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The Thesis Submitted for the Degree of DVM

Investigating the Presence of Efflux Genes in Urinary Isolates of Klebsiella Pneumoniae in Clinical Samples in the city of Zahedan

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Abstract

Introduction: Klebsiella pneumoniae is one of the most important opportunistic pathogens that cause hospital infections. The new mechanisms used by bacteria for their survival have caused the emergence of antibiotic resistance and have led to the death of many people due to infections resistant to antibiotic treatment. One of the most important mechanisms of antibiotic resistance is the expression of efflux pump systems in bacteria. By removing extracellular compounds, efflux pump systems prevent the creation of lethal concentrations of toxic compounds for cells and by creating resistant mutated strains in bacteria, they cause the survival of bacteria.

Aim: The aim of this study is to investigate the presence of efflux genes in Klebsiella pneumoniae clinical isolates.

Materials and methods: The study was conducted on 96 isolates of Klebsiella pneumoniae isolated from patients hospitalized in Zahedan Hospital. DNA extraction was done by boiling method. Multiplex PCR *TolC* and *AcrAB* efflux pump genes and PCR reaction is used to detect the *MdtK* gene.

Conclusion and discussion: Klebsiella pneumoniae are the cause of many infectious diseases. Wide use of antibiotics has caused high resistance of Klebsiella pneumoniae strains. The level of antibiotic resistance among isolates obtained from the community and hospitals is increasing and this is a big and global problem. In Gram-negative bacteria, efflux pumps are an efficient drug efflux structure and cause multiple drug resistance phenotypes. Antibiotic efflux pumps are one of the most important antibiotic resistance mechanisms that are also used in Klebsiella pneumoniae clinical isolates. *AcrAB* efflux pump gene was observed in 97.91% of isolates and *TolC* gene in 95.83% of isolates and *MdtK* gene in 42.70% of isolates; that in 98.9% of isolates there is at least one efflux pump coding gene. The prevalence of antibiotic efflux pump genes in this study is a cause for concern, therefore, the treatment of Klebsiella pneumoniae infections can be directed towards inhibition the expression of these pumps in bacteria.

Key words: Klebsiella pneumoniae, Efflux genes, Urinary isolates, Zahedan.