Norwegian
Veterinary Institute

Report 41 – 2025

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REPORT 41/2025

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Suggested citation

Grøntvedt, Carl Andreas, Nordstoga, Anne, Hamnes, Inger Sofie, Ptochos, Sokratis, Bergsjø, Bjarne, Urdahl, Anne Margrete, Rolandsen*, Christer Moe, Odden*, John, Rivrud*, Inger Maren, Våge, Jørn, Madslien, Knut and Attila Tarpai. The surveillance programme for diseases in wild boars in Norway 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: Martin Blom/Runhild Gjelsvik
www.vetinst.no

Content

Summary

Wild boar health surveillance was re-established in August 2018 to gain insight into the incidence of pathogens of importance for animals and humans and to enable early detection of notifiable diseases in this expanding species.

In 2024, samples from 362 wild boars were submitted to the Norwegian Veterinary Institute. This is a slightly higher number than the number of harvested wild boar (n=351) reported to Hjorteviltregisteret (Norwegian Cervid Register). In addition to samples from hunted wild boars, carcasses or relevant sample material from six wild boars found dead (n=4) or killed in traffic accidents (n=2) were submitted by the Norwegian Food Safety Authority (NFSA) as a part of passive surveillance for African swine fever virus (ASFV) and classical swine fever virus (CSFV), with no agents detected.

Furthermore, all samples were negative for antibodies against the following notifiable pathogens: Aujeszky's disease virus (ADV), transmissible gastroenteritis virus (TGEV), porcine respiratory and reproductive syndrome virus (PRRSV), porcine epidemic diarrhoea virus (PEDV) and swine influenza virus (SIV) (these are part of the surveillance programme for specific viral diseases in domestic pigs). Antibodies against *Mycoplasma hyopneumoniae*, an agent that was eradicated from the domestic pig population in 2008 and has not been detected since, were not detected.

Serum from a single male wild boar was positive for antibodies against porcine respiratory corona virus (PRCV). It was concluded that the seroreaction most likely was a false positive, as no other wild boar from the same area had antibodies against PRCV.

The following species and serotypes (n) of *Salmonella* spp. were detected in faeces from 11 hunted wild boars: *S.* Typhimurium (5), *S. enterica* subsp. *diarizonae* serovar 42:r:z (2), *S. enterica* subsp. *diarizonae* serovar 38:r:z (1), *S.* Abony (1), *S.* Hessarek (1), and *Salmonella* sp. serovar 4,5,12:-:- (1). Nine of these were tested for their susceptibility to antimicrobial agents, all nine were fully susceptible to all antimicrobial agents included in the test panel.

Parasitological analysis did not demonstrate presence of *Trichinella* larvae.

Sammendrag

Villsvinhelseovervåkning for 2018 ble initiert og gjennomført av Veterinærinstituttet, og fra 2019 reetablert som et løpende overvåkningsprogram i regi av Mattilsynet for å øke kunnskapen om forekomst av patogene mikroorganismer med betydning for dyre- og folkehelse, og for tidlig å kunne oppdage meldepliktige dyresykdommer hos en art på fremmarsj i Norge.

I 2024 ble det sendt inn prøver fra 362 villsvin til Veterinærinstituttet. Dette er noen flere enn antall felte villsvin rapportert til Hjorteviltregisteret (n=351). Seks villsvin som var påtruffet døde (n=4) eller trafikkdrept (n=2) ble sendt inn av Mattilsynet som en del av den passive overvåkningen for afrikansk og klassisk svinepest, og disse virussykdommene ble ikke påvist.

Det ble ikke påvist antistoff mot de alvorlig meldepliktige svinepatogenene Aujeszky's disease virus (ADV), smittsom gastroenterittvirus (TGEV), porcint respiratorisk og reproduksjonssyndromvirus (PRRSV), porcin epidemisk diarévirus (PEDV) eller influensa A virus (SIV). Dette er smittestoff som også er gjenstand for overvåking i overvåknings- og kontrollprogrammet for spesifikke virussykdommer hos tamsvin. Det ble heller ikke påvist antistoff mot *Mycoplasma hyopneumoniae*, et agens som forårsaker smittsom grisehoste hos tamsvin og som har vært gjenstand for systematisk bekjempelse i den norske svinepopulasjonen. Siste påvisning av smittsom grisehoste i Norge var i 2008.

I prøver fra ett hanndyr av villsvin felt under jakt i Marker ble det påvist antistoff mot porcint respiratorisk koronavirus (PRCV). Det vurderes som mest sannsynlig at antistoffpåvisningen skyldes en falsk positiv reaksjon, da det ikke har vært påvist antistoff mot PRCV i prøver fra andre villsvin felt i samme område.

