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Surveillance of wild boar health in Norway - results from 2018 and 2019

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Content

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Summary

Wild boar health surveillance was re-established in August 2018 to gain insight about the incidence of pathogens of importance for animals and humans and to enable early detection of notifiable diseases in this recently emerging species. By the end of 2019, samples from 92 hunted wild boar have been submitted to the Norwegian Veterinary Institute. This represents approx. 31% of harvested wild boar, as reported to Statistics Norway (SSB) during the hunting year of 2018/2019.

Antibodies for the following notifiable pathogens were not detected: Aujeszky's disease virus (AD), transmissible gastroenteritis virus (TGE), porcine respiratory corona virus (PRCV), porcine respiratory and reproductive syndrome virus (PRRS), porcine epidemic diarrhoea virus (PED) and swine influenza virus (SI) (these are also included in the surveillance programme for specific viral diseases in domestic pigs), and *Mycoplasma hyopneumoniae*. However, antibodies against *Actinobacillus pleuropneumoniae*, pathogenic *Yersinia* spp., and hepatitis E virus were detected in 64%, 53% and 1.1% of the samples, respectively.

Salmonella Typhimurium was detected in faeces from one hunted wild boar. Parasitological analysis did not demonstrate presence of *Trichinella* larvae or *Alaria alata* mesocercariae.

Analysis for antimicrobial resistance showed that 2.5% of the *Escherichia coli* isolates tested displayed reduced susceptility to gentamicin and colistin (no plasmid mediated nor chromosomal mutations detected), respectively. Quinolone-resistant *E. coli* was detected in 22.4% of the samples, of which several isolates were multidrugresistant. Extended-spectrum cephalosporin-resistant *E. coli* was detected in 4.4% of the samples. Methicillin-resistant *Staphylococcus aureus*, *Campylobacter coli*, colistin-resistant *E. coli* and carbapenem-resistant *Enterobacteriaceae* were not detected in any samples investigated.

Sammendrag på norsk

Villsvinhelseovervåkning ble re-etablert i august 2018 for å øke kunnskapsgrunnlaget om forekomst av patogene mikroorganismer med betydning for dyre- og folkehelse, og for å tidlig kunne oppdage meldepliktige dyresykdommer hos en art på fremmarsj i Norge. I løpet av høsten 2018 og hele 2019 ble det sendt inn prøver fra til sammen 92 villsvin felt under jakt til Veterinærinstituttet. Dette representerer om lag 31% av antallet felte villsvin som ble rapportert til Statistisk sentralbyrå (SSB) i jaktåret 2018/2019.

Det ble ikke påvist antistoff for de alvorlig meldepliktige svinesykdommene Aujeszky's disease (AD), smittsom gastroenteritt (TGE), porcint respiratorisk korona virus (PRCV), porcint respiratorisk og reproduksjonssyndrom (PRRS), porcin epidemisk diaré (PED) eller influensa A (SI). 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. Det ble påvist antistoff mot *Actinobacillus pleuropneumoniae*, sykdomsfremkallende *Yersinia* spp., og hepatitt E virus i henholdsvis 64%, 53% og 1.1% av undersøkte prøver. Disse er smittestoff som også er utbredt i den konvensjonelle tamsvinpopulasjonen i Norge.

Salmonella Typhimurium ble påvist i avføringsprøve fra ett villsvin. Parasittologiske undersøkelser påviste ikke forekomst av *Trichinella* spp. larver eller *Alaria alata* mesocercarier i innsendte prøver.

Undersøkelser for antimikrobiell resistens hos tilfeldige *Escherichia coli* viste at kun 2,5% av isolatene var resistente. Kinolonresistente *E. coli* ble påvist fra 22,4% av prøvene, og flere av disse var multiresistente. Utvidet spektrum cefalosporin-resistent *E. coli* ble påvist i 4,4% av prøvene. Meticillin-resistent *Staphylococcus aureus*, *Campylobacter coli*, kolistin-resistent *E. coli* og karbapenem-resistent *Enterobacteriaceae* ble ikke påvist i noen av de undersøkte prøvene.

