

TITLE: MOLECULAR EPIDEMIOLOGY, FREQUENCY OF VIRULENCE AND ANTIMICROBIAL RESISTANCE GENES OF *SHIGELLA SONNEI* STRAINS ISOLATED DURING 1983-2014 IN THE SÃO PAULO STATE IN BRAZIL

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ABSTRACT:

Shigella sonnei is an important causative agent of bacillary dysentery worldwide that has recently emerged in developing countries. Specifically, in Brazil there are few published studies that molecularly characterized this species. The aims of this study were to analyze the efficacy of the Multiple-locus Variable-number tandem-repeat Analysis (MLVA) typing method, to study the phylogeny by Multilocus Sequence Typing (MLST) and, to assess by PCR the presence of some resistant extended-spectrum β -lactamases (ESBLs) genes and 12 virulence genes in *S. sonnei* strains isolated from human diarrhoeic faeces in the São Paulo State in Brazil between 1983-2014. Seventy-two *S. sonnei* strains were typed by MLVA and grouped in two clusters, both presenting isolates from 1983-2014. Furthermore, the discrimination index of MLVA was 0.996. All the 72 *S. sonnei* strains presented the *ipaH*, *iuc* and *sigA* virulence genes. The *ipaBCD* gene was detected in 19% of the strains, the *ial* and *virF* genes in 18% and the *sen* gene in 10% of the strains. The *set1A*, *set1B*, *pic*, *sepA* and *sat* genes were not detected. The ST152 was assigned to all the 20 *S. sonnei* strains typed by MLST. Also, eight (72.7%) of 11 *S. sonnei* strains that previously showed to be resistant to β -lactams presented the bla_{TEM} gene. However, bla_{CTX-M-1group}, bla_{CTX-M-9} and bla_{SHV} genes were not found in these strains. MLVA results suggested the existence of two prevalent subtypes in the *S. sonnei* strains studied. Furthermore, MLVA could discriminate efficiently the monomorphic *S. sonnei* species. In conclusion, the pathogenic potential of the strains studied was highlighted by the presence of important virulence genes related to the pathogenesis of the disease. The MLST results suggested that the *S. sonnei* studied descend from a common precursor. Although, the β -lactams resistance rates found were not high, the frequency of bla_{TEM} gene may represent a risk for patients that need treatment.

Keywords: *Shigella sonnei*, MLVA, virulence genes, MLST, antimicrobial resistance genes.

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