

# The surveillance programme for methicillin resistant *Staphylococcus aureus* in pigs in Norway 2019



**Veterinærinstituttet**  
Norwegian Veterinary Institute



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## Summary

The surveillance programme in 2019 detected one pig herd with MRSA. In total, 722 herds were included in the survey, of which 79 were genetic nucleus or multiplier herds, 12 herds were central units of the sow pool herds, 22 were of the largest farrow to grower or farrow to finish herds, and the remaining 609 were herds with more than 10 sows. Additional samples from six farrow to finish herds were received, though not included in the 2019 surveillance, and MRSA was detected from one of these.

## 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 pig 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. 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 or 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.

The commercial Norwegian pig population is characterized by being essentially closed due to negligible imports of live pigs (1). The population is based on a pyramidal structure with genetic nucleus herds at the apex, and with a unidirectional downward trade of live animals. The number of herds with breeding sows were about 1050 during 2019, while the number of specialized fattening pig herds were about 1830 during 2018 (2).

Surveys that were conducted in 2008 (3), 2011 (4) and 2012 (5) indicated a very low prevalence of MRSA-positive pig herds in Norway. The MRSA belonging to the animal associated clonal complex CC398 *spa*-type t034 was detected in pig samples for the first time in 2011 (anonymous study). In 2013/14, three clusters of MRSA CC398 positive pig herds were detected, in eastern and southwestern Norway, respectively, and measures to eradicate LA-MRSA from positive pig herds were imposed. The rationale behind this strategy was to avoid the pig 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 pig 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 pig 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 (6). In 2015, a total of 821 herds were included, of which 86 were nucleus or multiplier herds and 735 was finishing herds (7). 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 neither detected in any of the genetic nucleus or multiplier herds, nor in the central units of the sow pool herds (8). The surveillance programme in 2017 did not detect any pig herds with LA-MRSA CC398. However, MRSA CC7, and CC130 and CC425 were detected in one multiplier herd and in two farrow to finish herds, respectively (9). MRSA was not detected in samples from any of the total 716 herds included in the 2018 surveillance (10).

In total, ten pig herds have been found through the surveillance programmes from 2014 to 2019. Additionally, contact tracing from positive herds or from persons have detected a total of 73 MRSA positive herds, bringing the total number of pig herds found positive for MRSA to 83 in this time period (6-11). In all LA-MRSA positive herds, measures to eradicate MRSA were imposed.

## Aims

The objective of the surveillance programme is to identify methicillin resistant *Staphylococcus aureus* (MRSA) positive pig 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 2019, all of the genetic nucleus and multiplier herds (n = 85), 12 sow pool herds, the 22 largest farrow to grower or farrow to finish herds with more than 10 sows, and herds with more than 10 sows (n =737) according to the Registry of Production subsidies as of 1st of March 2018, were to be sampled by the Norwegian Food Safety Authorities. The genetic nucleus and multiplier herds, as well as the sow pool herds and the 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 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, 10 µL were streaked on Brilliance™ MRSA2 Agar (Oxoid) and incubated at 37°C for 18-24 h. The 95% confidence interval (CI) was calculated based on a binomial distribution.

## Results and Discussion

Samples were received from 79 of the 85 genetic nucleus and multiplier herds. From these 79 herds, samples were received twice from 65 herds, and once from 14 herds.

Samples were received from all the 12 sow pool herds. One herd was sampled three times, 8 were sampled twice, and three were sampled once. Samples were also received from the 22 largest farrow to grower or farrow to finish herds, of which 15 were sampled twice and seven were sampled once.

Samples were received from a total of 612 herds with more than 10 sows (the herds included in the category largest farrow to grower or farrow to finish herds not included among these). From three of these herds, the samples were not suitable for analyses, leaving samples from 609 herds for further investigation.

Altogether 722 herds were included in the 2019 MRSA surveillance. This constitute a total coverage of 95.1%.

MRSA was detected in samples from one sow herd of the total 722 herds included in the 2019 surveillance (0.1 %, 95% CI [0.003-0.77%]). The MRSA isolate belonged to clonal complex 398 *spa*-type t034. Two more herds were found MRSA positive through contact tracing, and eradication was imposed in all three herds.

Table 1. Number of pig herds included in the MRSA surveillance per Norwegian Food Safety Authorities (NFSA) Region in 2019.

NFSA Region	No. genetic nucleus and multiplier herds	No. sow pool herds	No. herds > 10 sows*
Stor-Oslo	8	3	46
Øst	28	4	184
Sør og Vest	17	4	228
Midt	20	2	137
Nord	6	-	36
Total	79	12	631

\*Including data from the largest farrow to grower or farrow to finish herds.

In addition, samples from six farrow to finish herds were received. These are not included in the statistics, although MRSA was detected from one of these farrow to finish herds. The MRSA isolate belonged to clonal complex 398 *spa*-type t011. Four more herds were found MRSA positive through contact tracing, and eradication was imposed in all five herds.

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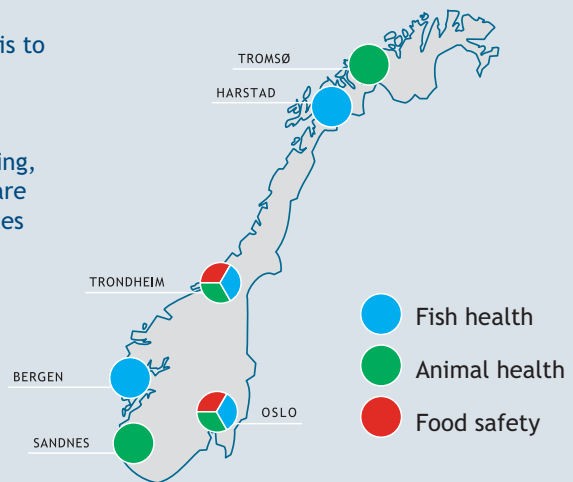
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