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Role of *rmpA, wabG, uge, Ycfm, fimh1, EntB, Ybt-irp2 and kfu* genes in pathogenicity of *Klebsiella pneumoniae*: An overview.

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Abstract: *Klebsiella pneumoniae* is one of the most important pathogenic bacteria, its gram negative, bacilli, non-motile and causative agent of many diseases, such as pneumonia, urinary tract infections, bacteremia, burns and wounds infections and pyogenic liver abscesses. Pathogenicity of *K. pneumoniae subsp. pneumoniae* is due to many virulence genes can encoded many virulence factors that allow it to attack the immune system of mammalians and cause many kind of diseases, some of these virulence factors are: biofilm formation, hypermucoviscosity, capsule synthesis, adhesions, iron uptake and lipopolysaccharides formation.

Objective:The aim of this study was to an overview study about the role of some gens in pathogenicity of *K.pneumoniae*.

Conclusions: The study concluded that *rmpA, wabG , uge , Ycfm , fimh1, EntB , Ybt-irp2 and kfu* genes have an important role in classic pathogenicity of *K. pneumoniae.*

Keywords : Klebsiella pneumoniae, rmpA, wabG, uge, Ycfm , fimh1, EntB , Ybt-irp2 and kfu genes.

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