

Molecular Detection of the Virulence Genes in *Escherichia coli* Isolated from Healthy and Diarrheic Calves in Southern Iraq

ABSTRACT

Aim: To investigate the *stx1*, *stx2*, *hly*, *cnf2*, *sfa/foc*, *afaI*, *papC*, and *afaC* virulence-associated genes of pathogenic *Escherichia coli*, isolated from diarrheic and non-diarrheic calves.

Materials and Methods: The genes to be investigated were first isolated from the stool samples obtained from 150 diarrheic and non-diarrheic calves, between the ages of one day and six months, during the period 2016 to 2017. Rectal swabs were aseptically and randomly collected from several herds, from different regions in the province of Basra.

Results of Research: The polymerase chain reaction (PCR) results showed that pathogenic *E. coli* were detected in a total of 34 out of 41 (82.9%) distributed as 23 out of 26 (88.5%) and 11 out of 15 (73.3%) of the diarrheagenic and non-diarrheagenic calves, respectively. The results also showed that *stx1*, *hlyA*, and *stx2* genes showed a higher incidence of distribution in both diarrheagenic and non-diarrheagenic calves, in a percentage rate of 69.6%, 65.2%, 56.5% and 63.6%, 63.6%, 45.5%, respectively. Moreover, eight different virulence gene profiles were established in the present study. Most of the isolates analyzed had at least two or three gene arrangements and only four isolates were seen in a combination of four genes *stx1*, *stx2*, *hlyA*, and *afaI*.

Conclusion: It is concluded that *E. coli* isolates from healthy and diarrheic calves that carried various virulence genes, of which the most frequent were

stx1, *stx2*, and *hlyA*. A high percentage of these isolates are found in both diarrheic and non-diarrheic calves.

1. INTRODUCTION

In veterinary medicine, diarrhea is considered as one of the most common and critical diseases that causes huge economic losses in neonatal animals. Diarrhea can be caused by bacteria, virus, parasites, and other etiological agents, even as *Escherichia coli* bacteria are being recognized as the leading cause of diarrhea. This microorganism was first described by Theodor Escherichia in 1885. It is a part of the normal gut flora in warm-blooded animals, human beings, and birds. However, some strains are pathogenic and cause different clinical illnesses and diseases (1) *E.coli* also causes septicemia and diarrhea in a wide range of hosts, including man, avian species, and animals such as cattle, piglets, goats, foals, lambs, and buffaloes, as well as children in developing countries, (2) the diarrheagenic form of *E. coli* (DEC) is generally distinguished into Enteropathogenic *E. coli* (EPEC), Enterotoxigenic *E. coli* (ETEC), Enteroinvasive *E. coli* (EIEC), Shiga toxin-producing *E. coli* (STEC), Enteroaggregative *E. coli* (EAEC), and adherent *E. coli* (DAEC) (3). Generally, the diarrheagenic form of *E.coli* is known as colibacillosis. Colibacillosis has been linked to clinical symptoms, such as, diarrhea, dehydration, fatigue, fever, malaise, and depression. Calves between three and five days old can also develop colisepticemia, when the bacterial infection spreads into the bloodstream of the host (4,5,6,7). ETEC infection is the most common type of colibacillosis in young animals especially in calves and piglets (8). Moreover, STEC strains are also well-recognized as a cause of colibacillosis in newborn calves. Even though both healthy and diarrheic calves harbor STEC in their

intestine, natural outbreaks and experimental infections have documented the association of STEC with diarrhea and dysentery in young calves (9,10).

Pathogenic *E.coli* can be categorized based on serogroups, pathogenicity mechanisms, clinical symptoms, or virulence factor genes. The pathogenicity of *E. coli* based on virulence factors occurs through plasmids, transposons, bacteriophages, and/or pathogenicity islands (3,11). On the other hand, evidence and information about the *E. coli* occurrence and distribution in neonatal calves in the Basra Governorate is limited based on molecular technique. Thus, it is necessary to develop modern methods or tools to monitor the prevalence of different *E. coli* pathotypes in neonatal calves, in Basra, through the detection of wide-ranging virulence genes. Therefore, in this particular study, the *E.coli* from calves was isolated using the PCR technique and screened through a wide range of virulence genes including the *stx1*, *stx2*, *hly*, *cnf2*, *sfa/foc*, *afaI*, *papC*, and *afaC* genes.

