https://www.mediresonline.org/

ISSN: 2836-2306

Open Access

International Journal of Genetics and Genomic Science

Research Article

# Genomic Characterization of Antimicrobial Resistance in Foodborne Diarrheagenic Escherichia coli from Chifeng, China

**Yanbo Bai[1#], Jia Yu[1#], Chunru Wei[1], Haoran Yang[2], Lei Yang[1*]**

[1]Microbiology Laboratory, Chifeng Center for Disease Control and Prevention, Chifeng, China
[2]The First Clinical Medical College, Inner Mongolia Medical University, Hohhot, China
[#]Co-first author:Yanbo Bai and Jia Yu contributed equally to this paper

***Corresponding Author:** Lei Yang, Chifeng Center for Disease Control and Prevention, Chifeng, China

**Received Date:** 11 April 2025; **Accepted Date:** 02 May 2025; **Published Date:** 19 May 2025



## Abstract

**Objective:** Recent studies have revealed the increasing severity of antimicrobial resistance (AMR) in diarrheagenic Escherichia coli (DEC), but relevant data remain limited in the Chifeng, China. This study aimed to investigate the AMR profiles and resistance gene distribution of foodborne DEC isolates in our city, providing critical insights for monitoring DEC and guiding rational antibiotic use.

**Methods:** From 2023 to 2024,240 diarrheal stool samples were collected from sentinel hospitals. DEC isolates were identified by PCR. Antimicrobial susceptibility to 29 antibiotics was determined using broth microdilution method. Whole genome sequencing (WGS) was performed to analyze resistance genes and plasmid types with bioinformatics tools.

**Results:** The DEC detection rate is 9.6% (23/240), predominantly enteroaggregative E. coli (EAEC, 69.5%) and enteropathogenic E. coli (EPEC, 30.5%). Resistance phenotypes show the highest rates to TET (60.9%) and nalidixic acid (56.5%), with 30.4% of isolates classified as multidrug-resistant (MDR). Genomic analysis identified nine classes of resistance genes, primarily tet(A), blaTEM-1B, and aph(3'')-Ib. The most prevalent plasmid type was IncF (47.8%).

**Discussion:** The findings highlight a severe AMR burden in Chifeng's DEC strains, underscoring the urgent need for enhanced surveillance and antibiotic stewardship to curb their dissemination.

**Keywords:** Diarrheagenic Escherichia coli, Antimicrobial resistance, Whole genome sequencing, Resistance genes.

## Background

*Escherichia coli* belongs to the family Enterobacteriaceae, which is a commensal in the intestines of humans and animals. Some pathogenic strains of Escherichia coli contaminate food and can be cause severe diarrhoea when ingested by humans, so, they are referrd to as DEC.DEC are divided into five categories, namely enteropathogenic E.coli (EPEC), enterotoxigenic E.coli (ETEC), enteroinvasive E.coli (EIEC), enterohaemorrhagic E.coli (EHEC) and enteroaggregative E.coli (EAEC) [1]. Epidemiological studies have demonstrated that DEC serves as a primary etiological agent of bacterial infectious diarrhea. Recent surveillance data from multiple regions in China have reported a significant upward trend in AMR among DEC strains. This phenomenon is generally attributed to the overuse of broad-spectrum antibiotics, which accelerates the dissemination of resistance genes. Furthermore, horizontal gene transfer (HGT) via plasmids, transposons, and other mobile genetic elements (MGEs) facilitates the spread of AMR determinants. Additional contributing factors may include host immune compromise and environmental selection pressures [2]. However, in the context

of Chifeng, China, critical knowledge gaps persist regarding the local AMR profiles, distribution patterns of resistance genes, and molecular mechanisms underlying their transmission. This study aims to elucidate the AMR characteristics of DEC isolates in this region through integrated phenotypic susceptibility testing and genomic analysis. The findings will provide actionable insights for optimizing clinical therapeutic strategies and informing targeted public health interventions to mitigate AMR proliferation [3].

## Materials and Methods

### *Source of strains*

The 240 samples used in this study were collected from two sentinel hospitals in our city, namely *Chifeng Maternal and Child Health Hospital* and *Chifeng Hospital*. Between 2023 and 2024, the two sentinel hospitals collected samples according to the requirements of the *National Active Surveillance of Foodborne Diseases:* cases were collected on the principle that they were caused by food or suspected to be caused by food, and the main complaint was diarrhoea. Diarrhoea is defined as having three or more bowel movements per day with abnormal stool characteristics such as watery, loose, bloody, purulent or mucoid stools [4]. The two sentinel hospitals sent the above samples together with the case information to the laboratory of a *Center for Disease control and Prevention* for pathogenetic testing of the samples. The central laboratory performed isolation, identification, virulence factor gene detection, Antimicrobial Susceptibility Test and WGS of the samples according to the *National Foodborne Disease Surveillance Work Manual*.

