Basrah Journal of Veterinary Research 2026; 25(2):162-178.

BASJVETRES

Print ISSN: 1813-8497
Online ISSN: 2410-8456
https://bjvr.uobasrah.edu.iq/

Investigation of Colibacillosis and Antibiotic Resistance Genes in Neonate Lambs in Basrah Governorate, Iraq

Article Info.

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Article History

Received: 6 February 2026
Revised: 19 March2026
Accepted: 26 March 2026
e Published: 30 June 2026
Article type: **Research Article**

https://doi.org/10.23975/bjvr.2026.169253.1282

Abstract

Colibacillosis is a common infectious bacterial disease affecting neonatal lambs and leading to substantial economic losses. This study aimed to diagnose *Escherichia coli* as a causative agent in diarrheic lambs and to assess its antibiotic resistance and associated resistance genes. A total of 30 faecal and blood samples were collected from diseased lambs with diarrheic symptoms. The faecal samples were initially subjected to the bacteriological test, disc diffusion test, and molecular method, while blood samples were haematologically analysed. The molecular test utilized 16srRNA with the specific primers targeted to the gene resistance for Polymerase chain reaction (PCR). All samples in the selective media were initially found to be positive for *E. coli*. According to the antibiotic-sensitivity results, the bacterial colonies were sensitive to all antibiotics, with inhibition zones showing different degrees. The susceptibility rate of ciprofloxacin, norfloxacin, and chloramphenicol was evaluated to be 40%, whereas gentamycin and amoxicillin was 60%, 50%, respectively. PCR targeting 16S rRNA indicates the amplification of DNA products at 1492 bp in the 10 isolated samples. The PCR amplification also identified the class 1 integron, with the bands detected at the 160 bp marker. The haematological analyses revealed an increase in the levels of WBC (14×10^9/L) and granulocyte (10×10^9/L), whereas the erythrocyte indices remained unchanged. Additionally, the level of the comprehensive metabolic panel (CMP) did not show significant modification. In conclusion, *E. coli* is a major pathogen in neonatal lambs, showing variable antibiotic resistance that is related to the presence of resistance genes. Improving farm management and introducing an effective therapy is important to mitigating the bacterial infections in lambs.

Keywords: Colibacillosis, diarrheic lambs, 16sRNA, antibiotic resistance, Integrons.

Publisher: University of Basrah,
College of Veterinary Medicine, Basrah, Iraq

Introduction

Escherichia coli causes watery diarrhea in neonatal lambs with significant economic losses due to high morbidity and mortality. *E. coli* is a Gram-negative, rod-shaped, and facultative anaerobic bacterium that colonises in the gut. This bacterium causes severe inflammation in the intestinal mucosal membranes and is a more complicated urinary tract infection (UTI) and meningitis. *E. coli* is an extant survival in the environment, water, sewage, undercooked food, and fresh milk (1,2). Bacterial contamination can arise from animal waste or food chain exposure, supported by complex genetic mechanisms that enable them to survive in environmental stress and nutrient limitations (3). The strains of *E. coli* are classified into different pathotypes based on its antigenicity structure and virulence factors. The principal antigens of *E. coli* include the heat-stable O antigen, the heat-labile H antigen, and various fimbrial antigens (4,5). Based on disease symptoms, target host, and virulence genes, *E. coli* strains are classified into enteropathogenic *E. coli* (EPEC),enterohemorrhagic *E. coli* (EHEC), enterotoxigenic *E. coli* (ETEC), enteroinvasive *E. coli* (EIEC), enteroaggregative *E. coli* (EAEC), and diffusely adherent *E. coli* (DAEC) (6). Molecular identification and characterization of virulence genes are crucial for understanding the dynamics of infection and developing effective therapies.

Enteropathogenic *E. coli* (EPEC) is an important pathogenic strain having multiple virulence factors and associated genes, causing severe pathological changes in the host tissues. EPEC leads to a deleterious impact on epithelial cells by adhering to enterocytes and through the expression of multiple virulence-associated genes (7). EPEC can produce attaching and effacing (A/E) lesions, which is the most effective virulence factor leading to complete effacement of microvilli (8). EPEC carries a unique pathogenic island known as the locus of enterocyte effacement (LEE), which encodes a type III secretion system (T3SS) and is mainly responsible for injecting effector proteins into host cells (9). Among key virulence proteins, intimin is encoded by the *eae* gene and functions as a mediator of adherence to the host cell surface (10). The translocated intimin receptor (Tir) is an encoded protein that is injected into host cells through T3SS and serves as a receptor for intimin and pedestal beneath adherent bacteria (11). Additionally, the bundle-forming pilus (BFP), is encoded by the *bfp* gene cluster located on the EAF plasmid and facilitates the initial adhesion of EPEC to epithelial cells and promotes microcolony formation. EPEC strain can also produce Lymphostatin, a protein that inhibits the immune response and sustains adherence mechanisms (12).