2. MATERIALS AND METHODS

Collection of Stool Samples and Isolation of *E.coli*

E. coli was isolated from rectal stool samples obtained from 150 diarrheic and non-diarrheic calves, between the ages of one day and six months, during the period December 2016 to June 2017. Rectal swabs were aseptically and randomly collected from several herds that were found in different regions in the province of Basra. The samples were collected in sterile screw-capped containers and labeled, to show their serial numbers, as well as time and date of collection. Next, the samples were transported in ice-cooled containers to the Laboratory of Microbiology at the College of Veterinary Medicine, for immediate analysis. The *E. coli* from the samples were isolated and identified using the standard technique (12). All stool samples were inoculated into tubes of freshly prepared Brain Heart Infusion (BHI) broth and incubated aerobically at 37°C overnight, followed by

subculturing on MacConkey agar plates for 24 hours, at 37°C. Of the resulting colonies, the lactose-fermenting colonies were sub-cultured immediately on Eosin methylene blue (EMB) agar and incubated at 37°C for 24 to 48 hours. A colony with a metallic sheen appearance was picked for further analysis using bacteriological and biochemical tests and the API-20E system (bioMérieux, Marcy l'Etoile, France). The bacteriological and biochemical tests included were: Gram staining and culturing on Triple Sugar Iron, Oxidase test, Catalase test, Indole test, and the Urease test, which were carried out for further identification of *E.coli*, according to the previous methods of (12). Following the purification and subculturing on the BHI agar, the isolated bacterial colonies were further identified using the PCR technique.

Bacterial DNA Extraction and PCR analysis

Bacterial DNA was obtained using the boiling method, through the following steps: Five colonies of *E. coli* were transferred into Eppendorf tubes containing 100 µl distilled water after being incubated in a BHI agar. The tubes were vortexed and incubated at 100°C for 20 minutes. Next, 900 µl of distilled water was added and mixed well until the solution was homogeneous. The solution was centrifuged at 12,000 rpm for 10 minutes. The supernatant that contained the genomic DNA was transferred into new Eppendorf tubes, ready for PCR.

The *E.coli* isolates were screened for the following virulence genes: *stx1*, *stx2*, *hlyA*, *cnf*, *sfa/foc*, *afaI*, *papC*, and *afaC*, using conventional PCR, to confirm the identification of *E.coli* isolates on the previously extracted DNA samples, using a master mix (Bioneer, Korea) and a specific set of oligonucleotide primers (Bioneer, Korea), which is illustrated in Table 1. The PCR reaction consisted of: the Master Mix of 5 µl, 1 µl Forward Primer (Bioneer, Korea), 1 µl Reverse Primer (Bioneer, Korea), and 5 µl DNA

Templates. The final volumes of the reaction were adjusted to 20 µl by adding 8 µl of nuclease-free water. The PCR amplification process was accomplished by using a Thermocycler (*Esco*, Singapore), with cycling conditions consisting of initial denaturation at 94°C for two minutes, followed by 35 cycles of amplification (denaturation at 94°C for 30 seconds, annealing for 30 seconds, extension at 72°C for one second, and final elongation at 72°C for seven minutes). The analysis of the PCR products was performed in 2% agarose gel electrophoresis. A 100-bp DNA ladder (Bioneer, Korea) was used as a molecular weight marker and the gels were stained with ethidium bromide, examined, and photographed under ultraviolet (UV) illumination (E-graph – ATTO/Japan). Fragment sizes of approximately 180 bp, 255 bp, 565 bp, 839 bp, 410 bp, 750 bp, 328 bp, and 672 bp, were verified as positive for *stx1*, *stx2*, *hly*, *cnf2*, *sfa/foc*, *afaI*, *papC*, and *afaC* genes, respectively.