### *Main Instruments and Reagents*

MALDL-TOF-MS(*Bruker*); Quantitative Real-time PCR(*Thermo Fisher*); Ion geneStudioTM S5 Series System(*Thermo Fisher*); Multiplex fluorescent quantitative PCR kit(*ABT*); Gram Negative MIC plate (*Fosun Diagnostics*); ATCC25922 (*Nanjing LeZhen*); ATCC700603 (*Nanjing LeZhen*); QIAmp DNA Mini Kit (QIAGEN); Ion 510 & Ion 520 & Ion 530 Kit-Chef (*Thermo Fisher*). All reagents were used within the stated expiry date and after having passed Quality Control.

### *Quantitative Fluorescence PCR Experiment*

Performed nucleic acid extraction and PCR amplification according to the instructions using the multiplex fluorescent quantitative PCR kit.

### *Antimicrobial Susceptibility Testing*

Antimicrobial susceptibility testing is a test that determines whether an antimicrobial drug has an inhibitory or killing effect on a pathogen in vitro. In this study, 29 antibiotics in 11 categories were selected to monitor resistance in Gram-negative bacteria with reference to the 2023 *National Foodborne Illness Surveillance Manual*. Antimicrobial susceptibility testing was performed using the broth microdilution method recommended by *Clinical and Laboratory Standards Institute* (CLSI)for the quantitative determination of the *Minimal Inhibitory Concentration* (MIC) of pathogenic bacteria [5]. A commercially available antibiotic susceptibility plate containing the following antibiotics was used: *Ampicillin/Sulbactam* (AMS), *Azithromycin*(AZM), *Ceftazidime*(CAZ), *Ceftazidime/Clavulanic Acid*(CAZ/C), *ceftiofur*(CEF), *Amoxicillin/Clavulanic Acid*(AMC), *Amikacin*(AMK), *Ampicillin*(AMP), *cefoxitin*(CFX), *cefazolin*(CFZ), *chloramphenicol*(CHL), *ciprofloxacin*(CIP), *cefepime*(CPM), *polymyxin*(ECT), *ceftizoxime*(CTX), *ceftizoxime/clavulanicacid*(CTX/C), *cefuroxime*(CXM), *ceftazidime/avibactam*(CZA), *ertapenem*(ETP), *florfenicol*(FFC), *gentamicin*(GEN), *imipenem*(IPM), *meropenem*(MEM), *nalidixicacid*(NAL), *polymyxin*(BPB), *streptomycin*(STR), *trimethoprim/sulfamethoxazole*(SXT), *tetracycline*(TET), *tigecycline* (TIG). The tests were performed and results interpreted according to the instructions, while the quality control strains were selected from ATCC25922 and ATCC700603. The results of antimicrobial susceptibility testing are of great reference value for the rational clinical use of antimicrobial agents.

### Whole Genome Sequencing (WGS)

Selected the qualified DEC, used the QIAmp DNA Mini Kit to extracted the *Escherichia coli* DNA, prepared the DNA library, ensuring that the library concentration was approximately 40pM and the library reads was 200-400bp. Sequenced the library on the *Ion geneStudioTM S5 Series System* sequencing platform and finally analysed the data: The genomic sequence coverage was ≥95%, Scaffold<100 Mismatch/100kb≤20, Q20≥1GB Q30≥85%.

### Analysis of Resistance Genes

The assembled sequence was used to identify resistance genes, using the Resfinder v4.6.0 database from the Center for Genomic Epidemiologe (CGE) services, and the plasmid replicon type carried by the isolate was identified using the Plasmid-finder v2.1 database.

## Result

### Detection Status of DEC

A total of 240 stool specimens were collected from two sentinel hospitals in our city (From 2023 to 2024), and 23 strains of DEC are detected, with a detection rate of 9.6%. The 23 isolates sequence in this study are identified as belonging to five DEC categories: EAEC (69.5%, 16/23), EPEC (30.5%, 7/23), EIEC (0), EHEC (0) and EPEC (0). The date show in Table1.

| Year | Number of specimens (copies) | Number of detections (copies) | Detection rate (%) | Category (strain) | |
|---|---|---|---|---|---|
| | | | | EAEC | EPEC |
| 2023 | 120 | 12 | 10% | 7 | 4 |
| 2024 | 120 | 11 | 9.10% | 9 | 3 |
| **Total** | **240** | **23** | **9.60%** | **16** | **7** |

***Table 1:*** Detection Status of DEC

### *Antimicrobial Susceptibility Test Results*

The antimicrobial susceptibility analysis of 23 DEC strains show that 21 strains exhibit AMR, while 2 strains remain fully susceptible, yielding a resistance rate of 91.3%. Among them, 7 strains (30%) are MDR strains. (Multi-drug resistance (MDR) refers to a bacterial strain demonstrating resistance to three or more classes of antimicrobial agents [6].)

