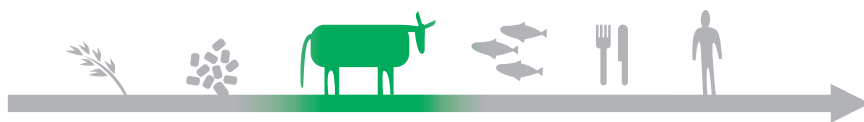


The surveillance programme for methicillin resistant *Staphylococcus aureus* in pigs in Norway 2017



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Summary

The surveillance programme in 2017 did not detect any pig herds with LA-MRSA CC398. However, MRSA CC7, and CC130 and CC425 was detected in one multiplier herd and in two farrow to finish herds, respectively. MRSA was not detected in any of the genetic nucleus herds, nor in the central units of the sow pool herds. In total, 826 herds were included in the survey, of which 85 were genetic nucleus or multiplier herds, 12 herds were the central units of sow pool herds, and 741 were herds with more than 10 sows.

Introduction

There are several varieties of Methicillin resistant *Staphylococcus aureus* (MRSA) some of which are associated with animals (especially pigs), and are collectively referred to as LA-MRSA (Livestock Associated - MRSA). Within a few years, LA-MRSAs have become widespread in swine populations around the world, thereby representing a risk for dissemination to the human population.

All types of MRSA can be transmitted between humans and animals and vice versa. However, not all types are well adapted for establishing in other species than their original host specie. MRSA is not typically associated with disease in animals and healthy humans, but it is important to prevent transmission especially to health institutions such as hospitals and nursing homes where the bacteria can cause severe infections that are difficult to treat.

Surveys that were conducted in 2008 (1), 2011 (2) and 2012 (3) indicated a very low prevalence of MRSA-positive swineherds in Norway. The MRSA belonging to the animal associated clonal complex CC398 *spa*-type t034 was detected in swine samples for the first time in 2011 (anonymous study). In 2013/14, three clusters of MRSA CC398 positive swine herds were detected, in eastern and southwestern Norway, respectively, and measures to eradicate LA-MRSA from positive swineherds were imposed. The rationale behind this strategy was to avoid the swine population becoming a reservoir of MRSA with the potential of zoonotic transmission. The LA-MRSA eradication strategy includes restrictions on trade of live animals upon suspicion, depopulation of pigs in LA-MRSA positive swine herds, thorough cleaning and disinfection of premises, negative samples from the environment and mandatory down-time before restocking with pigs from MRSA negative herds. After restocking, samples are collected from animals and the environment several times to assess the effectiveness of MRSA eradication.

From 2014, a yearly surveillance program of MRSA in the swine population was implemented. The first year, all sow herds with more than ten sows were examined (n=986 herds) and a single positive herd with MRSA CC398, t11 was identified (4). In 2015, a total of 821 herds were included, of which 86 were nucleus or multiplier herds and 735 was finishing herds (5). LA-MRSA was identified in four herds; three finishing herds and one multiplier herd. The isolates from two finishing herds were typed as CC1, t177 and further outbreak tracing showed that the two herds belonged to the same cluster of positive herds. The last two herds were not linked, but both positive for MRSA CC398, t034. The surveillance programme in 2016 detected one farrow to finish pig herd and two contact pig herds with LA-MRSA CC398 t034, and during this year MRSA was not detected in any of the genetic nucleus or multiplier herds, nor in the central units of the sow pool herds (6).

In total, six herds have been found through the surveillance programmes from 2014 to 2016. Additionally, contact tracing from positive herds or from persons have detected a total of 62 MRSA positive herds, bringing the total number of pig herds found positive for MRSA to 68 in this time period (Grøntvedt, CA. et al 2016, NORM-VET 2014, NORM-VET 2015, NORM-VET 2016). In all these positive herds, measures to eradicate MRSA were imposed.

Aims

The objective of the surveillance programme is to identify methicillin resistant *Staphylococcus aureus* (MRSA) positive swine herds with the intention of contact tracing and eradication of LA-MRSA, as the overall goal is to keep the Norwegian pig population free of LA-MRSA.

Materials and methods

In 2017, genetic nucleus and multiplier herds (n = 87), as well as all farrow to grower or farrow to finish herds with more than 10 sows (n~840) of which 12 consisted of sow pool herds, were to be sampled by the Norwegian Food Safety Authorities. The genetic nucleus and multiplier herds, as well as the twelve sow pool herds and the twenty largest commercial sow herds, were to be sampled twice. Sampling was conducted throughout the whole year.