E. coli can resist multiple antimicrobial drugs, which poses an extreme challenge to human health and diseased animals. Extended-spectrum β-lactamases (ESBLs) are important enzymes produced by *E. coli* and can reduce the efficacy of β-lactam antibiotics, such as penicillin and cephalosporins (13). Numerous genes responsible for antibiotic resistance were identified in *E. coli*, and these genes are located on the mobile genetic elements such as plasmids and integrons, which contribute to the spread of horizontal gene transfer (HGT) among bacterial populations (14). The extent of

antimicrobial resistance (AMR) varies according to geographic location and host-related factors. The rate of resistance has been observed to exceed 50% for second- and third-generation antibiotics (15). Livestock meat serves as an important reservoir for AMR, with high prevalences reported in developing and middle-income countries (16,17). BlaTEM and blaCTX-M are commonly detected resistance genes in *E. coli*, especially in poultry and ruminants, with prevalence rates estimated from 30% to 60% in several meat markets in Asian countries (18,19). Other resistance genes, such as tetA and tetB (conferring resistance to tetracyclines) and aadA and aphA1 (associated with aminoglycoside resistance), have been frequently reported (20).

To ensure public health safety and lower antibiotic resistance, monitoring of *E. coli* in the environment, food, and animals is a strategic goal of the One Health approach. Molecular methods, especially qualitative PCR, offer unparalleled precision and efficiency for the detection *of E. coli* in different sample types (21). Bacteriological and biochemical tests remain indispensable tools for screening coliform bacteria, including *Enterobacteriaceae*, *Klebsiella pneumoniae*, and *E. coli*. Selective media, for instance CHROMagar™ and Violet Red Bile Lactose (VRBL) agar, are employed to advocate the selective growth and differentiating *E. coli* colonies (22). MALDI-TOF mass spectrometry is an advanced technique that has also been employed for *E. coli* identification, relying on the generation of protein profiles in the organisms (23). UidA and 16S rRNA are common genes used to confirm the presence of *E. coli* by microbiological laboratories (24). Sequencing of 16S rRNA is a highly sensitive and gold-standard method for identifying *E. coli* and genetic relationships, and host specificity (25). Furthermore, whole-genome sequencing (WGS) is a lucrative method and provides a comprehensive insight into *E. coli* genotyping and phenotypic characteristics, enabling detailed analysis of virulence factors, antimicrobial resistance genes, and evolutionary relationships (26). Information on the infection with *E. coli* in neonate lambs and antibiotic gene resistance is limited in Basrah province. To the best of our knowledge, the use of antibiotics is accessible to farmers for the treatment of seasonal infection, and this can highlight the risk of antimicrobial resistance in small ruminates and through the food chain. The results may help veterinarians and farmers to limit the use of antibiotics, improve farm management, and seek alternative therapy. Therefore, this study aims to identify *E. coli* in neonate lambs with diarrhea and to assess its antibiotic resistance and associated resistance genes.

Materials and Methods

Area of study and sample collection

This research was carried out in the Safwan subdistrict, located in the southwestern area of Basrah Governorate, approximately 51 km from Basrah city. The area is known as a major zone for extensive sheep and camel farming. The study took place between January and April 2025 and included 30 neonatal lambs (under two weeks old) from two different farms. All the lambs showed

clinical signs of watery diarrhea. Rectal swab samples were collected directly from the affected lambs using sterile cotton swabs. The swabs were placed in sterile containers and transported in an ice box to the Bio-Vet Laboratory, a private microbiological and veterinary facility situated in the centre of Basrah. The samples underwent bacteriological examination and antibiotic susceptibility testing. Initially, they were cultured on nutrient agar, followed by selective media, including MacConkey and Eosin Methylene Blue (EMB) agars, and incubated at 37 °C for 24 hours. The isolated results were presumptively identified as *E. coli*, and molecular techniques were subsequently employed to confirm the bacterial identification.