As indicate in Table 2, the resistance prevalence to TET reaches 60.9%, while NAL exhibits a resistance rate of 56%. Resistance frequencies for APM, CTX, CFZ, CIP, FFC, and CHL range between 30% and 35%. All isolates remain fully susceptible to IPM, MEM, ETP, AMK, and TIG. Notably, 100% of strains demonstrate intermediate resistance to ECT and BPB.

| Types of antibiotics | Antibiotics | Resistant strains | | Intermediate | | sensitive strain | |
|---|---|---|---|---|---|---|---|
| | | No.of strains | No. of resistant strains (%) | No.of strains | No. of Intermediate strains (%) | No.of strains | No. of sensitive strains (%) |
| Beta-lactams | AMC | 4 | 17.4% | 1 | 4.3% | 17 | 73.9% |
| | AMP | 10 | 43.5% | 0 | 0.0% | 13 | 56.5% |
| | AMS | 3 | 13.0% | 4 | 17.4% | 16 | 69.6% |
| | CAZ | 4 | 17.4% | 0 | 0.0% | 19 | 82.6% |
| | CAZ/C | 1 | 4.3% | 0 | 0.0% | 22 | 95.7% |
| | CEF | 5 | 21.7% | 0 | 0.0% | 18 | 78.3% |
| | CFZ | 7 | 30.4% | 0 | 0.0% | 16 | 69.6% |
| | CPM | 3 | 13.0% | 0 | 0.0% | 20 | 87.0% |
| | CTX | 6 | 26.1% | 0 | 0.0% | 17 | 73.9% |
| | CTX/C | 1 | 4.3% | 0 | 0.0% | 22 | 95.7% |
| | CXM | 6 | 26.1% | 0 | 0.0% | 17 | 73.9% |
| | CZA | 0 | 0.0% | 0 | 0.0% | 23 | 100.0% |
| Aminoglycosides | AMK | 0 | 0.0% | 0 | 0.0% | 23 | 100.0% |
| | GEN | 4 | 17.4% | 0 | 0.0% | 19 | 82.6% |
| | STR | 8 | 34.8% | 0 | 0.0% | 15 | 65.2% |
| | GEN | 4 | 17.4% | 0 | 0.0% | 19 | 82.6% |
| Quinolones | CIP | 6 | 26.1% | 0 | 0.0% | 17 | 73.9% |
| | NAL | 13 | 56.5% | 0 | 0.0% | 10 | 43.5% |
| Polypeptides | ECT | 0 | 0.0% | 23 | 100.0% | 0 | 0.0% |
| | BPB | 0 | 0.0% | 23 | 100.0% | 0 | 0.0% |
| Carbapenems | IPM | 0 | 0.0% | 0 | 0.0% | 23 | 100.0% |
| | MEM | 0 | 0.0% | 0 | 0.0% | 23 | 100.0% |
| | ETP | 0 | 0.0% | 0 | 0.0% | 23 | 100.0% |
| Chloramphenicols | FFC | 6 | 26.1% | 0 | 0.0% | 17 | 73.9% |
| | CHL | 7 | 30.4% | 0 | 0.0% | 16 | 69.6% |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| Cephamycins | CFX | 1 | 4.3% | 4 | 17.4% | 18 | 78.3% |
| Sulfonamides | SXT | 3 | 13.0% | 0 | 0.0% | 20 | 87.0% |
| Tetracyclines | TET | 14 | 60.9% | 0 | 0.0% | 9 | 39.1% |
| Glycylcyclines | TIG | 0 | 0.0% | 0 | 0.0% | 23 | 100.0% |
| Macrolides | AZM | 4 | 17.4% | 1 | 4.3% | 18 | 78.3% |

***Table 2:*** AMR of DEC isolates to 29 antimicrobial agents

### *AMR spectrum of 23 DEC strains*

The AMR spectrum of DEC show that 2 of the 23 DEC strains are fully sensitive to the test antibiotics, while the remaining 21 DEC strains show 12 kinds of AMR spectra. The higher resistance rates are observed for NAL (34.7%, 8/23) and the combination STR+TET (13%, 3/23). The remaining 10 resistance profiles are each identify in a single strain, with NAL resistance being the predominant profile. MDR is observed in 30.4% (7/23) of the 23 strains. As show in Fig 1.

