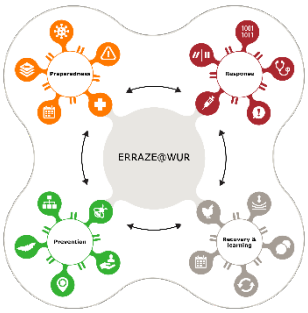
Paradigm Shifts for Global One Health

Greater resilience requires transformation and integration

Book of Abstracts

International symposium
23-25 April 2024
Wageningen, The Netherlands



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One Health MRSA surveillance: the Dutch experience

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1) RIVM National Institute for Public Health and the Environment, the Netherlands, 2) WBVR Wageningen Bioveterinary Research (WBVR), the Netherlands, 3) WFSR Wageningen Food Safety Research, the Netherlands, 4) NVWA Netherlands Food and Consumer Product Safety Authority

Aim: In 2018 a joined One Health livestock (LA)-MRSA surveillance in animals and humans in the Netherlands was started with a consortium of the Public Health Institute RIVM, the veterinary and food institute Wageningen Bioveterinary Research (WBVR), Wageningen Food Safety Research (WFSR), and the Netherlands Food and Consumer Product Safety Authority (NVWA) to monitor the nature of MRSA transmission between these two sources.
Approach: Every year another livestock sector was sampled. Sampling was done at farms including farmers and persons working on the farm. In addition, LA-MRSA from former research projects were included as well as isolates from meat and caeca samples collected during the national monitoring of antimicrobial resistance in animals and food. Human LA-MRSA were obtained from national surveillance via Type-Ned MRSA. Genomes were analysed using next-generation sequencing (NGS). MRSA genogroup 0398 (LA-MRSA) isolates collected were compared to LA-MRSA isolates of the national human surveillance using whole-genome multi-locus sequence typing (wgMLST). In addition, resistance and virulence genes were compared.
Results: A high MRSA farm prevalence was observed on finishing pig farms (76%), whereas the prevalence was lower on veal calf farms (25%), dairy farms (6%) and MRSA was not found on broiler farms. NGS data from 1770 LA-MRSA from Type-Ned MRSA and 811 animal-related isolates were collected and compared.
The wgMLST minimum spanning tree (MST) showed that some animal-related isolates were closely related to human ones. None of the MST branches contained animal isolates only. One branch only comprised of LA-MRSA from humans, and these isolates were often positive for the virulence factor Panton Valentine Leucocidin (PVL). PVL-positive LA-MRSA originating from animals were not found. However, two PVL positive isolates from two other MST branches were derived from persons that reported contact with pigs.
The multiresistance gene cfr was detected in an isolate from one pig farm and in seven isolates from the national human MRSA surveillance. wgMLST comparison of these cfr-positive LA-MRSA showed no relatedness, although two plasmids were genetically similar.
Conclusions: As there were no clusters containing animal isolates only and some animal-related isolates were closely related to human isolates, it is likely that transmission between animals and humans occurred. In addition, (indirect) transmission between different animal species also occurred as some isolates differed by less than 16 wgMLST alleles.
OneHealth surveillance of LA-MRSA is important to monitor genomic epidemiology of LA-MRSA in animals and humans.

Keywords: LA-MRSA, NGS, livestock, surveillance, OneHealth