Abstract

The first stage of the infection with Escherichia coli is the binding phase. For this, Fimbria Factor plays a major role in the bacterial binding. In this study, the prevalence of Fimbria virulence genes of Escherichia coli isolates isolated from Poultry meat in Sistan province was investigated. From 1,500 , 100 isolates of Escherichia coli were studied. After the biochemical examination of the isolated bacteria, DNA extraction was performed from isolates. Subsequently, polymerase chain reaction was performed for *fim*, *pap*, *foc*, *afa* and *sfa* genes. The results showed that *fim* gene with 100% frequency had the highest statistical percentage And then the *Pap* gene is the most frequent statistically. In the present study, the prevalence of Escherichia coli *fim* gene in Poultry meat in the Sistan region was high. After that, the prevalence of the virulence gene of *Pap* Escherichia coli in Poultry meat in the high Sistan region, which accounts for 22% of the frequency of this gene, and the remaining virulence genes Zero percentages were observed. In the PCR reaction, three *foc*, *afa* and *sfa* genes did not show any bands and were negative. In the present study, the reaction was based on the distribution of virulence genes from 100 isolates of Escherichia coli isolated from Poultry meat referred to 2 Different genetic distribution patterns were observed. This study showed that the prevalence of Viverulence fimbriae genes of Escherichia coli isolated from Poultry meat in Sistan region for *fim* and *Pap* genes.

key words:
Escherichia coli, Virulence, Polymerase Chain Reaction, patterns of genes Poultry meat

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The Thesis Submitted for the Degree of Master of Science

(In the field of Veterinary Bacteriology)

Title:

Prevalence of virulence genes fimbriae in Escherichia coli strains isolated from poultry meat in sistan

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October 2019