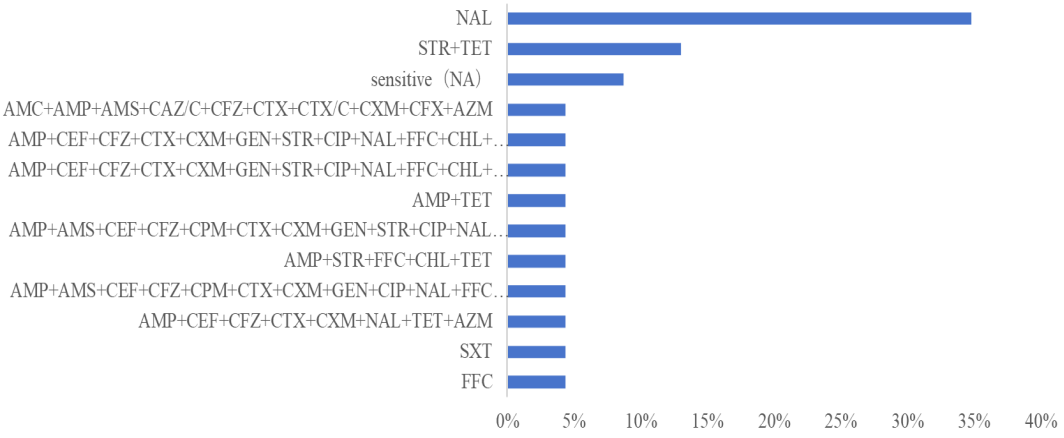


***Figure 1:*** AMR spectrum of 23 DEC strains

### *AMR Gene Status*

As illustrated in Figure 2, the 23 strains of diarrheagenic *Escherichia coli* (DEC) collectively harbor nine classes of AMR genes. The TET resistance gene tet(A) demonstrates the highest prevalence, followed by the β-lactamase gene blaTEM-1B and aminoglycoside resistance genes aph(6)-1d and aph(3'')-Ib. Figure 2 further reveals that Extended-Spectrum β-Lactamases (ESBL)-encoding genes exhibit the greatest diversity, with 19 distinct variants detected, including TEM, CTX-M, AP, and DHA-type genes. Among these, TEM-type ESBLs display the broadest genetic variation, encompassing subtypes such as blaTEM-1B, blaTEM-104, blaTEM-126, blaTEM-148, blaTEM-176, blaTEM-186, blaTEM-198, blaTEM-207, blaTEM-217, blaTEM-220, blaTEM-230, blaTEM-234, blaTEM-30, and blaTEM-70. Notably, blaTEM-1B emerges as the most prevalent subtype, occurring in 21% of isolates. CTX-M-type ESBLs are represented by blaCTX-M-65, blaCTX-M-55, and blaCTX-M-27, with blaCTX-M-65 showing the highest detection frequency. Aminoglycoside resistance genes comprise nine variants, among which aph(3'')-Ib demonstrates a notable prevalence of 22%. The high occurrence of blaTEM-1B (21%) and aph(3'')-Ib (22%) underscores the potential risk of plasmid-mediated dissemination of these resistance determinants.

