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# Outbreak and dissemination of the international high-risk NDM-5-producing *Escherichia coli* ST410 clone in companion animal hospitals in China

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## ABSTRACT

Carbapenemase-producing *Enterobacterales* (CPEs) have increasingly been detected in companion animals, posing potential risks to both animal and public health. We investigated $bla_{NDM-5}$-positive *Escherichia coli* from fecal and environmental samples collected between 2019 and 2025 from 12 companion animal hospitals across six cities in China. A total of 41 $bla_{NDM-5}$-positive *E. coli* isolates were recovered from six hospitals, with 36 (87.8%) belonging to sequence type (ST) 410. The 36 *E. coli* ST410 isolates belonged to B4/H24RxC or B5/H24RxC sub-lineages and displayed close phylogenetic relatedness. Isolates from the same facility differed by only 0–7 cgSNPs, supporting clonal outbreaks. The environmental *E. coli* ST410 isolate showed 3–7 cgSNPs difference from fecal isolates from the same hospital. Global analysis incorporating 129 pet-derived $bla_{NDM}$-positive *E. coli* from GenBank revealed ST410 as the predominant sequence type (38.0%, *n*=49). Phylogenetic analysis of 85 pet-derived *E. coli* ST410 strains from seven countries, incorporating both genomes of our isolates and genomes from GenBank, revealed that they predominantly clustered within B4/H24RxC (*n*=35) and B5/H24RxC (*n*=47) sub-lineages. These strains were closely related, indicating limited genomic diversity despite wide geographic distribution. Importantly, pet-derived strains shared high genetic similarity (≤25 cgSNPs) with human-derived *E. coli* ST410 isolates, supporting cross-species transmission. Plasmid analysis identified IncX3 and hybrid IncFII/IncFIA/IncFIB plasmids as major $bla_{NDM-5}$ vehicles. Notably, a $bla_{NDM-5}$-carrying IncHI2-IncY plasmid was newly detected in companion animals. The frequent occurrence and outbreaks of NDM-5-producing *E. coli* ST410 in companion animal hospitals highlight its dominant role in $bla_{NDM-5}$ dissemination in veterinary settings and further indicate companion animals as reservoirs for high-risk CPE clones. These findings underscore the practical need for strengthened nosocomial infection control, regular environmental disinfection, and integrated AMR surveillance in veterinary hospitals to prevent hospital-acquired infections and their further spread to the community.

**Keywords:** Antimicrobial resistance; Carbapenemase-producing *Enterobacterales*; NDM-5; Companion animals; ST410; One Health

## INTRODUCTION

Antimicrobial resistance (AMR) has emerged as a critical public health threat of the 21st century, jeopardizing the effective prevention and treatment of infections in both humans and animals. Carbapenems have long been utilized as a last line of defense against severe bacterial infections, especially multidrug-resistant *Enterobacterales*. However, the rapid emergence and dissemination of carbapenemase-producing *Enterobacterales* (CPEs), which have been listed as critical priority pathogens by the World Health Organization (WHO), pose an increasingly severe challenge to human health (Jesudason, 2024).

NDM-producing *Escherichia coli* represents one of the most prevalent CPEs. Among them, sequence type (ST) 410 has emerged as one of the predominant lineages, increasingly replacing ST167 and ST131 as a major NDM-producing clone in recent years (Ba et al., 2024). *Escherichia coli* ST410 constitutes one of the major lineages of extraintestinal pathogenic *E. coli* (ExPEC), responsible for both nosocomial and community-acquired infections in humans, and is distinguished by its extensive intercontinental dissemination



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and multidrug-resistant phenotype (Manges et al., 2019). Thus, it has been identified as one of the particularly concerning international high-risk clones (Roer et al., 2018). ST410 has been divided into several subclones, including A/H53, B1/H24, B2/H24R, B3/H24Rx, B4/H24RxC, and B5/H24RxC (Ba et al., 2024; Chen et al., 2022; Feng et al., 2019; Roer et al., 2018). Hospital-associated subclones, particularly B4/H24RxC and B5/H24RxC, frequently harbor multiple resistance genes including *bla*$_{\text{CTX-M-15}}$, *bla*$_{\text{NDM-5}}$, and *bla*$_{\text{OXA-181}}$, together with virulence determinants like the high pathogenicity island (HPI) encoding the yersiniabactin iron acquisition system, thereby evolving into multidrug-resistant and hypervirulent strains that pose substantial therapeutic challenges (Ba et al., 2024; Feng et al., 2019). Beyond human clinical settings, ST410 has also been reported to cause nosocomial infections in companion animals, and it is increasingly regarded as a truly interspecies and inter-ecosystem transferable clone (Caddey et al., 2025; Nigg et al., 2019; Oh et al., 2020; Ramadan et al., 2020).

Despite the global ban on the use of carbapenems in animals, reports of carbapenemase genes in companion animals have been increasing in recent years, with the *bla*$_{\text{NDM}}$ gene being the most prevalent (Caddey et al., 2025; Chanchaithong et al., 2025; Moon et al., 2024), followed by *bla*$_{\text{OXA-181}}$ (Brilhante et al., 2020; Nigg et al., 2019). To date, *bla*$_{\text{NDM}}$ -positive *E. coli* strains of pet origin have been reported in multiple countries including China, Thailand (Chanchaithong et al., 2025), the United States (Cole et al., 2020), Japan (Harada et al., 2024), South Korea (Kyung et al., 2022), and Egypt (Ramadan et al., 2020). Likewise, *bla*$_{\text{OXA-181}}$ has been identified in pet-derived *E. coli* isolates from Portugal (Ramadan et al., 2020), Switzerland (Nigg et al., 2019), and Egypt (Ramadan et al., 2020). Numerous studies have shown that NDM-producing *E. coli* from companion animals are largely confined to a few internationally disseminated high-risk clones, particularly ST410 and ST167 (Caddey et al., 2025; Nigg et al., 2019; Oh et al., 2020; Ramadan et al., 2020).

Given the intimate human-companion animal contact, the emergence of CPE in pets poses potential risks to public health. Currently, there are only sporadic reports on the occurrence of CPE in companion animals, comprehensive surveillance on the epidemiological characterization of CPE in companion animals remain limited. Here we investigated the prevalence of CPE in companion animal hospitals across six cities in China, revealing NDM-5-producing *E. coli* ST410 as the predominant clone with evidence of nosocomial outbreaks.

## MATERIALS AND METHODS

### Sample collection, bacterial isolation, and detection of *bla*$_{\text{NDM}}$

During 2019 to 2025, a total of 341 fecal samples were collected from hospitalized or healthy companion animals (185 dogs and 156 cats) from 12 companion animal hospitals in Shanghai, Guangzhou, Shenzhen, Foshan, Suzhou, and Nanchang in China. Additionally, 392 environmental swab samples were collected at Hospital A in February 2025 from seven functional areas including animal ward areas, examination areas, public areas, and other clinical zones. Sampling areas included high-contact surfaces such as floors, cages, sinks, examination tables, and medical equipment. Detailed sampling distribution is provided in Supplementary Table S1. The samples were selectively cultured on MacConkey agar supplemented with 0.5 μg/mL meropenem. From each agar plate, one or two morphologically distinct colonies were randomly selected for further analysis. The presence of *bla*$_{\text{NDM}}$, *bla*$_{\text{KPC,}}$ and *bla*$_{\text{OXA-48}}$ genes was assessed by PCR using primers previously described (Poirel et al., 2011). Bacterial species were identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS; Bruker Daltonik GmbH, Germany).

