

Phylogenetic analysis and antibiotic resistance of *Shigella sonnei* isolates

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Abstract

Shigellosis is one of the most important gastric infections caused by different species of *Shigella*, and has been regarded as a serious threat to public health. Lineage/sublineage profile of *Shigella sonnei* is strongly associated with the antibiotic resistance and population structure of this pathogen. In this study, we determined the phylogeny and antibiotic resistance profiles of *S. sonnei* strains, isolated from 1246 stool and 580 food samples, using multiplex PCR-HRMA genotyping and Kirby-Bauer disk diffusion methods, respectively. A total of 64 *S. sonnei* strains were isolated (13 food and 51 clinical isolates). Multiplex PCR-HMR assay was able to differentiate the lineages II and III, and sublineages IIIb and IIIc strains successfully considering the definite melting curves and temperatures. Lineage I and sublineage IIIa strain were not isolated in this study. We also demonstrated that most of the *S. sonnei* strains isolated from both food and clinical samples clustered within the lineage III and sublineage IIIc. Resistance against trimethoprim-sulfamethoxazole, tetracycline, chloramphenicol, and streptomycin antibiotics were the most prevalent phenotypes among the *S. sonnei* lineage III and sublineage IIIc strains.

Keywords: *Shigella sonnei*; PCR-HMRA; antibiotic resistance; phylogenetic group.