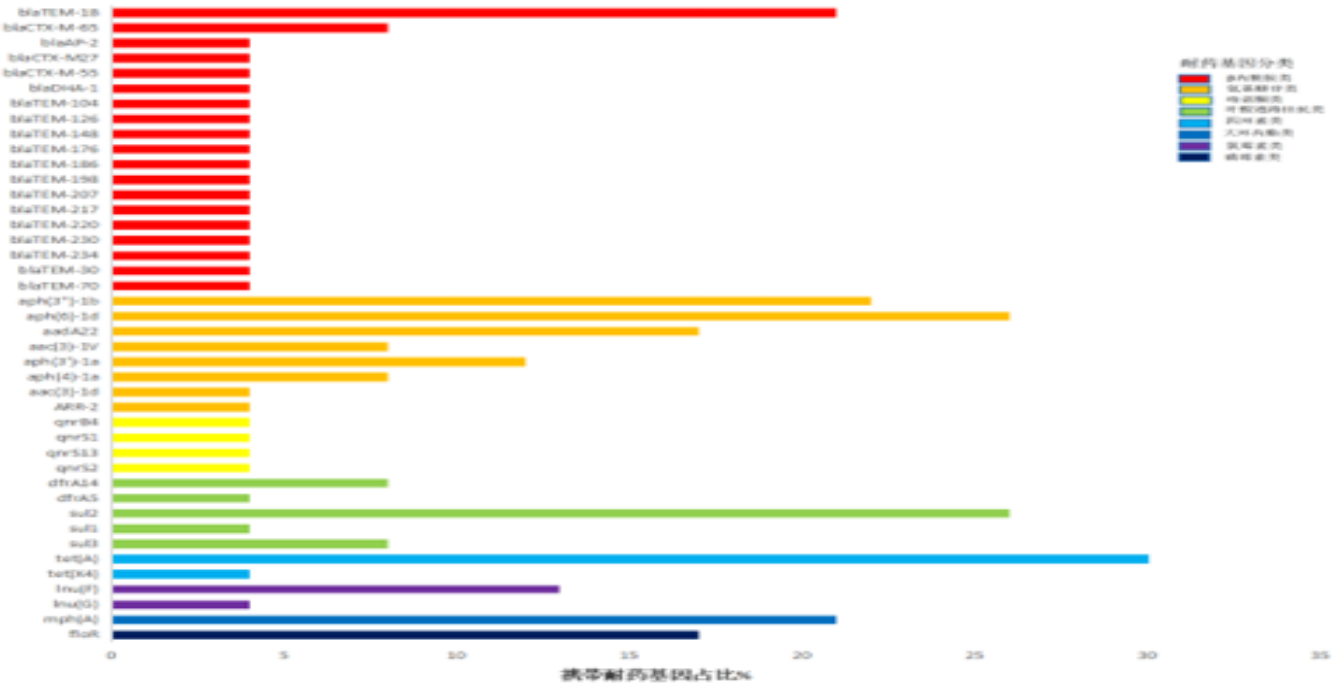

***Figure 2:*** Proportional distribution of AMR Genes in Diarrheagenic *E.coli* isolates

For folate pathway antagonists and macrolides, *sul2 and mph(A)* are the most frequently detected resistance genes. Quinolone resistance genes (*qnrS1, qnrS2, qnrS13, qnrB4*) each show a 4% carriage rate. Notably, none of the 23 DEC strains harbor polymyxin E/B resistance genes, and all demonstrate susceptibility to glycylcyclines and carbapenems, with no detect carbapenemase encoding genes (*blaOXA-48, blaNDM* e.g.,). Polymyxins exhibit intermediate susceptibility. As show in Table 3.

| Strains | Antibiotics | Resistance Genes |
|---|---|---|
| F48 | AMP+CEF+CFZ+CTX+CX-M+NAL+TET+AZM | blaCTX-M27、mph(A)、tet(A) |
| F156 | AMP+STR+FFC+CHL+TET | aadA22、blaTEM-1B、lnu(G)、floR、qnrS2、qnrS1、sul3、tet(X4)、tet(A) |
| F179 | STR+TET | aph(6)-1d、aph(3'')-1b、sul2、tet(A) |
| F185 | AMP+AMS+CEF+CFZ+CPM+CTX-+CXM+GEN+STR+CIP+NAL+FF-C+CHL+SXT+TET+AZM | aph(6)-1d、aac(3)-1d、aadA22、aph(3')-1a、blaCTX-M-55、blaTEM-1B、blaAP-2、mph(A)、lnu(F)、floR、qnrS13、ARR-2、sul3、tet(A)、dfrA14 |
| F189 | STR+TET | aph(6)-1d、aph(3'')-1b、sul2、tet(A) |
| F191 | STR+TET | aph(6)-1d、aph(3'')-1b、sul2、tet(A) |
| F201 | AMP+TET | aph(6)-1d、aph(3'')-1b、blaTEM-1B、sul2、tet(A)、dfrA14 |
| F209 | AMP+CEF+CFZ+CTX+CX-M+GEN+STR+CIP+NAL+FF-C+CHL+TET | aph(4)-1a、aph(3')-1a、aac(3)-1V、aadA22、aph(6)-1d、aph(3'')-1b、blaCTX-M-65、mph(A)、lnu(F)、floR、-sul2、tet(A) |
| F210 | AMP+CEF+CFZ+CTX+CX-M+GEN+STR+CIP+NAL+FF-C+CHL+TET+AZM | aph(4)-1a、aph(3')-1a、aac(3)-1V、aadA22、blaCTX-M-65、blaTEM-234、blaTEM-230、blaTEM-220、blaTEM-217、blaTEM-207、blaTEM-198、blaTEM-186、blaTEM-176、blaTEM-148、blaTEM-126、blaTEM-104、blaTEM-70、blaTEM-30、blaTEM-1B、mph(A)、lnu(F)、floR、sul2 |

| | | |
|---|---|---|
| F223 | AMC+AMP+AMS+CAZ/C+CFZ+CTX+CTX/C+CXM+CFX-+AZM | blaDHA-1、blaTEM-1B、mph(A)、qnrB4、sul1 |
| S209 | SXT | sul1、dfrA5 |

***Table 3:*** AMR spectrum and resistance genes of the main DEC strains

### *Plasmidtypes carried in diarrheagenic E.coli isolates*

The plasmid replicon types identify in 23 DEC isolates by Plasmid Finder analysis predominantly comprised 17 families, with *Col and Inc* being the most prevalent. Specifically, the IncF group exhibit the highest carriage rate, including subtypes *IncFIB* (detected in 11 strains), *IncFIC* (5 strains), and *IncFII* (3 strains). Additional replicon types identify are *ColR-IncX1*, *IncHI2*, and *p0111*, among others (Figure 3).

