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Antibiotic resistance profiles of *Escherichia coli* isolated from the floating islands and water of Çat Dam Lake, Adiyaman, Turkey

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Antibiotics, metabolites of the antibiotics, and resistant bacteria reach the aquatic environment through treated and untreated sewage, hospital waste, aquaculture discharges and agricultural irrigation. Therefore, aquatic environments have a significant role in spreading the antibiotic-resistance genes. The current study demonstrates the prevalence of antibiotic-resistant bacteria in surface water and floating islands of Çat Dam Lake, Adiyaman, Turkey. A total of 79 *E. coli* colonies were isolated from Çat Dam Lake water samples and the floating islands, of which 36 were from the first period (August 2021), 28 were from the second period (November 2021), and 15 were from the third period (May 2022), which were also confirmed as *E. coli* by polymerase chain reaction (PCR). The confirmed isolates were tested for susceptibility using the EUCAST protocol. The results showed that the prevalence of resistance to erythromycin (E), ceftaroline (CPT) and cefazolin (CZ) was significantly higher than other tested antibiotics. In total, 96.2% of the isolated bacteria from all three periods were resistant to E, 77.21% to CPT and 48.1% to CZ, 12.65% to tetracycline (TE), 8.86% to cefuroxime (CXM), 6.32% to chloramphenicol (C) and cefotaxime (CTX), 2.53% to cefepime (FEP) and 1.26% to imipenem (IPM) and gentamicin (CN). Thirteen (16.5%) isolates were found with a high multiple antibiotic resistance (MAR) index. The observed MAR index could be due to the contamination of water sources with antibiotics used in the surrounding areas. It throws a potential risk to the local population from antimicrobial-resistant infections that can lead to serious side effects such as organ failures.

Keywords: Antibiotic-resistance genes, Aquatic pollution, Artificial floating ecosystem, Bacterial identification, Multiple antibiotic resistance (MAR), Soil