Within-farm prevalence and environmental distribution of livestock-associated methicillin-resistant Staphylococcus aureus in farmed mink (Neovison vison)

The aim of the present study was to identify the animal prevalence and environmental reservoir of livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) in mink farms. LA-MRSA on mink constitutes a human health hazard to farmers and farm workers, who handle the animals and are at risk of bites and scratches from colonized sites. The primary route of LA-MRSA colonization of mink is suspected to be by ingestion of contaminated pig by-products.

We performed a cross-sectional study with repeated measurements during May-July 2017. A total of 644 mink carcasses (542 mink kits and 102 breeding animals) from five Danish farms were sampled. From each carcass, pharynx was swabbed and the right forepaw dissected. In addition, environmental samples covering feed, air, glove, cages (top and between) and nest boxes were collected on the farms. MRSA was selectively cultured from each sample and suspect colonies were assessed using matrix-assisted laser desorption ionisation (MALDI-TOF) for species confirmation. Further, from each farm, three isolates from mink and one isolate per positive environmental site were sent for whole genome sequencing.

We isolated LA-MRSA from mink in four out of the five farms, but LA-MRSA bacterium was detected on all farms. On farms with LA-MRSA positive animals, the overall apparent animal prevalence ranged from 20% [13;29] CI95% to 29% [22;38] CI95%. LA-MRSA was isolated from kits before weaning, most likely due to a contaminated environment or transfer from the dam. Further, the apparent prevalence of LA-MRSA in kits tended to increase during the first months of age. On farms where LA-MRSA was isolated from mink, LA-MRSA was also isolated from the environment. LA-MRSA was isolated from all environmental sites tested (i.e. glove, on top of and between the cages and in the nest boxes), apart from air. The negative air samples contrast with the high concentrations of LA-MRSA in air found in the pig production. Hence, the risk of human exposure to LA-MRSA on mink-farms tends to be associated mainly with direct contact with contaminated environmental sites and the handling of colonized mink. All sequenced isolates were confirmed as LA-MRSA CC398 and genetically similar to clones previously isolated from the Danish pig production, supporting the hypothesis of LA-MRSA being transmitted by contaminated pig by-products.

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