Background

During the last decade, wild boar (*Sus scrofa*) populations have established mainly in the south-eastern parts of Norway, in areas bordering Sweden. Hunting statistics (Statistics Norway (SSB), www.ssb.no) report a steadily increasing number of wild boars harvested in the same period. The Norwegian Veterinary Institute (NVI) initiated a comprehensive wild boar health surveillance in 2018. This was based on a surveillance programme in 2014, financed by the Norwegian Food Safety Authority (NFSA) and discontinued because of low sample submission rate. From 2019, the Norwegian Food Safety Authority included parts of the wild boar health surveillance in their surveillance programmes for terrestrial animals, and the surveillance now run in collaboration with the NVI. Furthermore, additional pathogens were included through project-based financing. Specifically, the serological investigation for antibodies against *Mycoplasma hyopneumoniae* (*M. hyopneumoniae*) was financed by Animalia (The Norwegian Pig Health Service) and serology for zoonosis like hepatitis E virus and pathogenic *Yersinia* spp. and the porcine respiratory opportunistic pathogen *Actinobacillus pleuropneumoniae* was financed through regional qualification support from Oslofjordfondet (project 304090, *Wild boar – knowledge needs in regional management*). In addition, the NVI self-funded analyses for antimicrobial resistance (AMR).

The wild boar health surveillance includes the same pathogens as the national surveillance programme for specific viral infections in domestic pigs, but also analyses for parasites (*Trichinella* spp. and *Alaria alata*), AMR in bacteria (*E. coli* and *Campylobacter* spp.) and *Salmonella* spp. The national surveillance programme for specific viral infections in domestic swine was launched in 1994, and documents the status of Aujeszky's disease (AD), 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.

The aims of the wild boar health surveillance are to investigate the health status and the prevalence of selected agents, as well as AMR, in the emerging wild boar population in Norway. The surveillance is designed with a particular focus on notifiable diseases, zoonosis, 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 kits were distributed to hunters, including submission forms that contained questions about the sampled animal, geographic reference to the location where the animal was harvested and estimated population densities. Distribution of kits was done via municipal wildlife managers and also upon request, directly to hunters and personnel involved in searching for animals wounded by hunting or traffic accidents. Before distribution of sample collection material, the NVI hosted an open seminar in August 2018 to provide wildlife management personnel and hunters with background information about wild boar and health surveillance and to demonstrate sampling of wild boar carcasses. In addition to the submission forms, the sample collection kits included sterile bacteriological swabs with transport medium, sterile 25ml screw-cap containers for collection of skeletal muscle, faeces and blood, disposable gloves and an insulated pre-paid return envelope.

Data on wild boar harvest statistics was retrieved from SSB. These data are reported by hunters to SSB following the hunting year (i.e., April 1st–March 31st the following year). Wild boar-vehicle collisions data was obtained from the national deer register (www.hjorteviltregisteret.no), which also contains reported wild boar-vehicle collisions. Observations of wild boars from camera traps are based on a network of 600 cameras, with one camera per 50 km^2 originally designed for lynx (*Lynx lynx*)-monitoring, covering parts of Norway including areas where most wild boars are harvested during hunting.

Laboratory analyses

All serological and bacteriological analyses, including AMR, and analysis for *Alaria alata* were performed at the NVI. Skeletal muscle samples were submitted to the National Veterinary Institute (SVA) in Uppsala, Sweden for *Trichinella* spp. analysis. 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). The test detects antibodies against glycoprotein B (previously glycoprotein II) found on the surface of the virus.

Transmissible gastroenteritis virus (TGEV) and porcine respiratory coronavirus (PRCV)
A commercial blocking ELISA from Svanova (SVANOVIR® TGEV/PRCV-Ab) was used to detect antibodies against TGEV/PRCV. The ELISA test enables 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 European and American strains of PRRSV. In cases of positive or inconclusive results, the samples were sent to the National Veterinary Institute (DTU-Vet) in Denmark for confirmatory testing using ELISA and immunoperoxidase tests for detection of antibodies against EU- and US-strains of the PRRSV and real-time PCR for PRRSV.

