

Abstract

Although *Escherichia coli* is present in the natural intestinal flora and other host mucosal surfaces and in the bird environment, only some of these species, which have specific virulence characteristics, are known as pathogenic *Escherichia coli*. They cause disease. APEC, or avian pathogenic *Escherichia coli*, is more likely to be associated with intestinal infections, respiratory tract infections or systemic infections, leading to a variety of diseases that are responsible for the severe economic damage to the poultry industry. Iron is an essential factor for many cellular biochemical activities, such as the electron transport chain. Aerobactins are the iron-absorbing bacterial agent found in *Escherichia coli*. The main objective of this study was to evaluate the frequency of *feoB*, *ireA*, *fyuA*, *prfA*, *modD*, *fepC*, *hlyB* and *hlyC* pathogenic iron transmitter genes as effective genes in iron uptake process in *Escherichia coli* by Multiplex-PCR technique. The *fyuA* gene, with 60% of observations, was the most abundant among the 100 isolates. Then *feoB* genes with 53%, *fepC* with 53%, *hlyC* with 39%, *hlyB* with 36%, *modD* with 21%, *ireA* with 11% and *prfA* with 10% were observed. Therefore, it was found that the *fyuA* gene with 60% had the highest frequency and the *prfA* gene with 10% had the lowest gene frequency among APEC isolates in Sistan region. By identifying APEC pathogenic genes in chronic infections and at the expense of costly treatment each year, vaccine design against this disease can be suggested.

Keywords: Pathogenic *Escherichia coli*, Iron transmitter genes, poultry.



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**Frequency of Iron transmitter genes in E. coli
isolation in poultry or APEC**

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