### Antimicrobial susceptibility testing and conjugation experiments

The minimum inhibitory concentrations (MICs) of 16 antimicrobial agents, including imipenem, ampicillin, cefotaxime, ceftiofur, ceftazidime, amikacin, neomycin, gentamicin, ciprofloxacin, colistin, tetracycline, doxycycline, tigecycline, fosfomycin, trimethoprim-sulfamethoxazole, and florfenicol, were determined following the guidelines of CLSI (https://clsi.org/) and EUCAST (http://www.eucast.org/clinical_breakpoints/). MIC testing was performed using the agar dilution method, except for colistin and tigecycline, which were assessed by broth microdilution. Tigecycline MICs were interpreted using the US Food and Drug Administration MIC breakpoints (≥8 μg/mL) for *Enterobacterales* (https://www.fda.gov/drugs/development-resources/antibacterial-susceptibility-test-interpretive-criteria). All testing plates were incubated at 37 ℃ under aerobic conditions. *Escherichia coli* ATCC 25922 was included as the quality control strain.

In this study, streptomycin-resistant *E. coli* C600 was used as the recipient, and each *bla*$_{\text{NDM-5}}$-positive isolate was used as the donor for the conjugation experiment by broth mating at 37℃ for 16–20 h.

### Whole-genome sequencing and bioinformatics analysis

The whole genome DNA of *bla*$_{\text{NDM}}$-positive isolates was sequenced using the Illumina HiSeq X Ten and Oxford Nanopore MinION platforms. High-quality genome assemblies were generated through hybrid assembly with Unicycler v.0.4.7 (Wick et al., 2017). Multi-locus sequence typing (MLST) analysis was conducted using mlst v.2.19 (https://github.com/tseemann/mlst). Plasmid replicons, antimicrobial resistance genes, and heavy metal resistance genes were analyzed with ABRicate v.1.0 (https://github.com/tseemann/abricate), and AMRplusFinder (https://github.com/ncbi/amr). Core-genome single nucleotide polymorphism (cgSNP) analysis was executed using Snippy v.4.6.0 (https://github.com/tseemann/snippy). The population structure of the *bla*$_{\text{NDM-5}}$-carrying *E. coli* ST410 was determined through hierarchical Bayesian analysis of population structure (hierBAPS) (Cheng et al., 2013), with the final phylogenetic trees visualized using the interactive Tree of Life (iTOL) platform (https://itol.embl.de/). Comparative genomics of *bla*$_{\text{NDM}}$-harboring plasmids was performed using the BLAST Ring Image Generator (BRIG) (Alikhan et al., 2011). Detailed examination of *bla*$_{\text{NDM}}$ genetic environments and plasmid architecture was conducted through integrated analysis using blastn, BRIG, and Easyfig v.2.2.5 (http://mjsull.github.io/Easyfig/files.html).

To investigate the global epidemiological patterns of carbapenemase-producing *E. coli* originating from companion animals, we retrieved and downloaded genomic data from the Pathogen Detection Microbial Browser for Identification of Genetic and Genomic Elements (MicroBIGG-E) using the keywords "pet", "companion animal", "dog", "canine", "cat", and "feline". Carbapenemase-carrying *E. coli* isolates were

subsequently screened using MLST (Multilocus Sequence Typing) and ResFinder analysis.

## RESULTS

### Characterization of *bla*$_{NDM}$-carrying isolates

From 341 fecal samples collected across 12 companion animal hospitals, a total of 38 *bla*$_{NDM-5}$-positive *E. coli* isolates were recovered from 36 (10.6%) fecal samples, including 23 isolates from canine feces and 15 from feline feces across six companion animal hospitals located in three cities (Guangzhou, Shanghai, and Nanchang). Environmental surveillance at Hospital A yielded 48 *bla*$_{NDM}$-positive isolates from 44 (11.2%) samples, representing ten species with *Leclercia adecarboxylata* (*n*=26) being predominant, followed by *Pseudescherichia vulneris* (*n*=6), *Enterobacter hormaechei* (*n*=5), and *E. coli* (*n*=3) (Supplementary Table S1). The three environmental *E. coli* isolates all carried *bla*$_{NDM-5}$. Thus, a total of 41 *bla*$_{NDM-5}$-positive *E. coli* were obtained. Further antimicrobial susceptibility testing revealed that all 41 *bla*$_{NDM-5}$-positive *E. coli* isolates exhibited resistance to imipenem, ampicillin, cefoxitin, ceftazidime, and cefotaxime. Resistance rates to gentamicin and ciprofloxacin exceeded 97.6%, and 95.1%, respectively. Additionally, resistance rates for doxycycline, amikacin, florfenicol, and colistin were 73.2%, 58.5%, 9.8%, and 2.4%, respectively. All isolates remained susceptible to tigecycline (Table 1; Supplementary Figure S1A).

### Genotypic profiles of *bla*$_{NDM}$-positive isolates

All 41 *bla*$_{NDM-5}$-positive *E. coli* isolates were subjected to whole-genome sequencing for molecular characterization. Among the 38 *bla*$_{NDM-5}$-positive *E. coli* isolates of fecal origin, 35 (92.1%) belonged to the high-risk international clone ST410, while the remaining three isolates belonged to ST648, ST167, and ST5229, respectively. Interestingly, all isolates from hospitals A (*n*=11), D (*n*=15), and E (*n*=6), were ST410, and 3 of the 4 *bla*$_{NDM-5}$-positive *E. coli* isolates from hospital C belonged to ST410. However, the remaining two isolates, one ST167 and one ST648, were recovered from other hospitals, respectively. In addition, the three *E. coli* isolates obtained from environmental samples in Hospital A were identified as ST410, ST189, and ST17885. All *bla*$_{NDM-5}$-positive isolates harbored multiple ARGs and heavy metal-resistant gene clusters (Table 1). The positive rates of *bla*$_{CMY-2}$, *rmtB*, *bla*$_{CTX-M-55}$, *bla*$_{CTX-M-15}$, *fosA3*, and *floR* were 90.2%, 58.5%, 39.0%, 34.1%, 19.5%, and 7.3%, respectively (Supplementary Figure S1B). Notably, the environmental ST17885 *E. coli* GDG25A341 additionally harbored the colistin resistance gene *mcr-1*. Mutations of quinolone resistance-determining regions (QRDRs) were observed at the amino acid level in GyrA (D87N/S83L, 95.1%) and ParC (S80I, 95.1%). Additionally, 92.7% and 95.1% of the isolates carried metal resistance genes *pco* and *sil* clusters. Notably, all 36 *bla*$_{NDM-5}$-carrying *E. coli* ST410 isolates co-harbored *bla*$_{CMY-2}$ gene and exhibited QRDRs mutations at the amino acid level in GyrA (D87N/S83L) and ParC (S80I). These findings are consistent with the multidrug-resistant phenotypes observed in antimicrobial susceptibility testing, highlighting the clinical challenge posed by these strains.