Antibiotic susceptibility testing of the isolates was carried out using the disk diffusion method (Kirby–Bauer test). Five antibiotics were evaluated: amoxicillin, norfloxacin, ciprofloxacin, gentamicin, and chloramphenicol. The diameters of the inhibition zones were measured and interpreted according to the breakpoint values that classify bacterial responses as susceptible, intermediate, or resistant. The interpretation was conducted following the guidelines established by the Clinical and Laboratory Standards Institute (27).

Measurement of hematobiochemical parameters

Blood samples were submitted to the laboratory for complete haematological and biochemical analyses. A full blood count (FBC) was performed to determine red blood cell (RBC) count, white blood cell (WBC) count, platelet count, haemoglobin concentration (Hb), and haematocrit (HCT) values using a Veterinary Hematology Auto-Analyzer (Exigo 400H, Sweden).

To assess the overall health and metabolic status of the diarrheic lambs, a comprehensive metabolic panel (CMP) was conducted using a Veterinary Chemistry Analyzer (Mindray, China). The panel included quantification of total protein (TP), albumin (ALB), globulin (GLB), total bilirubin (T-BIL), alanine aminotransferase (ALT), aspartate aminotransferase (AST), blood urea nitrogen (BUN), creatinine (CREA), glucose (GLU), and total cholesterol (CHOL).

Molecular testing for isolates

Individual bacterial colonies were inoculated into nutrient broth and incubated for 24 hours. Subsequently, 2 mL of each culture was centrifuged at 10000 rpm for 2 minutes to pellet the bacterial cells. Genomic DNA was extracted from the pellets using the Wizard® Genomic DNA Purification Kit (Promega, USA), following the manufacturer's protocol. The amount of extracted DNA was quantified in ng/µL, and its purity was checked using a NanoDrop spectrophotometer based on the A260/A280 absorbance ratio. Ratios ranging from 1.8 to 2.0 indicated that the DNA was appropriate for PCR testing.

Polymerase Chain Reaction (PCR) was performed to amplify the *16sRNA* gene from ten samples, by which a specific primer to identify *E. coli (Table 1)*. Each PCR reaction was prepared in a total volume of 25 µL, containing 12.5 µL of 2X GoTaq® Hot Start Green Master Mix (Promega, USA), along with the respective primers and DNA template. Amplification was performed using

a SimpliAmp™ Thermal Cycler under the following conditions: an initial denaturation at 95 °C for 5 minutes; 35 cycles of denaturation at 95 °C for 30 seconds, annealing at 55.0 °C for 30 seconds, and extension at 72 °C for 45 seconds; followed by a final extension at 72 °C for 7 minutes. The PCR products were separated by electrophoresis on a 1.5% agarose gel prepared in 1× TAE buffer and stained with ethidium bromide. DNA fragments were visualized under UV illumination, and a GeneRuler DNA ladder was used as a molecular size marker. Subsequently, the products of the 16s RNA gene were sent for sequencing of ten isolates.

We also conducted additional PCR amplification to detect antibiotic resistance genes in the same samples used for *E. coli* detection. Three sets of primers were utilized to target the integrons segment, as shown in Table 1. The procedure was similar to the PCR protocol used for 16S rRNA, but the differences are only in the thermal cycling timing conditions. Briefly, the reaction included an initial denaturation at 95 °C for 5 minutes, followed by 35 cycles of denaturation at 95 °C for 20 seconds, annealing at 55 °C for 20 seconds, and extension at 72 °C for 45 seconds, with a final extension step at 72 °C for 10 minutes.

Table 1: Primer sets used for the detection *of E. coli* using 16sRNA and three classes of integrons.

Gene	Primer sequence (5'-3')	PCR product (bp)	References
16SrRNA	AGAGTTTGATCMTGGCTCAG TACCTTGTTACGACTT	1492	(28)
Class 1 integrons	CAGTGGACATAAGCCTGTTC-CCCGAGGCATAGACTGTA-3′	160	(29)
Class 2 integrons	CAACGGAGTCATGCAGATG CATTTGTGTTGTGGACGGC	403	(30)
Class 3 integrons	AGTGGGTGG CGAATGAGTG-TGTTCTTGTATCGGC AGGTG	600	(31)

Results

Colonies of bacteria appeared in the pink colour on MacConkey agar (Figure 1). The examined culture on the EMB agar was coloured with a metallic green sheen. This primarily indicates the presence *of E. coli*. Based on the antibiotic-sensitivity results, the colonies were sensitive to all antibiotics tested, but the degree of sensitivity varied. Ciprofloxacin, norfloxacin, and chloramphenicol showed 40% for each of them as susceptibility rate, while gentamycin (60%) and amoxicillin (50%) were classified as intermediate of microbial sensitivity.

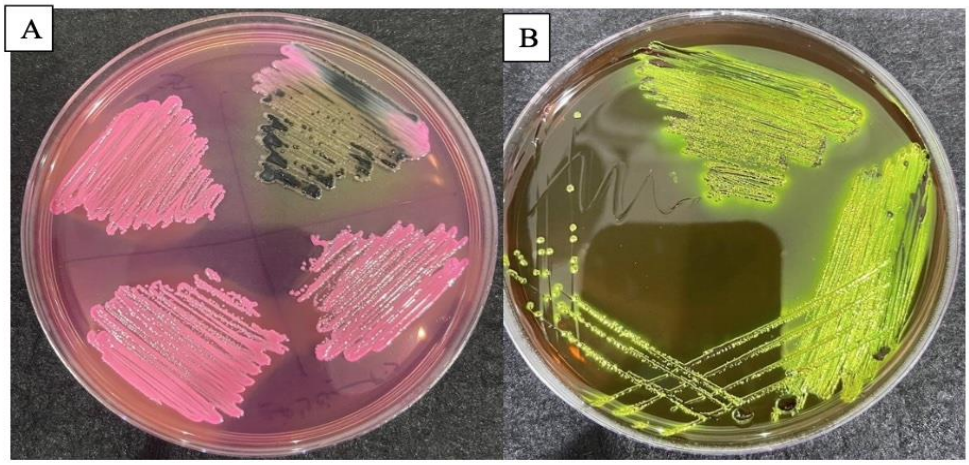

Figure 1: Shows colonies of *E. coli* on MacConkey (A) and EMB (B) agars.

Hematobiochemical analyses results

Based on hematological parameters, the infected lambs showed an increase in the leukocyte levels, including WBC (14 x 10^9/L) and granulocyte (10 X 10^9/L), compared with the reference values (Table 2). RBC, HTC, platelets, and HGB did not show any exaggeration. Also, the level of erythrocyte indices (MCH, MCV, and MCHC) did not exhibited changing. According to the biochemical analyses, neither proteins (e.g, albumin, globulin and blood urea nitrogen) nor the liver enzymes were significantly overwhelmed by the infection in sick animals (table 3).

Table 2: Measures of the hematological parameters in lambs infected with colibacillosis.

Parameters	Infected	References
WBC	14.78±3.66	4.0-12.0 10^9/L
Lymphocyte	3.04±0.36	2.0-9.0 10^9/L
Monocytes	0.68±0.13	0 0-0.8 10^9/L
Granulocyte	10.98±3.26	0.7-6.0 10^9/L
Red Blood Cell (RBC)	10.35±0.60	9.0-15.0 10^{12}/L
Haematocrit (HCT)	31.28±1.24	27.0-45.0 %
Platelet	621±126	200-800 10^9/L
Haemoglobin (HGB)	11.34±0.71	9.0-15.0 g/dL
Mean Corpuscular Haemoglobin (MCH)	11.70±0.15	8.0-12.0 pg
Mean Corpuscular Volume (MCV)	30.32±0.38	25.0-40.0 FL
Mean Corpuscular Haemoglobin Concentration (MCHC)	37.60±0.93	31.0-34.0 g/dL

Table 3: Measurement of biochemical parameters and liver enzymes in infected lambs.

Parameters	Infected	References
Albumin	27.98±1.66	20-49 g/L
Total Protein	48.12±5.39	39-99 g/L
Globulin	20.14±5.48	13-74 g/L
Glucose	5.38±0.59	2.6.17.5 mmol/L
Blood Urea Nitrogen	4.38±0.73	3.9-17.5 mmol/L
Total Cholesterol	1.92±0.44	0.2-6 mmol/L
Alanine Aminotransferase	11.16±1.11	0-70 U/L
Aspartate Aminotransferase	44.60±5.32	0-530 U/L
Total Bilirubin	5.36±0.76	0-36 umol/L
Creatinine	43.20±9.88	45-290 umol/L

Molecular findings and species identification

Where is the concentration and purity of DNA extraction of bacterial colonies. The PCR amplification of the target gene (16s rRNA) in the ten samples resulted in the distinct amplicons of approximately 1492 bp, as visualized by electrophoresis on agarose gel (Figure 2). The band size was determined by comparison with a standard molecular DNA ladder and corresponded precisely to the expected product size for the specific gene region of *E. coli*. This result confirms the successful and specific amplification of the target gene, which supports the molecular identification of the bacterial isolates as *E. coli*. The PCR for the detection of antibiotic resistance gene was identified only in class 1 integrons in the isolates (Figure 3).

