

Molecular and biological Study of Colibacillosis Susceptibility in broiler

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Abstract

This study was aimed to Detection of virulence genes(*rfbE*) It was carried in College of Veterinary Medicine at Baghdad university, During a time span of November (2021) to March (2022). (100) samples were collected from diarrheal chicken . 100 chicks were used in the present study, One day old chicks were weighed (Average of chicken weight was 160 gm±2) then transferred to the poultry house. Chickens in wards that were divided by wood barriers. Diagnosis of bacterial colonies were first done by the bacteriological methods. From (100) fecal samples of diarrheal cases of chicken , 90(90%) isolates were *Escherichia coli*. In the present study using vitek 2 compact system and Api 20 *Escherichia coli*. for the identification isolated bacteria. PCR technique was used to Detection of *virulence genes(rfbE)* ,The result for *rfbE* gene in this study was showed that this gene was detected in(60) isolates of (90) samples of chicken observed carried the *rfbE* gene which represent (67%).

Keywords: Diarrhea, *rfbE*, chicken, PCR.

I. INTRODUCTION

Avian pathogenic *Escherichia coli* (APEC), an extra-intestinal pathogenic *E. coli* (ExPEC), causes diverse local and systemic infections in poultry, including chickens, turkeys, ducks, and many other avian species (Mellata.,2013).The most common infections caused by APEC in chickens are perihepatitis, airsacculitis, pericarditis, egg peritonitis, salphingitis, coligranuloma, omphalitis, cellulitis, and osteomyelitis/arthritis; these are commonly referred as avian colibacillosis (Bandyopadhyay *et al.*, 2011). Colibacillosis in poultry includes systemic and localized infections. The localized infections were; omphalitis, swollen head syndrome, cellulitis, and diarrhea. Whereas systemic infection including; respiratory colisepticemia, enteric colisepticemia, and neonatal colisepticemia. (Ewers *et al.*,2003) reported that *E. coli* pathogenicity was generally enhanced or initiated by several influencing factors such as; environmental

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factors, viral infections, mycoplasma infections, and immune-suppression. Susceptibility to APEC infection increased after exposure to many intrinsic and extrinsic factors. Extrinsic factors involve environment; exposure to other infections, virulence, duration and levels of exposure, whereas intrinsic factors involve age; route of exposure, passive and active immune status, in addition to strain and breed of chickens. Generally, young birds were more susceptible to severe infections than adult (Rodriguez *et al.*, 2005). *Escherichia coli* O157:H7 has been associated with many outbreaks of diarrhea and haemolytic uraemic syndrome (HUS). The main pathways for the infection of this pathogen are contaminated food (including water), environmental, and person to person contact (Verma *et al.*, 2007). Lipopolysaccharide (LPS), the characteristic of outer membrane of gram-negative bacteria, is an important virulence factor for *E. coli* O157:H7. It serves to protect the pathogen from the host's defense system such as hydrophobic agents, serum-mediated killing, phagocytosis, and cationic peptides. LPS is composed of three domains: lipid A, core oligosaccharide and O-antigen. O-antigen is located at the outer layer of LPS and is almost specific to each gram-negative bacterium. The modification/alteration of LPS by various O-antigens likely aids the success of the pathogens during human infection. Some research suggested that the mutation on O-antigen synthesis could improve the adhesion of *E. coli* O157 to epithelial cells seven fold more than the wide-type bacteria. The *rfb* gene cluster has a lower GC content (30–40%) than that of *E. coli* chromosome (51%) with the exception of *manB* gene, which suggests that these genes are originated from a non-*E. coli* species. In the *rfb* gene cluster, *per* gene is predicted to encode GDP-perosamine synthetase. The gene is essential for the O-antigen synthesis. The mutation in *per* gene made bacteria deficient on the O-antigen, (Kalb., 2022)

II. MATERIALS AND METHODS

100 chicks were used in the present study, One day old chicks were weighed (Average of chick weight was 160 gm±2) then transferred to the poultry house. Chicks in wards that were divided by wood barriers, area of each barrier were 1×1.5 m. The ground bed was a sawdust and its thickness was 7cm. Drinking water and food being freely accessed (*ad libitum*) made of plastic manhels and with using of continuous lighting system. The chicks were neither vaccinated nor medicated throughout the 35-day of study. The chicks were neither vaccinated nor medicated throughout the 35-day of study.

