

## Abstract

Avian pathogenic *Escherichia coli* (APEC), is the pathogenic factor of various systemic and local infections in birds. This strain, an important pathogenic factors including inosin, siderophore and toxins carry, which will help to disease progression. The first step to deal with and inhibit these pathogen, is identifying it pathogenic virulence factors. The main objective of this study was to determine the frequency of genes encoding virulence factors of toxins (iss, cdtB, astA, cvi/cva), iron uptake system (iutA), lipopolysaccharide capsules (KpsII and neuS) and inosin (ibeA and tsh) Based on the way Multiplex-PCR. A total of 100 *E. coli* studied, iutA gene with 93% highest frequency and gene neuS was observed in any of the samples and has the lowest frequency of the gene. Gene frequency for genes iss, cvi/cva, kpsII, astA, tsh, ibeA, vat, cdtB, 40%, 26%, 23%, 22%, 19%, 6%, 3%, 1% respectively, were observed.

Keywords: inosin, siderophore, toxins, disease-causing genes, avian pathogenic *E. coli*



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**Study of the Frequency of Toxin Coding Genes of  
eschrechia coli, the causative agent of poultry  
Collibacillosis, by multiplex PCR**

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