MOLECULAR CHARACTERIZATION OF *Shigella* spp. STRAINS ISOLATED IN FORTALEZA, CEARA, BRAZIL

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Shigella spp. are listed as one of the most prevalent etiological agents of childhood enteric infection. This study aimed to characterize the profile of virulence-related genes (VRGs) of *Shigella* spp. strains isolated in the course of children epidemiologic studies conducted in Fortaleza, Brazil, between 2010 and 2014. Strains were derived from the collections of the Institute of Biomedicine for Brazilian Semiarid. Standard microbiological methods followed by immunoagglutination assay were used for identification of *Shigella* spp. from stool specimens. Isolates were stored in trypticase soy broth added by glycerol at -20°C until molecular tests were performed. Four Multiplex-PCRs were developed to detect 16 VRGs. Approximately 76.2% (16/21) of the isolates were identified as *S. sonnei* and 23,8% (5/21) as *S. flexneri*. The invasion plasmid antigen H (*ipaH*) gene was detected in 95.2% (20/21) of the isolates. Other highly prevalent genes included the protease with hemagglutinin activity encoded by *sigA*, the enterotoxin 2 encoded by *sen*, the invasion plasmid antigens (*ipaA-D)*, the evasion autophagy protein encoded by *icsB*, the regulator of *ial* (*virB*), the regulator of *virB* (*virF*) and actin nucleator (*icsA*), with frequencies ranging from 70% to 91%. Cell invasion protein encoded by *sepA* gene and the shiga toxin (*stx*) genes were the least prevalent (9.5% and 0%, respectively). The genes *pic* (protease associated with mucosal binding) and *sepA* (protein associated with cell invasion) were significantly more detected in *S. flexneri* than in *S. sonnei* (*pic*: 60% vs. 0%, p=0.0075; *sepA*: 40% vs. 0%, p=0.0476, respectively), while *sigA* was significantly more frequent in *S. sonnei* (100% vs. 60%, p=0.0476). *S. sonnei* was the most prevalent serogroup from this collection, confirming the trend of the dominance of this serogroup regarding to S. flexneri in our population evidenced by previous studies. Most virulence genes were highly prevalent but *stx* was not detected, which it was expected since there was no record of *S. dysenteriae* in the tested collection. These data also suggest that *pic* and *sepA* genes could play an important function on *S. flexneri* pathogenesis, and *sigA* gene would be relevant for *S. sonnei* infection. Clinical analysis are under way to verify the role of these genes in the pathogenesis of each infection.

Keywords: *Shigella* spp., virulence genes, molecular characterization

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