Salmonella spp. med følgende serotyper (n) ble påvist i avføringsprøve fra 11 villsvin felt under jakt: *S.* Typhimurium (5), *S. enterica* subsp. *diarizonae* serovar 42:r:z (2), S. *enterica* subsp. *diarizonae* serovar 38:r:z (1), *S.* Abony (1), *S.* Hessarek (1) og *Salmonella* sp. serovar 4,5,12:-:- (1). Ni av disse ble testet for følsomhet mot antibakterielle midler, og alle ni var fullt følsomme for de antibakterielle midlene de ble testet for.

Parasittologiske undersøkelser påviste ikke forekomst av *Trichinella* spp. larver.

Background

During the last decade wild boar (*Sus scrofa*) populations have been established mainly in a core area, the south-eastern part of Norway, bordering Sweden. A few solitary animals have also been observed or shot by hunters several hundred kilometres north of this. Hunting statistics (Statistics Norway (SSB), www.ssb.no and later the National Cervid Register, Hjorteviltregisteret) documented a steadily increasing number of wild boars harvested since 2014/2015, however this number seems to have stabilised since 2020/2021. The Norwegian Veterinary Institute (NVI) initiated a comprehensive wild boar health surveillance in 2018. This was based on a surveillance in 2011-2014, financed by the Norwegian Food Safety Authority (NFSA), discontinued because of low sample submission rate. From 2019, the NFSA included parts of the wild boar health surveillance in their surveillance programmes for terrestrial animals, and the surveillance is now run in collaboration with the NVI. Furthermore, additional pathogens were included through project-based financing and self-funding by the NVI. Specifically, the serological investigation for antibodies against *Mycoplasma hyopneumoniae* (*M. hyopneumoniae*) was financed by Animalia (The Norwegian Pig Health Service) and the NVI funded the analyses for antimicrobial resistance (AMR).

To promote the submission of samples for testing, the NFSA, since July 2020, pays a compensation to hunters for the submission of samples. From October 2023, land-owners of properties where wild boars are harvested, are also eligible for compensation by the NFSA. Free-of-charge testing for *Trichinella* spp. has also been included since 2018.

The wild boar health surveillance includes the same pathogens as the national surveillance programme for specific viral infections in domestic pigs, with additional analyses for *M. hyopneumoniae*, the parasite *Trichinella* spp., and bacteriological analyses for *Salmonella* spp. The national surveillance programme for specific viral infections in domestic swine was launched in 1994, and documents Norway's disease-free status for Aujeszky's disease, and the status of transmissible gastroenteritis (TGE), porcine respiratory corona virus (PRCV), porcine respiratory and reproductive syndrome (PRRS), porcine epidemic diarrhoea (PED) and swine influenza (SI) in the Norwegian swine population.

Aims

The aims of the wild boar health surveillance are to investigate the health status, the prevalence of selected agents, and the early detection of disease in the wild boar population in Norway. The surveillance is designed with a particular focus on notifiable diseases, zoonoses, agents under active surveillance in the domestic pig population and agents with a potential for transmission between wild and domestic pigs.

Material and methods

Sampling and data collection

Purpose-built sample collection kits were distributed to hunters, including sample collection and submission information forms. These forms also had a printed QR-code that linked to the Norwegian Cervid Register (Hjorteviltregisteret, the national database for data from hunted cervids and wild boar), where data on the sampled animal (incl. gender, age group, dressed weight and carcass weight), geographic reference to the location where the animal was harvested and the number of wild boars observed in the immediate vicinity of the harvested wild boar, was collected. Distribution of kits was done via municipal wildlife managers, the local offices of the NFSA and also upon request directly to hunters and personnel involved in searching for animals injured by hunting or traffic accidents. Before distribution of sample collection kits, the NVI hosted an open seminar in August 2018 to provide wildlife management personnel and hunters with background information about wild boars and health surveillance, and to demonstrate sampling of wild boar carcasses. The forms also included contact information to the NVI and NFSA. In addition to the written information, the sample collection kits included, sterile 25 ml screw-cap containers for collection of skeletal muscle, faeces and blood, disposable gloves and an insulated pre-paid return envelope.