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. In cases of positive or inconclusive results, the serum samples were retested using the haemagglutination inhibition (HI) test, for the detection of antibodies against the A/Swine/California/07/09 (A/H1N1/pdm09), A/Swine/Belgium/1/98 (H1N1), A/Swine/Gent/7623/99 (H1N2) and A/Swine/Flanders/1/98 (H3N2) subtypes as described in the OIE Manual of Diagnostic Tests and Vaccines for Terrestrial Animals (1). The antigens for the tests were produced at the NVI.

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). In cases of positive or inconclusive results, the samples were sent to the DTU-Vet in Denmark for confirmatory testing using an in-house ELISA.

Mycoplasma hyopneumoniae
Serological examinations for antibodies against *M. hyopneumoniae* were performed with the use of a blocking ELISA produced by Oxoid (*Mycoplasma hyopneumoniae* ELISA).

Hepatitis E virus (HepEV)
All serum samples were tested for antibodies against HepEV using a commercial Indirect ELISA from IDvet (ID Screen® Hepatitis E Indirect Multi-species).

Actinobacillus pleuropneumoniae **(APP)**
A commercial Indirect ELISA from IDvet (ID Screen® APP Screening Indirect) was used to detect antibodies against APP. The test detects antibodies against APP serotypes 1-12.

Yersinia spp.

The presence of antibodies against pathogenic *Yersinia* spp., was determined using an indirect ELISA produced by Qiagen (*pigtype*® Yersinia Ab ELISA). Antigens used in the test are produced by pathogenic strains only, spanning all serotypes.

Bacteriological analyses and antimicrobial resistance
From each wild boar, nose swabs were taken for detection of methicillin-resistant *Staphylococcus aureus* (MRSA) and faecal samples for detection of *Salmonella* spp., *Campylobacter coli*, *Escherichia coli*, extended-spectrum cephalosporin-resistant (ESC) *E. coli*, quinolone-resistant *E. coli* (QREC), colistin-resistant *E. coli* and carbapenem-resistant *Enterobacteriaceae* (CRE).

Methicillin-resistant *Staphylococcus aureus* **(MRSA)**
Nasal swabs were analysed for MRSA by incubation in Mueller-Hinton broth (Difco Laboratories, Fisher Scientific, Thermo Fisher Scientific, Waltham, Massachusetts, USA) with 6.5% NaCl (Merck KGaA, Darmstadt, Germany) at 37±1.0°C for 18-24 hours. A loopful of the overnight broth (10 µL) was plated onto Brilliance™ MRSA2 agar plate (Oxoid, Oslo, Norway) (EFSA journal 2012:10(10):2897). Suspected colonies were subjected to species identification using the MALDI-TOF MS (Bruker Daltonics GmbH, Bremen, Germany) before further phenotypical testing by disc diffusion (EUCAST, www.eucast.org).

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

Campylobacter coli
Faecal content from the wild boars were plated directly onto mCCDA (Oxoid) agar and incubated under microaerobic conditions at 41.5±0.5°C for 48h. Typical colonies were subcultured on blood agar and confirmed as *Campylobacter coli* using MALDI-TOF MS.

E. coli
Antimicrobial resistance in *E. coli* is used as an indicator on AMR levels within a population. For this purpose a random picked *E. coli* per animal was susceptibility tested. Faecal content were plated directly onto MacConkey agar (Difco) and incubated at 44.0±0.5°C for 20±2h. Typical colonies were subcultured on blood agar (Heart infusion agar, Difco) containing 5% bovine blood and incubated at 37±1°C for 20±2h. Colonies were identified as *E. coli* by typical colony appearance and a positive indole reaction before susceptibility tested.