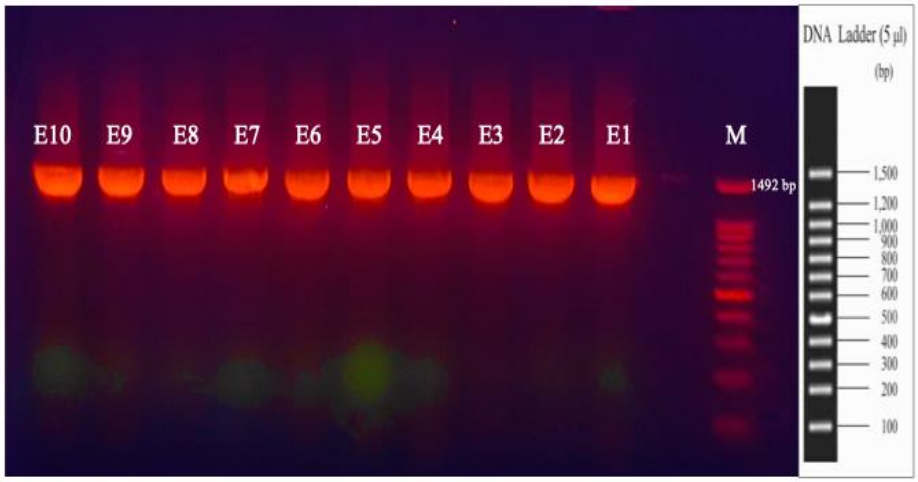

Figure 2: Amplicon band of agarose gel electrophoresis detected *E. coli* utilizing 16S rRNA. The band size of ten samples characterized by 1492 bp.

The PCR products of ten isolates were sequenced, and each strain was given an accession number where they were deposited in the NCBI database. The sequence data confirmed the *E. coli* bacterium identification from the samples. The constructed phylogenetic tree is illustrated in Figure 4. The tree splits into upper and lower clades, with 100% shared similarity of these strains. The upper clade includes three isolated strains (1,2,10). These strains are very close to what was reported in the USA (CP074863.1, CP104539.1), Japan (AP027790.1), and Germany (CP181646.1). The second clade includes seven isolated strains (3,4,5,6,7,8,9) that are closely related to each other.

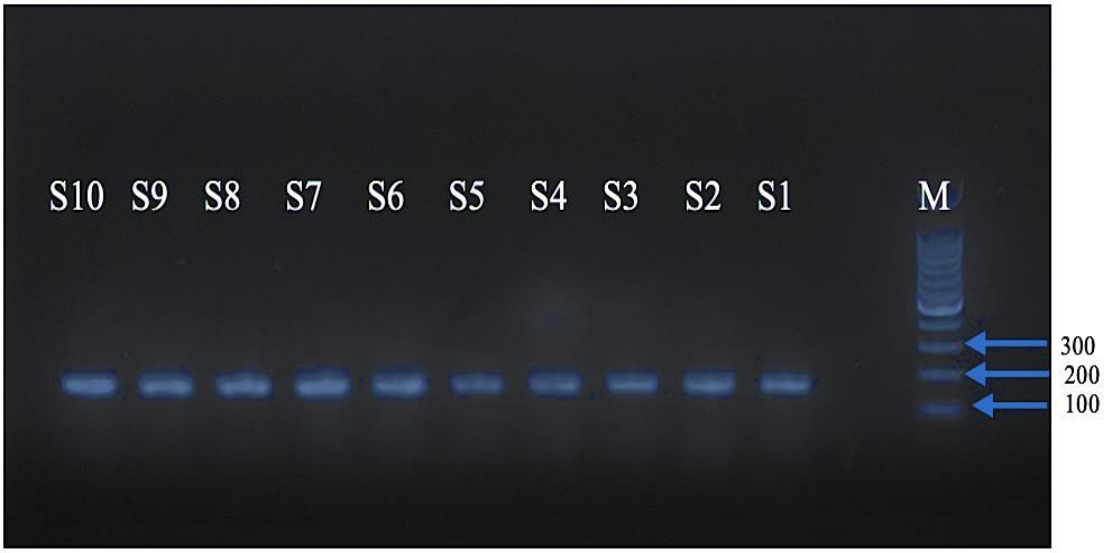

Figure 3: Amplicon band of agarose gel electrophoresis for amplification of class 1 integrons for a wide range of antibiotic resistance in *E. coli* samples. The band size of ten samples characterized by 160 bp.

Discussion

This study investigated the infection of neonate lambs with *E. coli*, with identification of antibiotic resistance and resistance genes. The classical culture-based media were used to isolate and differentiate Gram-negative bacteria, primarily *E coli*. Although these media have relatively low specificity and sensitivity (32), they are still valuable for suppressing Gram-positive bacteria and serve as a preliminary screening method. The PCR-based method is an important tool for confirming and accurately identifying the presumptive bacterial colonies (33

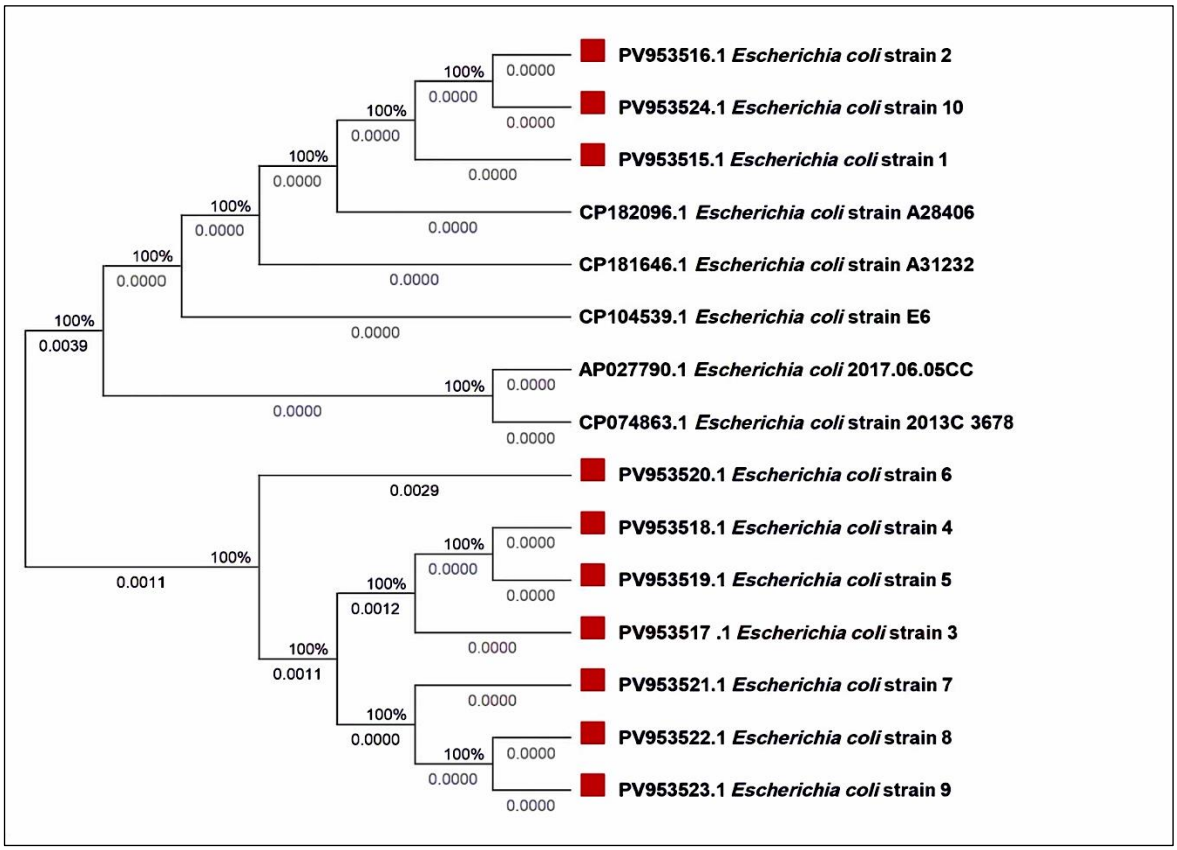

Figure 4: Phylogenetic tree of sequencing ten isolations confirming *E. coli* strains. Each strain has a specific accession number deposited on the NCBI website.

The extracted DNA products from the media were subjected to sequencing after targeting the 16sRNA gene, as it is the most accurate and reliable method for diagnosing *E. coli* or other pathogenic organisms (33,34). Evaluating the antibiotic susceptibility of colonies was carried out using the disc diffusion method, which is a widely used method in laboratories that provides a qualitative assessment of whether a bacterial isolate is susceptible, intermediate, or resistant to antimicrobial drugs. This technique remains low accurate unless the isolates undergo molecular analyses for the detection of specific gene resistance (35).

In the present study, the thirty neonate lambs (≤ weeks) were diagnosed with *E. coli* infection in the winter time. *E. coli* is an opportunistic bacterium, and exposure mostly occurs due to lack of sanitation, inadequate colostrum intake, and overcrowded conditions (36). An epidemiological study was conducted in two locations in Egypt, Al -Sharkia and Al-Ismailia, reported that 45% of a total of 95 neonate lambs were apparently diagnosed with *E. coli*, due to improper farm management (37). The infection rate varies geographically based on *E. coli* strains. For instance,

the highest infection rate with *E. coli* disease in lambs was estimated in the Kashmir valley (85.33%), while the lowest infection rate was observed in Iran, estimated as 4.3% (38,39). Seasonal patterns are a key meteorological factor influencing *E. coli* transmission and outbreakduringng the winter season, which enhances bacterial growth and increases environmental contamination (40,41).

The diarrheic lambs showed an increase in the leucocytic counts compared to their normal levels. This finding is contrary to a previous study done by Mokhbatly et al. (42), who indicated that lambs with diarrhoea suffered from neutropenia, monocytopenia and lymphopenia, which was attributed to a malnutrition condition. Adequate feeding of neonate lambs with colostrum from dams, which mainly contains a high amount of IgG, can transfer good passive immunity and protect them from possible death or boost their immunity against pathogenic bacteria **(**43). Therefore, it is important to ensure newborn lamb sufficient amount of colostrum for early two weeks of life. Several researchers recommended feeding probiotics to enhance both immunity and growth (44,45)**.**

For precise identification of *E. coli*, the 16S rRNA (1492 bp) was amplified and sequenced. Consistent with the present findings, (46) reported that 100 samples obtained from sheep in Baghdad Province were positive for the *E. coli/* O157:H7 strain, based on 16S rRNA gene detection. The 16S rRNA gene is an important genetic marker present in a wide range of bacterial species, including *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Streptococcus* spp., and *Pseudomonas* spp., and has been extensively utilized for bacterial identification from diverse sources such as human, animal, food, milk, and water samples (47-49). In Indonesia, Kusumaningrum et al. (50) applied partial sequencing of the 16S rRNA gene to monitor *S. aureus* contamination in food products. (51) and (52) employed 16S rRNA-based molecular screening of stool and urine samples for the detection of *E. coli* and *S. aureus*. Sequencing of the 16S rRNA gene represents not only a precise and reliable diagnostic approach but also is an essential molecular marker for bacterial genus and species identification, providing a valuable insight into phylogenetic and taxonomic relationships (25). Compared with the conventional PCR method, 16S rRNA gene sequencing remains a highly sensitive method for bacterial detection and can differentiate between pathogenic and non-pathogenic *E. coli* strains (53,54).

According to another finding, only class 1 integrons were detected among bacterial isolates. This explains why 40% to 60 of our isolates showed resistance to fluoroquinolone and aminoglycoside group drugs on the disc diffusion test. Class 1 integrons are important genetic segments associated with multidrug resistance (MDR), mostly found in the *Enterobacteriaceae* family (55,56). This gene is highly prevalent in environmental samples and animal sources. A Norwegian study reported that class 1 integron was detected in 12% of a total of 241 samples isolated from meat and meat by-products in the marketplaces (57). Another study from Iran indicated that class 1

integron was found in 16% of *E. coli* isolates from all of 200 samples gathered from faecal matter of humans, chicken, cattle, and sheep (58). In fact, this indicated how widely antibiotics are misused in animals and humans, which has contributed to the spread of this gene in *E. coli* and among other bacterial species.

Our study has a few limitations. The sample size was small, as samples were collected only from sick lambs. In addition, samples from ewes and the environment were not included, but will be considered in future studies. Other virulence genes of *E. coli* were not detected, and will be investigated in further study using a set of sequence primers.

Conclusions

The present study identified *E. coli* in diarrheic lambs from Basrah governorate using bacteriological and molecular methods. All samples were diagnosed as *E. coli* based on quantitative assessment. Out of ten isolates, *E. coli* was confirmed by 16S rRNA gene by PCR and sequence, which facilitates the diagnosis of sick animals. The isolated strains showed a high level of resistance to antibiotics, and only the class 1 integron resistance gene was identified in all samples. This study provides baseline information on *E. coli* infection in neonatal lambs and is associated with antibiotic resistance, which may support future large-scale studies to better understand the epidemiological characteristics of *E. coli* in Basrah. Additionally, the study highlights resistance genes carried by *E. coli* that are responsible for antimicrobial resistance, emphasizing the need for further research to develop new treatment approaches or alternative therapies to antibiotic use. Mitigation strategies should be implemented to reduce colibacillosis in lambs, including improving farm management practices, vaccinating ewes, and developing alternative therapeutic options.

Conflict of interests

The authors declare that there is no conflict of interest.

Ethics Approval

Ethical approval was obtained from the scientific committee in the College of Veterinary Medicine, University of Basrah (No: 85/37/2025) on January 4, 2024. The agreement was obtained from sheep farmers before collecting the samples.

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الاستقصاء عن داء الإشريكية القولونية والجينات المقاومة للمضادات الحيوية في الحملان حديثة الولادة في محافظة البصرة, العراق

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الخلاصة

داء القولونيات مرض بكتيري معدٍ شائع يصيب الحملان حديثة الولادة ويؤدي إلى خسائر اقتصادية كبيرة. هدفت هذه الدراسة إلى تشخيص بكتيريا الإشريكية القولونية كعامل مسبب للإسهال في الحملان، وتقييم مقاومتها للمضادات الحيوية وجينات المقاومة المرتبطة بها. جُمع ما مجموعه 30 عينة من البراز والدم من حملان مصابة بأعراض الإسهال. خضعت عينات البراز في البداية لاختبارات بكتيرية، واختبار انتشار القرص، والتشخيص الجزيئي، بينما خضعت عينات الدم لتحليل معلمات الدم والكيمياء الحيوية. استخدم الاختبار الجزيئي 16srRNA مع بادئات محددة تستهدف جينات المقاومة لتفاعل البوليميراز المتسلسل (PCR) . تبين في البداية أن جميع العينات في الأوساط الانتقائية إيجابية للإشريكية القولونية. وفقًا لنتائج حساسية المضادات الحيوية، كانت مستعمرات البكتيريا حساسة لجميع المضادات الحيوية، مع اختلاف درجات مناطق التثبيط. بلغت نسبة حساسية البكتيريا للمضادات الحيوية سيبروفلوكساسين، ونورفلوكساسين، وكلورامفينيكول 40%، بينما بلغت 60% للجنتاميسين و50% للأموكسيسيلين. يشير تفاعل البوليميراز المتسلسل الذي يستهدف 16srRNA إلى تضخيم منتجات الحمض النووي عند 1492 زوجًا قاعديًا في العينات العشر المعزولة. كما كشف تضخيم PCR عن وجود الإنتغرون من الفئة الأولى، حيث تم الكشف عن الحزم عند علامة 160 زوجًا قاعديًا. أظهرت التحاليل الدموية ارتفاعًا في مستويات خلايا الدم البيضاء (14 × 10^9/لتر) والخلايا المحببة (10 × 10^9/لتر)، بينما لم تتغير مؤشرات خلايا الدم الحمراء. بالإضافة إلى ذلك، لم تظهر لوحة التمثيل الغذائي الشاملة (CMP) لمصل الدم أي تغيير يُذكر. في الختام، تُعد الإشريكية القولونية من مسببات الأمراض الرئيسية في الحملان حديثة الولادة، وتُظهر مقاومة متفاوتة للمضادات الحيوية ترتبط بوجود جينات المقاومة. يُعد تحسين إدارة المزارع وإدخال علاج فعال أمراً مهماً لتقليل من العدوى البكتيرية في الحملان.

الكلمات المفتاحية: داء الاشريكية القولونية، الحملان المصابة بالإسهال, الحامض النووي الريبي 16S, مقاومة المضادات الحيوية, الانتغرونات .