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MLVA ANALYSIS OF SALMONELLA

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Background

Salmonella enterica consists of 1500 serovars and causes salmonellosis in humans and animals. Multiple-Locus Variable-number of tandem repeats Analysis (MLVA) has successfully been used for epidemiological investigations of S. Enteritidis and S. Typhimurium. A range of serovars causes salmonellosis, but since most MLVA protocols are serovar specific, no efficient method can genotype several serovars simultaneously. In this study we developed a general 5-locus MLVA assay for typing of several Salmonella serovars.

Method

66 unique VNTRs were investigated and the polymorphisms of seven promising VNTRs were evaluated with a panel 163 diverse isolates/14 serovars. Five VNTRs were selected for MLVA analysis. The discriminatory power was evaluated within the 14 serovars and compared with that of PFGE. Six pairs (six serovars) of outbreak-related strains were included.

Results

MLVA exhibited 100% in vitro stability and contained only true repeats. When analyzing 163 isolates MLVA obtained 79 genotypes (DI of 0.98 ) and PFGE revealed 86 genotypes (DI of 0.99). Each serotype displayed 2-8 different MLVA-profiles and MLVA identified the isolates from potential outbreaks.

Conclusion

This MLVA
• provides a good discrimination within all serovars, equal to that of PFGE,
• is fast, cheap and provides straightforward genotype identification,
• can be used as a single method for routine subtyping of isolates for surveillance and outbreak investigations, and
• enables rapid cross-country surveillance of multiple Salmonella serovars, which may improve the effectiveness of global Salmonella surveillance.