TRANSCRIPTOMIC ANALYSIS OF *SALMONELLA* TYPHIMURIUM ST313 FROM HOSPITAL BLOOD CULTURES IN THE STATE OF SÃO PAULO- BRAZIL

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Salmonella enterica serovar Typhimurium sequence type (ST)313 strains have been recently associated to invasive non-typhoidal (iNTS) emergent infections broadly associated with multidrug-resistant (MDR) and a broad mortality rate. ST313 strains are able to evade the gastrointestinal tract and reach the bloodstream of patients with comorbidities with HIV and malaria via unknown mechanisms. However, the ST313 in Brazil was recently detected, but only few studies have approached virulence mechanisms. The aims of this study were to evaluate the antimicrobial resistance profile of ST313 strains isolated from human blood cultures between 1998 and 2011 at the University Hospital of Unesp, survival in J774 macrophages and transcriptome via RNASeq under growth in Luria Bertani supplemented with blood at 37°C. The resistance profiles against 11 antimicrobials were assessed of Brazilian S. Typhimurium ST313 strains were resistant to at least two antimicrobials tested ampicillin and streptomycin or kanamycin and just one strain was resistant to all (ampicillin, streptomycin and kanamycin). All ST313 strains studied were able to survive in J774 macrophages in comparison with SL1344 (ST19) no evidence of statistically significant differences was found, thus demonstrating that ST strains were similar to the prototype strain, which is classically considered a model pathogen. The transcriptome showed upregulated genes related to maltodextrin and maltose transport responsible for the uptake and efficient catabolism glucose polymers. Conversely, the downregulated genes are responsible for propanediol metabolism and produced by by intestinal microbiota and cell motility linked to stimulating the inflammatory response in the host. Our results contribute to a better understanding of iNTS pathogenesis during systemic environment and they are essential for development of novel therapies.

Keywords: Salmonella Typhimurium ST313, antimicrobial resistance, macrophages, RNASeq.

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