Paradigm Shifts for Global One Health

Greater resilience requires transformation and integration

Book of Abstracts

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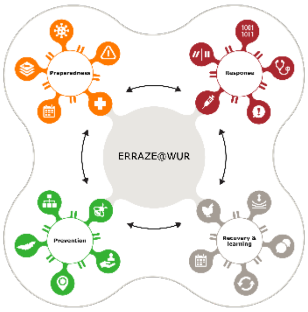

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Evaluation of One Health integrated WGS-based surveillance of foodborne diseases

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Aim Near real-time integrated monitoring of whole genome sequences (WGS) of Listeria monocytogenes, Salmonella and Shiga toxin-producing Escherichia coli (STEC) from food and human patients has been implemented in the Netherlands since 2019. We here evaluate the effectiveness of WGS-based One Health surveillance with regard to source-finding in food-related outbreak investigation and preventing further illness.

Approach Clinical isolates are obtained by the National Institute for Public Health and the Environment (RIVM) from microbiological laboratories for national infectious disease surveillance purposes. Commissioned by The Netherlands Food and Consumer Products Safety Authority (NVWA), food isolates are obtained by Wageningen Food Safety Research (WFSR) within the framework of monitoring programs. Assessment of the core genome multilocus sequence typing (cgMLST) is done using Ridom SeqSphere+.

Results Identifying joint patient-food clusters and their subsequent investigation has led to finding the source of the contaminated food products in at least nine clusters of L. monocytogenes with a minimum of five human cases per cluster. Control measures taken during an investigation always led to a reduction in cases with that particular strain, in most cases even leading to elimination of that strain from subsequent surveillance data. Within the Salmonella surveillance, the shared database did not lead to direct source finding, but was in several occasions informative for the possible food source. Moreover, matches between human and non-human STEC isolates are rare and detected clusters contain up to a maximum of only four human cases.

Conclusions The integration of WGS data from clinical and food isolates clearly enabled the identification of (direct and indirect) links between food and cases of listeriosis and salmonellosis. Although such a link gives a clear indication of the source of the outbreak, it is important to validate this link via subsequent investigation at food producers and epidemiological data confirming actual consumption of the implicated products by human cases. Once transmission of a specific strain from a food product or production facility to consumers is sufficiently established, the NVWA can act based on the statement in the General Food Law that food should be safe for consumption. Differences in the added value of One Health surveillance between the three pathogens could be due to persistence or reoccurrence of strains versus new introductions, type of reservoir, sampling schemes, under-recognized sources, multiple-strain contamination of one food product or location, ease of laboratory detection, and availability of isolates for WGS typing.

Keywords: One Health surveillance systems , Whole Genome Sequencing, collaborations between sectors