Genotyping of Shigella sonnei strains isolated from Iranian paediatric patients

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Background: S. sonnei has become the dominant species in certain parts of Iran. Although PFGE is still a gold standard for genotyping and source tracking of food-borne pathogens, it is laborious, expensive, time-consuming, and often difficult to interpret. However, MLVA is a PCR-based method, which is rapid, relatively inexpensive and easy to perform. The aims of this study were to characterize Iranian Shigella sonnei strains isolated from pediatric cases and evaluate the utility of multilocus variable-number tandem-repeat (VNTR) analysis (MLVA) for genotyping of local S. sonnei strains.

Materials and Methods: A total of 47 S. sonnei isolates were obtained from sporadic cases of pediatric shigellosis in Tehran, Iran, during the years 2002-2003 (n=10) and 2008-2010 (n=37). Bacterial isolation and identification had been achieved through standard biochemical and serological methods. A MLVA scheme based on 7 VNTR loci was established to assess the diversity of 47 S. sonnei isolates.

Results: Overall, 47 S. sonnei isolates were discriminated into 21 different genotypes. Analysis of the MLVA profiles using a minimum spanning tree (MST) algorithm showed the usefulness of the MLVA assay in discriminating S. sonnei isolates collected over different time periods. However, no correlation was found between the MLVA genotypes and age, gender or clinical symptoms of the patients.

Conclusions: It is assumed that our S. sonnei isolates are derived from a limited number of clones that undergo minor genetic changes in the course of time. The present study has provided some valuable insights into the genetic relatedness of S. sonnei in Tehran, Iran.