### Phylogenetic relationships of *bla*$_{NDM-5}$-carrying *E. coli* ST410 isolates

Phylogenetic analysis revealed that the 36 *bla*$_{NDM-5}$-carrying ST410 strains clustered predominantly into two sub-clades, B4/H24RxC (*n*=10) and B5/H24RxC (*n*=26), as previously defined (Ba et al., 2024; Roer et al., 2018). To investigate the global phylogenetic relationships of *bla*$_{NDM}$-positive *E. coli* ST410 strains of companion animal origin, we retrieved a total of 129 pet-derived *bla*$_{NDM}$-positive *E. coli* isolates from GenBank. Among these, ST410 (38.0%, *n*=49) was the predominant sequence type, which included isolates from the United States (*n*=8), the United Kingdom (*n*=1), Egypt (*n*=7), South Korea (*n*=11), Thailand (*n*=6), and China (*n*=16) (Figure 1). Phylogenetic analysis was performed on 85 *bla*$_{NDM-5}$-carrying *E. coli* ST410 strains of companion animal origin, combining our 36 isolates with 49 GenBank isolates. The results revealed that most of the isolates (82/85) belonged to B4/H24RxC (n=40) and B5/H24RxC (*n*=42) and differed by only 0–100 cgSNPs within each of the two sub-clones, indicating close genetic relatedness (Figure 2). Notably, GZA9A16M differed by only 13 to 25 cgSNPs from pet-origin strains in Hangzhou, China, and South Korea. Importantly, isolates from hospitals A, C, and D exhibited only 0–7 cgSNPs differences, while strains from the same veterinary hospital retrieved from GenBank also showed minimal cgSNP variation, indicating clonal dissemination of *E. coli* ST410 within veterinary settings (Figure 2). Interestingly, the environmental isolate GDG25A380-1, obtained from hospital A in February 2025, differed by only 3–7 cgSNPs from isolates recovered from the same hospital in October 2024. These findings suggest that *E. coli* ST410 can persist in the veterinary hospital environment over time, highlighting its potential for sustained transmission in clinical settings.

In addition, to investigate the global phylogenetic relationships and provide evidence for cross-ecological transmission of *bla*$_{NDM}$-positive *E. coli* ST410 strains, we performed a phylogenetic analysis comparing the pet-origin strains with B4/H24RxC and B5/H24RxC sub-clade *E. coli* ST410 strains from diverse ecological niches in the GenBank database. The results demonstrated that the pet-origin isolates exhibited close genetic relatedness to human-origin strains. For example, strain GZA9A16M showed ≤9 cgSNP differences from a human-origin isolate from Guangzhou (GCA_029854555.1) and differed by only 16–19 cgSNPs from human-origin strains from Australia (GCA_012482135.1), Vietnam (GCA_018260215.1), and Switzerland (GCA_021371395.1), providing strong molecular evidence for cross-species transmission between human and companion animal populations (Figure 3). Furthermore, *E. coli* ST410 isolates recovered from companion animals in hospital D in Nanchang differed by only 16 to 19 cgSNPs from genetically related human-derived strains from multiple countries, including China, Germany, the USA, Thailand, and Finland, demonstrating the global clonal dissemination of this high-risk clone between companion animals and humans, which poses significant zoonotic risks.

### Characteristics of *bla*$_{NDM-5}$-carrying plasmid

Conjugation assays showed that, among the 41 *bla*$_{NDM-5}$-positive isolates, only 12 *bla*$_{NDM-5}$-carrying transconjugants were obtained. Of these, 10 harbored IncX3 plasmids, while the remaining two carried IncHI2 plasmids (Table 1). To comprehensively characterize the genetic context of *bla*$_{NDM-5}$, we randomly selected five representative strains for complete plasmid sequencing, including those carrying the predominant IncF plasmids as well as the less common IncY and IncHI2

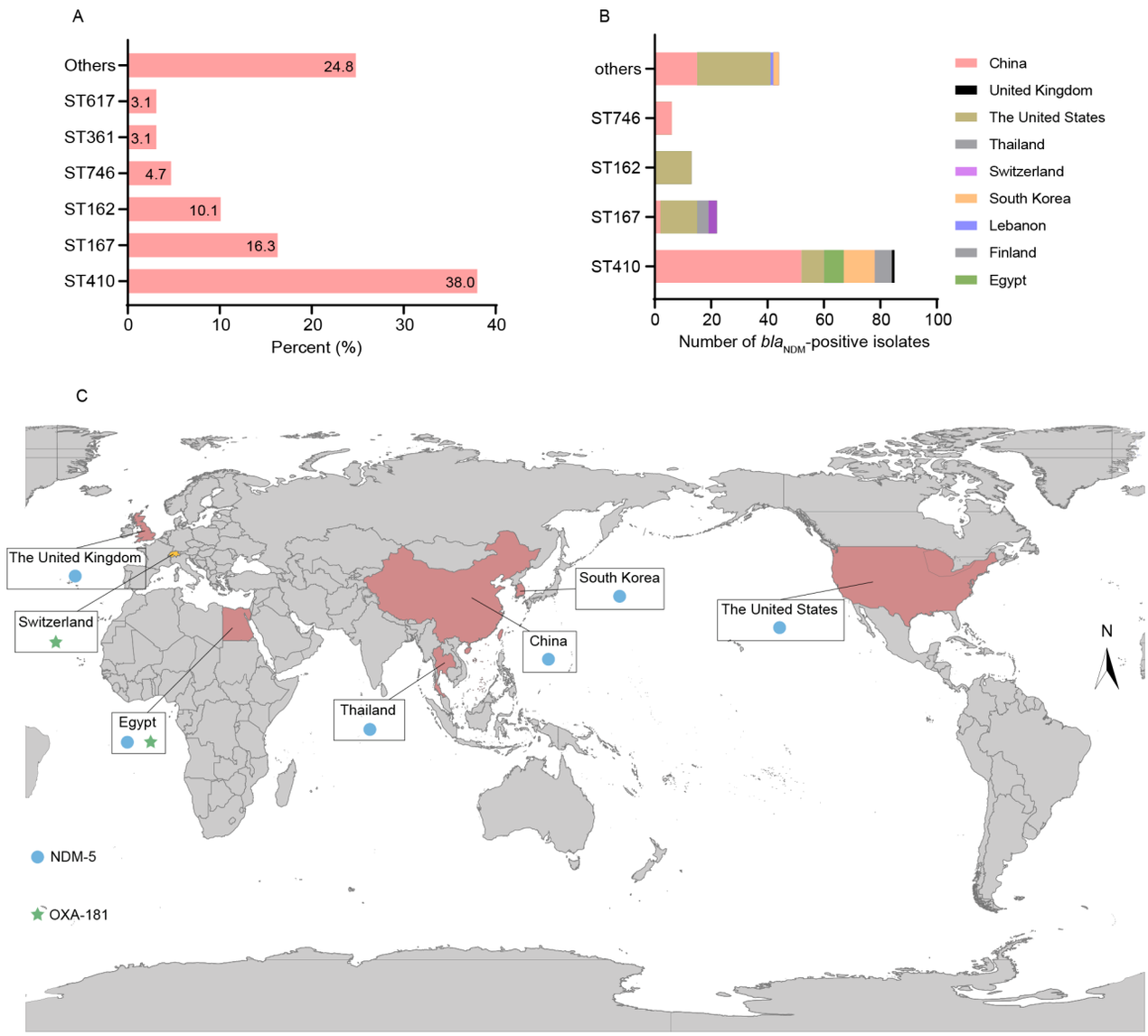


**Figure 1 Distribution of carbapenemase-producing *Escherichia coli* from companion animals**

A: Distribution of sequence types (STs) of 129 $bla_{NDM}$-positive *E. coli* isolates from companion animals in GenBank databases. B: Geographic distribution of sequence types among pet-derived $bla_{NDM}$-positive *E. coli* isolates from this study and GenBank databases. C: Geographic distribution of pet-derived *E. coli* ST410 harboring $bla_{NDM}$ or $bla_{OXA-181}$.

plasmids. Complete sequences of five $bla_{NDM}$-carrying plasmids, including pHNJXA36-1, pHNJXA32-1, pHNGDGA36-1, pHNGDGA39-1, and pHNGDGA71I-1, were obtained using both Illumina and Oxford Nanopore sequencing platforms.

