka Y. Evolution and ecology of influenza A viruses. Microbiol Rev 1992; 56: 152-79. https://doi.org/10.1128/mr.56.1.152-179.1992
3. Dhingra MS, Artois J, Dellicour S, Lemey P, Dauphin G, Von Dobschuetz S, Van Boeckel TP, Castellan DM, Morzaria S, Gilbert M. Geographical and Historical Patterns in the Emergences of Novel Highly Pathogenic Avian Influenza (HPAI) H5 and H7 Viruses in Poultry. Front Vet Sci 2018; 5: 84. https://doi.org/10.3389%2Ffvets.2018.00084
4. Olsen B, Munster VJ, Wallensten A, Waldenström J, Osterhaus ADME, Fouchier RAM. Global patterns of influenza A virus in wild birds. Science 2006; 312(5772): 384-8. https://doi.org/10.1126/science.1122438
5. The global consortium for H5N8 and related influenza viruses. Role for migratory wild birds in the global spread of avian influenza H5N8. Science 2016; 354(6309): 213-17. https://doi.org/10.1126/science.aaf8852
6. Plaza PI, Gamarra-Toledo V, Eugui JR, Lambertucci SA. Recent Changes in Patterns of Mammal Infection with Highly Pathogenic Avian Influenza A(H5N1) Virus Worldwide. Emerg Infect Dis 2024; 30(3): 444-452. https://doi.org/10.3201/eid3003.231098
7. Madslien K, Moldal T, Gjerset B, Gudmundsson SH, Follestad A, Whittard E, Tronerud OH, Dean KR, Åkerstedt J, Jørgensen HJ, das Neves CG, Rømo G. First detection of highly pathogenic avian influenza virus in Norway. BMC Veterinary Research 2021; 17(218). https://doi.org/10.1186/s12917-021-02928-4
8. Veterinærinstituttet. (2022, 30. juli). Høypatogen fugleinfluensa-virus påvist hos rødrev. https://www.vetinst.no/nyheter/hoypatogen-fugleinfluensa-pavist-hos-rodrev
9. Gjevre AG, Handeland K, Jansen PA, Lyngstad TM, Ytrehus B. Risiko for smitte med høypatogen aviær influensa (HPAI) H5N1 fra ville fugler til fjørfe i Norge. Veterinærinstituttets rapportserie 1-2006. Oslo: National Veterinary Institute; 2006. https://www.vetinst.no/rapporter-og-publikasjoner/rapporter/2006/rapport-risiko-for-smitte-med-hypatogen-avir-influensa-hpai-h5n1-fra-ville-fugler-til-fjrfe-i-norge
10. Granstad S, Rømo G, Falk M, Reiersen A, Ytrehus B, Åkerstedt J. Risikovurdering – Høyrisikoområder for introduksjon av høypatogen fugleinfluensa (HPAI) til fjørfe i Norge. National Veterinary Institute; 2022. https://www.vetinst.no/dyr/vilt/fugleinfluensa-i-norge/_/attachment/download/c02a92a1-44bd-46c3-a32f-3918a225ed57:93c6de1e0452892e90337899aec92ee7ebbf24f0/20221219_Risikovurdering_h%C3%B8yrisikoomr%C3%A5der_HPAI_Norge%20(1).pdf
11. EFSA (European Food Safety Authority), ECDC (European Centre for Disease Prevention and Control), EURL (European Union Reference Laboratory for Avian Influenza), Brown I, Kuiken T, Mulatti P, Smietanka K, Staubach C, Stroud D, Therkildsen OR, Willeberg P, Baldinelli F, Verdonck F and Adlhoch C, 2017. Scientific report: Avian influenza overview September – November 2017. EFSA Journal 2017; 15(12), e05141. https://doi.org/10.2903/j.efsa.2017.5141
12. Spackman E, Senne DA, Myers TJ, Bulaga LL, Garber LP, Perdue ML, Lohman K, Daum LT, Suarez DL. Development of a real-time reverse transcriptase PCR assay for type A influenza virus and the avian H5 and H7 hemagglutinin subtypes. J Clin Microbiol 2002; 40(9): 3256-60. https://doi.org/10.1128/jcm.40.9.3256-3260.2002
13. James J, Seekings AH, Skinner P, Purchase K, Mahmood S, Brown IH, Hansen RDE, Banyard AC, Reid SM. Rapid and sensitive detection of high pathogenicity Eurasian clade 2.3.4.4b avian influenza viruses in wild birds and poultry. J Virol Methods 2022; 301:114454. https://doi.org/10.1016/j.jviromet.2022.114454
14. Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe). Diagnostic protocols for the detection, identification and typing of AI. https://www.izsvenezie.com/reference-laboratories/avian-influenza-newcastle-disease/diagnostic-protocols/
15. Granstad S, Fosse JH, Åkerstedt J. The surveillance programme for avian influenza (AI) in poultry in Norway 2024. Surveillance program report. Veterinærinstituttet 2025.
https://www.vetinst.no/en/surveillance-programmes/avian-influenza-in-poultry/_/attachment/inline/cce7becb-3476-4891-b6e3-ed3ea437df46:18c7bab1d939ccca840b162936fbef955dc35f11/2025_34_OK_AI%20in%20poultry%20in%20Norway%202024%20KOMPLETT.pdf

Health and well-being for animals and people

Norwegian Veterinary Institute

Ås ▪ Sandnes ▪ Bergen ▪ Trondheim ▪ Harstad ▪ Tromsø

postmottak@vetinst.no

vetinst.no