Table 1: List of primers, annealing temperatures, and predicted sizes used for the detection of virulence genes of *E. coli* isolates

| Target gene | Primers | size of PCR products (bp) | Annealing temperature | Reference |
|-------------|--|---------------------------|-----------------------|-----------|
| stx1 | ATAAATCGCCTATCGTTGACTAC AGAACGCCCACTGAGATCATC | 180 bp | 60°C | 13 |
| stx2 | GGCACTGTCTGAACTGCTCC TCGCCAGTTATCTGACATTCTG | 255 bp | 60°C | 13 |
| hly | F-AGATTCTTGGGCATGTATCCT R- TTGCTTTGCAGACTGTAGTGT | 565 bp | 55 °C | 14 |
| cnf2 | GTGAGGCTCAACGAGATTATGCACTG CCACGCTTCTTCTTCAGTTGTTCCCTC | 839 bp | 65 °C | 15 |
| sfa/foc | F:CTCCGGAGAACTGGGTGCATCTTAC R:CGGAGGAGTAATTACAAACCTGGCA | 410 bp | 58 °C | 16,17 |
| afaI | F-GCTGGGCAGCAAAGTATACTCTC R-CATCAAGCTGTTTGTTCGTCGCCCG | 750 bp | 58 °C | 16 |
| papC | GACGGCTGTACTGCAGGGTGTGGCG ATATCCTTTCTGCAGGGATGCAATA | 328 bp | 63 °C | 18 |
| afaC | CGGCTTTTCTGCTGAACTGGCAGGC CCGTCAGCCCCACGGCAGACC | 672bp | 65 °C | 19 |

Statistical analysis

To demonstrate any association between the results, the exact Fisher test and Pearson's chi-squared test, with Yates correction, were used, with the limit of significance being 5%. Statistical analysis was performed using the Statistical Package for the Social Sciences SPSS software version 11.5.

Ethical responsibilities

Protection of human and animal subjects: The authors declare that the procedures followed were in accordance with the Animal Welfare Regulations and Ethics.

3. RESULTS AND DISCUSSION

Prevalence and detection of *E. coli* in rectal swabs collected from calves

Results in Table 2 show the bacterial isolates from the examined rectal swabs of diarrheic and non-diarrheagenic calves. In this Table, a total of 150 rectal swabs were collected from calves (75 diarrheagenic and 75 non-diarrheagenic calves). The samples were cultured on specific and selective media for isolation of *E. coli* and subjected to biochemical tests and the results were confirmed by using the API-20E system. Gram-negative rods were detected by Gram staining, and the isolates produced colonies with a black metallic sheen on the EMB agar and a pink appearance on the MacConkey agar. Therefore, on the basis of bacteriological, biochemical, and API-20E system tests, the *E. coli* was isolated from 26 out of 75 (34.7%) diarrheagenic calves and from 15 out of 75 (20%) non-diarrheagenic calves, with a total percentage of 27.4% (41/150). Additionally, a total of 34 (82.9%) isolates were obtained from the PCR-positive samples and were found to be positive for at least one of the virulence genes as revealed in

Table 2. The results of the conventional PCR analysis are shown in Figures 1(a,b,c,d,e,f,g and h).

On the other hand, Table 3 reveals the prevalence of virulence gene distribution among diarrheagenic and non-diarrheagenic calves. In this Table, the *stx1*, *hlyA*, and *stx2* genes showed a higher incidence of distribution in both diarrheagenic and non-diarrheagenic calves in a percentage rate of 69.6%, 65.2%, 56.5% and 63.6%, 63.6%, 45.5%, respectively. Moreover, Table 4 shows the virulence gene arrangements in each *E.coli* isolate. It shows that eight different virulence profiles were established in the present study. Most of the isolates analyzed have at least two or three gene arrangements, and only four isolates show a combination of four genes with a profile of *stx1*, *stx2*, *hlyA*, and *afal*.

Table (2): Prevalence of *E. coli* among diarrheagenic and non-diarrheagenic calves based on the API-20E system and PCR detection results.

| Type of sample | <i>E.coli</i> Isolation based on API 20 E system | | <i>E.coli</i> Isolation based on PCR results | |
|-------------------|--|----------------------------|--|----------------------------|
| | <i>E.coli</i> Isolation no. | <i>E.coli</i> isolation(%) | <i>E.coli</i> Isolation no. | <i>E.coli</i> isolation(%) |
| Diarrheagenic | 26/75 | 34.7 | 23/26 | 88.5% |
| non-diarrheagenic | 15/75 | 20 | 11/15 | 73.3 |
| Total | 41/150 | 27.3 | 34/41 | 82.9 |
| P-value | *0.0919 | | **0.0131 | |
| P-value | ***0.0580 | | | |

