Multilocus variable number of tandem repeats analysis (MLVA) - a reliable tool for rapid investigation of Salmonella Typhimurium outbreaks

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Salmonella enterica subsp. *enterica* serovar Typhimurium is a frequently occurring foodborne pathogen which causes many sporadic cases worldwide and is frequently the responsible agent in outbreaks of gastroenteritis. In elucidating outbreaks involving consumption of contaminated food, source tracing in a timely manner is imperative. Furthermore, it is important for risk managers to be able to accurately attribute sporadic cases to specific animal host species and to understand transmission routes of S. Typhimurium. Epidemiological meaningful subdivision of this serotype is therefore indispensable.

Phage-typing and pulsed field gel electrophoresis (PFGE) are among the methods most frequently applied. Both have been used sucessfully but have the disadvantage that reading the typing results is difficult to standardise, which hampers the exchange of typing results between laboratories and the construction of international reference databases. Source tracing or attribution using these methods fails when a frequently occurring important phagetype like DT104 (or PT 4 within *Salmonella* Enteritidis) that may have different sources, cannot be further subdivided.

Unambiguous typing results are critical in both detecting outbreaks and determining their source. Multilocus variable number of tandem repeats analysis (MLVA) is a PCR-based method that has recently become a widely used highly discriminatory molecular method for typing S. Typhimurium. It is based on amplification and fragment analysis of five repeat loci. MLVA has the advantages of typing methods based on PCR (low cost, short time, and easy to perform) that are independent of equipment and yield unambiguous typing data. For the latter purpose, the authors of the article published in today's issue of Eurosurveillance [1] developed a set of reference strains that can be used for easy normalisation of fragment sizes in each laboratory. According to the authors MLVA turned out to have a discriminatory power similar to that of phage typing and PFGE. Their results suggest that MLVA are reliable in epidemiological studies, including analyses of outbreaks and transmission routes. The authors propose a simple and definitive universal nomenclature based on the fragment size of tandem repeat loci allowing the comparison of MLVA profiles between laboratories. A further advantage of this nomenclature is that it allows easy recognition of related but slightly different MLVA-profiles that may be epidemiologically linked.

We strongly believe that molecular typing is the way forward and MLVA is a step in that direction. Nevertheless, at present it cannot fully replace the older typing techniques irrespective of all its advantages. Still faster methods are necessary for timely intervention both in outbreaks and during quality control along the food chain. Furthermore, epidemiological significance of related strains would be greater if molecular methods more fully exploited the phylogenetic information in the DNA of *Salmonella*.

References

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