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Surveillance programmes for terrestrial and aquatic animals in Norway

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The surveillance programme for methicillin resistant *Staphylococcus aureus* in pigs in Norway 2015

Anne Margrete Urdahl, Bjarne Bergsjø, Madelaine Norström, Carl Andreas Grøntvedt

In 2015, a total of 821 swine herds were tested for MRSA, four herds were positive and MRSA eradication was initiated.

Introduction

MRSA (Methicillin Resistant Staphylococcus aureus) are special variants of 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 - animal associated - MRSA). LA-MRSA has within a few years become common in the global swine population.

All MRSA variants can be transmitted between humans and animals. The bacteria 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 conducted in 2008 (1), 2011 (2) and 2012 (3) indicated a very low prevalence of MRSA-positive swine herds 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 swine herds 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 was identified (4). A few additional herds were not included in the survey as they were involved and sampled in ongoing outbreak investigations in the same time period.

Aim

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 2015, all pure breed nucleus herds and multiplier herds (n = 95), as well as all finishing swine herds with an annual production more than 70 pigs (n = 877) the preceding year were to be sampled by the Food Safety Authorities. Sampling was conducted throughout the whole year, with the exception of July.

Pigs were sampled by using sterile SodiBox[™] cloths 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 μ L were inoculated on BrillianceTM 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 verification and typing. The 95% confidence interval (CI) was calculated based on a binomial distribution.

Results and discussion

A total of 821 herds were included in the survey, of which 86 were nucleus or multiplier herds and 735 was finishing herds. Of the nucleus or multiplier herds not sampled in the survey, four were sampled in ongoing outbreak investigations in the same time period and three had closed down their swine production.

LA-MRSA was identified in four herds; situated in the counties Rogaland, Hordaland and Nordland (0.5%; 95% CI: 0.01-1.2). From two herds (finishing herds), both samples from animals and the environmental were positive, whereas only animal samples were positive for the other two herds (one finishing herd and one multiplier herd). The isolates were typed as CC1, t177 (Rogaland and Hordaland), and CC398, t034 (Rogaland and Nordland). Outbreak tracing showed that the two herds with MRSA CC1, t177 belonged to the same cluster of positive herds, while the two MRSA CC398, t034 positive herds were not linked.

County	Number of sampled herds	Number of positive herds	Clonal complex (CC), spa type (t)
Østfold	53	0	
Akershus	25	0	
Hedmark	92	0	
Oppland	81	0	
Buskerud	3	0	
Vestfold	54	0	
Telemark	8	0	
Aust-Agder	6	0	
Vest-Agder	10	0	
Rogaland	271	2	CC1, t177 / CC398, t034
Hordaland	27	1	CC1, t177
Sogn og Fjordane	13	0	
Møre og Romsdal	13	0	
Sør-Trøndelag	14	0	
Nord-Trøndelag	96	0	
Nordland	48	1	CC398, t034
Troms	7	0	
Total	821	4	

Table 1. Number of herds sampled and positive herds by county in 2015.

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