Annual Report

The surveillance programme for methicillin resistant *Staphylococcus aureus* in pigs in Norway 2016

Veterinærinstituttet
Norwegian Veterinary Institute

The surveillance programme for methicillin resistant *Staphylococcus aureus* in pigs in Norway 2016

Content

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Summary

The surveillance programme in 2016 detected one multiplier pig herd with LA-MRSA CC398 t034. MRSA was not detected in any of the genetic nucleus or multiplier herds, nor in the sowpool herds. In total, 872 herds were included in the survey, of which 87 were genetic nucleus or multiplier herds, 12 herds were the sow pool herds and 773 were herds with more than 10 sows.

Introduction

MRSA (Methicillin Resistant *Staphylococcus aureus*) are *Staphylococcus aureus* that are resistant to antibiotics. There are several varieties of MRSA, and some of these are carried by animals, especially pigs, and are called LA-MRSA (Livestock Associated - MRSA). Within a few years, LA-MRSAs have become common in the global swine population.

All types of MRSA can be transmitted between humans and animals and vice versa. However, not all types are well fitted for establishing a reservoir in other species than their original host specie. MRSA rarely produces disease in animals and healthy humans, but it is important to prevent the spread to health institutions such as hospitals and nursing homes where the bacteria can cause serious infections that are difficult to treat.

Surveillance programs 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, two clusters of MRSA CC398 t034 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 swineherds, 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.

Aims

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

Materials and methods

In 2016, genetic nucleus and multiplier herds (n = 89, as well as all farrow to grower or farrow to finish herds with more than 10 sows of which 12 consisted of sow pool herds (n=12) , were to be sampled by the Norwegian Food Safety Authorities. The genetic nucleus and multiplier herds, as well as the twelve sow pool herds, were to be sampled twice; 1. and 3. tertial. One extra sampling performed by the industry was voluntary and set to take place during the 2. tertial. Sampling was conducted throughout the whole year, with the exception of July.

Pigs were sampled by using sterile SodiBox™ cloths (Sodibox™, Pont C'hoat 29920 Nevez, France) moistened with sterile saline water. A point on 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 taken 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 contact 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 16-20 h. Then 1 mL was transferred into 9 mL tryptone soya broth with cefoxitin (3.5 mg/L) and aztreonam (75 mg/L). After incubation at 37°C for 16-20 h, 10 µL were inoculated on Brilliance™ MRSA2 Agar (Oxoid) and incubated at 37 °C for 24-48 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 872 herds were included in the survey, of which 87 were genetic nucleus or multiplier herds, 12 herds were the sow pool herds and 773 were herds with more than 10 sows.

Nucleus and multiplier herds, and sowpool herds

MRSA was not detected in any of the genetic nucleus or multiplier herds, nor in the sowpool herds. Two multiplier herds were not sampled in the survey, though these were sampled through an ongoing outbreak investigation in the same time period and found negative. Table 1 shows an overview of the number of sampled herds included per county.

Farrow to grower and farrow to finish herds

LA-MRSA was identified in one of the multiplier herds (n=773); situated in Hordaland (0.13%; 95% CI: 0.0 - 0.72) (Table 2). Only the pooled environmental sample was positive. The isolate was typed as CC398 t034. Follow up testing of contact herds, revealed two other herds positive for the same CC and spa-type.

Table 1. Number of genetic nucleus and multiplier herds, and sow pool herds, sampled per county in 2016. Number of positive herds is also shown.

County	Number of herds	Number of positive herds	Clonal complex (CC), spa type (t)
Østfold	6	0	
Akershus	7	0	
Hedmark	11	0	
Oppland	13	0	
Buskerud	2	0	
Vestfold	10	0	
Telemark	3	0	
Aust-Agder	-	0	
Vest-Agder	1	0	
Rogaland	13	0	
Hordaland	3	0	
Sogn og Fjordane	3	0	
Møre og Romsdal	2	0	
Sør-Trøndelag	5	0	
Nord-Trøndelag	18	0	
Nordland	2	**0**	
Troms	-	**0**	
Total	99	0	

Table 2. 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	45	0	
Akershus	24	0	
Hedmark	91	0	
Oppland	50	0	
Buskerud	23	0	
Vestfold	51	0	
Telemark	9	0	
Aust-Agder	8	0	
Vest-Agder	8	0	
Rogaland	213	0	
Hordaland	16	1	CC398 t034
Sogn og Fjordane	25	0	
Møre og Romsdal	22	0	
Sør-Trøndelag	20	0	
Nord-Trøndelag	122	0	
Nordland	39	0	
Troms	6	0	
Finnmark	1	0	
Total	773	1	CC398 t034

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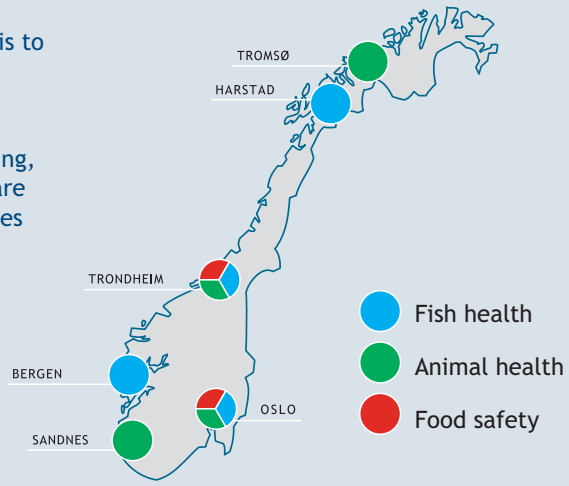

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