Plasmids pHNJXA32-1 and pHNJXA36-1 were 108 271 bp and 108 280 bp in length, respectively, and both belonged to the IncF1:A1:B49-IncQ1 hybrid plasmids. BLASTn analysis indicated that both plasmids lacked a conjugative transfer region but possessed a multidrug resistance (MDR) region containing 16 resistance genes including $bla_{CTX-M-15}$, $bla_{NDM-5}$, and *aac(6')-Ib-cr*. Notably, these two plasmids showed 100% query coverage and >99.9% nucleotide identity with plasmids previously identified from human isolates in diverse regions, including pYJ1-NDM5 (Thailand; AP023225), pAMA1167-NDM-5 (Denmark; CP024805), and pE22P1 (China; CP123037) (Figure 4). Plasmid pHNGDGA39-1 (92 434 bp), although non-conjugative, shares a conserved backbone with pHNJXA32-1 and pHNJXA36-1 but carries only seven resistance genes, including $bla_{NDM-5}$ and *rmtB* (Supplementary Figure S1). Furthermore, all NDM-producing *E. coli* ST410 isolates carried similar IncF or IncF–IncQ replicons, consistent with the plasmid lineage typically associated with ST410 strains (Pitout & Chen, 2023; Pitout et al., 2024; Chanchaithong et al., 2025).

Plasmid pHNGDGA36-1, identified from the ST648 *E. coli* strain GDG24A36, is a phage-like IncY plasmid with a length of 88 678 bp. This non-conjugative plasmid harbors 12 resistance genes, including *rmtB* and $bla_{NDM-5}$. BLASTn analysis revealed that pHNGDGA36-1 shares high similarity to *E. coli* plasmid pCUVM3.3 (CP116973.1, pig, Thailand) and *Shigella flexneri* SWHIN_110_plasmid1 (CP055093.1, wastewater, Hong Kong), with over 90% coverage and >99.97% nucleotide identity (Supplementary Figure S2).

Plasmid pHNGDG71-1 is a 372 134 bp hybrid IncHI2-IncY plasmid recovered from the ST189 *E. coli* isolate GDG25A71. This plasmid exhibits high sequence similarity to pNDM-M121 (CP083586, meat, China) and pNDM-33 (CP076648, duck, China) (Supplementary Figure S3). The genetic context of $bla_{NDM-5}$ gene in pHNGDG71-1 resembled that of the duck-

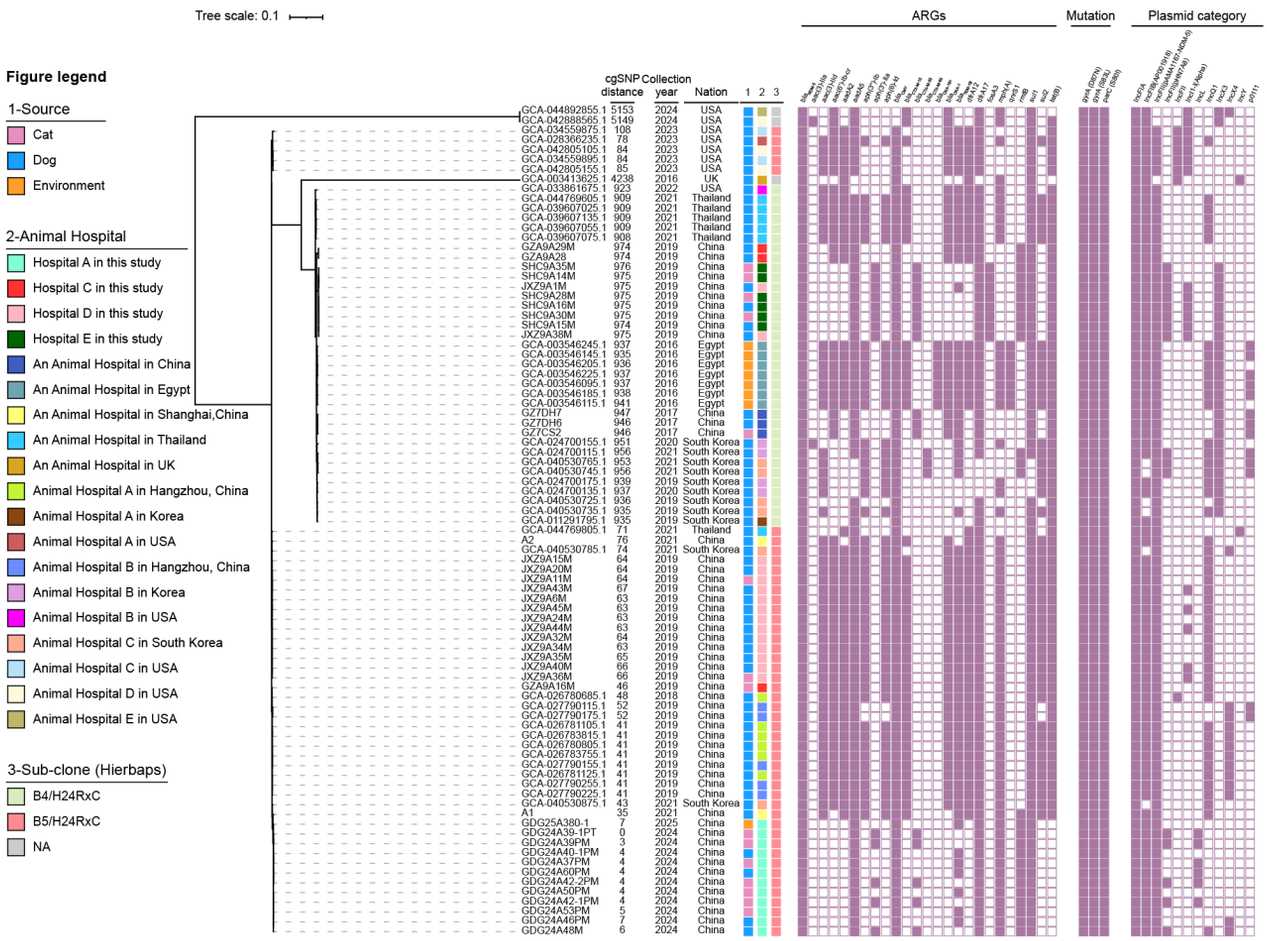


**Figure 2 Phylogenetic tree of *bla*$_{NDM-5}$-positive *E. coli* ST410 isolates from companion animal hospitals**

NA: Not applicable.

derived plasmid pNDM-33 from Guangdong Province, although the Tn*7051* transposon was truncated (He et al., 2023; Lv et al., 2024; Zhao et al., 2021). The formation of this genetic environment is likely mediated by IS*26*-associated deletion and inversion events. This *bla*$_{NDM-5}$-harboring IncHI2 plasmid likely originated from duck-associated *E. coli* in Guangdong Province and has subsequently disseminated across diverse reservoirs, including humans, vegetables, fish, and poultry (He et al., 2023; Lv et al., 2022, 2024; Zhao et al., 2021). To our knowledge, this is the first report of *bla*$_{NDM-5}$-carrying IncHI2 plasmid in companion animals.