*For all diarrheagenic and non-diarrheagenic samples tested based on API-20E system the differences were not significant ($p > 0.05$)

**For all diarrheagenic and non-diarrheagenic samples tested based on PCR results the differences were significant ($p < 0.05$)

***For all diarrheagenic and non-diarrheagenic samples tested based on API-20E system and PCR results the differences were significant ($p < 0.05$)

Table 3: Prevalence of virulence gene distribution among diarrheagenic and non-diarrheagenic calves

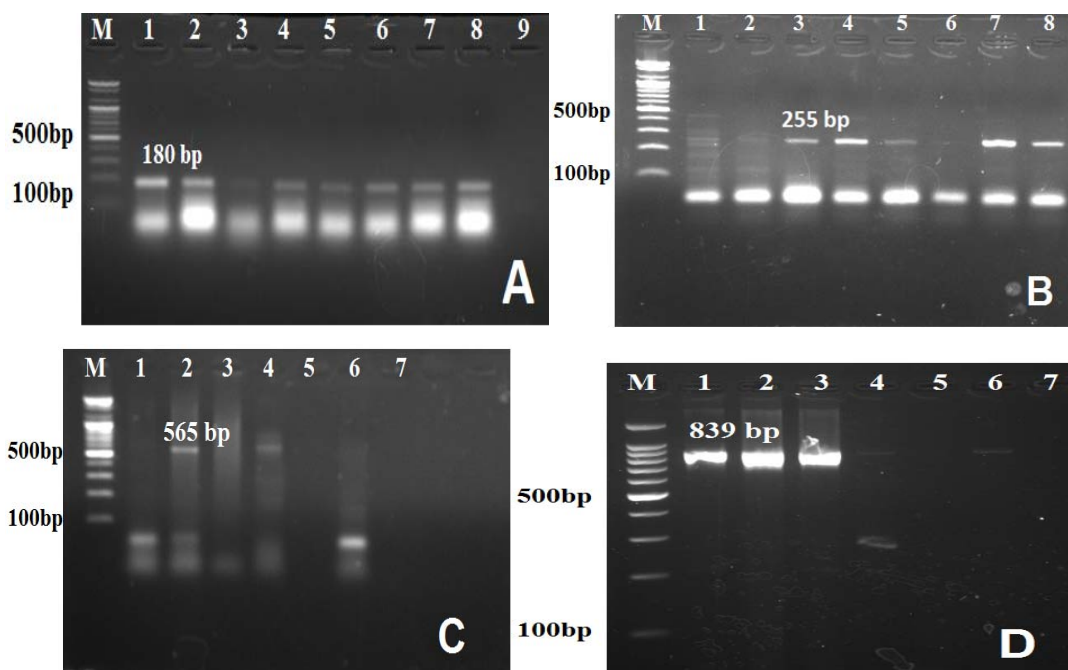
| Virulence gene | Diarrheagenic calves Isolates 23 | Non-Diarrheagenic calves Isolates 11 | Total 34 | P-value |
|----------------|-------------------------------------|---|-------------|---------|
| Stx1 | 16 (69.6) | 7(63.6) | 23(7.82) | 0.0392 |

| | | | | |
|---------|----------|---------|----------|--------|
| Stx2 | 13(56.5) | 5(45.5) | 18(52.9) | 0.0526 |
| hlyA | 15(65.2) | 7(63.6) | 22(64.7) | 0.0684 |
| Cnf | 5(21.7) | 3(27.3) | 8(32.5) | 0.7090 |
| Sfa/foc | 4(17.4) | 2(18.2) | 6(17.6) | 0.6728 |
| afaI | 3(13.0) | 1(9.1) | 4(11.8) | 0.6135 |
| PapC | 3(13.0) | 3(27.3) | 6(17.6) | 1.0000 |
| afaC | 2(8.7) | 1(9.1) | 3(8.8) | 1.0000 |