Pigs were sampled by using sterile SodiBox™ cloths (Sodibox™, Pont C'hoat 29920 Nevez, France) moistened with sterile saline water. A part of the cloth was rubbed firmly against the skin behind both ears of the pig (about 5x5 cm on each side). Each cloth was used for 20 pigs, and a total of three cloths, representing 60 pigs distributed on all rooms and all age groups (except suckling piglets), were used per herd. The three cloths were analyzed as one pooled sample. In addition, in each herd two cloths were used for environmental samples taken in all rooms with pigs. Each cloth was used on about 15 control points (about 10x10 cm per location) representing furnishings, feeders, water nipples, window sills, door handles, tools, boots, ventilation system etc. These two cloths were analyzed as one pooled sample.

The samples were submitted to the Norwegian Veterinary Institute's laboratory in Oslo and analysed for MRSA by a method described by the EU reference laboratory on antimicrobial resistance (DTU Food, National Food Institute, Copenhagen, Denmark): Pre enrichment in 300 mL Mueller Hinton broth with 6.5% NaCl at 37°C for 18-24 h. From the culture obtained in the Mueller Hinton Broth 1 mL was transferred to 9 mL tryptone soya broth (TSB) with cefoxitin (3.5 mg/L) and aztreonam (75 mg/L). After incubation of the TSB at 37°C for 18-24 h, 10 µL were streaked on Brilliance™ MRSA2 Agar (Oxoid) and incubated at 37 °C for 18-24 h. Suspect colonies were isolated on 5 % blood agar and submitted to the Norwegian human reference laboratory for MRSA at St. Olavs Hospital in Trondheim for *spa* typing.

The 95% confidence interval (CI) was calculated based on a binomial distribution.

Results and Discussion

A total of 826 herds were included in the surveillance, of which 85 were genetic nucleus or multiplier herds. One multiplier herd was not sampled due to a recent barn fire. A total of 729 commercial sow herds with more than 10 sows were sampled, of which 18 of the largest sow herds were sampled twice. The remaining 12 sampled herds were the central units of the sow pools.

Nucleus and multiplier herds

MRSA was detected in one multiplier herd; situated in Vestfold (1.2%; 95% CI: 0.03 -6.4). The MRSA isolate belonged to clonal complex CC7 *spa*-type t091. One more herd was found MRSA positive through contact tracing, and eradication was imposed in both positive herds. MRSA was not detected in any of the genetic nucleus herds. Of the 85 sampled herds, 72 were sampled twice in 2017.

Sowpools, farrow to grower and farrow to finish herds

MRSA was identified in two farrow to finish sow herds (n=729); situated in Rogaland and Telemark (0.3%; 95% CI: 0.03 -1.0). In both herds the MRSA were *mecC* positive, although belonging to separate clonal complexes and *spa*-types (Table 1). Contact tracing did not detect any other positive herds. MRSA was not detected in any of the central units of the sowpool, nor the twenty largest sow herds. Table 1 shows an overview of the number of sampled herds included per county, and the MRSA positive sow herds detected through the surveillance program.

Table 1. Number of commercial sow herds sampled and number of positive herds per county in 2016.

County	No. of herds tested	Number of positive herds	Clonal complex (CC), spa type (t)
Østfold	54	0	
Akershus	22	0	
Hedmark	82	0	
Oppland	50	0	
Buskerud	16	0	
Vestfold	51	0	
Telemark	8	1	CC425 t6292
Aust-Agder	6	0	
Vest-Agder	5	0	
Rogaland	203	1	CC130 t843
Hordaland	16	0	
Sogn og Fjordane	21	0	
Møre og Romsdal	19	0	
Sør-Trøndelag	19	0	
Nord-Trøndelag	120	0	
Nordland	31	0	
Troms	6	0	
Finnmark	-	0	
Total	729	2	

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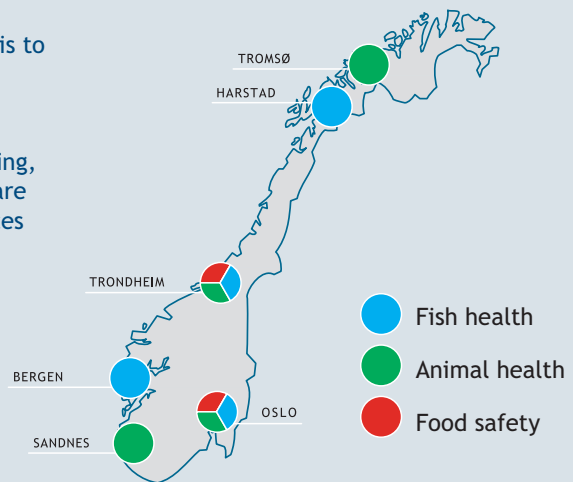
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