IAFP Latino 2024
Simpósio Latinoamericano em Segurança dos Alimentos
Santos - SP - Brasil
11 a 14 Nov, 2024

Genomic pathogenicity assessment of Shiga Toxin-producing (STEC) and Enterohemorrhagic Escherichia coli (EHEC) from the Brazilian Beef producing chain

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Cattle are considered reservoirs for pathogenic E. coli, especially STEC and EHEC. Although all STEC strains are considered potentially pathogenic, with the aid of whole genome sequencing it is possible to uncover important STs and some virulence genes present in specific isolates that are more often linked to severe illness, improving risk assessment. In this study, we characterized through genomic approach the virulence gene distribution of STEC, EHEC and commensal E. coli from beef production animals from Brazil. Whole genome sequences from 50 isolates from beef production chain (EHEC = 6, STEC = 13, commensal E. coli = 31) were processed and analyzed in silico through different platforms to identify phylotypes, serotypes and virulence genes. MLST identification according to Achtman scheme grouped EHEC in ST11 and ST14373, while STEC isolates were characterized as 10 STs and commensal E. coli in 24 STs. Phylotype distribution revealed that all EHEC isolates were type E, while STEC and commensal isolates were distributed in all phylotypes (A, B1, B2, D, E, F and U), with B1 as the higher prevalence. Regarding virulence factors, EHEC isolates harbored stx2, while STEC isolates carried both stx1 and stx2. Serotype identification confirmed O157 and H7 for EHEC isolates, while STEC strains were assigned to O7, O17, O79, O93, O105, O113, O130, O166, O175 and O178. Interestingly, O103 was identified among commensal isolates. Furthermore, major virulence factors were identified in all EHEC strains, that were also present in STEC isolates such as: astA, ehxA, gad, ompT, terC and traT. Results showed that the integration of WGS and epidemiological surveillance contributes to detect highly pathogenic E. coli naturally present in food producing animals, facilitating risk assessment and management, with more precise potential than conventional typing methods.

Agradecimentos: CNPq, CAPES and FAPEMIG.