P-value: calculated by exact Fisher's test

Table 4: Virulence gene profiles present in *E. coli* strains isolated from diarrheic calves

| No .of genes | Virulence profiles | Number of isolates | | Total |
|--------------|------------------------|----------------------|--------------------------|-------|
| | | Diarrheagenic calves | Non-Diarrheagenic calves | |
| 1 | Stx1, stx2 | 6 | 3 | 9 |
| 2 | Stx1, hlyA | 3 | 2 | 5 |
| 2 | hlyA, Cnf2 | 2 | 2 | 4 |
| 3 | Stx1, Stx2, hlyA, | 4 | 1 | 5 |
| 3 | hlyA, Cnf2, PapC | 1 | 0 | 1 |
| 3 | hlyA, Sfa/foc, afaC | 2 | 1 | 3 |
| 3 | Cnf2, Sfa/foc, PapC | 2 | 1 | 3 |
| 4 | Stx1, Stx2, hlyA, afaI | 3 | 1 | 4 |
| | Total | 23 | 11 | 34 |



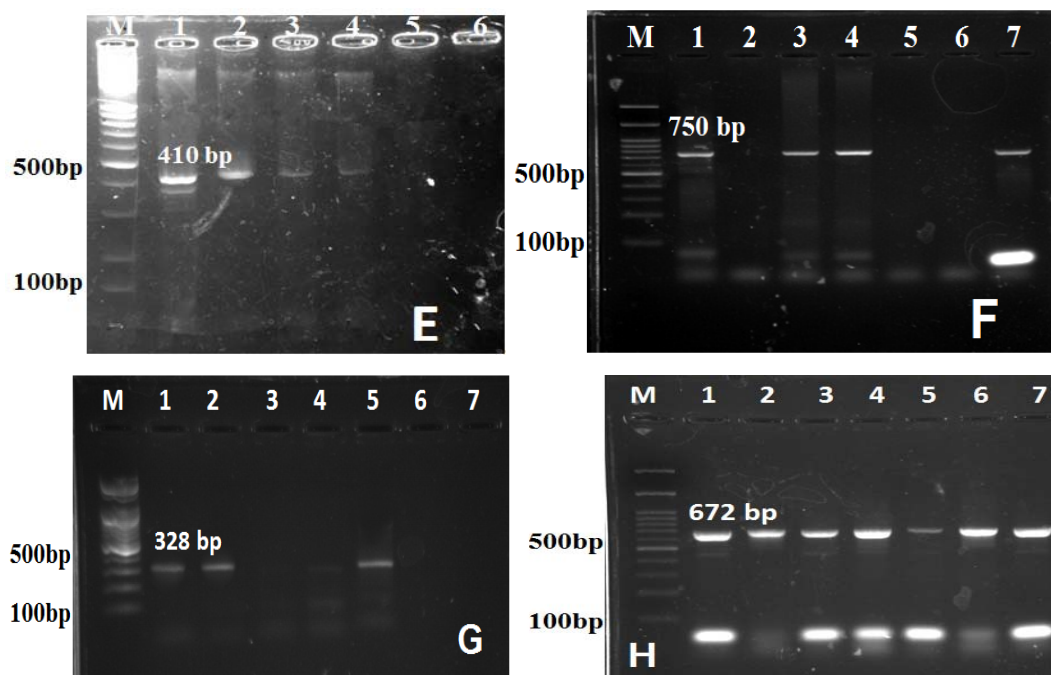


Figure 1. Agarose gel electrophoresis reveals the PCR products of : (A) Lane M: 100 bp DNA Ladder. Lanes 1- 8: PCR Products of 180 bp *stx1* gene. (B) Lane M: 100 bp DNA Ladder. Lanes 3,4,5,7 and 8: PCR Products of 255 bp *stx2* gene. (C) Lane M: 100 bp DNA Ladder. Lanes (2 and 4) PCR Products of 565 bp *hly* gene. (D) Lane M: 100 bp DNA Ladder. Lanes(1,2,3,4 and 6) PCR Products of 839 bp *cnf 2* gene.(E) Lane M: 100 bp DNA Ladder. Lanes (1-4) PCR Products of 410 bp *Sfa/foc* gene.(F) Lane M: 100 bp DNA Ladder. Lanes(1,3,4 and 7) PCR Products of 750 bp *afaI* gene.(G) Lane M: 100 bp DNA Ladder. Lanes (1,2 and 5) PCR Products of 328 bp *papC* gene.(H) Lane M: 100 bp DNA Ladder. Lanes (1-7) PCR Products of 672 bp *afaC* gene. All samples were run with control negative