Polymerase Chain Reaction

PCR assay was performed for detection The *Escherichia coli* O157 IQ1 *rfbE* gene for GDP-perosamine synthase in *E. coli* bacterium isolated from chicken

PCR master mix preparation

PCR master mix for each gene was prepared by using (Maxime PCR PreMix kit) and this master mix done according to company instructions as following table(3-12):



Table (1) PCR Master Mix preparation

PCR Master mix	Volume
DNA template 5-50ng	5 μ L
Forward primer (10pmol)	1 μ L
Reveres primer (10pmol)	1 μ L
PCR water	13 μ L

After that, these PCR master mix components that mentioned in table above placed in standard AccuPower PCR PreMix Kit that containing all other components which needed to PCR reaction such as (Taq DNA polymerase, dNTPs, Tris-HCl pH: 9.0, KCl, MgCl₂, and loading dye). Then, all the PCR tubes transferred into Exispin vortex centrifuge at 3000rpm for 3 minutes, and then placed in PCR Thermocycler (BioRad- USA).

PCR Thermocycler Conditions

PCR thermocycler conditions were done by using convential PCR thermo cyler system is same for each gene as following table(2)

Table (2):PCR Thermocycler Conditions

PCR step	Temp.	Time	Repeat
Initial Denaturation	94C	3min	1
Denaturation	94C	30sec.	30 cycle
Annealing	59C	60sec	
Extension	72C	1 min	
Final extension	72C	7min	1
Hold	4C	∞	-

III. RESULTS AND DISCUSSION

1) Isolation of *Escherichia coli*:

Fecal samples were inoculated on various bacteriological media such as Blood agar, Nutrient agar, MacConkey agar, and EMB agar then incubated at (37°C) for (18-24) hours to allow the growth of bacteria.

Diagnosis of bacterial colonies were first done by the bacteriological methods including colonial morphology, Gram's staining, and cultural and biochemical characteristics as described in (Cheesbrough .,2007).From (100) fecal samples of diarrheal cases of chicken , 90(90%) isolates were *Escherichia coli*.

(Alonso *et al.*,2012); (Amadi *et al.*,2015), reported prevalence rate of *E. coli* associated with diarrhea in chicken which accounted for 67%. These results were shown in Figure (1).

