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Genomic analysis of Avian pathogenic Escherichia coli (APEC) isolated from a Brazilian slaughterhouse

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Avian pathogenic Escherichia coli (APEC) is a pathogen that can cause extraintestinal infections responsible for many economic losses in the poultry food chain. Besides, APEC is also presumed to be a zoonotic pathogen, causing health risks to humans. This work aimed to provide a genomic portrait of APEC isolated from broiler chickens from a Brazilian slaughterhouse in Minas Gerais state. The Whole Genome Sequencing analysis was conducted using software for trimming, assembly, annotation, and virulence factors/antimicrobial resistance investigation (in order Trimmomatic v0.39, SPAdes v3.15.5, Prokka v1.13.3, BV-BRC v.3.35.5, CARD v3.2.9). Also, the isolates were screening for phylogroup (ClermoTyping), serotype (ECTyper - 1.0.0), and sequence type (BV-BRC v.3.35.5). A total of 35 isolates were characterized as APEC by the presence of at least 2 of the 5 virulence genes mostly associated with this pathotype (iroN, ompT, hlyF, iutA and iss). The most prevalent phylogroups were B1 (15/35), D and F (4/35 each). Most of the APEC belong to serogroup O9 (6/35). Sequence types ST155 (7/35), ST69, ST361, ST3258, and ST5459 (2/35 each) were the most identified. The highest levels of antimicrobial resistance were detected in the peptide and fluoroquinolone; macrolide, and penam classes. Peptides showed bacA, eptA, PmrF, OmpA and Yojl as frequent genes. Meanwhile fluoroquinolone; macrolide; and penam revealed gadX, gadW, CRP, mdtE and mdtF as predominant. Additionally, beta-lactamase genes, including blaTEM, blaCTX-M, blaSHV, and ampC were also identified, underscoring the concern given to the beta-lactam antibiotics as a human treatment for various diseases. This study provides a better characterization of this pathotype found in the Minas Gerais state, and contributes significantly to understanding the characteristics, circulation, and resistance genes among these isolates.

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