Genomic characterization and analysis of an uncommon Salmonella Saphra harboring the blaCTX-M-8 gene in Brazil

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Salmonellosis is a water and foodborne illness caused by the bacterium *Salmonella* spp. This infection can cause severe cases of diarrhea, vomiting, fever, and malaise which can lead to death. *Salmonella enterica* is divided into several distinct serovars, depending on their characteristics. Cases of salmonellosis are an emerging One Health problem due to the increase in antimicrobial-resistant isolates, especially those resistant to extended-spectrum cephalosporins (ESCs). Infections caused by *Salmonella enterica* serovar Saphra are rarely reported worldwide, with few outbreaks described. Therefore, this study aimed to genomically characterize an *S.* Saphra strain isolated by the Adolfo Lutz Institute, a regional reference laboratory for identification and serotyping for *Salmonella* spp. One isolate identified as *S.* Saphra, of environmental origin, was selected for this study; DNA was extracted using the Wizard Genomic DNA Purification kit (Promega) for bacterial culture. Whole-genome shotgun sequencing was performed using an Ion Torrent S5. Read trimming and assembly were performed using CLC Genomics Workbench v.11.0.1 software. For genomic analysis, online tools of the Center for Genomic Epidemiology were used to determine *in silico* serotype (SeqSero 1.2 version), MLST (MLSTFinder 1.0.1), resistance genes (Resfinder 4.7.2), and plasmid classification (PlasmidFinder 2.1). The SNP-analysis was performed by submitting the genomes to CSI phylogeny 1.4 online server. Comparative sequences of S. Saphra (n=35) were retrieved from the EnteroBase *Salmonella* database in April 2026, available at https://enterobase.warwick.ac.uk.The isolate carried the ESBL gene blaCTX-M-8 and belonged to sequence type ST1604. The blaCTX-M-8 gene was located on an IncI1 plasmid. Additionally, transferable resistance genes to aminoglycosides (aac(6\')-Iaa) and fosfomycin (fosA7) were identified. A point mutation in parC (p.T57S; ACC→AGC) was also detected, which may contribute to reduced susceptibility to quinolones and fluoroquinolones. Comparative SNP analysis demonstrated heterogeneous genetic diversity, with pairwise differences ranging from 89 to 29,449 SNPs, suggesting the presence of both relatively related and highly divergent lineages. These findings highlight the emergence of antimicrobial resistance in uncommon *Salmonella* serovars and reinforce the need for ongoing genomic surveillance to track resistance dissemination and support public health strategies.

Agradecimentos: