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Prevalence and Molecular Detection of Pks genotoxin Island in clinical *E. coli isolates* from Bovine and Human sources in Basra Governorate, Iraq

Article Info.

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Abstract

Escherichia coli is a major pathogen that possesses several virulence characteristics. The pks Island of E. coli, which codes the genotoxin called colibactin. The study aimed to investigate the distribution of Pks island genes in Escherichia coli isolated from both human and bovine sources in Basrah governorate. E.coli isolates are identified according to their morphological features on medium MacConkey agar, EMB agar, and chrome agar. E.coli was confirmed by the uidA as a species-specific gene by conventional PCR. The analysis revealed a 52.5% overall isolation rate. Specifically, the isolation rates were 50% (50/100) of human diarrhea, 50% (25/50) of animal diarrhea, and 50% (25/50) of bovine mastitis. The uidA gene PCR results of 60 isolates revealed that a 100% were E coli, which showed the band size of 162bp for the gene. This study was carried out to detect clbA, clbB, and clbQ genes in all 60 *E.coli* isolates using Specific primers for these genes. The outcomes demonstrated that two (10%) of the human diarrhea isolates tested positive for the clbA gene, while only one (5%) of the same samples tested positive for the clbB and clbQ genes. In contrast, one (5%) of the animal diarrhea samples tested positive for the clbA gene and negative for the clbB and clbQ genes

Keywords: Escherichia coli, Mastitis, Human and bovine diarrhea, clbA, clbB, and clbQ genes.

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Introduction

Escherichia coli is a gram-negative, facultative anaerobic, catalase-positive, oxidase-negative bacterium that ferments lactose and glucose. It does not generate spores. The majority of E. coli species are flagellated, motile, peritrichous members of the Enterobacteriaceae family (1). It is the primary resident of the large intestine in both humans and animals, and it is frequently utilized as a critical indicator of fecal pollution in water and environmental sources. (2). *E.coli is* an opportunistic pathogen that causes diarrhea in humans and animals, and it also causes urogenital tract infections in domestic animals and coliform mastitis in dairy cows (3, 4). In dairy cows, *Escherichia coli* also causes infection and inflammation of the mammary gland, primarily during the early stages, with noteworthy local and sometimes severe systemic clinical symptoms during lactation and surrounding parturition (5, 6). This so-called environmental kind of mastitis may have an effect on the productivity of high-producing cows in dairy herds. In the worst cases, it might even cause numerous deaths every year (7). *E. coli* enters the udder through the teat canal, grows there, and triggers an instant inflammatory response that leads to the emergence of more neutrophils [8]. Because it stops infections from leaving and proliferating, this neutrophil filtration is one of the initial stages of the inflammatory response (9, 10). Different phylogenetic groups (A, B1, B2, C, D, E, and F) are used to categorize *E. coli* strains. *Escherichia coli* is one of the most common bacteria-causing pathogens; it has several virulence factors. The *clb A-S* genes, which code for the secondary metabolite colibactin, are located on the 54-kb pathogenicity pks Island of *E. coli.* (11-13). Colibactin is a genotoxin that increases colorectal cancer and makes extra-intestinal pathogenic *Escherichia coli* more virulent (14). DNA damage and genetic instability are caused by *E.coli* strains that possess *pks islands* (15). According to epidemiological research, in wealthy countries, *pks+ E. coli* is increasingly prevalent in the human microbiome (16). The *pks Island* is home to up to 40% of B2 *E. coli* strains, and the population of *E. coli* is moving from phylogenetic group A to the more common group B2 (17). *PKS Island* carriage may provide a fitness advantage for long-term persistence in the human gut. Colibactin is another virulence factor of extra-intestinal pathogenic *E. coli* since its production increases lymphopenia and mortality in mice and newborn rats.

Because its synthesis exacerbates lymphopenia and death in mouse and neonatal rat systemic infection models, colibactin is also a virulence determinant of extra-intestinal pathogenic *E. coli* (18). DNA double-strand breaks are induced both in vitro and in vivo when mammalian cells are exposed to live *PKS* bacteria. Tumorigenesis is eventually fueled by chromosomal instability, gene mutation, and early senescence brought on by this DNA damage. The systemic infection module for mice and newborn rats (19). *The pks Island* is primarily found in the phylogenetic B2 strain of *E. coli*, and these strains have become much more common in industrialized nations (20). It's interesting to note that roughly 20% of healthy people, 40% of patients with inflammatory bowel disease, and 60% of patients with familial adenomatous polyposis or colorectal cancer have *E. coli* strains containing the *Pks Island*. Cows 3%-10% (21).

