Transmission of MRSA ST398 through the pork production chain


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Abstract

A distinct clone of MRSA, Multi Locus Sequence Type 398, was found in pigs and people in contact with pigs recently. In The Netherlands, a high prevalence of MRSA ST398 positive pig farms is reported. To quantify the role of animal trade on MRSA transmission within the pig production chain, results of 51 pig farms within 19 production chains were analyzed. Fifty-five percent of the farms were positive, including all kinds of farms. Complete positive and complete negative chains were found. Farms with a MRSA positive supplier had a much higher risk of being MRSA positive than farms with a MRSA negative supplier. These results indicate that trade of animals might be an important risk factor for the introduction of MRSA ST398 into pig farms.

Introduction

A distinct clone of methicillin resistant Staphylococcus aureus (MRSA ST398) was isolated recently in pigs and emerges in livestock [1]. Results of a Dutch study suggested that the purchase of animals from MRSA positive farms might be a risk factor for farrowing and finishing farms to become MRSA positive [2]. As breeding pigs are the top of the pig production pyramid, MRSA ST398 has the possibility to spread to a large number of other farms by the trade of animals. The objective of this study was to quantify the role of animal trade as a transmission route for MRSA ST398.

Material and methods

In 2007 and 2008, 38 farms were sampled, which included 11 breeding, 5 breeding-to-farrowing, 7 farrowing, 5 farrow-to-finish, and 10 finishing farms. All samples were convenience samples and farms within the same pig production chain were identified using the national Identification and Registration System. Time between sampling farms within a chain varied from 1 day to 6 months. Nasal swabs were collected from 60 to 80 pigs per farm. This sample size enables to detect the presence of MRSA on a farm with a within-herd prevalence of 2-5%. Analysis was performed on pooled samples (4-6 samples per pool), each pool containing swabs from just one section and age group. Samples were first enriched in Mueller Hinton Broth with 6.5% NaCl. After incubation for 18h at 37°C 1 ml of the Mueller Hinton Broth was put into 9 ml Phenol Red Mannitol Broth with aztreonam (75 mg/L) and cefitoxime (4 mg/L). After another 18h incubation time at 37°C a loopful was streaked out onto sheep blood agar and MRSA screen agar (Oxoid). Suspected colonies were confirmed by multiplex PCR for the S. aureus specific-gene [3], the mecA gene [4] and the Panton-Valentine-Leuococidin toxin genes [5]. Isolates were spa typed [6] and antimicrobial susceptibility was determined of at least one isolate per farm. A farm was classified positive
if at least one sample tested MRSA positive. On 25 of the 38 farms additional data on antimicrobial use was collected by a questionnaire.

Additionally, 13 positive farms out of another study on MRSA were used in the analysis [2]. In this study 10 individual nasal swabs were analyzed (see [2]). This sample size enables to detect the presence of MRSA on a farm with a within-herd prevalence of at least 25%. Therefore, farms classified negative in the latter study were excluded.

The association between MRSA status of farms within one chain was calculated with exact logistic regression [7].

Results

Fifty-five percent (28/51) of the farms were MRSA positive, including all kinds of farms. In 5 chains all farms tested MRSA-negative, in 8 chains all farms were MRSA-positive (including breeding farms), and in 6 chains positive and negative farms were found. Of farms that purchased animals from positive farms, 84.6% was MRSA positive compared to 26.7% of farms that purchased animals from negative farms (OR=13.4; 95% CI=1.8-177.2; P=0.006; exact logistic regression). The attributable proportion is 0.68, indicating that 68% of all MRSA-positive farms could have been prevented if their supplier had not been MRSA-positive. Seven spa types were identified, all belonging to ST398. Spa types t108 and t1011, the most common types in Dutch pigs, were found in several farms belonging to different chains, whereas more uncommon types (t567, t899, t943, t1939 and t2503) were found only on farms within one chain. All isolates were resistant to tetracycline and susceptible for mupirocin and linezolid.

Analysis of additional data on antimicrobial use will be performed and presented at the conference.

Discussion

An important finding is the existence of complete negative and positive pig production chains. The finding of mixed chains might be explained by the sometimes long period between sampling of farms within a chain. In this period the MRSA status of a farm might have changed.

The strong association between positive farms and positive suppliers might be the result of transmission of MRSA within a pig production chain by the trade of animals. The finding of the same spa types on farms within a chain supports this finding. These results support the choice for a top-down strategy in future control programs. However, transmission of MRSA by the purchase of animals from positive farms might not be the only risk factor, as breeding farms without supplier were found positive as well. Observational studies are currently performed to quantify additional risk factors for MRSA positive pig farms.

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References