## DISCUSSION

Companion animals serve as important reservoirs for antimicrobial-resistant bacteria, with various carbapenem resistance genes such as *bla*$_{NDM}$ and *bla*$_{OXA-181/-48}$, have been identified in *Enterobacterales* originating from pets (Caddey et al., 2025; Ramírez-Castillo et al., 2023; Rincón-Real & Suárez-Alfonso, 2022). However, most previous studies have focused on the prevalence of carbapenem-resistant *Enterobacterales* (CRE) in only a limited number of companion animal hospitals in local regions. In contrast to those sporadic reports, our study conducted multi-center surveillance across 12 companion animal hospitals in six Chinese cities from 2019 to 2025 and recovered *bla*$_{NDM-5}$-positive *E. coli* from hospitalized and outpatient animals in six hospitals, providing robust evidence that *E. coli* ST410 represents the predominant lineage among pet-derived carbapenemase-producing *E. coli* (PDCPE). In China, *bla*$_{NDM}$-positive *E. coli* was first detected in companion animals in 2015 (Cui et al., 2018), and *bla*$_{NDM-5}$-positive *E. coli* ST410 isolates were subsequently detected in pet feces collected in 2017 (Wang et al., 2021). Current limited data indicate that *E. coli* ST410 represents the predominant lineage among pet-derived carbapenemase-producing *E. coli* (PDCPE) isolates in China (Chen et al., 2025; Teng et al., 2023; Wang et al., 2021). The findings of this study further confirm that *E. coli* ST410 is the predominant *bla*$_{NDM-5}$-producing *E. coli* in companion animals in China. Interestingly, *E. coli* ST410 was also reported to be the dominant PDCPE in other countries, including South Korea and Thailand (Chanchaithong et al., 2025; Kyung et al., 2022; Moon et al., 2024). Considering the frequent emergence of *bla*$_{NDM-5}$-positive *E. coli* ST410 in companion animals, we suspect that *E. coli* ST410 might represent the dominant PDCPE globally. Thus, we conducted a genomic analysis of all PDCPE deposited in public databases. It revealed that *E. coli* ST410 did represent the most prevalent sequence type among PDCPE globally, exhibiting high frequency and broad geographic distribution (Figure 1). This global dominance raises important questions about its potential for cross-species transmission.

In human clinical settings, *E. coli* ST410 has emerged as an internationally recognized high-risk clone, becoming one of the predominant carbapenem-resistant *E. coli* lineages globally (Chen et al., 2022; Feng et al., 2019; Roer et al., 2018). In China, *E. coli* ST410 has gradually replaced ST167 and

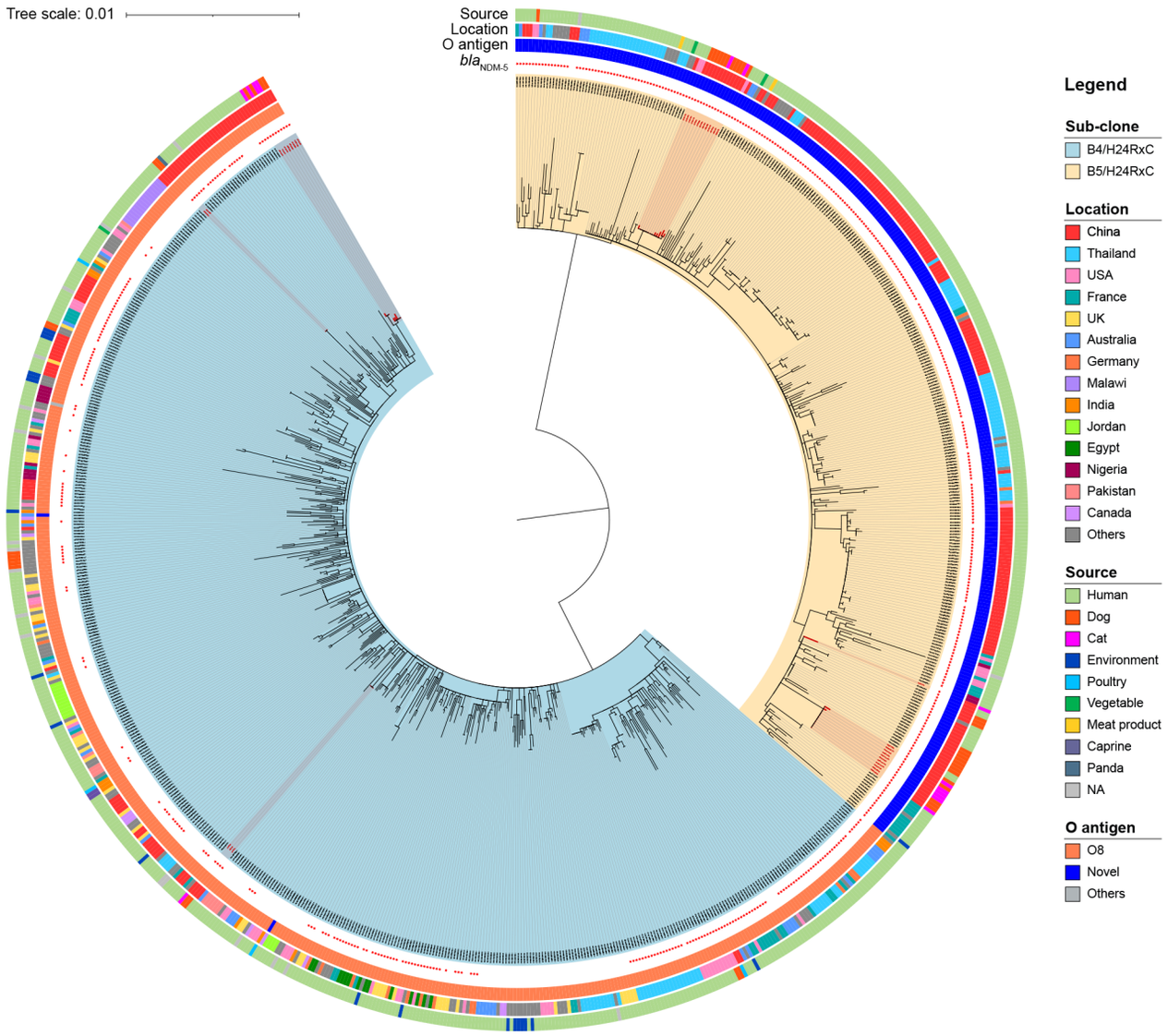


**Figure 3 Phylogenetic relationship of *Escherichia coli* ST410 sub-clones B4/H24RxC and B5/H24RxC from multiple sources and geographic locations**

ST131 and emerged as the most prevalent sequence type among NDM-producing *E. coli* isolates recovered from patients (Ba et al., 2024). Based on phylogenetic analysis, *E. coli* ST410 has been diversified into six subclones, including A/H53, B1/H24, B2/H24R, B3/H24Rx, B4/H24RxC, and B5/H24RxC (Ba et al., 2024; Chen et al., 2022; Feng et al., 2019; Roer et al., 2018). Among these, the B5/H24RxC sub-lineage represents a recently emerged hypervirulent and highly resistant clone, while both B4/H24RxC and B5/H24RxC pose significant threats to clinical treatment (Ba et al., 2024). Remarkably, our study revealed that pet-derived *E. coli* ST410 isolates from different countries exhibited high genetic relatedness, with 96.5% belonging to either the B4/H24RxC or the hypervirulent B5/H24RxC sub-lineages. By incorporating human-derived *E. coli* ST410 genomes into our phylogenetic analysis, we found that pet-origin *E. coli* ST410 isolates were highly related to human-derived strains from geographically distant regions, differing by fewer than 20 cgSNPs. This provides genomic evidence supporting clonal dissemination of *E. coli* ST410 across human and animal reservoirs. Given the close contact between humans and companion animals, the predominance of *E. coli* ST410 among pet-derived NDM-producing CREs suggests that companion animals may serve as critical reservoirs for the community-level transmission of CRE. This concern is further supported by our detection of other high-risk clinical lineages in pets, including *E. coli* ST167 and ST648, which are internationally recognized ExPEC lineages frequently associated with human clinical infections (Grönthal et al., 2018; Manges et al., 2019). Their presence in companion animals indicates that multiple high-risk lineages may circulate at the human–animal interface, highlighting the urgent need for integrated One Health strategies to control the spread of CRE between humans and pets (Caddey et al., 2025).

