Abstract

Colibacillosis in poultry birds is an infectious disease pathogen is the bacterium *Escherichia coli*. The ability of *E. coli* to cause UTI is associated with specific virulence determinants, some of which are encoded on *pathogenicity islands* markers (PAI). The first step is to confront and inhibit of this pathogen is the identification genetic traits associated with the pathogenicity of pathogenicity islands markers, virulence genes. The main objective of this study was to determine the frequency of pathogenicity islands include PAI of I536, II536, ICFT073, IJ96, IIJ96 which encoded the α-hemolysin and PAI of IJ96, ICFT073, IICFT073 that are fimbriae encoder. A total of the 100 *Escherichia coli* isolates, pathogenicity islands PAI IV536 with ٣٧% and PAI ICF073 with 1% were the highest and lowest frequencies, respectively. and Pathogenicity island PAI IICF073 also showed the frequency of 5%. also pathogenicity islands PAI I536 ، PAI II536 ،PAI Ij96 and PAI IIj96 were not detected in any of the isolates.

Key words: Colibasilosis, avian pathogenice *Escherichia coli* (APEC), *Pathogenicity island marker*s

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The Thesis Submitted for the Degree of DVM

Prevalence of *pathogenicity Island Marker* in
Escherichia coli isolated from avian colibasilosis in
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Sept 2016