We used observations from the SCANDCAM camera trap network, the species observation system (“Artsobservasjoner”), individuals dying from other causes than hunting (“fallviltregisteret”), and the location of harvested wild boar reported to NINA and NVI to estimate the wild boar distribution range. The main distribution of wild boar is today found along the Swedish border from Halden municipality in the south to Elverum municipality approx. 300km further north. The majority of observations are found in the far south in the municipalities of Aremark and Halden. Dispersing individuals can be expected to occur over larger parts of Southern Norway (Odden et al. 2023).

Laboratory analyses

All serological and bacteriological analyses were performed at the NVI. Skeletal muscle samples were submitted to the Swedish Veterinary Agency (SVA) in Uppsala, Sweden for *Trichinella* spp. analysis. Samples with positive or inconclusive results on serological analysis were retested in duplicate with the same test method. Samples were concluded as negative if the retests gave a negative result.

Serological analyses

Aujeszky’s disease/pseudorabies virus (ADV/PRV)

All serum samples were tested for antibodies against ADV using a commercial blocking ELISA from Svanova (SVANOVIR® PRV gB-Ab).

Transmissible gastroenteritis virus (TGEV) and porcine respiratory coronavirus (PRCV)

Samples were tested with either one or two commercial blocking ELISAs Swinecheck®TGEV/PRCV Recombinant, Biovet, and/or SVANOVIR® TGEV/PRCV-Ab, Svanova). The ELISA tests enable discrimination between antibodies to TGEV and PRCV in serum samples.

Porcine reproductive and respiratory syndrome virus (PRRSV)

All serum samples were tested for antibodies against PRRSV using a commercial indirect ELISA from IDEXX (IDEXX PRRS X3), which detects the most (pre)dominant type 1 and type 2 strains of PRRSV. PRRSV positive or inconclusive samples were tested with a confirmatory ELISA at the NVI (ID Screen® PRRS Indirect).

Swine influenza virus (SIV)

A commercial competitive ELISA from IDvet (ID Screen® Influenza A Antibody Competition, Multi-species) was used to screen serum samples from swine for antibodies against influenza A virus.

Porcine epidemic diarrhoea virus (PEDV)

All serum samples were tested for antibodies against PEDV using a commercial indirect ELISA from IDvet (ID Screen® PEDV Indirect).

Mycoplasma hyopneumoniae

Serological examinations for antibodies against *M. hyopneumoniae* were performed with the use of an indirect ELISA produced by IDvet (IDScreen Mycoplasma hyopneumoniae Indirect).

Bacteriological analyses and antimicrobial resistance

From each wild boar, faecal samples were taken for detection of *Salmonella* spp.

Salmonella spp.

Faecal content from the wild boars were analysed according to ISO 6579-1:2017, Detection of *Salmonella* spp. Serotyping was performed by seroagglutination, ISO 6579-3:2017.

Antimicrobial susceptibility testing was performed using EUVSEC3 plates from Sensititre® (TREK Diagnostic LTD). Epidemiological cut-off (ECOFF) values recommended by the European Committee on Antimicrobial Susceptibility Testing (EUCAST, accessed 24.01.2025) were used for classification of resistance.

Whole genome sequencing

Whole genome sequencing of seven *Salmonella* spp. isolates (i.e. *S*. Typhimurium (4), *S. enterica* subsp. *diarizonae* serovar 42:r:z (1), *S*. Hessarek (1), and *Salmonella* sp. serovar 4,5,12:-:- (1)) was performed at the NVI on an Illumina® MiSeq (Illumina, San Diego, California, USA). Paired end reads were subjected for analysis using ResFinder V.4.1 for both acquired genes and chromosomal mutations (PointFinder) using the online tool at the Centre for Genomic Epidemiology web site (https://cge.cbs.dtu.dk/services/ResFinder/).

Parasitological analyses

Trichinella spp.

Muscle samples from the front legs of wild boars were examined for the presence of *Trichinella* spp. larvae. The samples were packed with cooling elements and shipped overnight to the Swedish Veterinary Agency (SVA).

Five grams of each muscle sample were examined using the magnetic stirrer method to detect *Trichinella* larvae. This method follows the ISO 18743:2015 standard, the global benchmark for detecting *Trichinella* spp. larvae in meat from individual animal carcasses intended for human consumption. This standard has also been adopted as the *Trichinella* reference method within the EU, as outlined in regulation (EU) 2020/1478. This method, considered the gold standard for *Trichinella* testing, can be used for both individual and pooled muscle samples.

Results

Samples and locations of wild boar

Sample sets and completed submission forms from a total of 362 hunted wild boars were submitted to the NVI during 2024 (Figure 1) for inclusion in the health surveillance programme. In addition, six wild boars (four found dead and two killed in traffic accidents) were submitted by the Norwegian Food Safety Authority (NFSA) as a part of passive surveillance for African swine fever virus (ASF) and classical swine fever virus (CSFV).

