Note from the editors: Consensus paper on MLVA development, validation, nomenclature and quality control – an important step forward for molecular typing-based surveillance and outbreak investigation

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Molecular methods have greatly contributed to refining classical infectious disease epidemiology by adding a new dimension to tracing the source of an outbreak. In the last three decades, a multitude of such methods have been developed and a number of them have become firmly established in the tool set of epidemiologists, while others have become obsolete with the appearance of newer techniques. Pulsed-field gel electrophoresis (PGFE), for example, has for more than 20 years played a major role in the investigation of food-borne outbreaks. It has recently become more and more complemented by multiple-locus variable-number of tandem repeats analysis (MLVA).

A factor contributing to the success of PGFE, besides its high discriminatory power, has been a consensus on how the method could be applied a standardised manner for food-borne pathogens, enabling investigators to compare their results with those of other laboratories. Consequently PGFE has been considered the gold standard in many epidemiological studies of bacterial pathogens causing infectious disease. The application and usefulness of MLVA in outbreak investigations and molecular surveillance is well accepted and was covered recently in papers in *Eurosurveillance* and other journals [1-6]. For MLVA, however, a global consensus on how to apply it in a standardised fashion had been missing and rendered inter-laboratory comparability of results difficult. In this issue we present a paper that 'proposes an international consensus on the development, validation, nomenclature and quality control for MLVA used for molecular surveillance and outbreak detection based on a review of the current state of knowledge' [7].

The consensus paper, by Nadon et al., is the final outcome from a meeting of an international working group in 2011 in Copenhagen, Denmark. Besides representatives from the European Centre for Disease Prevention and Control, Stockholm, Sweden, the Public Health Agency of Canada, Winnipeg, and the United States Centers for Disease Control and Prevention, Atlanta, the working group consisted of representatives from several European (Denmark, France, Germany, Norway, United Kingdom) and non-European national public health institutes (Japan, South Africa, Taiwan). The paper is complemented by a proof-of-concept study that shows that researchers can compare MLVA results between different laboratories through use of a set of calibration strains in each laboratory [8].

Eurosurveillance welcomes the consensus as an important step forward for molecular typing-based surveillance and global outbreak investigations and we hope that such broad high-level consensus will lead to wide adoption of the proposed method and to similar consensus meetings on new fast-developing techniques, such as whole genome sequencing.

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