Abstract

In this study, we had developed a new PCR-based subtyping technique, called IS-PCR, for rapid genotyping of Shigella sonnei isolates. A total of 920 S. sonnei isolates collected from 1996 to 2004 were subtyped using both IS-PCR and PFGE to investigate clonal evolution among strains circulating for years. IS-PCR identified 30 IS types from the 920 isolates. Most of IS types circulated in a short time, five appeared in 2 or more year period, and four appeared intermittently. IS1, originating from India, was the most prevalent type, representing for 78% of the tested isolates. Since 2000, more than 90 PFGE patterns had developed among 713 IS1 isolates. These PFGE genotypes were highly divergent, the least similarity among the PFGE patterns was only 55%. Although numerous PFGE genotypes emerged, only few genotypes could exist for 2-3 years. Evolution was also observed among groups of isolates with identical PFGE patterns. For example, the J16N09.0015 family contained isolates of IS1, IS11, IS17, IS18 and IS23 genotypes. Isolates of these IS genotypes were collected from various geographic area in various time. This study demonstrates that subtyping of S. sonnei isolates by both less discriminatory IS-PCR and high discriminatory PFGE methods can be effective to identify clonal groups among isolates through circulation for years and, accompanying with epidemiologic data, can clearly delineate transmission patterns of the disease.

Keywords：Shigella sonnei；molecular subtyping；IS-PCR；PFGE；PulseNet Taiwan