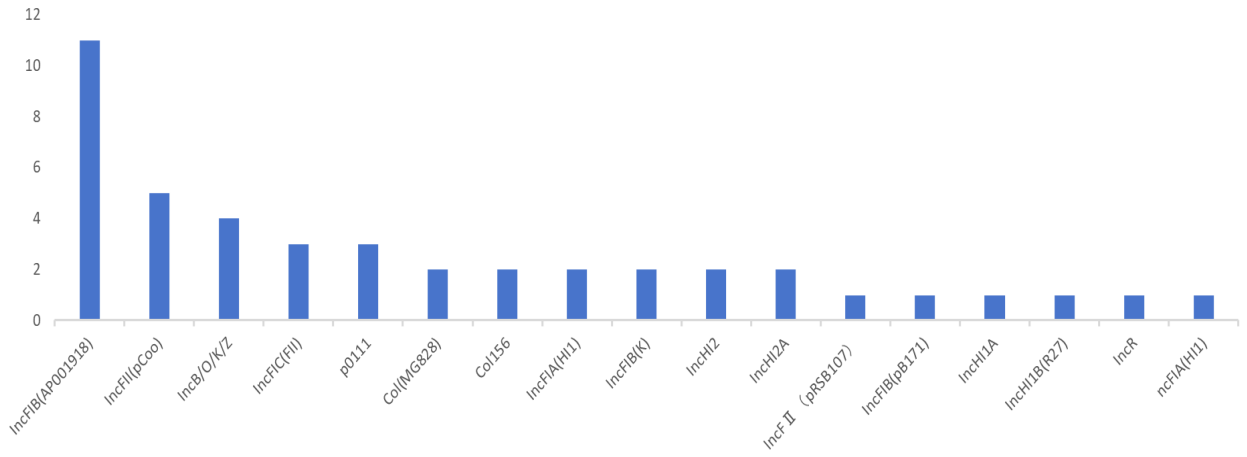


***Figure 3:*** Plasmidtypes carried in diarrheagenic *E.coli* isolates

## Discussion

### *Epidemiological Profile and Regional Variations*

*Diarrheagenic Escherichia coli* (DEC) has emerged as a predominant etiological agent of bacterial diarrhea [7]. In recent years, it has become a focal point in diarrheal disease research within developing countries. In this study, the detection rate of DEC among diarrheal patients in our city is 9.6%, which is lower than those reported in Beijing [9] (12%, 2019), Jiangsu Province [10] (20%, 2020), and Zibo City [11] (10.34%, 2023), but higher than the rate in Jiuquan City [12] (8.64%, 2020). The variability in detection rates may be attributed to climatic factors, dietary habits, among others. Furthermore, the predominant DEC subtypes in our city are identified as EAEC, whereas Beijing, Shanghai, Henan Province, and Ningxia Hui Autonomous Region are primarily associated with ETEC and EAEC. Fujian Province exhibits a higher prevalence of EPEC, while Guangzhou is dominated by EIEC. Studies indicate significant regional heterogeneity in DEC prevalence and dominant strains. Notably, EAEC remains the primary pathogenic subtype responsible for current diarrheal cases in our city.

### *AMR mechanisms of DEC*

The AMR genes in Escherichia coli exhibit a strong association with plasmids, which serve as pivotal vectors for HGT and play a central role in the dissemination of resistance determinants [7]. In this study, the DEC isolates demonstrated remarkable genetic diversity in resistance gene profiles, with the high prevalence of blaTEM-1B (21%) and aph(3'')-Ib (22%) underscoring the critical role of plasmid-mediated HGT in propagating β-lactam and aminoglycoside resistance. Analysis revealed that the ESBL genes carried by the 23 DEC strains predominantly belonged to TEM-type and CTX-M-type variants, where blaTEM-1B and blaCTX-M-65 (8%) were the most prevalent, consistent with epidemiological patterns observed in Huzhou [13] and Nanjing [14]. Notably, over 75% of ESBL resistance determinants are plasmid-borne, with IncF plasmids-conjugative elements widely distributed in Enterobacteriaceae-exhibiting multi-replicon architectures (e.g., *IncFIB/IncFII*) that facilitate efficient resistance gene transmission through conjugation [11]. In this cohort, the IncF plasmid family dominated (IncFIB: 47.8%;

