Use of multiple-locus variable-number of tandem repeats analysis (MLVA) to investigate genetic diversity of Salmonella enterica subsp. enterica serovar Typhimurium isolates from human, food, and veterinary sources

Salmonella enterica subsp. enterica serovar Typhimurium is the most common zoonotic pathogen in Bulgaria. To allow efficient outbreak investigations and surveillance in the food chain, accurate and discriminatory methods for typing are needed. This study evaluated the use of multiple-locus variable-number of tandem repeats analysis (MLVA) and compared results with antimicrobial resistance (AMR) determinations for 100 S. Typhimurium strains isolated in Bulgaria during 2008-2012 (50 veterinary/food and 50 human isolates). Results showed that isolates were divided into 80 and 34 groups using MLVA and AMR, respectively. Simpson's index of diversity was determined to 0.994 ± 0.003 and 0.945 ± 0.012. The most frequently encountered MLVA profiles were 3-11-9-NA-211 (n = 5); 3-12-9-NA-211 (n = 3); 3-12-11-21-311 (n = 3); 3-17-10-NA-311 (n = 3); 2-20-9-7-212 (n = 3); and 2-23-NA-NA-111 (n = 3). No clustering of isolates related to susceptibility/resistance to antimicrobials, source of isolation, or year of isolation was observed. Some MLVA types were found in both human and veterinary/food isolates, indicating a possible route of transmission. A majority (83%) of the isolates were found to be resistant against at least one antimicrobial and 44% against ≥4 antimicrobials. Further studies are needed to verify MLVA usefulness over a longer period of time and with more isolates, including outbreak strains.

General information
Publication status: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Research Group for Analytical and Predictive Microbiology, Research group for Genomic Epidemiology, National Food Institute, National Diagnostic and Research Veterinary Medical Institute, National Center of Infectious and Parasitic Diseases Bulgaria, Bulgarian Academy of Sciences
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Publication date: 2017
Peer-reviewed: Yes

Publication information
Journal: MicrobiologyOpen
Volume: 7
Issue number: 1
Article number: e00528
ISSN (Print): 2045-8827
Ratings:
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.63 SJR 1.158 SNIP 0.909
Web of Science (2017): Impact factor 2.682
Web of Science (2017): Indexed yes
Original language: English
Keywords: MLVA, Salmonella genetic diversity, antimicrobial resistance, laboratory surveillance, public health, zoonoses
Electronic versions:
Mateva_et_al_2018_MicrobiologyOpen.pdf
DOIs:
10.1002/mbo3.528

Bibliographical note
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Source: FindIt
Source-ID: 2373297985
Research output: Contribution to journal › Journal article – Annual report year: 2017 › Research › peer-review