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Prevalence of Beta-lactam Resistance Genes (Bla Genes) in Multidrug-Resistant Strains of *Escherichia coli* and *Klebsiella pneumoniae* Isolated from Infections at a University Hospital in Abidjan, Ivory Coast

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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Abstract

Aim: The overall objective of this study was to characterise the bla genes responsible for beta-lactam resistance in two major strains of Enterobacteriaceae (*Escherichia coli* and *Klebsiella pneumoniae*) involved in bacterial infections and producing extended-spectrum beta-lactamases.

Study Design: The resistance of Enterobacteriaceae to various classes of antibiotics in general, and to the beta-lactam class in particular, is showing a worrying trend in Côte d'Ivoire and around the world. This resistance is due to the production of extended-spectrum beta-lactamases (ESBLs) encoded by bla genes.

Place and Duration of Study: This study was conducted from August 2022 to February 2024 in Abidjan (Ivory Coast) at the Pasteur Institute of Ivory Coast (IPCI), at the Cocody site, specifically within the Unit for Antibiotics, Natural Substances, and Surveillance of Microorganisms and Anti-Infective Agents (ASSURMI).

Methodology: These strains were isolated from biological samples collected from various hospital departments. A total of 40 Enterobacteriaceae strains were identified using MALDI-TOF mass spectrometry (MS), and antibiotic susceptibility testing (antibiogram) was performed using the Mueller-Hinton agar diffusion method. Genes conferring resistance to Beta-lactams were detected using conventional PCR.

Results: The strains studied were *Escherichia coli* (25) and *Klebsiella pneumoniae* (15). Seventy-five per cent of the strains were multidrug-resistant (*Escherichia coli*: 19/25; *Klebsiella pneumoniae*: 11/15). High resistance rates ranging from 52.63% to 100% to amoxicillin-clavulanic acid, aztreonam, and third-generation cephalosporins (cefepime, ceftriaxone, cefotaxime, cefixime) were observed. The Beta-lactam resistance genes detected were *blaTEM, blaCTX-M-1, blaCTX-M-8, blaSHV, and blaCTX-M- with prevalence rates of* 60%, 50%, 35%, 32.5%, and 7.5%, respectively. The co-expression rate of the resistance genes was 22,5 %, 17,5 %, 15 %, 12,5 %, 7,5 % et 2,5 %, respectively, for the associations bla_{TEM} /$bla_{CTX\text{-}M\text{-}8}$, bla_{TEM} /$bla_{CTX\text{-}M\text{-}1}$, bla_{SHV} /$bla_{CTX\text{-}M\text{-}1}$, bla_{SHV} /$bla_{CTX\text{-}M\text{-}8}$, bla_{TEM} / bla_{SHV}, bla_{TEM} / bla_{SHV} / $bla_{CTX\text{-}M\text{-}1}$.

Conclusion: This study revealed the presence and persistence of bla genes that have been under surveillance for many years, with an increase in the prevalence of certain genes.

Keywords: Escherichia coli; Klebsiella pneumoniae; bla resistance genes; multidrug-resistant bacteria.

1. Introduction

Hospitals, communities, farms, fish farming, and agriculture are sectors where the constant use and misuse of antibiotics significantly alter the microbial ecosystem. These practices tend to increase the prevalence of antibiotic-resistant bacteria (Dosso et al., 2000). The emergence and spread of resistant bacteria are due to their adaptability, which manifests itself in their ability to acquire new properties. This occurs through changes either in their genome (mutations) or through the acquisition of genetic information via mobile genetic elements such as plasmids and transposons (Carattoli, 2008; Leverstein-Van Hall et al., 2011). As a result, the spread of resistance genes among bacteria has led to the emergence of bacteria resistant to multiple classes of antibiotics (multidrug-resistant bacteria, or MDR bacteria). The species in question include, in particular, methicillin-resistant *Staphylococcus aureus* (MRSA), ceftazidime-resistant *Pseudomonas* (CRP), ticarcillin-resistant *Acinetobacter* (TRA), vancomycin-resistant enterococci (VRE), and extended-spectrum beta-lactamase-producing Enterobacteriaceae (ESBL-producing Enterobacteriaceae) (Bourgeois-Nicolaos et al., 2006; Canton et al., 2008). In human medicine, antibiotics in the beta-lactam class (penicillins, cephalosporins, monobactams, and carbapenems) are the most commonly used for treating Gram-negative bacterial infections. Indeed, these antibiotics have a broad antibacterial spectrum, time-dependent bactericidal activity, low toxicity, and a wide range of available compounds (Ferech & Coenen, 2006; Vander & Elseviers, 2006; Pitout & Laupland, 2008). In the early 1980s, the introduction of new antibiotics such as third- and fourth-generation cephalosporins into human medicine was seen as a major victory in the fight against the beta-lactam-resistant Enterobacteriaceae of the time. However, three years after their discovery, the first plasmids encoding beta-lactamases capable of hydrolysing broad-spectrum cephalosporins were described (Knothe et al., 1983). The production of a beta-lactamase is believed to be the primary mechanism of resistance to beta-lactams in Gram-negative bacteria. Since the early 1980s, the emergence of numerous and diverse new extended-spectrum beta-lactamases (ESBLs) has conferred acquired resistance to cephalosporins, particularly third- and fourth-generation cephalosporins. This situation constitutes a significant public health problem (Canton & Coque., 2006; Canton et al., 2008). In Ivory Coast, the emergence of extended-spectrum beta-lactamase-producing Enterobacteriaceae (ESBL-producing Enterobacteriaceae) in hospitals has been widely reported for several years in numerous studies (Dadie et al., 2003; Gbonon et al., 2007; Guessennd et al., 2008a; Katy et al., 2013; Ouattara, 2016). The