A key finding of this study is the occurrence of clustered outbreaks of NDM-5-producing *E. coli* ST410 in multiple veterinary hospitals, highlighting its role in clonal dissemination within veterinary settings. Notably, our environmental monitoring revealed close genetic relatedness between *E. coli* ST410 isolates from hospital environments and those from animals, with genetically related strains (0–10 cgSNPs) persisting for at least four months in the same hospital. These findings align with documented nosocomial outbreaks in human healthcare settings, where ST410 dissemination has been attributed to environmental contamination and inadequate infection control measures (Ba

**Table 1 Characteristics of *bla*$_{NDM-5}$-carrying *E. coli* from this study**

| Isolate ID | Time | Hospital | Animal | Outpatient/ Hospitalized animal | Sequence Type | ST410 Sub-clone | O antigen | Resistance gene | Heavy metal resistance genes | Plasmid |
|---|---|---|---|---|---|---|---|---|---|---|
| GDG24A36-2PT | 2024 | B | cat | hospitalized | ST648 | / | O83 | *aac(3)-IId*, *aadA2*, *aadA22*, *aph(3'')-Ib*, *aph(3')-Ia*, *aph(6)-Id*, *bla*$_{CMY-2}$, *bla*$_{CTX-M-55}$, *bla*$_{NDM-5}$, dfrA12, *erm*(B), *floR*, *mph*(A), *parC* (S80I), *rmtB*, *sul1*, *sul3*, *tet*(A) | *merCPRRT* | IncFII, IncY |
| GDG24A37PM | 2024 | A | cat | hospitalized | ST410 | B5/H24RxC | Novel | *aadA5*, *bla*$_{CMY-2}$, *bla*$_{NDM-5}$, *bla*$_{TEM-1B}$, *dfrA17*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncL |
| GDG24A39-1PT | 2024 | A | cat | hospitalized | ST410 | B5/H24RxC | Novel | *aadA5*, *aph(3')-IIa*, *bla*$_{CMY-2}$, *bla*$_{CTX-M-55}$, *bla*$_{NDM-5}$, *bla*$_{TEM-214}$, *dfrA17*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncL |
| GDG24A39PM | 2024 | A | cat | hospitalized | ST410 | B5/H24RxC | Novel | *aadA5*, *aph(3')-IIa*, *bla*$_{CMY-2}$, *bla*$_{CTX-M-55}$, *bla*$_{NDM-5}$, *bla*$_{TEM-214}$, *dfrA17*, *erm(B)*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncL |
| GDG24A40-1PM | 2024 | A | dog | hospitalized | ST410 | B5/H24RxC | Novel | *aadA5*, *bla*$_{CMY-2}$, *bla*$_{NDM-5}$, *bla*$_{TEM-1B}$, *dfrA17*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5) |
| GDG24A42-1PM | 2024 | A | cat | hospitalized | ST410 | B5/H24RxC | Novel | *aadA5*, *aph(3')-IIa*, *bla*$_{CMY-2}$, *bla*$_{CTX-M-55}$, *bla*$_{NDM-5}$, *bla*$_{TEM-216}$, *dfrA17*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncL |
| GDG24A42-2PM | 2024 | A | cat | hospitalized | ST410 | B5/H24RxC | Novel | *aadA5*, *aph(3')-IIa*, *bla*$_{CMY-2}$, *bla*$_{CTX-M-55}$, *bla*$_{NDM-5}$, *bla*$_{TEM-216}$, *dfrA17*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncL |
| GDG24A46PM | 2024 | A | dog | hospitalized | ST410 | B5/H24RxC | Novel | *aadA5*, *bla*$_{CMY-2}$, *bla*$_{NDM-5}$, *bla*$_{TEM-1B}$, *dfrA17*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | Col(MG828), IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncX4 |
| GDG24A48M | 2024 | A | dog | hospitalized | ST410 | B5/H24RxC | Novel | *aadA5*, *aph(3')-IIa*, *bla*$_{CMY-2}$, *bla*$_{CTX-M-55}$, *bla*$_{NDM-5}$, *bla*$_{TEM-216}$, *dfrA17*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | Col(MG828), IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncQ1, IncX4 |
| GDG24A50PM | 2024 | A | cat | outpatient | ST410 | B5/H24RxC | Novel | *aadA5*, *bla*$_{CMY-2}$, *bla*$_{NDM-5}$, *bla*$_{TEM-1B}$, *dfrA17*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5) |
| GDG24A53PM | 2024 | A | cat | hospitalized | ST410 | B5/H24RxC | Novel | *aadA5*, *bla*$_{CMY-2}$, *bla*$_{NDM-5}$, *bla*$_{TEM-1B}$, *dfrA17*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5) |
| GDG24A60PM | 2024 | A | dog | hospitalized | ST410 | B5/H24RxC | Novel | *aadA5*, *bla*$_{CMY-2}$, *bla*$_{NDM-5}$, *bla*$_{TEM-1B}$, *dfrA17*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncL |
| GDG25A341I | 2025 | A | environment | N/A | Novel | / | O113 | *aadA1*, *aadA2*, *bla*$_{CARB-2}$, *bla*$_{CTX-M-55}$, *bla*$_{NDM-5}$, *bla*$_{TEM-70}$, *cmlA1*, *dfrA16*, *floR*, *mcr-1.1*, *sul3*, *tet*(A) | *merCPRRT* | IncFII(pHN7A8), IncHI2, IncHI2A, IncI1, IncQ1, p0111 |
| GDG25A380-1KI | 2024 | A | environment | N/A | ST410 | B5/H24RxC | Novel | *aadA5*, *bla*$_{CMY-2}$, *bla*$_{NDM-5}$, *bla*$_{TEM-1B}$, *dfrA17*, *mph*(A), *rmtB*, *sul1* | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5) |
| GDG25A71I | 2024 | A | environment | N/A | ST189 | / | O80 | *aac(3)-IV*, *aadA2*, *aadA24*, *aph(3'')-Ib*, *aph(3')-Ia*, *aph(4)-Ia*, *aph(6)-Id*, *ARR-3*, *bla*$_{NDM-5}$, *bla*$_{OXA-10}$, *bla*$_{TEM-70}$, *cmlA1*, *dfrA14*, *floR*, *lnu*(F), *qnrS1*, *sul3*, *tet*(A) | *merCPRRT* | IncHI2, IncHI2A, IncY |
| GZA9A02M | 2019 | C | dog | hospitalized | ST5229 | / | Novel | *aac(3)-IId*, *aadA1*, *aadA2b*, *aph(3')-Ia*, *blaDHA-1*, *bla*$_{NDM-5}$, *blaTEM-30*, *cmlA1*, *dfrA12*, *dfrA17*, *floR*, *lnu(F)*, *mph*(A), *qnrB4*, *sul1*, *sul2*, *sul3*, *tet*(A) | *pcoABCDRS silABCEFPRS* | IncX3 |