Extended-spectrum cephalosporin (ESC)-resistant *Escherichia coli***, quinolone-resistant** *E. coli* **(QREC), colistin-resistant** *E. coli* **and carbapenem-resistant** *Enterobacteriaceae* **(CRE)**
The faecal samples were enriched prior to plating onto selective media for detection of ESC-resistant *E. coli*, QREC, colistin-resistant *E. coli* and CRE. A total of 1±0.1 g faecal material was homogenised with 9 mL of BPW-ISO (Oxoid), and incubated at 37±1°C for 20±2h according to the protocol from the European reference laboratory on antimicrobial resistance (EURL-AR, http://www.eurl-ar.eu/233-protocols.htm). After incubation, 10-20 µL of the enrichment broth was plated onto each of the different selective media; MacConkey agar (Difco) containing 1 mg/L cefotaxime and MacConkey agar (Difco) containing 2 mg/L ceftazidime for ESC-resistant *E. coli*, MacConkey agar (Difco) containing 0.06 mg/L ciprofloxacin for QREC, SuperPolymyxin agar (Oxoid) for colistin-resistant *E. coli*, and CHROMID® CARBA and CHROMID® OXA-48 agar (bioMérieux, Marcy l'Etoile, France) for CRE. The agar plates were incubated at 44.0±0.5°C (35±2°C for CRE and 37±0.5°C for 21±3h for colistin-resistant *E. coli*) for 20±2h. Presumptive colonies were subcultured on both selective media and blood agar and confirmed using MALDI-TOF MS before susceptibility tested.

Susceptibility testing
Isolates were tested for antimicrobial susceptibility using a broth microdilution method. Minimum inhibitory concentration (MIC) values were obtained using plates from Sensititre® (TREK Diagnostic LTD) with different panels depending on the tested bacteria as shown in Table 1. Susceptibility data were

recorded and stored in the sample registration system at NVI as discrete values (MIC). Epidemiological cut-off (ECOFF) values recommended by the European Committee on Antimicrobial Susceptibility Testing (EUCAST, accessed 25.03.2020) were used. For antimicrobial agents were ECOFFs are not defined by EUCAST, cut-offs recommended by the European Food Safety Authorities was used. Data management was performed both in SAS-PC System® v 9.4 for Windows (SAS Institute Inc., Cary, NC, USA) and in R version 3.6.2 Copyright (C) 2019 (The R Foundation for Statistical Computing Platform), while the statistical analysis was performed in R. The 95% confidence intervals were calculated using the exact binomial test.

Table 1. Overview of antimicrobial groups and agents used in the susceptibility testing of *E. coli* and *Salmonella* spp. with respective EUCAST epidemiological cut-off values (ECOFF).

Antimicrobial group	**Antimicrobial agents**	**ECOFF for** *E. coli**	**ECOFF for** *Salmonella spp.*
Tetracyclines	Tetracycline	>8	>8
	Tigecycline	>0.5	>1**
Amphenicols	Chloramphenicol	>16	>16
Penicillins with extended spectrum	Ampicillin	>8	>8
	Temocillin	(>16)	
2nd generation cephalosporins	Cefoxitin	(>8)	
3rd generation cephalosporins	Cefotaxime	>0.25	>0.5
	Ceftazidime	>0.5	>2
Combinations of 3rd generation cephalosporins and clavulanic acid	Cefotaxime/clavulanate	(>0.25)	
	Ceftazidime/clavulanate	(>0.5)	
4th generation cephalosporins	Cefepime	(>0.125)	
Carbapenems	Meropenem	>0.125	>0.125
	Ertapenem	(ND)	
	Imipenem and enzyme inhibitor	(>0.5)	
Trimethoprim and derivatives	Trimethoprim	>2	>2
Sulfonamides	Sulfamethoxazole	>64	>256**
Macrolides	Azithromycin	ND	ND
Other aminoglycosides	Gentamicin	>2	>2
Fluoroquinolones	Ciprofloxacin	0.064	0.064
Other quinolones	Nalidixic acid	>8	>8
Polymyxins	Colistin	>2	>2**

*(ECOFF) = only ESC-resistant *E. coli* and CRE suspected isolates are tested with these antimicrobial agents.
**ECOFF defined by European Food Safety Authorities.
ND = ECOFF not defined