The study aims to investigate the distribution of *Pks* island genes in *Escherichia coli* isolated from both human and bovine sources in Basrah governorate.

Material and Method

Specimen collection

Between September 2024 and December 2025, 200 samples were gathered from various locations within the Barah governorate. 100 people with diarrhea, 50 cows with diarrhea, and 50 people with milk mastitis made up these samples.

Bacterial cultures identification

All types of samples are cultivated on MacConkey Agar, Eosin-methyl blue agar, and chrome agar at 37 °C for a 24-hour incubation period (22). Whereas milk mastitis, the primary inoculated on BHI broth medium to activate the samples, and then cultured on other media (23). All isolates are examined for the color, shape, size, and Gram stain reaction (24). *E.coli* isolates are identified according to their morphological features on medium (MacConkey agar, EMB agar, and chrome agar), and Gram stain (25). The *UidA* gene was utilized to identify isolated E. coli using polymerase chain reaction (PCR).

DNA extraction

The following technique was followed in order to extract the genomic DNA using the boiling method: From the *E.coli* selective medium, pure colonies were selected and cultivated in 5 milliliters of nutritional broth. Following an overnight incubation period, the tubes were centrifuged at 4000 rpm for five minutes, the supernatants were discarded, and then 100µl of free nuclease water was added to the tubes to dissolve the pellet. The suspensions were then transferred to a 1.5 ml Eppendorf and placed in a water bath at 100°C for ten minutes. Each Eppendorf was filled with 600 µl of free nuclease water and centrifuged at 12000 rpm for 10 minutes. The supernatant, which stands for the pure the supernatant, which represents the pure DNA, was taken carefully and transferred to another Eppendorf. Purity and quantity of the DNA were tested by the Nano Drop device, and then stained; the concentration ranged from (1.08 to 2.1) ng/µl. In addition, the DNA bands are observed in the electrophoresis (26). The product was stored at -20 until further examination. The pure DNA is represented by the supernatant, which was carefully collected and moved to another Eppendorf.

The Nano Drop instrument was used to evaluate the quantity and purity of the DNA before it was dyed; the concentration ranged from 1.08 to 2.1 ng/µl. Furthermore, the electrophoresis shows the DNA bands (26). The product was kept at -20 till it was examined further.

PCR amplification of the *UidA* gene and *clb* genes

Amplification of the DNA was done using the PCR for the detection of *uidA, E.coli* was confirmed by the *uidA* as a species-specific gene. The specific pair of primers' sequence was employed (see Table 1). PCR reactions are used to detect bacteria that possess the *clb* genes. The PCR reactions were conducted in a 20µl volume and contained 5µl of DNA template, 1µl of each primer (10 pmol), and 10µl of master mix (Promega, USA, Solarbio, China, and Bioneer, Korea). The reaction volume was increased to 20µl using nuclease-free water (Promega, USA). Agarose gel electrophoresis was performed (2 %) of agarose powder, 50 ml of TBE buffer, 5 ul of safety dye, Solarbio, China, and 1.5 ethidium bromide, Promega) with a 100bp DNA ladder (Promega, USA) to detect bands under UV trans illuminator (27).

Table 1: primers used for *UidA* and *Clb gene* detection

Name of primers	Sequence of primers	Product size pb	Annealing temperature.	Ref.
UidA	F: TGGTAATTACCGACGAAAACGGC R: ACGCGTGGTTACAGTCTTGCG	162pb	58	28
ClbA	F-AAGCCGTATCCTGCTCAAAA R-GCTTCTTTGAGCGTCCACA	342pb	56	29
ClbB	F-GCGCATCCTCAAGAGTAAATA R-GCGCTCTATGCTCATCAACC	283pb	57	29
ClbQ	F-GCAC GATCGGACAGGTTAAT R-TAGTCTCGGAGGGATCATGG	308pb	57	29

Table 2: The PCR Amplification Conditions of the gene (*UidA*)

Stage	Steps	Temperature (C°)	Time (min)	No. of cycle
I.	Initial denaturation	95	3 min	1
II.	Denaturation	95	30 sec	35
	Annealing	58	30 sec	
	Extension	72	1 min	
III.	Final extension	72	10min	1

Table 3: The PCR Amplification Conditions of the *clb* genes

Stage	Steps	Temperature (C°)	Time (min)	No. of cycle
I.	Initial denaturation	94	4 min	1
II.	Denaturation	94	30 sec	30
	Annealing	Table (1)	30 sec	
	Extension	72	1 min	
III.	Final extension	72	4 min	1

Results

E. coli isolation and identification

A total of 200 clinical samples were screened for *E. coli* using differential media, including MacConkey, EMB, and Hichrom agar. The analysis revealed a 52.5% overall isolation rate. Specifically, the isolation rates were 50% (50/100) of human diarrhea, 50% (25/50) of animal diarrhea, and 50% (25/50) of bovine mastitis (Table 4).

Table 4: *E. coli* isolation rates in different sources

Source of the samples	Number of samples	Number of isolates	Percentage of *E.coli*
Humans diarrhea	100	55	55 %
Animals' diarrhea	50	25	50 %
Bovine mastitis	50	25	50 %
Total	200	105	52.5 %

After a 24-hour aerobic incubation period at 37°C, the initial culture of the samples on MacConkey agar revealed bacterial colony formation. The growing colonies were medium in size, had a consistent circular form, and were pink due to their capacity to digest lactose (Figure 1A). The characteristic pink colonies were re-cultured on eosin-methylene blue agar (EMB agar) in order to verify the diagnostic feature. Following incubation, the bacteria showed typical development in the form of colonies with a green metallic sheen, which is highly characteristic of E. coli bacterium that results from intense lactose fermentation (Figure 1B). Hichrome agar, a differential selective medium, was used for the final confirmation of the diagnosis. On this medium, bacteria grew and produced a blue-green color (Figure 1C).

Microscopic Examination

Gram staining was performed on all 105 isolates, which revealed that all isolates were Gram-negative, rod-shaped organisms (Figure 1D).

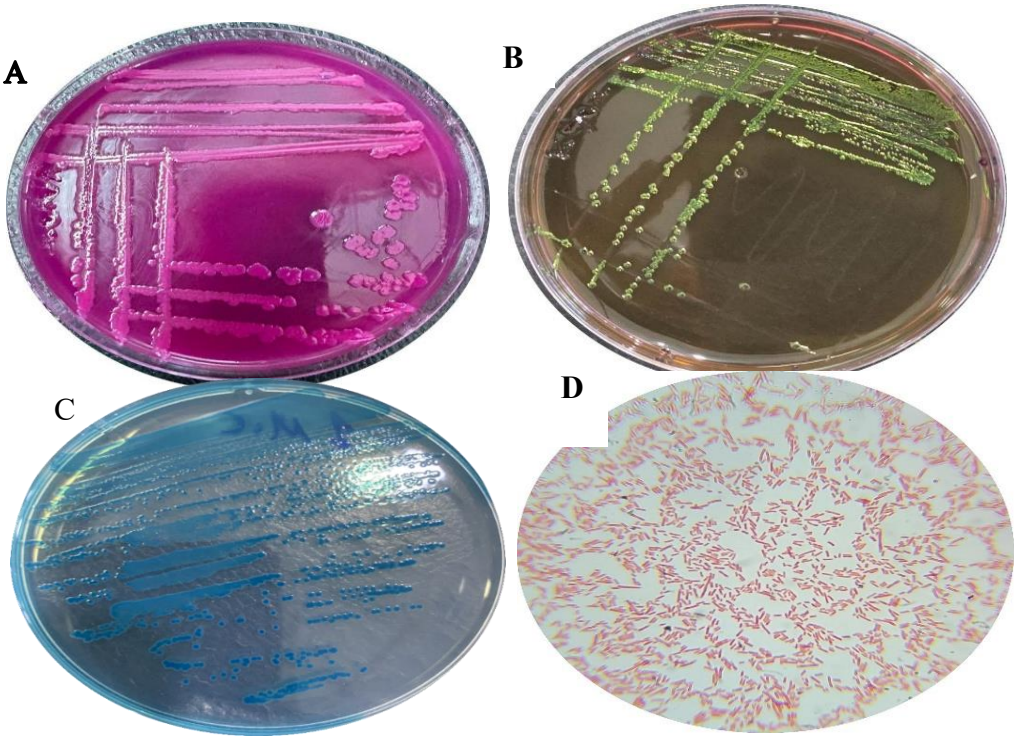

Figure 1: Primary *E.coli Identification.* A*:* MacConkey agar colonies *of E.coli* that are reddish pink . B: *E.coli* colonies on EMB, displaying dark centers with a characteristic metallic greenish appearance. C: E.coli on Hichrome agar, producing blue-green color due to the interaction of specific bacterial enzymes (such as β-glucuronidase) with the chromogenic substrate. D: Gram stain *E. coli* under light microscope (1000X).

Molecular identification of *E.coli UidA* gene by PCR:

The *uidA* gene PCR results of 60 isolates revealed that a 100% were *E coli,* which showed the band size of 162bp for the gene. (Figure 5) shows a shine band on gel electrophoresis of positive isolates compared with a 100bp ladder (Table 7).

Table 7: Prevalence of uidA and Pks island genes according to the source of samples

Source of samples	*UidA gene*	*clbA (%)*gene	*clbB* (%)gene	*clbQ (%)*gene
Humans diarrhea	20	2 (10%)	1 (5%)	1 (5%)
Animals diarrhea	20	1 (5%)	0%	0%
bovine mastitis	20	0%	0%	0%
Total	60	3 (5%)	1 (1.6%)	1 (1.6%)

Detection of Pks island genes by PCR:

This study was carried out to detect *clbA, clbB, and clbQ* genes in all 60 *E.coli isolates* using Specific primers for these genes. The outcomes demonstrated that two (10%) of the human diarrhea isolates tested positive for the *clbA gene*, while only one (5%) of the same samples tested positive for the *clbB* and *clbQ* genes. In contrast, one (5%) of the animal diarrhea samples tested positive for the *clbA* gene and negative for the *clbB* and *clbQ genes*. Consequently, the bovine mastitis isolates showed negative results for *Pks island* genes. The product of PCR was detected by using gel electrophoresis, as shown in Figures 2, 3, and 4.

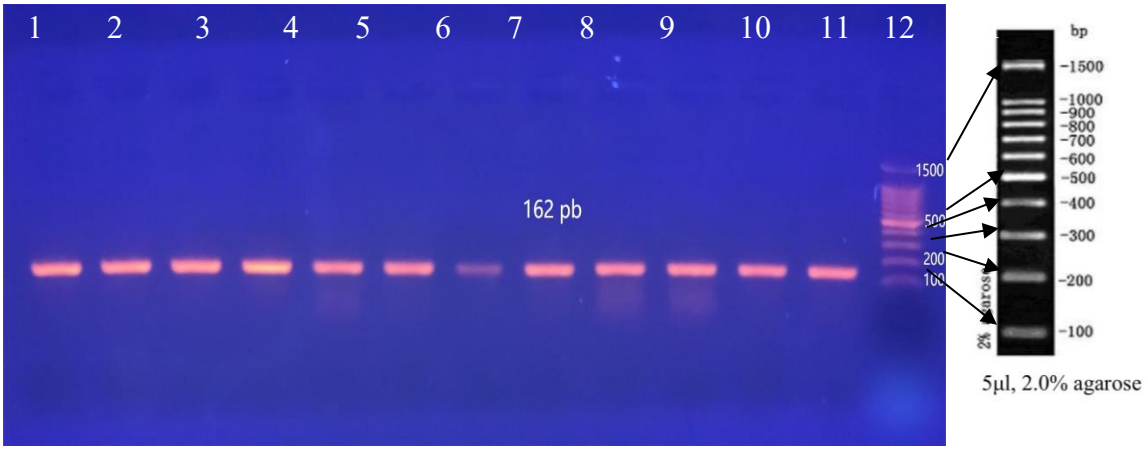

Figure 2: The PCR product used to identify the *UidA gene* (162bp) in isolates of E.coli. Lane M: marker, (100bp); Lanes 1-12: positive sample.

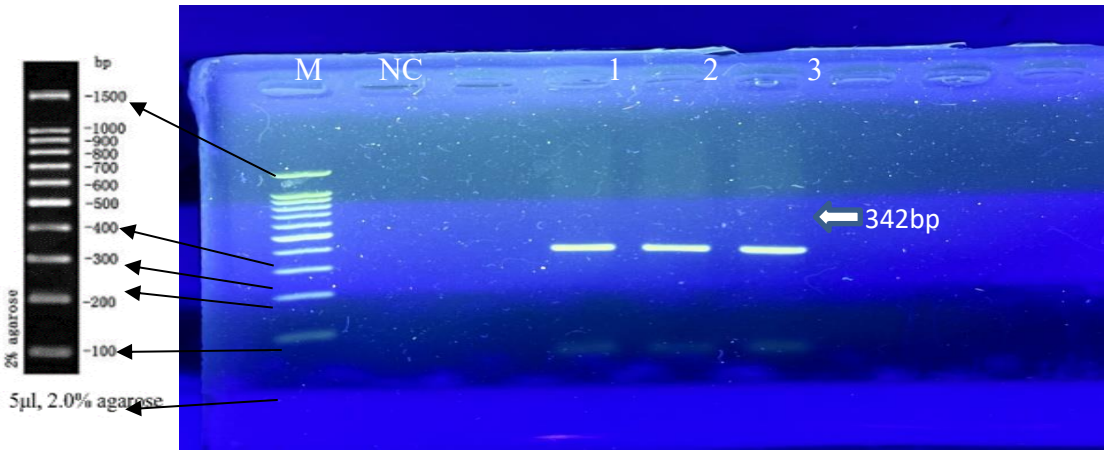

Figure 3:The PCR product used to identify the *clbA gene* (342 bp) in isolates of *E.coli*. Lane M: marker, (100bp); Lanes 1-3: positive sample.

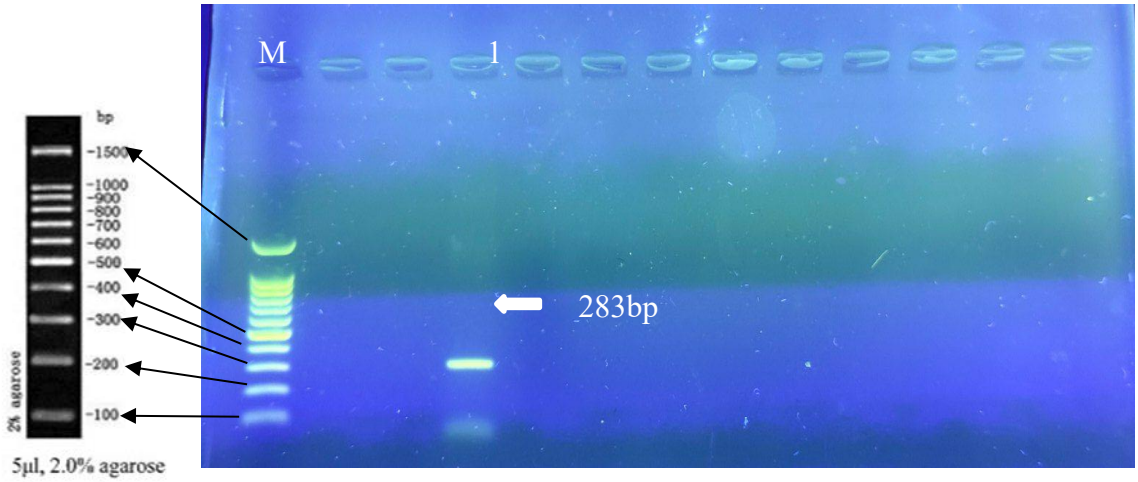

Figure 4:The PCR product used to identify the *clbB gene* (283 bp) in isolates of *E.coli*. Lane 1: positive sample, Lane M: marker (100bp)

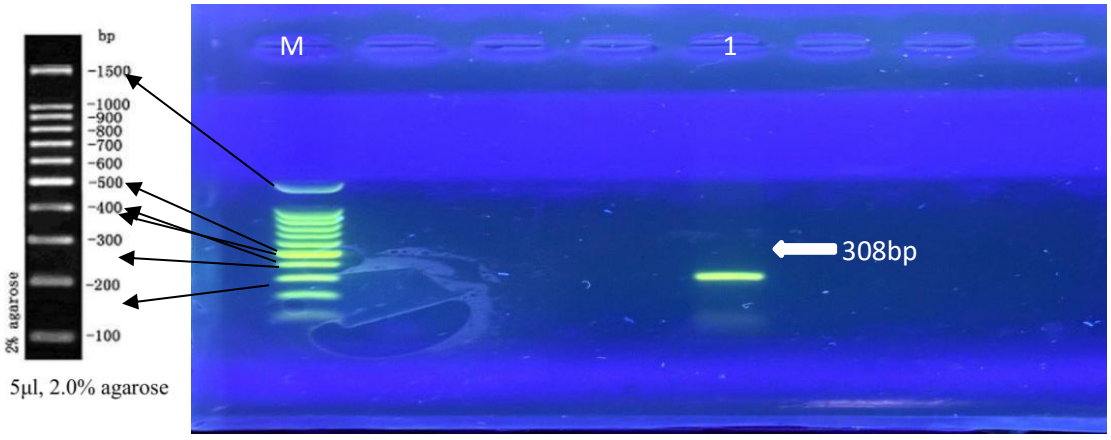

Figure 5: The PCR product used to identify the (308 bp) *clbQ* gene in isolates of *E. coli*. Lane 1: positive sample; Lane M: marker (100 bp).

Discussion

The presence of *pks+ Escherichia coli* across human and animal populations is a significant public health concern due to its ability to produce colibactin, a genotoxin linked directly to DNA damage and the development of colorectal cancer (30). Our study focused on investigating the *pks Island genes* in *Escherichia coli* isolated from both human and bovine sources in Basrah governorate. To achieve these goals, the *E.coli* was primarily isolated from three sources: diarrhea in humans, animal diarrhea, and bovine mastitis. The results revealed that the largest isolation rate of *E.coli* was from human diarrhea, 55%, where the isolation rate reached 50% in animal diarrhea and 50% in bovine mastitis. This study's *E.coli* isolation rate from milk is higher than previous research, which found that *E. coli* isolation rates from milk were 26.6% in Ethiopia and 18.5% in India (32). Those who isolate these germs with 8% disagree with these findings (31). The physical properties of *E.coli* isolates are used to identify them. When cultivated on MacConkey agar, the isolate showed up as brilliant pink colonies; on EMB media, the colonies had a green metallic shine. MacConkey agar's crystal violet and bile salts, which encourage the growth of Gram-negative bacteria while inhibiting the growth of Gram-positive bacteria, are responsible for these results. It was discovered that the bacterium fermented sugar (1). Eosin Methylene Blue (EMB), a differential medium for E. coli that was used to separate it from other Enterobacteriaceae members, revealed green metallic sheen colonies. This suggests that the colonies fermented lactose and glucose to create organic acids, which give the colonies a green metallic shine when eosin and methylene are present (2,4). *E. coli's* importance is concentrated on human public health and animals because of its multiple virulence traits that raise morbidity and mortality as well as its resistance to many antibiotics, which lowers treatment chances (5, 6). *E.coli* can spread from animals to people through consumer milk and its products, direct animal contact, and indirect environmental transfer (7). There is a connection between the *E. coli* that was identified in humans

and animals. The results of our investigation are in contrast to previous studies that reported recovering 4.7% and 5% of *E. coli* from dairy farms (8, 9). Cleaning the farm's floor, all used utensils, and providing safe water for dairy farms are essential to preventing *E. coli* from developing and multiplying among cows, which reduces the risk of bacterial contamination and illness (10). Several studies have shown that bedding, dung, and flies are important factors in the infection and spread of *E. coli* on dairy farms. Several studies have shown that flies, bedding, and dung are important factors in the spread of *E. coli* on dairy farms and the infection of dairy cows. That is not in agreement. However, the genetic study using the specific *uidA* in a PCR reaction eliminated the uncertainty in the diagnosis confirmation process (28). This process has been used in numerous investigations since it is faster and more reliable. As a result, a specific gene known as *uidA* has been essential to the effective identification of bacterial isolates; in many cases, specific primers were used to locate and identify the bacteria. Colibactin is a genotoxin that can damage host DNA and induce increased virulence and severe disease consequences. Enzymes encoded by the *Pks Island* produce it (11-13). Since colibactin was initially identified, many studies have been carried out to fully comprehend this bacterial genotoxin (14). The *Pks Island*-harboring *Escherichia coli* is intimately associated with bacteremia and human colorectal tumors (15). Previous studies have shown that the *pks Island* was mostly present in *E.coli* phylogenetic group B2 strains, which are mainly recognized as extra-intestinal pathogens (29). Recent findings showed that mice infected with isogenic colibactin-negative mutants had much greater survival rates than mice infected with colibactin-positive E. coli (21). Additional research has demonstrated that *pks-positive E. coli* infection induces cellular senescence and concurrently produces growth factors that promote tumor development (16, 17). The *Pks Island* encodes the enzymes needed to produce the genotoxin colibactin, which makes Escherichia coli strains more virulent and may cause colorectal cancer (18). *E.coli* strains obtained from individuals with extra-intestinal illnesses have been the focus of research on *Pks Island* (19, 20).

Conclusion

The study concludes that colibactin-producing *E.coli* (associated with clbA, B, Q) may play a specific role in intestinal pathogenesis rather than mammary infections, implying a difference in virulence mechanisms between diarrhea-associated and mastitis-associated *E.coli*.

Recognition

The authors thank the College of Veterinary Medicine at the University of Basrah for providing all the resources required to finish the experiment in their labs.

Conflicts of interest

The authors declare that there is no conflict of interest.

Ethical Clearance

This work is approved by The Research Ethical Committee

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انتشار جزيرة السموم الجينية Pks والكشف الجزيئي عنها في عزلات الإشريكية القولونية المعزولة من مصادر بقرية وبشرية في محافظة البصرة، العراق

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فرع الاحياء المجهرية، كلية الطب البيطري، جامعة البصرة ،البصرة ،العراق.

الخلاصة

تُعدّ الإشريكية القولونية من مسببات الأمراض الرئيسية التي تمتلك العديد من خصائص الضراوة. تحتوي هذه الإشريكية على جزيرة جينية تُسمى pks ، والتي تُشفّر السم الجيني المعروف باسم الكولييباكتين.هدفت هذه الدراسة إلى التحقق من توزيع جينات جزيرة pks في الإشريكية القولونية المعزولة من مصادر بشرية وحيوانية في محافظة البصرة. تمّ تحديد عزلات الإشريكية القولونية بناءً على خصائصها المورفولوجية على أوساط ماكونكي، وإي إم بي، وكروم. تمّ تأكيد هوية الإشريكية القولونية من خلال جين uidA كجين نوعي باستخدام تفاعل البوليميراز المتسلسل التقليدي .(PCR) كشف التحليل عن معدل عزل إجمالي قدره 52.5%. وبالتحديد، كانت معدلات العزل كالتالي: 50% (100/50) لحالات الإسهال البشري، و50% (50/25) لحالات الإسهال الحيواني، و50% (50/25) لحالات التهاب الضرع البقري. أظهرت نتائج تفاعل البوليميراز المتسلسل (PCR) لجين uidAفي 60 عزلة أن جميعها (100%) كانت من نوع الإشريكية القولونية، حيث بلغ حجم الشريط 162 زوجًا قاعديًا. أُجريت هذه الدراسة للكشف عن جينات clbA و clbB و clbQ في جميع عزلات الإشريكية القولونية الستين باستخدام بادئات نوعية لهذه الجينات. وأظهرت النتائج أن عزلتين (10%) من عزلات الإسهال البشري كانت إيجابية لجينclbA ، بينما كانت عزلة واحدة فقط (5%) من نفس العينات إيجابية لجيني clbB و .clbQ في المقابل، كانت عزلة واحدة (5%) من عينات الإسهال الحيواني إيجابية لجين clbA وسلبية لجيني clbB و.clbQ

الكلمات المفتاحية: الإشريشيا القولونية، التهاب الضرع، الإسهال البشري والبقري، جينات clbA و clbB و clbQ