

## Phenotypic and genotypic aminoglycoside resistance patterns of *Escherichia coli* strains isolated from Bovine Mastitis

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Mastitis caused by *E. coli* is the most common cause of toxic mastitis causes a high incidence of cow death or culling of cows. Resistance phenotypes arise from many different genetic determinants and each determinant may present specific epidemiological features. Therefore, in the present study phenotypic and genotypic antimicrobial resistance determined for better controlling of *E. coli* mastitis. A total of 57 *E. coli* collected in 15 dairy farms belonging to three different province of Iran (Tehran, Khorasan razavi and Kohgiluyeh). The sensitivity testing of clinical isolates was performed by disc diffusion on Muller-Hinton agar. Template DNA for PCR was extracted from all bacterial cultures by the boiling method. To further characterize the resistance mechanisms associated with aminoglycoside resistance genes encoding for the aminoglycoside adenylyltransferase (*aadA*) and streptomycin phosphotransferases (*strA* and *strB*) was determined. Antibacterial resistance rates for streptomycin, gentamicin and neomycin were 57.9%, 8.7% and 33.3%, respectively. The most prevalent gene was *aadA* found in 49.1% of the isolates. Although resistance to gentamicin and neomycin in *E. coli* isolated from bovine mastitis is low but high genotypic resistance showed that increasing resistance is expected in the future.

**Keywords:** aminoglycoside resistance patterns, *Escherichia coli*, mastitis