Genotyping

For genotyping of suspected resistant isolates, the procedure was either performed by conventional PCR or whole genome sequencing from November 2019. For *E. coli* isolates with an AmpC beta-lactamase resistance profile, PCR was performed for the identification of plasmid-mediated AmpC genes by multiplex PCR (Pérez-Pérez et al. 2002). If no plasmid-mediated AmpC genes were detected, amplification of the promoter and attenuator regions of the chromosomal *ampC* gene was performed to detect any mutation causing an upregulation of the chromosomally located *ampC* gene in *E. coli* (Agersø et al. 2012, Peter-Getzlaff et al. 2011, Tracz et al. 2007). For presumptive MRSA isolates, realtime PCR for the detection of *mecA* and *nuc* genes together with a conventional PCR for the *mecC* gene was performed (Tunsjø et al. 2013, Stegger et al. 2012). Whole genome sequencing was performed at the NVI on an Illumina® MiSeq (Illumina, San Diego, California, USA). Paired end reads were subjected for analysis using ResFinder V.3.2 for both aquired 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 front leg of wild boars were examined for the presence of muscle larvae of *Trichinella* spp. Muscle samples was packed with cooling element and shipped as express-over-night parcel to SVA (Swedish National Veterinary Institute). For samples arriving at VI on Thursday evening and Friday the samples were refrigerated until Monday morning and shipped to SVA. Five grams of muscle per sample was examined using the magnetic stirrer method for the detection of *Trichinella* larvae in muscle samples This is the international accepted reference method (https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=celex%3A32015R1375; https://www.oie.int/fileadmin/Home/eng/Health_standards/tahm/3.01.20_TRICHINELLOSIS.pdf). This method is considered the gold standard for *Trichinella* testing of meat and can be used for single or pooled muscle samples.

Alaria alata

Mixed soft-tissue samples (from front leg, around the mandible, tongue) from wild boar were examined for the precence of *Alaria alata* mesocercaria by a modified *A. alata* mesocercariae migration technique, AMT (Riehn et al 2010).

Results

Samples and locations of wild boar

Sample kits and completed submission forms from a total of 92 hunted wild boar were submitted to the NVI during 2018 and 2019 for inclusion in the health surveillance programme. The locations of where the wild boars were harvested during 2019 as reported by the hunters are shown in Figure 1.

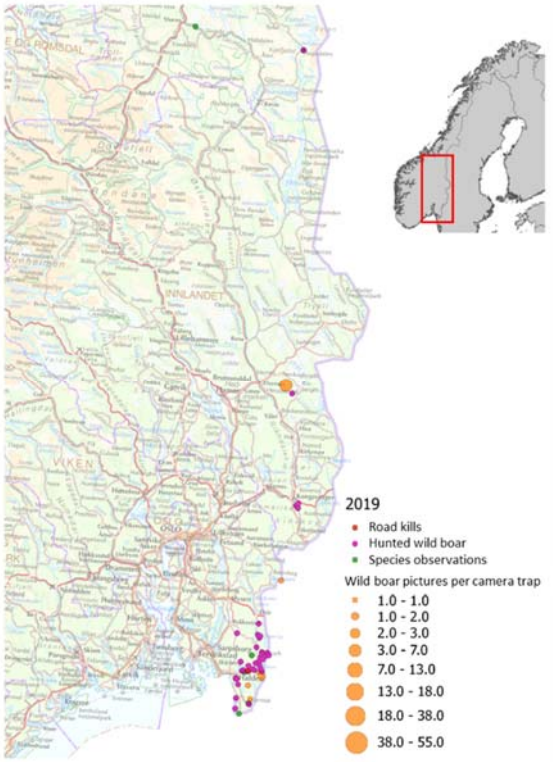

Figure 1. Geographical distribution of road kills, hunted wild boar, species observations and camera trap observations of wild boar in Norway during 2019. Plotted map prepared by NINA, inserted map prepared by NVI showing area of interest in red box.

Serological analyses

Blood samples from 92 wild boars were included in the serological analyses. In a few 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 2. Antibodies against the notifiable infectious diseases included in the analyses and *Mycoplasma hyopneumoniae* were not detected. Sixty-four percent of the samples were seropositive for *Actinobacillus pleuropneumoniae* (APP, serotypes 1-12). Further serological investigations to distinguish between serotypes/serogroups were not performed. Furthermore, antibodies against pathogenic *Yersinia* spp. bacteria and hepatitis E virus were detected in 53% and 1% of the analysed samples, respectively.