IncFIC: 21.7%; IncFII: 13.0%), and blaTEM-1B, a classical β-lactamase gene, frequently co-occurred with blaCTX-M-65 (a third-generation cephalosporin resistance determinant) within mobile genetic elements of IncF plasmids. For instance, zoonotic E. coli strains often harbor blaCTX-M-65 integrated into IncF plasmid backbones via IS26 transposase-mediated recombination [9]. Furthermore, the elevated carriage rate of aph(3'')-Ib (22%) directly correlated with gentamicin resistance phenotypes, as IncF plasmid-bearing strains demonstrated 88% aminoglycoside resistance rates and synergistic dissemination with blaCTX-M-65. The emerging TET resistance gene tet(X4) showed strong linkage to HGT mediated by IncFII and IncQ1 plasmids. Although no mcr genes were detected in BPB [7] E/B-intermediate isolates (100%), resistance mechanisms likely involve chromosomal mutations (e.g., pmrAB modifications) or lipopolysaccharide remodeling-a membrane permeability regulatory phenomenon aligning with Asia's epidemiological trend of low carbapenemase-producing Enterobacteriaceae (CRE) prevalence but increasing adaptive resistance [5].

### *Clinical Significance of AMR Results*

The escalating MDR in DEC has become a critical public health challenge under the pressure of extensive antibiotic use. In this study, 23 DEC isolates demonstrated an overall AMR rate of 91.3% against 29 antibiotics, with 30% exhibiting MDR phenotypes. High resistance prevalence was observed for TET (60.9%) and NAL (56%), followed by AMP (43%), aligning with resistance patterns reported in Beijing and nationwide surveillance data [9]. These findings underscore the clinical obsolescence of traditional first-line therapies (e.g., third-generation cephalosporins and fluoroquinolones) for empirical DEC management. Notably, carbapenems (ETP, IPM, MEM) and AMK retained full susceptibility (100%), consistent with the global low prevalence of carbapenem-resistant Enterobacteriaceae (CRE). However, a 100% intermediate resistance rate to polymyxin E/B signals emerging adaptive resistance risks, likely driven by evolutionary pressures such as membrane permeability modifications (pmrAB mutations or lipopolysaccharide remodeling). The study reveals complex resistance profiles in DEC, with some strains resistant to over 10 antibiotic classes, necessitating tailored therapeutic regimens based on regional resistance dynamics. Sustained surveillance is imperative, particularly for nalidixic acid in intermediate resistance states, alongside stringent stewardship of high-resistance agents. Despite preserved carbapenem susceptibility, vigilance against regional resistance gene reservoir evolution remains crucial to preempt potential resistance gene dissemination. These insights highlight the urgency of integrating robust AMR monitoring and evidence-based intervention frameworks into clinical and public health strategies.

### *Limitations of the Study*

The current investigation is constrained by limited sample size and geographically restricted strain sources (solely clinical isolates from a single region), which may not comprehensively reflect the diversity of AMR gene dissemination or plasmid-mediated transmission dynamics. To address these constraints, future studies will involve expanded specimen collection across diverse epidemiological settings and systematic genomic surveillance of both clinical and environmental isolates to enhance dataset robustness and generalizability.

## Conclusion

Comprehensive analysis of AMR phenotypes and resistance genes in DEC isolates from this study revealed a high prevalence of MDR, characterized by diverse resistance determinants and plasmid-mediated dissemination mechanisms [11]. Notably, plasmid-mediated HGT has accelerated the emergence and dissemination of MDR-DEC strains. Current therapeutic options such as carbapenems (e.g., MEM) and AMK remain effective against DEC infections; however, judicious use is imperative to mitigate further resistance evolution. Future AMR surveillance should prioritize dynamic tracking of high-risk resistance genes, including *blaTEM-1B, blaCTX-M-65* and aph(3'')-Ib, as well as dominant plasmid types (e.g., *IncF family*), combined with WGS to elucidate resistance gene transmission networks and pathways. Enhanced molecular diagnostics for diarrheal pathogens and strict implementation of antibiotic stewardship programs (ASPs) are critical to reducing selective pressures driving MDR-DEC proliferation. These strategies will inform clinical decision-making and safeguard public health against the escalating threat of plasmid-driven resistance evolution [14].

