

Application of Molecular Typing Results in Source Attribution Models: The Case of Multiple Locus Variable Number Tandem Repeat Analysis (MLVA) of Salmonella Isolates Obtained from Integrated Surveillance in Denmark - DTU Orbit (08/11/2017)

Application of Molecular Typing Results in Source Attribution Models: The Case of Multiple Locus Variable Number Tandem Repeat Analysis (MLVA) of Salmonella Isolates Obtained from Integrated Surveillance in Denmark

Salmonella is an important cause of bacterial foodborne infections in Denmark. To identify the main animal-food sources of human salmonellosis, risk managers have relied on a routine application of a microbial subtyping-based source attribution model since 1995. In 2013, multiple locus variable number tandem repeat analysis (MLVA) substituted phage typing as the subtyping method for surveillance of *S. Enteritidis* and *S. Typhimurium* isolated from animals, food, and humans in Denmark. The purpose of this study was to develop a modeling approach applying a combination of serovars, MLVA types, and antibiotic resistance profiles for the Salmonella source attribution, and assess the utility of the results for the food safety decisionmakers. Full and simplified MLVA schemes from surveillance data were tested, and model fit and consistency of results were assessed using statistical measures. We conclude that loci schemes STTR5/STTR10/STTR3 for *S. Typhimurium* and SE9/SE5/SE2/SE1/SE3 for *S. Enteritidis* can be used in microbial subtyping-based source attribution models. Based on the results, we discuss that an adjustment of the discriminatory level of the subtyping method applied often will be required to fit the purpose of the study and the available data. The issues discussed are also considered highly relevant when applying, e.g., extended multi-locus sequence typing or next-generation sequencing techniques.

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