Table 2. Overview of serological results from samples submitted from wild boar hunted in Norway during 2018 and 2019.

Agent-specific antibodies	**Number of analysed / positive (%) samples**
Suid Herpesvirus 1/Aujeszky's disease/pseudorabies virus (SuHV1/ADV/PRV)	92 / 0
Transmissible gastroenteritis virus (TGEV) and porcine respiratory coronavirus (PRCV)	88 / 0
Porcine reproductive and respiratory syndrome virus (PRRSV)	92 / 0
Swine influenza virus (SIV)	91 / 0
Porcine epidemic diarrhoea virus (PEDV)	92 / 0
Mycoplasma hyopneumoniae (MHYO)	92 / 0
Hepatitis E virus (HepEV)	86 / 1 (1.1%)
Actinobacillus pleuropneumoniae (APP)	87 / 56 (64%)
Pathogenic *Yersinia* spp.	86 / 46 (53%)

Bacteriological analyses and antimicrobial resistance

Samples from a total of 86 wild boars were screened for the presence of MRSA. MRSA was not detected from any of the samples. Out of 86 investigated animals, *Salmonella* Typhimurium was detected from one sample. The isolate was fully sensitive to all antimicrobials included in the test panel (Table 1). No *Campylobacter coli* was detected from any of the 91 animals investigated.

Altogether, 80 indicator *E. coli* isolates were susceptibility tested. Of these, 2.5% showed reduced susceptibility to the antimicrobials included in the test panel (Table 1). These were two isolates showing reduced susceptibility to gentamicin and colistin, respectively. For the isolate showing reduced susceptibility to colistin, no plasmid mediated genes nor chromosomal point mutations were detected after whole genome sequencing of the isolate.

Samples from a total of 90 wild boars were investigated for ESC-resistant *E. coli* by selective media. Of these, ESC-resistant *E. coli* was detected from four animals (4.4%, [95% CI: 1.2-11.0]). The four isolates displayed resistance to the beta-lactams (i.e. ampicillin, and cefotaxime and/or ceftazidime). Three of the isolates had an AmpC beta-lactamase phenotype and the resistance was due to mutations in the promoter and attenuator region of the chromosomally encoded *ampC* gene causing an up-regulation of the gene. The last isolate displayed an ESBL phenotype and was genotyped as $bla_{\text{CTX-M-14}}$.

Samples from a total of 85 wild boars were investigated for QREC by selective media, and 19 QREC (22.4%, [95% CI: 14.0-32.7]) were detected (i.e. *E. coli* displaying resistance to ciprofloxacin and/or nalidixic acid). Table 3 gives an overview of the antimicrobials these 19 QREC show reduced susceptibility to.

Table 3. Overview of antimicrobial resistance in 19 quinolone-resistant *E. coli* from wild boars.

Antimicrobial classes	Number of isolates
Quinolones	8
Quinolones + Trimethoprim	1
Quinolones + Ampicillin	1
Quinolones + Tetracycline + Ampicillin	1
Quinolones + Tetracycline + Sulfamethoxazole	1
Quinolones + Tetracycline + Trimethoprim + Ampicillin	4
Quinolones + Tetracycline + Trimethoprim + Ampicillin + Sulfamethoxazole	2
Quinolones + Tetracycline + Trimethoprim + Sulfamethoxazole + Gentamicin	1

Samples from a total of 82 wild boars were investigated for colistin-resistant *E. coli* by selective media. No colistin-resistant *E. coli* was detected (0%, [95% CI: 0.0-4.4]).

Analyses for detecting CRE by selective media was performed on samples from a total of 85 wild boars. No CRE were detected (0%, [95% CI: 0.0-4.2]).

Parasitological analyses

Trichinella spp. larva were not detected in muscle samples from 92 wild boars. Mixed soft tissue samples from 15 animals were investigated for *A. alata* mesocercariae, all were negative.

