

**Title: CHARACTERISTICS OF *SHIGELLA* SPP. ISOLATED IN THE DIFFERENT REGIONS OF BRAZIL FROM 2009 TO 2014.**

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**Abstract:**

The *Shigella* genus is a common cause of diarrhea in developing countries with high rates of morbidity and mortality, especially in children under five and elderly. Poor sanitary conditions are the transmission way from person to person or by food or water when are contaminated by the organism. The aim of the present study was to evaluate the characteristics of *Shigella* sp isolated in Brazil from 2009 to 2014 received by NRLED. The strains were submitted to antigenic characterization and antimicrobial susceptibility testing by disk diffusion method according to CLSI (updated annually) using 13 antimicrobial drugs representative of the classes beta-lactams, phenicols, tetracyclines, aminoglycosides, fosfomicin, quinolones, antifolates, and nitrofurans. The research of *ipaH* gene by PCR was performed in the strains received from 2012. A total of 391 strains (195 *S. flexneri*, 195 *S. sonnei* and 1 *S. boydii*) have been received of which. 92 strains (40 *S. flexneri*, 52 *S. sonnei*) from outbreaks in the south region. *S. flexneri* is divided in 20 serotypes which the serotype 2a is the prevalent. An important aspect is that the newly epidemic serotypes reported weren't identified among the strains. The *ipaH* gene associated with invasiveness was confirmed in all the strains. 90.5% were resistant to ≥1 drugs. SXT (76%) was the most common followed by AMP (65%), TCY (64.3%), STR (33.7%) and CHL (33.7%). Resistance to CIP was observed in one strain from RS (2010) and one strain to CAZ from SC (2012) while six multidrug-resistant strains, presented in their profiles, resistance to FOX. None of the isolates were resistant to imipenem. All strains *S. flexneri* 2a exhibited multidrug-resistant (MDR - resistant to three or more classes of antimicrobials). The increasing antibiotic resistance showed the importance of horizontal transfer of integrons which may account for the dissemination of resistance genes and resistance to same antibiotics is associated with the presence of class 1 and class 2 integrons, plasmids, etc. The high percentage of resistance to aminoglycosides points to the presence of genetic elements involved in resistance to other drugs. Although most strains have shown susceptibility to drug of last generation these results should not be underestimated when considering aspects of relevance involving shigellosis, indicating a need continuous monitoring to strengthen the actions prevention and control.

**Keywords:** Shigella, serovars, antimicrobial resistance, virulence genes,