The economy of many developing countries is dependent on the production of livestock animals, which continues to make important contributions to the local food supply. In recent years, animals have been increasingly raised on farms and have spread, particularly in southern Iraq. As a result, several livestock diseases have occurred. Diarrhea in calves, caused by *E. coli*, is one of these diseases, which often occurs as an outbreak and is still one of the most common causes of death in newly born calves (20,21,22,23). Additionally, the findings of the current study are similar to those found in the previous data, which has found that *E. coli* is the most common bacteria isolated from the fecal samples of diarrheic and healthy calves (24). Besides, the presence of pathogenic *E. coli* strains in diarrheic animals is of greater

significance because of the high possibility of zoonotic transmission following widespread environmental contamination with these organisms (25,26,27).

In the current study, two diagnostic tools were required API- 20E system and PCR. On the basis of the API -20E system, the prevalence of *E. coli* infection in the examined calves was 27.3%, distributed as 34.7% in calves with diarrhea and 20% in non-diarrheagenic calves. According to the Table 2 there was no significant difference ($p > 0.05$) between diarrheagenic and non-diarrheagenic calves based on the API-20E system results. On the other hand, the PCR technique was also used to confirm the *E. coli* infection using eight virulence genes, which included *stx1*, *stx2*, *hlyA*, *cnf*, *sfa/foc*, *afaI*, *papC*, and *afaC*. The prevalence of *E. coli* infection in the examined calves was 82.9% (88.5% in calves with diarrhea and 73.3% in non-diarrheagenic calves). With regard to the PCR results there was a significant difference ($p < 0.05$) between diarrheagenic and non-diarrheagenic calves. The explanation of this result is attributed to the fact that the PCR test is more current and specific to detect the pathogenic *E. coli* from clinical and random samples. Moreover, in the current study, seven *E. coli* isolates that were isolated from diarrheic and non-diarrheic samples have no virulence factors. The possible explanation for this finding is the fact that maybe these strains are non-pathogenic *E. coli* and the animals had diarrhea due to some other infectious agents (28).

On the basis of the PCR results, eight virulence genes were used to detect the presence of pathogenic *E.coli* (*stx1*, *stx2*, *hlyA*, *cnf*, *sfa/foc*, *afaI*, *papC*, and *afaC*). Four of them encoded the toxic factors (*stx1*, *stx2*, *hlyA*, and *cnf*) and the other four encoded the adhesion factors (*sfa/foc*, *afaI*, *papC*, and *afaC*). The prevalence of toxic virulence genes was 23(7.82), 18(52.9), 22(64.7), and 8(32.5) for *stx1*, *stx2*, *hlyA*, and *cnf* genes, respectively. Many previous

studies identified that the *stx1* and *stx2* genes were the most toxic genes detected in the *E.coli* from colibacillosis. Studies by (29) were designed to determine the prevalence of STEC and STEC/O157:H7 in healthy sheep.

According to (29), the prevalence of *stx1*, *stx2*, and *cnf1* toxic genes in the STEC isolates was higher: 52.2% (47/90), 33.3% (30/90), and 32.2% (29/90), respectively. Similarly, (30,31) observed that 46.5% (20/43) and 55% (213/384) of the STEC isolates carried *stx1*, even as (32) revealed that 17% of all diarrheic and healthy calves of Australian herds were infected by *E. coli*, and 15.2% of the *E. coli* strains harbored the shiga toxin genes including *stx1*, *stx2*, *ehly*, and *eae* genes.

The presence of a hemolysin-encoding *hlyA* gene, from the Shiga toxin-producing *Escherichia coli* (STEC) was detected by PCR in each of the 41 strains tested. Fifteen (65.2%) and seven (63.6%) of the *E.coli* isolates from healthy and diarrheic calves, respectively, had the *hlyA* gene. This finding is in contrast to a majority of previous epidemiological studies by (33) who developed a multiplex PCR assay for the rapid detection of virulence factor genes in the Enterohemorrhagic *Escherichia coli* (EHEC) in the fecal samples derived from healthy and clinically affected cattle, sheep, pigs, and goats. Hemolysin genes play a critical role in *E.coli* pathogenicity, as they are considered the main factors responsible for cell detachment, and have damaging effects on the epithelial integrity (34,35). Moreover *E. coli* produce several other hemolysin genes. Enterohaemolysin of the enterohemorrhagic *E. coli* (EHEC), designated *Ehx* or *hly* EHEC, is very similar to *hlyA* with regard to its genetic organization and calcium ion dependency, although it is cell-bound (36).