The samples were submitted from 13 municipalities and correspond well with the estimated distribution of wild boar in 2021 (Figure 2).

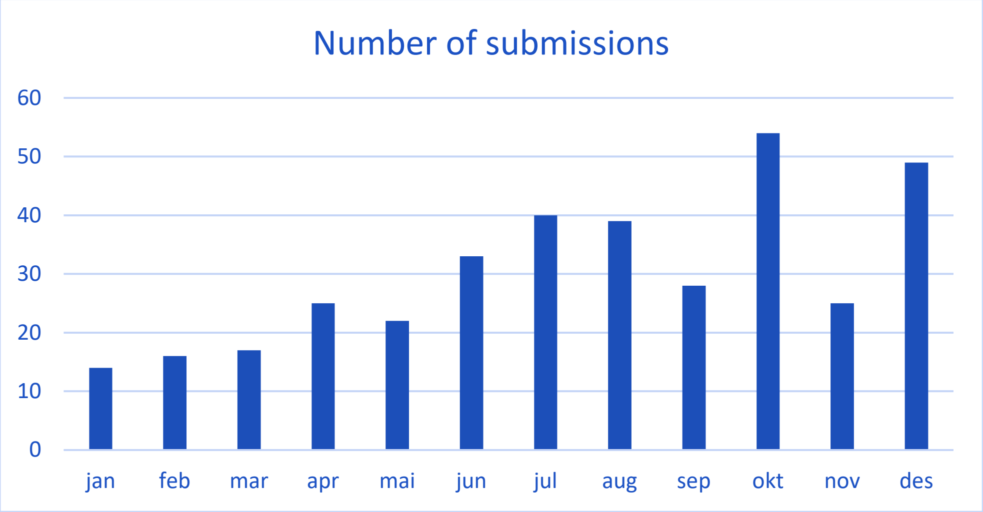

Figure 1. Number of submissions from wild boar per month during 2024.

Figure 2. Estimated distribution of wild boar in 2023. The map shows the probability that wild boar is present in a blue (low probability) to red (high probability) scale. The model is based on observations of wild boar from the SCANDCAM camera trap network, species observations and locations of wild boar shot during hunting and reported dead from other causes (Odden et al. 2023, Rivrud et al. 2024). Black dots represent new observations in 2024. The map is prepared by NINA.

Serological analyses

Blood samples from 347 wild boars were included in the serological analyses. In some cases, samples were unsuitable for one or more specific serological tests, hence not all samples were subject to every serological analysis. The results of the serological analyses are shown in Table 1.

Antibodies against the notifiable infectious diseases included in the analyses and *M. hyopneumoniae* were not detected.

Table 1. Overview of serological results from samples submitted from wild boar hunted in Norway during 2024.

Agent-specific antibodies	Number of positive / analysed samples
SuHV1/ADV/PRV	0 / 347
TGEV	0 / 347
PRCV	1* / 347
PRRSV	0 / 346
SIV	0 / 345
PEDV	0 / 347
MHYO	0 / 346

*Serum from a single male wild boar was positive for antibodies against porcine respiratory corona virus (PRCVV). It was concluded that the seroreaction most likely was a false positive, as no other wild boar from the same area had antibodies against PRCV.

Bacteriological analyses and antimicrobial resistance

Out of 362 available fecal samples, the following species and serotypes (n) of *Salmonella* spp. were detected in faeces from 11 hunted wild boars: *Salmonella* Typhimurium (5), *S. enterica* subsp. *diarizonae* serovar 42:r:z (2), *S. enterica* subsp. *diarizonae* serovar 38:r:z (1), *S*. Abony (1), *S*. Hessarek (1), and *Salmonella* sp. serovar 4,5,12:-:- (1). Nine of these were tested for their susceptibility to antimicrobial agents, all nine were fully susceptible to all antimicrobial agents included in the test panel. Although phenotypically sensitive to aminoglycosides, whole genome sequencing detected presence of the gene *aac(6')-laa* that confer resistance to aminoglycodides in the seven sequenced *Salmonella* spp. isolates.

Parasitological analyses

Trichinella spp. larva were not detected in muscle samples from 349 wild boars, while samples from 13 wild boar were not subject to *Trichinella* spp. analysis due to inadequate or inappropriate material submitted.