Discussion

Wild boar populations are establishing in south-eastern Norway. 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 through hunting have increased from 70 in the hunting year 2014/2015 to 295 in the hunting year 2018/2019 (data from SSB). With an increasing number of animals being harvested annually through hunting, it is possible and important to gain insight regarding the presence of notifiable diseases, as well as zoonoses and AMR. Additionally, knowledge is needed about agents with a potential to transmit between wild boar and domestic pigs. Hence, wild boar health surveillance was reinitiated by NVI during 2018 with a goal of increasing the number of samples submitted from hunted wild boar. During 2018 and 2019, samples from 92 wild boar were submitted. This constitutes approx. 31% of hunted wild boar as reported by SSB during the hunting year of 2018/2019. Although these periods do not completely overlap, and as such are not entirely comparable, it provides an indication that the hunters' willingness to submit samples was fairly high. Moreover, the locations of sampled wild boar coincides 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 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, African swine fever (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. No such notifications were made during 2018 and 2019.

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 in the current report indicate a lower incidence of *Salmonella* spp., *Mycoplasma hyopneumoniae* and swine influenza virus than what has been recently reported from Sweden (Malmsten, Magnusson et al. 2018, Sanno, Rosendal et al. 2018). Nonetheless, the detection of *Salmonella* Typhimurium in faecal samples of wild boar hunted in Norway highlights the importance of maintaining strict hygiene during carcass and meat handling, as to prevent zoonotic infections.

With regard to AMR, the results indicate an overall low occurrence of AMR. However, multidrug resistant isolates (i.e. resistant to >3 antimicrobial classes) were identified, as well as isolates with an ESBL phenotype, showing that wild boar may contribute in dissemination of such AMR bacteria.

Maintaining a focus on notifiable agents and other pathogens, including AMR bacteria, in wild boar, is important to recognise their potential significance as a reservoir of transmission to domestic animals and humans, and facilitate early detection of emerging diseases. Furthermore, this may inform policy regarding risk-mitigation measures, such as population management and biosecurity.

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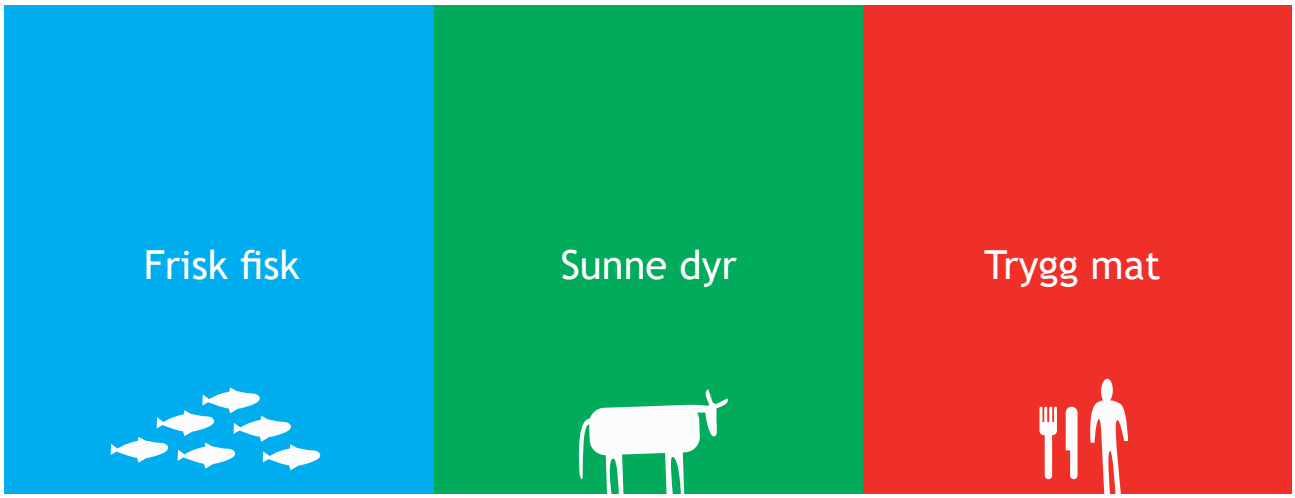

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