Alternatively, the current results are also consistent with the results found in the study of (37) and (38) where their *E.coli* isolates were PCR-positive for

the *hlyA* Hemolysin gene. Similarly, a high occurrence of the *hlyA* gene with *stx1* and/or *stx2* was also detected in the study of (39). The possible explanation for the occurrence of a particular gene combination is the fact that a particular gene is carried by a plasmid and has the ability to transfer among the related bacteria (39). Also, in the current study, the prevalence of the *cnf* gene was low and this finding agreed with the previous studies (40).

According to (40) the distribution of the *cnf* gene in the *E.coli* isolates from diarrheic and healthy animals, and humans, was also detected, but was rare, and the occurrence of the *cnf* gene was not clear, as this gene contributed more to the uropathogenic *Escherichia coli* (UPEC) outbreaks in humans. Hence, the most accepted hypothesis for the existence of the *cnf* gene, which was more related to the necrotoxic *E.coli* (NTEC) strains, was that it occurred as an extraintestinal infection from UPEC and also confirmed the significance of the *cnf* gene isolated from diarrheic and healthy animals as a potential threat to human health (29).

On the other hand, four fimbriae adhesion genes were also detected. The finding of these fimbriae factors in a diarrheal condition is rare, but they are indicators to extraintestinal pathogenic *E.coli* infection (41,42). Moreover, (43,44) they finding the significant association between the occurrence of fimbriae genes detection with strains that produced cytotoxic necrotizing factor that isolated from calves with septicemia or diarrhea. In addition, the Fisher's exact test has also been applied to determine if there is a significant difference between a particular gene occurrence and the calf diarrhea, Table 3. According to Table 3 there is a significant difference ($p = 0.0392$) in the case of the *stx1* gene and no statistically significant difference ($p > 0.05$) in the case of *stx2*, *hlyA*, *cnf*, *sfa/foc*, *afaI*, *papC*, and *afaC* genes. This result indicates that the *stx1* gene is related more to the *E.coli* isolated from diarrheagenic than non-diarrheagenic calves and this finding agrees with the

finding of (20,45), who detected that the *stx* gene in healthy in diarrheagenic calves

The current study has also revealed eight different combinations of the virulence-associated genes in each *E.coli* isolate. Most of these isolates have at least two or three gene arrangements, and only four isolates show a combination of four genes with profiles of *stx1*, *stx2*, *hlyA*, and *afaI*. However, many researchers have attempted to correlate the existence of recognized virulence profile factors with a disease or severity of a disease and concluded that no single factor is responsible for the virulence of STEC(46,47,78). These variations in gene virulence and severity may contribute to the overuse and misuse of antibiotics in intensive animal production as well as in the crowded and stressful conditions of factory farms. Moreover, the geographical differences and climate conditions also play an important role and influence the shedding of STEC in calves (49,50).

4. CONCLUSION

It is concluded that *E. coli* isolates from healthy and diarrheic calves carry various virulence genes, of which the most frequent are *stx2*, and *hlyA*, which are present in a higher percentage in isolates from both diarrheic and non-diarrheic calves. Additionally *Stx1* was isolated more in diarrheagenic than non-diarrheagenic calves.

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34. Secretion of Alpha-Hemolysin by *Escherichia coli* Disrupts Tight Junctions in Ulcerative Colitis Patients Hengameh Chloé Mirsepasi-Lauridsen, PhD^{1,2,6}, Zhengyu Du, MSc^{3,6}, Carsten Struve, PhD¹, Godefroid Charbon, PhD², Jurgen Karczewski, PhD³, Karen Angeliki Krogfelt, PhD¹, Andreas Munk Petersen, PhD^{1,4,5} and Jerry M Wells, PhD³. *Clinical and Translational Gastroenterology* (2016) 7, e149; doi:10.1038/ctg.2016.3

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