Discussion

Wild boar populations have been establishing in south-eastern Norway, with several solitary animals also being observed or shot by hunters far north and west of this (Figure 2). Wild boar health surveillance focusing on viral diseases and *Trichinella* spp. was conducted from 2011 to 2014, but was discontinued from 2015 due to very few samples being submitted. Number of wild boars harvested by hunters have increased from approx. 70 in the hunting year 2014/2015 to a preliminary maximum of 450 in the hunting year 2020/2021 (Statistics Norway, www.ssb.no). For the current calendar year of reporting, the number of wild boars harvested through hunting and reported to the National Cervid Register was 351.

With the establishment of wild boar in Norway and a stable number of animals being harvested annually it is feasible and important to gain insight regarding the presence of notifiable diseases, as well as zoonoses and AMR. Knowledge is also needed about agents with a potential to transmit between wild boar and domestic pigs. Hence, wild boar health surveillance was reinitiated by the NVI during 2018. In the years from 2018 up to and including 2020, samples from a total of 295 wild boars were submitted. In 2020 the NFSA also implemented a financial incentive to report sick or dead wild boars and to submit samples from hunted wild boar. Since October 2023, this financial incentive has been increased to 3000 NOK for male wild boars and 5000 NOK for female wild boars and expanded to include eligibility for the land-owner to receive 4000 NOK per wild boar harvested on their property. These incentives seem to have motivated sample submissions as samples were submitted from 362 wild boars during 2024. This constitutes more than the number of hunted wild boars reported to the National Cervid Register during the same period. This indicates that hunters are highly motivated to collect and submit samples, but also that most of the sampled wild boar are also registered through the appropriate national registry. The locations of sampled wild boars coincide with areas where wild boar was registered based on other data, such as road kills, species observations and camera traps, indicating that the availability of sample kits and geographical coverage of surveillance was adequate.

As the re-establishment (absent for about 1000 years) of wild boar in Norway is fairly recent, collecting health information from this species is important to be able to monitor changes over time and for early detection of notifiable diseases. Specifically, ASF has emerged as a major cause of disease and death in affected wild boar populations across several European countries during the last decade, proven very hard to control and eliminate. The most effective and efficient method for early detection of ASF in wild boar is passive surveillance (More, Miranda et al. 2018), where diseased and "found-dead"-wild boars are subjected to notification to the competent authority (i.e. NFSA) and tested for ASF. Six notifications and submissions for passive surveillance of ASF and CSF were made during 2024, all with subsequent negative laboratory analyses for ASF and CSF.

In September 2023, the Swedish Board of Agriculture and the Swedish Veterinary Agency, reported the first case of African swine fever in the municipality of Fagersta, Sweden (https://jordbruksverket.se/djur/djurskydd-smittskydd-djurhalsa-och-folkhalsa/aktuellt-lage-for-smittsamma-djursjukdomar/afrikansk-svinpest-asf (in Swedish)), but Sweden regained its ASF-free status in September 2024 after a comprehensive disease eradication campaign. African and classical swine fever was not detected through passive surveillance in wild boar in Norway during 2024.

Since the present wild boar population in Norway originate from Sweden, it is of interest to compare the status of infectious agents between these populations, building on data from research and surveillance in Sweden. Although not entirely comparable, the results presented here indicate a lower incidence of *Salmonella* spp., *M. hyopneumoniae* and swine influenza virus than what has been recently reported in Sweden (Malmsten, Magnusson et al. 2018, Sanno, Rosendal et al. 2018). Nonetheless, the detection of zoonotic *Salmonella* spp. in faecal samples of wild boar hunted in Norway highlights the importance of maintaining strict hygiene during carcass and meat handling. Furthermore, in Sweden, *Salmonella* Choleraesuis were detected in domestic pigs and wild boar during the fall of 2020 and onwards (https://www.sva.se/djurhalsa/smittlage/overvakning-av-salmonella-choleraesuis-hos-vildsvin / (in Swedish)). This important pig pathogen with zoonotic potential was not detected in samples from wild boar in Norway during any years after 2020, including 2024.

Maintaining a focus on notifiable agents and other pathogens in wild boar is important to recognise their potential significance as a reservoir of transmission to domestic animals and humans, and further facilitate early detection of emerging (e.g. ASF) and re-emerging (e.g. S. Choleraesuis) diseases. This information is important for biosecurity evaluations and risk-mitigation measures, like population management.

Acknowledgement

The authors would like to thank the technical staff for preparing the sample submission kits and performing the analyses with excellence. We would also like to acknowledge all the municipal wildlife managers and personnel from the Norwegian Food Safety Authority for distributing sample submission kits and the hunters for collecting and submitting data and samples from wild boars.

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