## References

1. Zhu, Yinchu, Wenyang Dong, Jiale Ma, Lvfeng Yuan, Hassan MA Hejair, Zihao Pan, Guangjin Liu, and Huochun Yao. "Characterization and virulence clustering analysis of extraintestinal pathogenic Escherichia coli isolated from swine in China." *BMC veterinary research* 13 (2017): 1-10.
2. Bai, Xiangning, Hong Wang, Youquan Xin, Rongjie Wei, Xinyuan Tang, Ailan Zhao, Hui Sun et al. "Prevalence and characteristics of Shiga toxin-producing Escherichia coli isolated from retail raw meats in China." *International Journal of Food Microbiology* 200 (2015): 31-38.
3. Yu, Jianxing, Huaiqi Jing, Shengjie Lai, Wenbo Xu, Mengfeng Li, Jianguo Wu, Wei Liu et al. "Etiology of diarrhea among children under the age five in China: results from a five-year surveillance." *Journal of Infection* 71, no. 1 (2015): 19-27.

4. Zhu Y, Dong W, Ma J, Yuan L, Hejair HM, Pan Z, Liu G, Yao H. Characterization and virulence clustering analysis of extraintestinal pathogenic Escherichia coli isolated from swine in China. *BMC Vet Res*. 2017;13(1):94.
5. Clinical and Laboratory Standards Institute (CLSI).M100-performance standards for antimicrobial suscepibility testing twenty-second informational supplement [M]. Wayne: CLSI,2022:34-47.
6. Wang, Yang, Chunyan Xu, Rong Zhang, Yiqiang Chen, Yingbo Shen, Fupin Hu, Dejun Liu et al. "Changes in colistin resistance and mcr-1 abundance in Escherichia coli of animal and human origins following the ban of colistin-positive additives in China: an epidemiological comparative study." *The Lancet Infectious Diseases* 20, no. 10 (2020): 1161-1171.
7. Bueno, Maria Fernanda C., Gabriela R. Francisco, Jessica A. O'Hara, Doroti de Oliveira Garcia, and Yohei Doi. "Coproduction of 16S rRNA methyltransferase RmtD or RmtG with KPC-2 and CTX-M group extended-spectrum β-lactamases in Klebsiella pneumoniae." *Antimicrobial agents and chemotherapy* 57, no. 5 (2013): 2397-2400.
8. Zhang, Z. K., S. J. Lai, J. X. Yu, W. Q. Yang, X. Wang, H. Q. Jing, Z. J. Li, and W. Z. Yang. "Epidemiological characteristics of diarrheagenic Escherichia coli among diarrhea outpatients in China, 2012-2015." *Zhonghua liu Xing Bing xue za zhi= Zhonghua Liuxingbingxue Zazhi* 38, no. 4 (2017): 419-423.
9. Wen, Jing, Tian-Chi Zheng, Lin Ma, Guang-Yuan Feng, Yue Hu, and Ying Zhao. "Analysis of detection results of diarrheagenic Escherichia coli in patients with diarrhea in daxing district, Beijing, 2018-2020." (2021): 3418-3422.
10. Qin, S., Y. Shen, and K. Ma. "Epidemiological characteristics and drug resistance of diarrheal Escherichia coli in foodborne diseases in Jiangsu, 2018–2019." *Modern Preventive Medicine* 47 (2020): 3884-3888.
11. Yuan P., Yang L., Li S., Zhang S.F., Fu P.Y. (2018): Foodborne disease surveillance research status and management suggestions. China Health Industry, 15: 136–137.
12. Yu Z.R., Wang Y., Wang L.M., Si J.X., Gan Z.Q. (2022): Molecular typing and drug resistance analysis of diarrheagenic Escherichia coli in Jiuquan City, 2019–2020. Bulletin of Disease Control & Prevention, 37: 78–81.
13. Xu, Deshun, Lei Ji, Wei Yan, and Yuehua Shen. "Characteristics of cases with foodborne diarrheagenic Escherichia coli infection in Huzhou, China." *Czech Journal of Food Sciences* 41, no. 6 (2023).
14. Zhou, Shi-Xia, Li-Ping Wang, Meng-Yang Liu, Hai-Yang Zhang, Qing-Bin Lu, Lu-Sha Shi, Xiang Ren et al. "Characteristics of diarrheagenic Escherichia coli among patients with acute diarrhea in China, 2009–2018." *Journal of Infection* 83, no. 4 (2021): 424-432.

**Citation:** Yanbo Bai, Jia Yu, Chunru Wei, Haoran Yang, Lei Yang. Genomic Characterization of Antimicrobial Resistance in Foodborne Diarrheagenic Escherichia coli from Chifeng, China. *Int. J. Genet. Genom. Sci*. Vol. 4, Iss. 1, (2025). DOI:10.58489/2836-2306/009