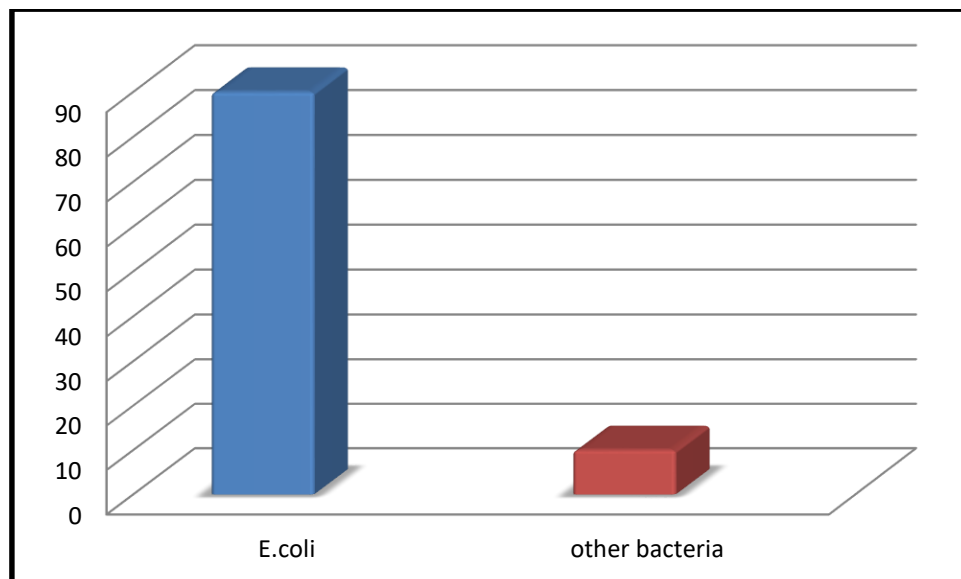


Figure (1): Percentage of Bacterial Isolates of diarrhea cases in chicken

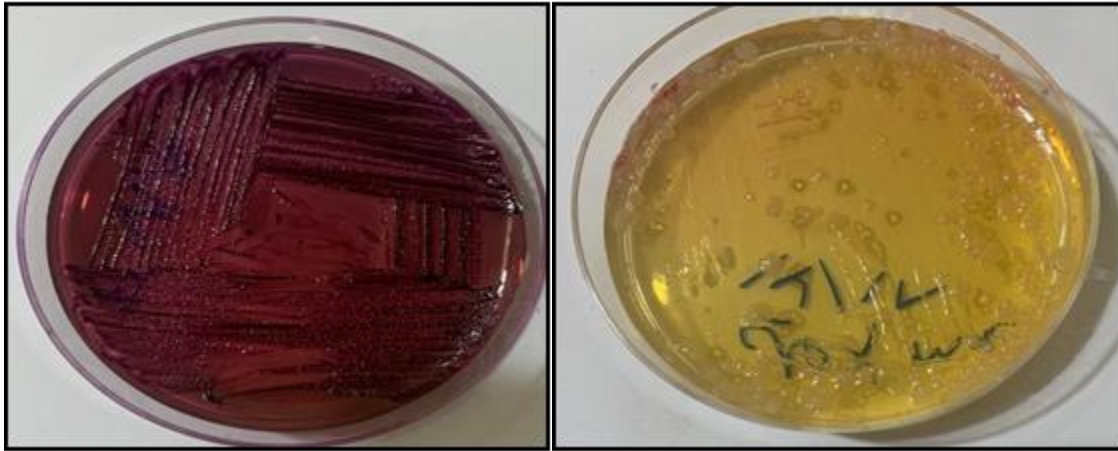


Figure (٢): Bacterial Isolates of diarrhea cases in chicken

The results of this study are similar to the findings of (Abbassi *et al.*,2017) who found that prevalence of 67% and 100% was reported in rectal swabs of indigenous and caecal samples of broiler chicken respectively.

(Adelaide *et al.*,2008) found that about 99% of diarrheal cases caused by *E.coli* , while other bacteria about for 1% of cases.

Mixed infection of samples with other microbes has been reported to affect prevalence of some bacteria such as *E. coli* and this could possibly be the cause of different prevalence from other studies. Environmental conditions, geographical location and other host factors affect prevalence of *E. coli* among related animals and could also account for the differences (Gambushe *et al.*,2022).

2) Detection and Characterization of (*rfbE*) Gene

To determine if *E.coli* isolates was *E.coli* o157H7 ,we characterized the isolates on the basis of the presence of virulence genes(*rfbE*) by using real time PCR technique. Figure (3) shows Agarose gel electrophoresis image that showed the PCR product analysis of *rfbE* gene in *Escherichia coli* isolated from feces samples. Figure (4) shows Agarose gel electrophoresis image that showed the PCR product analysis of *rfbE* gene in *Escherichia coli* isolated from feces samples

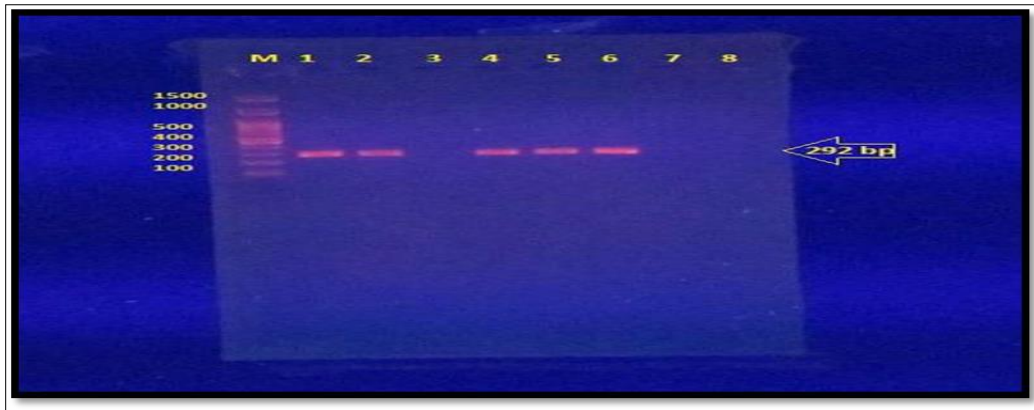


Figure (3): Agarose gel electrophoresis image that showed the PCR product analysis of *rfbE* gene in *Escherichia coli* isolated from feces samples . Where Marker ladder (1500-100bp), Lane (1-7) some positive *rfbE* gene in *E. coli* isolates at 292bp PCR product size.