Continued

| Isolate ID | Time | Hospital | Animal | Outpatient/ Hospitalized animal | Sequence Type | ST410 Sub-clone | O antigen | Resistance gene | Heavy metal resistance genes | Plasmid |
|---|---|---|---|---|---|---|---|---|---|---|
| GZA9A16M | 2019 | C | cat | hospitalized | ST410 | B5/H24RxC | Novel | *aac(3)-IId*, *aac(6')-Ib-cr*, *aadA2*, *aadA5*, *aph(3'')-Ib*, *aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3*, *dfrA12*, *dfrA17*, *mph*(A), *sul1*, *sul2*, *tet*(B) | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncQ1 |
| GZA9A28M | 2019 | C | dog | outpatient | ST410 | B4/H24RxC | O8 | *aac(6')-Ib-cr*, *aadA2*, *aadA5*, $bla_{CMY-2}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3*, *dfrA12*, *dfrA17*, *rmtB*, *sul1*, *tet*(B) | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5) |
| GZA9A29M | 2019 | C | dog | hospitalized | ST410 | B4/H24RxC | O8 | *aac(6')-Ib-cr*, *aadA2*, *aadA5*, $bla_{CMY-2}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3*, *dfrA12*, *dfrA17*, *rmtB*, *sul1*, *tet*(B) | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5) |
| JXZ9A01M | 2019 | D | dog | hospitalized | ST410 | B4/H24RxC | O8 | *aadA5*, *aph(3')-IIa*, $bla_{CMY-2}$, $bla_{CTX-M-55}$, $bla_{NDM-5}$, $bla_{TEM-1B}$, *dfrA17*, *fosA3*, *rmtB*, *sul1*, *tet*(B) | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncI1, IncX3 |
| JXZ9A06M | 2019 | D | dog | hospitalized | ST410 | B5/H24RxC | Novel | *aac(3)-IId*, *aac(6')-Ib-cr*, *aadA2*, *aadA5*, *aph(3'')-Ib*, *aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3*, *dfrA12*, *dfrA17*, *mph*(A), *sul1*, *sul2*, *tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncQ1 |
| JXZ9A11M | 2019 | D | cat | N/A | ST410 | B5/H24RxC | Novel | *aac(3)-IId*, *aac(6')-Ib-cr*, *aadA2*, *aadA5*, *aph(3'')-Ib*, *aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3*, *dfrA12*, *dfrA17*, *mph*(A), *sul1*, *sul2*, *tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncQ1 |
| JXZ9A15M | 2019 | D | dog | N/A | ST410 | B5/H24RxC | Novel | *aac(3)-IId*, *aac(6')-Ib-cr*, *aadA2*, *aadA5*, *aph(3'')-Ib*, *aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3*, *dfrA12*, *dfrA17*, *mph*(A), *sul1*, *sul2*, *tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncQ1 |
| JXZ9A20M | 2019 | D | dog | N/A | ST410 | B5/H24RxC | Novel | *aac(3)-IId*, *aac(6')-Ib-cr*, *aadA2*, *aadA5*, *aph(3'')-Ib*, *aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3*, *dfrA12*, *dfrA17*, *mph*(A), *sul1*, *sul2*, *tet*(B) | *pcoABCDRS silACEFPRS* | Col(MG828), IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncQ1 |
| JXZ9A24M | 2019 | D | dog | hospitalized | ST410 | B5/H24RxC | Novel | *aac(3)-IId*, *aac(6')-Ib-cr*, *aadA2*, *aadA5*, *aph(3'')-Ib*, *aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3*, *dfrA12*, *dfrA17*, *mph*(A), *sul1*, *sul2*, *tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncQ1 |
| JXZ9A32M | 2019 | D | dog | hospitalized | ST410 | B5/H24RxC | Novel | *aac(3)-IId*, *aac(6')-Ib-cr*, *aadA2*, *aadA5*, *aph(3'')-Ib*, *aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3*, *dfrA12*, *dfrA17*, *mph*(A), *sul1*, *sul2*, *tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncQ1 |
| JXZ9A34M | 2019 | D | dog | hospitalized | ST410 | B5/H24RxC | Novel | *aac(3)-IId*, *aac(6')-Ib-cr*, *aadA2*, *aadA5*, *aph(3'')-Ib*, *aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3*, *dfrA12*, *dfrA17*, *mph*(A), *sul1*, sul2, *tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncQ1 |
| JXZ9A35M | 2019 | D | dog | hospitalized | ST410 | B5/H24RxC | Novel | *aac(3)-IId*, *aac(6')-Ib-cr*, *aadA2*, *aadA5*, *aph(3'')-Ib*, *aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3*, *dfrA12*, *dfrA17*, *mph*(A), *sul1*, *sul2*, *tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncQ1 |

Continued

| Isolate ID | Time | Hospital | Animal | Outpatient/ Hospitalized animal | Sequence Type | ST410 Sub-clone | O antigen | Resistance gene | Heavy metal resistance genes | Plasmid |
|---|---|---|---|---|---|---|---|---|---|---|
| JXZ9A36M | 2019 | D | cat | hospitalized | ST410 | B5/H24RxC | Novel | *aac(3)-IId, aac(6')-Ib-cr, aadA2, aadA5, aph(3'')-Ib, aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3, dfrA12, dfrA17, mph*(A), *sul1, sul2, tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncI1, IncQ1 |
| JXZ9A38M | 2019 | D | dog | outpatient | ST410 | B4/H24RxC | O8 | *aadA5, aph(3')-IIa*, $bla_{CMY-2}$, $bla_{CTX-M-55}$, $bla_{NDM-5}$, $bla_{TEM-214}$, *dfrA17, fosA3, rmtB, sul1, tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncI1, IncX3 |
| JXZ9A40M | 2019 | D | dog | outpatient | ST410 | B5/H24RxC | Novel | *aac(3)-IId, aac(6')-Ib-cr, aadA2, aadA5, aph(3'')-Ib, aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3, dfrA12, dfrA17, mph*(A), *sul1, sul2, tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncI1, IncQ1 |
| JXZ9A43M | 2019 | D | dog | outpatient | ST410 | B5/H24RxC | Novel | *aac(3)-IId, aac(6')-Ib-cr, aadA2, aadA5, aph(3'')-Ib, aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3, dfrA12, dfrA17, mph*(A), *sul1, sul2, tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncI1, IncQ1 |
| JXZ9A44M | 2019 | D | dog | N/A | ST410 | B5/H24RxC | Novel | *aac(3)-IId, aac(6')-Ib-cr, aadA2, aadA5, aph(3'')-Ib, aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3, dfrA12, dfrA17, mph*(A), *sul1, sul2, tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncI1, IncQ1 |
| JXZ9A45M | 2019 | D | dog | N/A | ST410 | B5/H24RxC | Novel | *aac(3)-IId, aac(6')-Ib-cr, aadA2, aadA5, aph(3'')-Ib, aph(6)-Id*, $bla_{CMY-2}$, $bla_{CTX-M-15}$, $bla_{NDM-5}$, $bla_{OXA-1}$, $bla_{TEM-1B}$, *catB3, dfrA12, dfrA17, mph*(A), *sul1, sul2, tet*(B) | *pcoABCDRS silACEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncI1, IncQ1 |
| SHC9A14M | 2019 | E | cat | outpatient | ST410 | B4/H24RxC | O8 | aadA5, aph(3')-IIa, $bla_{CMY-2}$, $bla_{CTX-M-55}$, $bla_{NDM-5}$, $bla_{TEM-214}$, dfrA17, fosA3, rmtB, sul1, *tet*(B) | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncX3 |
| SHC9A15M | 2019 | E | dog | outpatient | ST410 | B4/H24RxC | O8 | aadA5, aph(3')-IIa, $bla_{CMY-2}$, $bla_{CTX-M-55}$, $bla_{NDM-5}$, $bla_{TEM-214}$, *dfrA17, fosA3, rmtB, sul1, tet*(B) | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncI1, IncX3 |
| SHC9A16M | 2019 | E | dog | outpatient | ST410 | B4/H24RxC | O8 | *aadA5, aph(3')-IIa*, $bla_{CMY-2}$, $bla_{CTX-M-55}$, $bla_{NDM-5}$, $bla_{TEM-214}$, *dfrA17, fosA3, rmtB, sul1, tet*(B) | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncI1, IncX3 |
| SHC9A28M | 2019 | E | cat | hospitalized | ST410 | B4/H24RxC | O8 | *aadA5, aph(3')-IIa*, $bla_{CMY-2}$, $bla_{CTX-M-55}$, $bla_{NDM-5}$, $bla_{TEM-214}$, *dfrA17, fosA3, rmtB, sul1, tet*(B) | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncI1, IncX3 |
| SHC9A30M | 2019 | E | cat | outpatient | ST410 | B4/H24RxC | O8 | *aadA5, aph(3')-IIa*, $bla_{CMY-2}$, $bla_{CTX-M-55}$, $bla_{NDM-5}$, $bla_{TEM-214}$, *dfrA17, fosA3, rmtB, sul1, tet*(B) | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncI1, IncX3 |
| SHC9A35M | 2019 | E | cat | outpatient | ST410 | B4/H24RxC | O8 | *aadA5, aph(3')-IIa*, $bla_{CMY-2}$, $bla_{CTX-M-55}$, $bla_{NDM-5}$, $bla_{TEM-214}$, *dfrA17, fosA3, rmtB, sul1, tet*(B) | *pcoABCDRS silABCEFPRS* | IncFIA, IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFII(pHN7A8), IncX3 |
| SHS9A09M | 2019 | F | dog | hospitalized | ST167 | / | O89 | *aac(3)-IId, aadA5*, $bla_{CTX-M-55}$, $bla_{NDM-5}$, $bla_{TEM-1B}$, dfrA17, *erm*(B), *mph*(A), *qepA1, rmtB, sul1, tet*(B) | *pcoABCDRS silABCEFPRS* | IncFIA, IncI1, IncX3 |

