Silent dissemination of multidrug-resistant Escherichia coli in drinking water: a One Health concern

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Water quality for human consumption is a fundamental pillar of the One Health approach, as it represents a critical link between the environment, animals, and humans. The presence of *Escherichia coli* in water not only indicates fecal contamination but may also reflect the dissemination of virulent and multidrug-resistant (MDR) strains within the ecosystem, posing a silent threat to public health. This study aimed to perform the phenotypic and genotypic characterization of *E. coli* isolates recovered from drinking water, investigating virulence-associated traits and antimicrobial resistance under a One Health perspective. A total of 50 bacterial isolates previously identified by biochemical tests and confirmed by MALDI-TOF MS were analyzed. Hemolytic activity was assessed on Blood Agar, while swarming motility was evaluated using semisolid medium. The detection of genes associated with diarrheagenic *E. coli* (DEC) was performed by real-time PCR. Antimicrobial susceptibility testing was carried out using the disk diffusion method for 15 antimicrobial agents from different classes according to BrCAST criteria. All isolates were confirmed as *E. coli*. Hemolytic activity was observed in 3 isolates (6%), while 6 isolates (12%) demonstrated swarming motility. No DEC-associated genes were detected. However, antimicrobial susceptibility analysis revealed clinically relevant resistance profiles: 12 isolates (24%) were classified as multidrug-resistant (MDR) according to international criteria. The highest resistance rates were observed for ampicillin/sulbactam (30%), tobramycin (26%), gentamicin (26%), and ampicillin (24%). Notably, the detection of an imipenem-resistant isolate highlights the concerning circulation of antimicrobial-resistant bacteria in drinking water systems, including resistance to last-resort carbapenems. Despite the absence of classical diarrheagenic *E. coli* genes, the occurrence of hemolytic activity, swarming motility, and multidrug resistance suggests the presence of environmentally adapted microorganisms with opportunistic potential and emerging clinical relevance. The detection of swarming-positive and MDR isolates further suggests adaptive mechanisms that may enhance persistence, colonization, and dissemination in aquatic environments. From a One Health perspective, drinking water systems may contribute to the environmental maintenance and transmission of clinically relevant antimicrobial resistance determinants. These findings reinforce the role of water as a potential reservoir and dissemination route for antimicrobial resistance, emphasizing the need for integrated microbiological surveillance based on phenotypic and molecular markers of resistance and virulence.

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