Sixteen of the 90 (66.7%) samples of chicken observed carried the *rfbE* gene .Figure (4)illustrate this results.

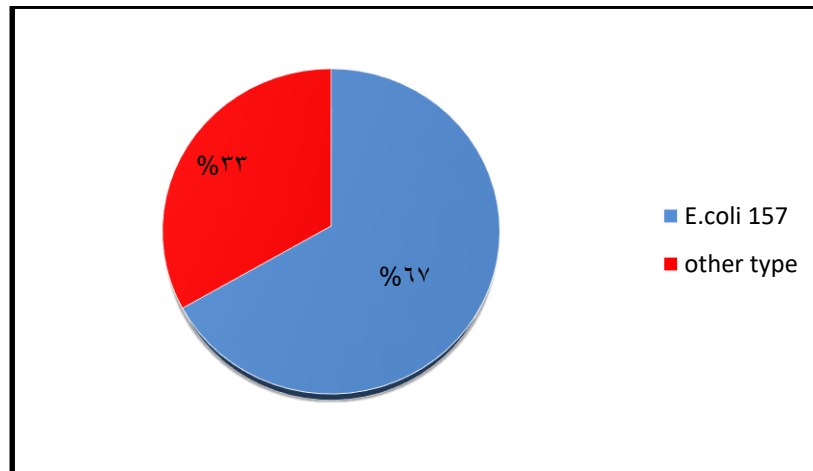


Figure (4): *rfbE* gene in chicken

The result in this study was agreement with study of (Abdulmawjood *et al.*,2004) ; (Jeshveen *et al.*,2012) , They focussed our method on the amplification of the *rfbE* gene to detect the presence of all *E. coli* O157 strains. they found that the The O157 *rfbE* PCR is a selective and rapid method for confirmation of the O15 serogroup.

The majority of *E. coli* strains are commensals inhabiting the intestinal tract of humans and warm-blooded animals

and rarely cause diseases, unless they acquire VFs carried by mobile genetic elements such as bacteriophages, pathogenicity islands and plasmids. Additionally, *E. coli* can form a reservoir of AMR genes that may be transferred among different bacterial species, including pathogenic bacteria for both humans and animals (Benameur *et al.*, 2021). The O-antigen was the immunodominant agent for the gram-negative bacteria, which can disguise the pathogen to escape from the defense system of the host. Previous studies showed that the deficient on O-antigen could make the pathogens sensitive to the killing mechanism of host.

(Bakhshi *et al.*, 2017) argued that the protein- encoding *rfbE* gene plays an essential role in the group of proteins involved in glucose-free biosynthesis and bacterial LPS synthesis. It is likely that the *rfbE* gene is involved in activating antibodies associated with *E. coli* antigen diseases and increases bacterial activity in the presence of sugar and LPS.

According to the knowledge obtained on the *rfb* gene function and its main activity as O antigens in *E. coli* through this study, creatinine, as a nutrient with a high level of nitrogen, can enhance the activities of O antigen and *rfbE* gene effectively.

The study by (Stevenson *et al.*, 1994) showed that O antigen is removed during in vitro culture that effectively reduces the expression of *rfb* cluster genes. Still, in the present study, the expression of *rfbE* gene was enhanced as one of the 11 *rfb* genes, which indicates the importance of creatinine amplification compared to the genes encoding O polysaccharide in this bacterium. The temperature changes lead to the expression of the *rfbE* gene.

3) Genetic analysis of *rfbE* gene:

Sequence analysis of *rfbE* gene of local *E. coli* isolates were found to be identical to the *rfbE* gene in (NCBI) Blast. The results of all tested samples have high identity to another global sequence data when compared to NCBI- Blast. In the present study, the phylogenetic trees of the isolated *rfbE* genes from tested isolates were very close to each other with 100 percent compatibility, Phylogenetic analysis were done on 5 isolate in a local tree analysis.

