

## **Abstract**

*Klebsiella pneumoniae* is an important nosocomial pathogen most frequently causing pneumonia, and urinary tract, wound or blood infections. These strains carry major virulence factors such as; polysaccharide capsule, adhesion, siderophore and toxins, which helps to develop infections. The first step to confront and inhibit of this pathogen is the identification of the major virulence factors. The main objective of this study was to determine the frequency of virulence factors genes encoding, capsular synthesis (*wcaG*), Iron acquisition systems (*irp2*), adhesions (*fimH*) and regulator of mucoid phenotype A (*rmpA*) using Multiplex PCR method. In this research the *16S-23S rRNA klebsiella pneumoniae* special marker gene was used as internal control. Among 100 *Klebsiella pneumoniae* isolates, *fimH* gene with 88% and *rmpA* with 6% were the highest and lowest frequencies, respectively. Gene frequency for *irp2* and *wcaG* genes were detected 87% and 33%, respectively. This study showed that genes *irp2*, *fimH* and *wcaG* are more abundant and important in isolates of zahedan.

**Keywords:** *Klebsiella pneumoniae*, Virulence factors, Multiplex PCR



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Frequency of virulence *fimH*, *irP2*, *wcaG* and *rmpA* genes  
in *Klebsiella pneumoniae* isolates collected from patient  
attending zahedan teaching hospitals

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