Observatory for the Surveillance of Microorganism Resistance to Antiinfectives in Côte d'Ivoire (ORMICI) has been monitoring the circulation of certain resistance genes, particularly bla genes, for several years. The objective of this study was to assess the prevalence of bla genes in the two main species of Enterobacteriaceae (*Escherichia coli* and *Klebsiella pneumoniae*) that produce Extended-Spectrum Beta-Lactamases.

2. Materials and Methods

2.1 Isolation and Identification of *Escherichia coli* and *Klebsiella pneumoniae* Strains

The biological material consisted of 40 strains of Enterobacteriaceae. These strains included 25 strains of Escherichia coli and 15 strains of Klebsiella pneumoniae. The strains were isolated from urine, wound drainage, blood cultures, catheter tips, bronchial aspirates, sputum, pleural fluid, ascites fluid, and nasal swabs. All strains of *Escherichia coli* and *Klebsiella pneumoniae* were isolated on Eosin Methylene Blue (EMB) agar (Isendahl et al., 2012) and were identified using spectrométrie de masse MALDI-TOF (MS) (Clark et al., 2013; Seng et al., 2013). Isolation was done in the laboratory of the Clinical Bacteriology Unit (CBU), and Identification of *Escherichia coli* and *Klebsiella pneumoniae* strains was carried out at the Biological Resource Centre (CereB) of the Institut Pasteur of the Ivory Coast.

2.2 Antibiotic Susceptibility Testing

Antibiotic susceptibility testing was conducted at the National Reference Centre for Antibiotics of the Institut Pasteur of Ivory Coast. The antimicrobial susceptibility profiles of *Escherichia coli* and *Klebsiella pneumoniae* isolates were determined using the Bauer–Kirby disk diffusion method, with commercial antibiotic discs (Bio-Rad, France), in accordance with previously described procedures (Schaumburg et al., 2013). Extended-spectrum β-lactamase (ESBL)-producing strains were identified using the double-disc synergy test (Bakour et al., 2014). Discs containing cefotaxime (30 µg), ceftazidime (30 µg), cefepime (30 µg), and ceftriaxone (30 µg) were positioned at a centre-to-centre distance of 20 mm around an amoxicillin/clavulanic acid disc (10/20 µg) on Mueller–Hinton agar (BioMérieux, France). This assay was performed for isolates exhibiting resistance to third-generation cephalosporins. A total of fourteen antimicrobial agents from six antibiotic classes, including β-lactams, quinolones, and aminoglycosides, were tested in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. Standardised procedures were followed for medium preparation, inoculum density, incubation conditions, and internal quality control using *Escherichia coli* ATCC 25922. Phenotypic screening for ESBL production was further confirmed using the standard double-disc synergy test, as previously described (Desta et al., 2016). The antimicrobial discs (concentration in µg) used included amoxicillin/clavulanic acid (10/20), ceftazidime (30), ceftriaxone (30), cefotaxime (30), cefepime (30), cefoxitin (30), meropenem (10), ertapenem (30), aztreonam (30), moxifloxacin (5), pefloxacin (5), amikacin (30), gentamicin (15), and nitrofurantoin (100). All antibiotics were obtained from Bio-Rad (France).

2.3 PCR Amplification of Beta-lactamase Genes

Plasmid DNA was extracted for the detection of β-lactamase genes using the STANDARD™ SPIN-X DNA/RNA Extraction Kit (SD BIOSENSOR, Republic of Korea). Extended-spectrum β-lactamase (ESBL) genes were characterised by polymerase chain reaction (PCR) as described by Farra et al. (2016). PCR amplification was performed in a final reaction volume of 50 µl. The primer sequences used in this study are presented in Table 1. The reaction mixture comprised 1× PCR buffer containing 20 mM $MgCl_2$, a PCR-grade nucleotide mix (2.5 mM each), gene-specific primers (20 pmol), and FastStart Taq DNA Polymerase (5 U/µl; Roche). Amplifications were carried out using a UNO II thermal cycler (BIOMETRA®). PCR products were resolved by electrophoresis on 2% (w/v) agarose gel (Invitrogen), stained with SYBR Green, and visualised using GELDOC software. The cycling conditions for blaTEM comprised an initial denaturation at 94 °C for 1 min, followed by 30 cycles of 94 °C for 1 min, 50 °C for 1 min, and 72 °C for 1 min, with a final extension at 72 °C for 7 min. For blaSHV and blaCTX-M, the protocol included an initial denaturation at 94 °C for 1 min, followed by 30 cycles of 94 °C for 1 min, 60 °C for 1 min, and 72 °C for 1 min, and a final extension step at 72 °C for 7 min.

Table 1. Primers used in this study

Bla genes	Priming	Sequence (5'->3')	Size (pb)
TEM	a216 (+)	ATAAAATTCTTGAAGACGAAA	1079
	a217 (-)	GACAGTTACCAATGCTTAATCA	
SHV	os-5 (+)	TTATCTCCCTGTTAGCCACC	795
	os-6 (-)	GATTTGCTGATTTCGCTCGG	
CTXM-1	ctxM1 (+)	GGTTAAAAAATCACTGCGTC	863
	ctxM1 (-)	TTGGTGACGATTTTAGCCGC	
CTXM-2	ctxM2 (+)	ATGATGACTCAGAGCATTCG	865
	ctxM2 (-)	TGGGTTACGATTTTCGCCGC	
CTXM-8	ctxM8 (+)	GCGGCGCTGGAGAAAAGCAG	608
	ctxM8 (-)	GCTGCCGGTTTTATCCCGA	
CTXM-9	ctxM9	ATGGTGACAAAGAGAGTGCA	869
	ctxM9	CCCTTCGGCGATGATTCTC	

3. Results and Discussion

3.1 Results

3.1.1 Identification of Enterobacteriaceae Strains by MALDI-TOF

Identification using MALDI-TOF mass spectrometry confirmed the identities of the 40 bacterial strains, including 25 strains of *Escherichia coli* (62.5%) and 15 strains of *Klebsiella pneumoniae* (37.5%).

3.1.2 Distribution of Extended-Spectrum Beta-Lactamase (ESBL)-Producing Enterobacteriaceae by Biological Sample

Table 2 shows the distribution of bacterial species isolated from various biological specimens, such as catheter tips, sputum, wound exudates, urine, pleural fluid, ascites fluid, and blood. They were most frequently isolated from two types of specimens: urine (55%) and catheter tips (22.5%). In contrast, these strains were rarely isolated from pleural fluid, ascites fluid, blood cultures, and pus, with rates of 5% and 2.5% for sputum samples (Table 4).

Table 2. Distribution of multidrug-resistant Enterobacteriaceae strains by biological product

Organic products	*Escherichia coli* (n=25)	*Klebsiella pneumoniae* (N=15)	Total (%)
Urine	15	7	22 (55)
Pus	1	1	2 (5)
Blood	1	1	2 (5)
Ascites fluid	1	1	2 (5)
Catheter tip	6	3	9 (22,5)
Sputum	-	1	1 (2,5)
Pleural fluid	1	1	2 (5)

3.1.3 Resistance of Extended-Spectrum Beta-Lactamase-Producing Enterobacteriaceae (ESBL-Producing Enterobacteriaceae)

Antibiotic susceptibility testing was performed on 40 Enterobacteriaceae strains isolated from human biological products against various classes of antibiotics. Of these, 30 (75%) strains were ESBL-producing, including 19 strains of *Escherichia coli* and 11 strains of *Klebsiella pneumoniae* (Table 3). Analysis of the resistance profile shows that all strains of *Escherichia coli* (100%) and *Klebsiella pneumoniae* (100%) that produce ESBL are resistant to ampicillin, amoxicillin–clavulanic acid, and aztreonam. Regarding cephalosporins, resistance was particularly high in *E. coli* for cefotaxime and cefixime (100% each) and cefepime (89.47%), while *K. pneumoniae* showed resistance rates of 81.81%, 63.63%, and 72.73%, respectively, for the same antibiotics.

