

**TITLE:** EVALUATION OF *Shigella* sp. ISOLATED IN BRAZIL IN THE PERIOD FROM 2012 TO 2016

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**ABSTRACT**

*Shigella* spp. is an intestinal infection whose etiological agent determines a high rate of morbidity and mortality worldwide, especially in countries where sanitary and hygienic conditions are precarious. We screened 262 strains received by NRLED from 2012 to 2016 isolated in different Brazilian regions to identify the serovars by antigenic characterization. The antimicrobial susceptibility profile were evaluated by disk diffusion according to CLSI (annually update) using 12 antimicrobial representative drugs the class of betalactams, phenicols, tetracyclines, aminoglycosides, quinolones, folate inhibitors and nitrofurans, and the virulence profile by ipaH gene by PCR. A total of 47.7% (125 strains) were identified as *S. flexneri* and 52.3% (137 strains) *S. sonnei*, being more prevalent in the South, Northeast and Southeast area. Ten *S. flexneri* serotypes were recognize, and the serovar prevalent were 2a detect in 72.8% of strains, and 27.2% distributed among serotypes 1a, 1b, 2b, 4a, 4c, 5, 6, IV, Y. The ipaH gene was confirmed in all strains. The antimicrobial resistance indicated that 90.3 % were resistant, 2.7% intermediary profile and 7% sensible. 32 different profiles were detected, ranging from 1 to 6 classes. *S. flexneri* and *S. sonnei* showed a high resistance for all the antimicrobial drugs tested, particularly to AMP, TCY, SXT, CHL and STR. Multi Drug Resistant (MDR) were observed in 94.8% of strains. In the present study, only one strain isolated in 2012 were resistant to cephalosporins 3<sup>rd</sup> (CAZ). 2013 and 2016 resistance and intermediate results observed to fluoroquinolones (CIP).The emergence of MDR strains has become a serious problem and has complicated the selection of empirical treatment for shigellosis. Resistance to some antibiotics is associated with the presence of some integrons and their horizontal transfer may account for the dissemination of resistance genes facilitated the survival of bacteria under the pressure of various antibiotics. Based the analysis, the serotype 2a was a prevalent serotype during the study period, and as MDR strains. Therefore, continuous surveillance will be needed to determine the distribution and resistance development of the prevalent serotype so as to understand the actual disease burden and provide guidance for the clinical treatment of shigellosis which has experienced changes to adapt to alter environmental conditions and represent a serious threat to public health in Brazil.

Keywords: Shigella; Antimicrobial Resistance