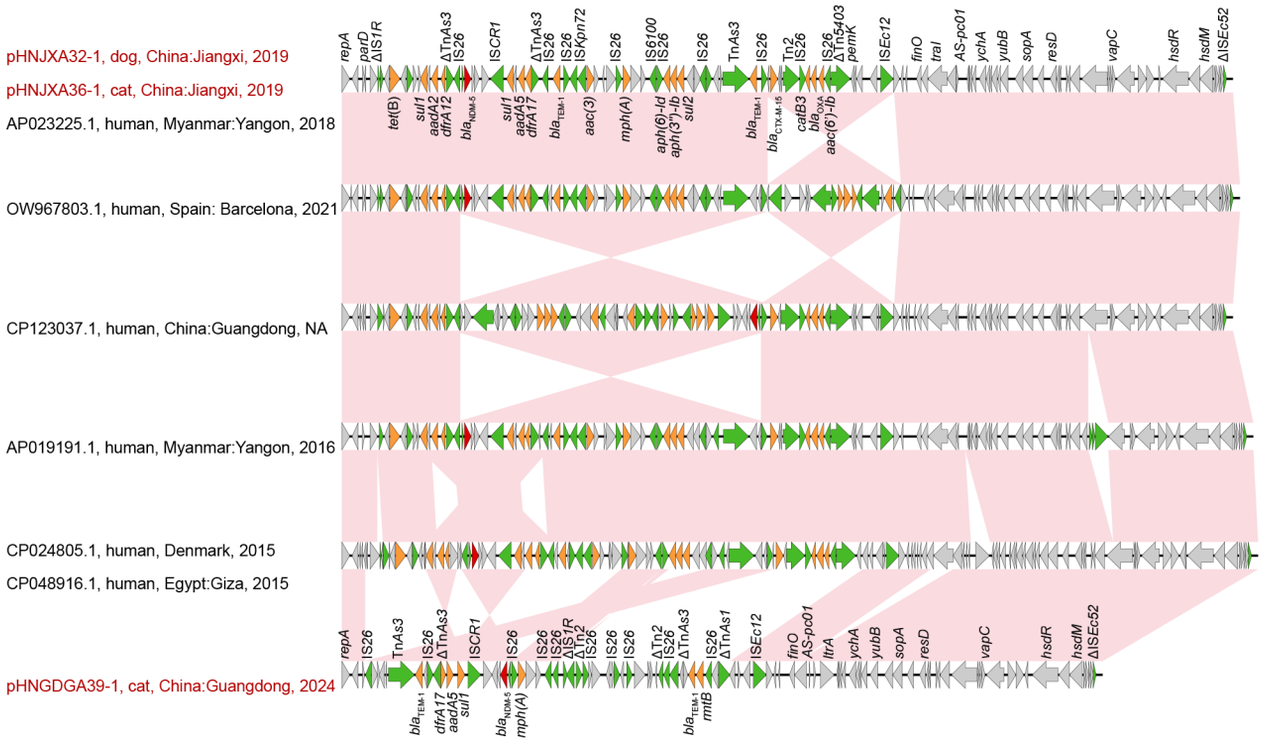


**Figure 4 Linear comparisons of the complete sequences of IncF1:A1:B49-IncQ1 and IncF1:A1:B49 plasmids**

et al., 2024; Pitout et al., 2024; Yao et al., 2025), and mirror the outbreak of *E. coli* ST410 in a Swiss pet hospital where environmental persistence facilitated transmission of hospitalized animals (Nigg et al., 2019). Overall, these findings highlight that *E. coli* ST410 can persist in companion animal hospital environments and is capable of transmission between animals and environment, thereby increasing the risk of nosocomial infections and spillover to humans. The demonstration of environment-mediated transmission in companion animal hospitals underscores the immediate need for hospital-level infection control strategies, including enhanced environmental disinfection protocols, strict hand hygiene practices, isolation of infected animals, proper waste management, and regular environmental surveillance to prevent hospital-acquired infections and their further spread to the community (Caddey et al., 2025; Conoscenti et al., 2024; Pinto et al., 2023). However, effective control strategies require further surveillance data and in-depth research to inform evidence-based interventions.

## CONCLUSION

In conclusion, our findings demonstrate the outbreak and wide dissemination of the international high-risk NDM-5-producing *E. coli* ST410 clone in companion animal hospital settings globally. This study reveals that companion animals serve as important reservoirs of CRE, with genomic evidence supporting cross-species transmission between pet and human isolates. The close genetic relatedness between pet- and human-derived *E. coli* ST410 strains highlights a significant “One Health” public health threat, underscoring the urgent need for comprehensive surveillance systems integrating veterinary and human healthcare settings, strengthened infection prevention measures in veterinary hospitals, enhanced antimicrobial stewardship, and coordinated cross-sector strategies to disrupt transmission at the human–animal–environment interface. These findings underscore the practical need for strengthened nosocomial infection control, regular environmental disinfection, and integrated AMR surveillance in veterinary hospitals to prevent hospital-acquired infections and their further spread to the community.

## DATA AVAILABILITY

All the data supporting the conclusions of this article are included within the article. The genomes of the 41 sequenced isolates have been deposited in NCBI database under Bioproject accession number PRJNA1269265, Genome Sequence Archive (GSA) (https://ngdc.cncb.ac.cn/gsa/) under PRJCA065114, and Science Data Bank (DOI: 10.57760/sciencedb.j00139.00328).

## COMPETING INTERESTS

The authors declare that they have no competing interests.

## AUTHORS’ CONTRIBUTIONS

J.H.L. and L.C.L. conceived the research. Z.P.C., B.Q. Z., W.H.L., J.Q.H., X.E.W., L.D.X., and Z.W.W. collected the data. L.C.L., J.H.L., Z.P.C., B.Q.Z., J.Y.T., and W.Y.H. analyzed and interpreted the data. L.C.L. and Z.P.C. drafted the manuscript, J.H.L. and L.C.L. revised the report. All authors read and approved the final version of the manuscript.

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