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Genotypic and phenotypic study of resistance to tetracycline and quinolone antibiotics in *Escherichia coli* isolated from cow and buffalo milk in Tabriz region

Abstract

Bacteria belonging to the Enterobacteriaceae family are Gram-negative bacilli, up to 3 microns in length. These bacteria ferment glucose and a wide range of sugars and are oxidase-negative. *Escherichia coli*, a member of this family, is considered part of the normal flora of the large intestine. When conditions are favorable for infection, it can cause clinical infections in humans and animals. The objective of the present study was to investigate the genotypic and phenotypic resistance to tetracycline and quinolone antibiotics in *Escherichia coli* isolated from cow and buffalo milk in the Tabriz region. In this study, 102 samples, including 74 from cow milk and 28 from buffalo milk, were randomly collected from traditional dairy farms in the villages of Tabriz from autumn 2024 to late spring 2025. Isolation of *E. coli* was performed using culture and biochemical tests. The 16S rRNA gene was used to confirm the *Escherichia* genus. The molecular method of PCR was performed to evaluate the *tetM* and *qnrS* resistance genes in the isolated *E. coli* strains. The results of microbial culture showed that out of the 102 samples studied, 24 samples (equivalent to 23.53%) from cows with mastitis and 11 samples (equivalent to 10.78%) from buffalos with mastitis were contaminated with *E. coli*. In the antibiogram test of isolates from cow mastitis, the highest frequency of drug resistance in *E. coli* was observed against tetracycline and erythromycin at 75%, and the lowest frequency of resistance was to norfloxacin at 4.16%. For isolates from buffalo mastitis, the highest frequency of drug resistance was to erythromycin at 90.90%, and the lowest frequency of resistance was observed against neomycin at 9.09%. The molecular analysis results for the 16S rRNA gene confirmed the *Escherichia* genus in 24 cow milk samples (23.53%) and 11 buffalo milk samples (10.78%). Six isolates (25%) from cow milk and 3 isolates (27.27%) from buffalo milk carried the *tetM* gene, while 8 isolates (33.33%) from cow milk and 4 isolates (36.36%) from buffalo milk carried the *qnrS* gene. The results of this study indicated that the rate of antibiotic consumption in dairy farms is relatively high, and the level of resistance observed in the isolated *E. coli* was genuinely higher than anticipated.

Keywords: Tetracycline, Quinolones, *Escherichia coli*, Cow and buffalo milk, Tabriz