

Abstract

Escherichia coli bacteria are as a normal flora in intestine of mammals and birds, and most strains are not pathogenic while some strains can cause different disease such as septicemia, peritonitis, salpingitis, synovitis, omphalitis, coligranuloma and yolk sac infection. The main goal of this study was to determine the abundance of virulence factor encoding genes including, toxins (*cnf1*) and hemolysins (*hlyA*), iron uptake system (*iucD*, *iroN* and *irp2*), adhesins (*fimH* and *iha*) and outer membrane protease (*ompT*) in *Escherichia coli* isolated from broiler flocks around Zabol. A total of 100 *Escherichia coli* isolates were obtained from broiler flocks and boiled for DNA extraction and then all genes were evaluated by Multiplex PCR. The results showed that among the 100 samples, *fimH* was the most abundant gene with 94% and the *iha* gene was the least abundant with 21%. The two *cnf1* and *hlyA* genes were not found in any of the isolates. Frequency of other genes were also observed for *iroN*, *irp2*, *ompT*, *iucD* genes with frequency of 74, 57, 48 and 42%, respectively. Since most of these genes have not been comprehensively studied in the region so far, the results of this study can be used to adopt preventive and therapeutic strategies and improve the poultry production efficiency and consequently the use of appropriate medicines widely used to control the disease in the area.

Keywords: • Virulence factor, Avian pathogenic *Escherichia coli* (APEC), broiler chickens, Zabol



University of Zabol

Graduate School

Faculty of Veterinary

Department of Nutrition and animal breeding

The Thesis Submitted for the Degree of M.Sc

(In the field of Veterinary)

Title:

**Prevalence of Virulence Genes in Avian pathogenic *Escherichia coli*
(APEC) Strains Isolated from broiler chickens around Zabol**

Supervisors:

Dr. Ahmad Rashki

Advisor:

Dr. Mohammad Jahantigh

Dr. Najmeh Sahebzadeh

By:

Rasoul saleki

Summer 2019