The alignment study of the *rfbE* gene in revealed a genotype similar to other strains, from USA, deposited in the Gen Bank (accession numbers documented in (Fig.5). Sequencing of the gene demonstrated 99% compatibility with the global standard gene in Gen Bank.

Global tree analysis were presented on figure (6) revealing that two cluster were shown one for our isolate and the other for the international gen bank isolate which revealing that the *rfbE* gene distantly a bit far from others isolates and to make it clear this might the effect of gene in producing EBLs effect. In addition, the gene sequencing and phylogenetic analysis from the *E. coli* isolates have reported 99 percent compatibility with the global standard genes of GenBank.

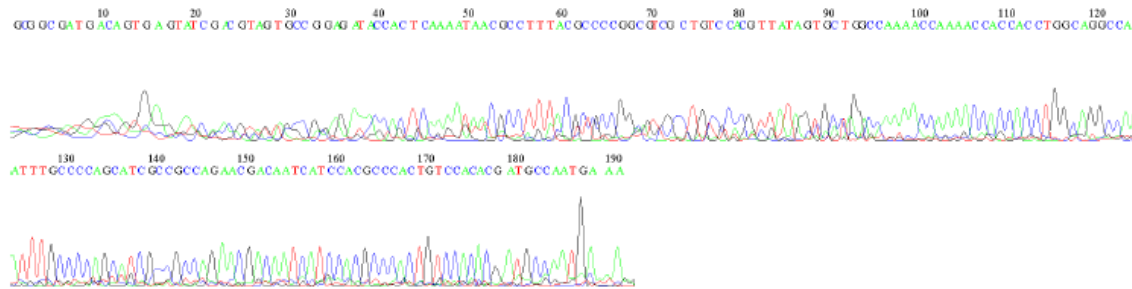


Figure (5): genetic analysis based on the *rfbE* gene for (5) isolates of *E. coli*

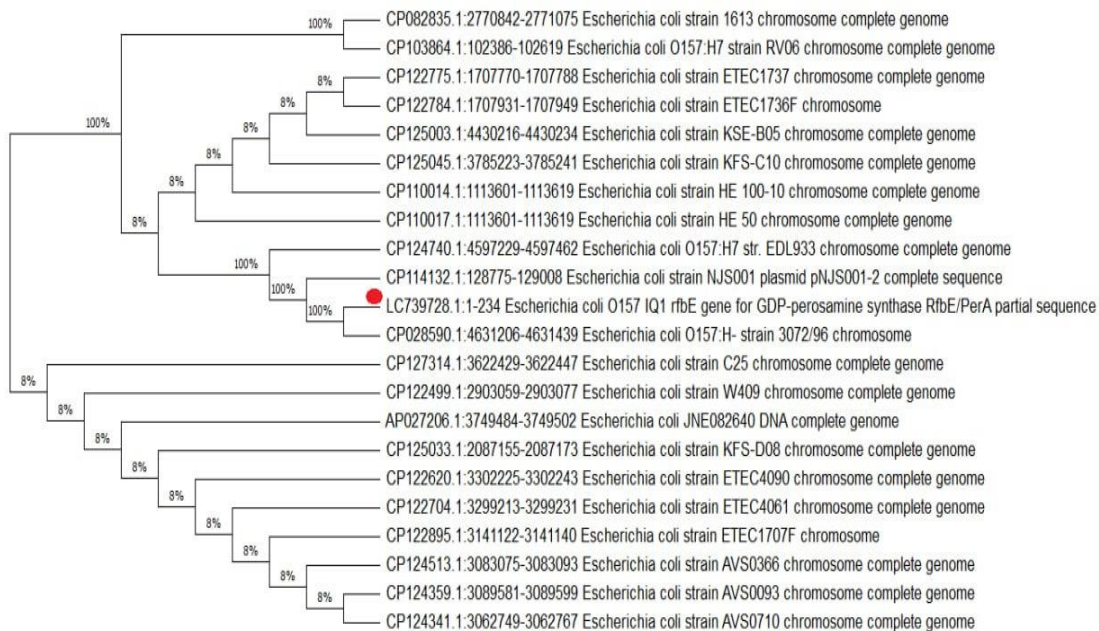


Figure (6): Phylogenetic tree based on the *rfbE* gene for (5) isolates of *E. coli*

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