

Title: Molecular and phenotypic characterization of *Salmonella* Typhi isolated from cases of typhoid fever in the State of Pará, in the period 1975-2009.

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Abstract:

The *Salmonella* Typhi is the causative agent of typhoid fever. Transmission of the disease occurs through ingestion of water and food contaminated. It's a relevant public health problem especially in developing countries. Considering demographic variables, time and space were selected 151 samples of *S. Typhi* isolated from 51 blood cultures and 100 stool cultures in 35 counties of Pará, Brazil, in the period of 1975-2009. For analysis of genomic DNA was used to Electrophoresis Pulsed Field Gel Electrophoresis (PFGE) using the restriction enzyme XbaI. Susceptibility analysis of the 11 antimicrobial agents (amoxicillin/clavulanic acid, ampicillin, ceftazidime, ciprofloxacin, Nalidixic acid, nitrofurantoin, tetracycline, sulfamethoxazole/trimethoprim, chloramphenicol, and gentamicin Cefotaxime) were performed using automated systems (Vitek II) and manual (disk-diffusion). The Polymerase Chain Reaction (PCR) was used for the detection of genes of the integrase *Int1* and *Int2* (class 1 and 2 integrons) and *VIAB* gene (virulence factor Vi). The profile macro-restriction defined by PFGE demonstrated the presence of 68 different pulsotypes with an average percentage of similarity of 71.7%; 66 pulsotypes were in five genomic groups (clusters) and two had become more distant. In the first cluster are grouped five pulsotypes with an average percentage of similarity of 81% in the second have been grouped pulsotypes 47 to 81.8% in the third pulsotypes were grouped eight to 85.8%; in the room we were grouped two pulsotypes with 83.9%; and fifth were grouped in four pulsotypes 83.4%. The The differences found in the studied clones may have been due to changes in the size of the macro-restriction fragments that can occur by insertions, deletions, substitutions or rearrangements. All samples independent of their origin, year of isolation or source, showed high genetic similarity which ranged from 80 to 100%. Nitrofurantoin resistance pattern was observed in 1.99% of samples and 6.62% of them presented intermediate resistance profile at the same antimicrobial. In any sample detected integron class 1 and 2; demonstrating that in the state of Pará, the circulating strains don't show resistance profile and multi-resistance at a high level as found in various regions of the world. In all of the samples 2.65% were Vi-negative, which may have been due to the long storage period because SPI-7 pathogenicity island is genetically unstable and can be lost after successive samplings.

Keywords: *Salmonella* Typhi, PFGE, Gene Integrase, Virulence factor Vi

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