

**Title :** Identification of antibiotic resistance gene (*qnrs*) in *Klebsiella* isolates from the feces of ornamental birds in Urmia city.

**Abstract:**

*Klebsiella* bacteria are recognized as opportunistic pathogens capable of affecting mucosal surfaces and invading other tissues. This bacterium can be transmitted to humans through ornamental birds and lead to various infections. Quinolones are the most common antibiotics used to treat infections caused by *Klebsiella*; however, resistance to these drugs, particularly plasmid-mediated resistance (PMQR), has become a significant issue. In this context, the present study aimed to investigate the prevalence of antibiotic resistance gene (*qnrs*) in strains of *Klebsiella* isolated from the feces of ornamental birds in Urmia County.

In this study, 100 fecal samples from birds were collected and analyzed after culturing and biochemical testing, using PCR and electrophoresis methods. Among these, 24 samples were identified as positive for *Klebsiella* DNA. The highest frequency of positive samples was found in cockatiels, budgerigars, pigeons, Brazilian parrots, cockatoos, and monk parakeets, while no positive samples were found from Malayan parrots, green cheek conures, and African grey parrots. Of the 24 positive samples, 5 contained the *qnrs* gene (related to quinolone resistance). The results indicate an expansion of quinolone resistance, which is likely to increase in the future, potentially impacting the effectiveness of treatments negatively.

**Keywords:** Antibiotic Resistance, *Klebsiella*, Feces, *Qnrs*, Ornamental birds, Quinolone