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ÁREA DO TRABALHO: MICROBIOLOGIA CLÍNICA

TÍTULO DO TRABALHO: Esbl-Producing Escherichia Coli Isolated From Community-Dwelling Individuals, Their Pet Dogs, And Household Dust

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RESUMO:

Antibiotic resistance is a global challenge driven by antibiotics misuse in humans and animals. Escherichia coli is an opportunistic pathogen, member of a variety of gut microbiota, including humans and dogs. We investigated the presence of E. coli producing Extended-Spectrum Beta-Lactamases (ESBL) in humans, dogs, and household dust in One Health approach. Bacteria were recovered from faeces (humans and dogs) and household dust of volunteers from three groups: group A (humans without dogs), group B (humans and healthy dogs), and group C (humans with dogs recently treated with antibiotics). The isolates were cultured on MacConkey agar with cefotaxime (2 mg/L) or ceftazidime (1 mg/L), identified, and tested for antimicrobial susceptibility using Phoenix M50, and minimum inhibitory concentration (MIC) by broth microdilution for tigecycline and polymyxin B. Bacterial genome was sequenced using Nanopore MinION. The assembled genomes were scanned for plasmids, antimicrobial resistance, and virulence genes. The core genome was aligned to obtain the pangenome and phylogeny of the isolates. Twenty-eight E. coli were isolated, and 24 were sequenced: 18 from humans (75%), with eight from group A, seven from group B, and three from group C; five from dogs (20.8%), where two were from group B, and three from group C; and one isolate from group B dust (4.2%). Fluoroquinolone resistance was found in nine isolates (37.5%). Eight isolates (34.8%) presented a multidrug-resistant profile, and one isolate from group B human was polymyxin resistant (MIC = 128 mg/L). The ESBL-producing phenotype was conferred by blaCTX-M-15 and blaCTX-M-55 in most of the isolates, and eleven isolates (46%) had IncFIB plasmids carrying antimicrobial resistance genes. The Jaccard index analysis showed the spread of a clone in dog and house dust. The E. coli isolated from dogs presented the highest number of virulence genes, such as the vacuolating autotransporter toxin vat, the PAIusp genomic island, and the serine protease pic. The phylogroup B1 was the most abundant (46.2%), followed by phylogroup A (23%), and phylogroups F, B2, G, and C, with two isolates each (7.7%). Several Sequence Types (ST) were found, and two dogs from group C presented ST372 and ST998 (phylogroup B2) serotypes O83:H31 and O2:H6, respectively, indicating a pathogenic extraintestinal E. coli (ExPEC). The serotype O27:H14 and fimbriae type fimH54 were the most prevalent.

The in-silico pathotype determination showed two ExPEC (8.3%) and five (20.8%) uropathogenic E. coli (UPEC) isolates, most of them isolated from dogs. In conclusion, the data showed a high occurrence of ESBL-producing E. coli and plasmid IncFIB-family spreading in the community, where dogs can contribute to dissemination in the household environment.