Among carbapenems, *E. coli* exhibits significant resistance to ertapenem (89.47%) and meropenem (84.21%), whereas *K. pneumoniae* shows lower rates (45.45% and 63.63%).

Among the fluoroquinolones, resistance to moxifloxacin was very high for both species (94.74% for *E. coli* and 90.90% for *K. pneumoniae*), followed by pefloxacin (78.95% and 72.73%) in these same strains. Regarding aminoglycosides, *E. coli* showed a higher resistance rate to gentamicin (73.68%) than to amikacin (42.10%), while *K. pneumoniae* exhibited lower resistance rates (36.36% and 18.18%). As for nitrofurans, resistance rates were limited (26.31% for *E. coli* and 18.18% for *K. pneumoniae*) (Table 3 and Fig. 1).

Table 3. Antibiotic resistance rates of ESBL-producing Enterobacteriaceae strains

Families	**Antibiotics**	***Escherichia coli* n=19** (%)	***Klebsiella pneumoniae* n=11** (%)
		BLSE strains	**BLSE strains**
Pénicillins	Ampicillin	19 (100 %)	11(100 %)
	Amoxicillin- clavulanic acid	19 (100 %)	11(100 %)
Céphalosporins	Cefotaxime	19 (100 %)	9 (81.81 %)
	Cefoxitin	10 (52.63 %)	6 (54.54 %)
	Cefepime	17 (89.47 %)	8 (72.73 %)
	Cefixime	19 (100 %)	7 (63.63 %)
Carbapenems	Ertapenem	17 (89.47 %)	5 (45.45 %)
	Meropenem	16 (84.21 %)	7 (63.63 %)
Fluoroquinolones	Pefloxacin	15 (78.95 %)	8 (72.73 %)
	Moxifloxacin	18 (94.74 %)	10 (90.90 %)
Aminoglycosides	Gentamicin	14 (73.68 %)	4 (36.36 %)
	Amikacin	8 (42.10 %)	2 (18.18 %)
Mono-bactam	Aztreonam	19 (100 %)	11 (100 %)
Others	Nitrofurans	5 (26.31 %)	2 (18,18 %)

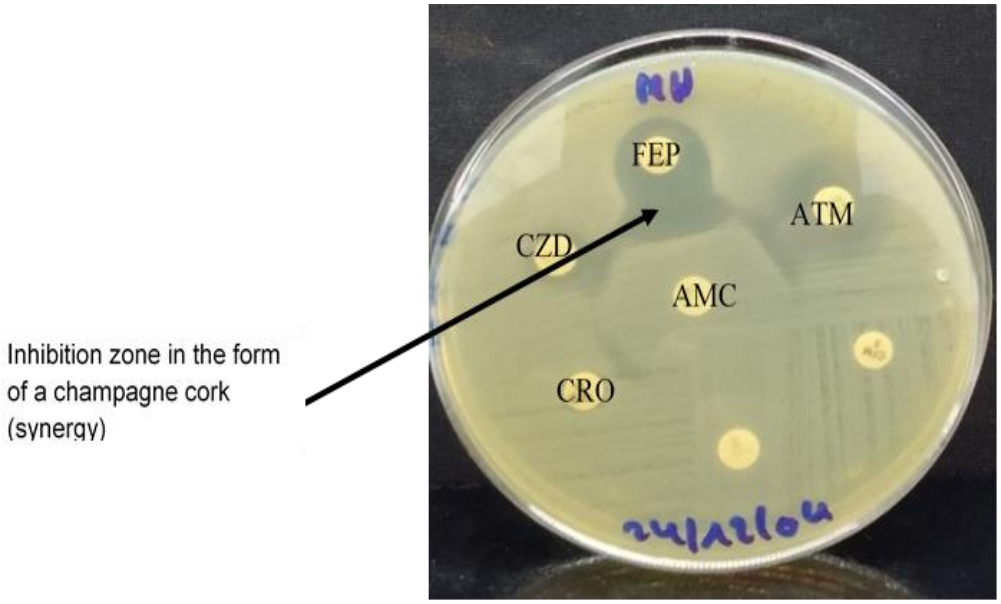

Fig. 1. Test De synergie d'une souche De Echerichia coli productrice de BLSE
FEP Cefépime; CZD: Ceftazidime; CRO: Ceftriaxone; AMC: Amoxicilline-acide clavulanique; ATM: Aztréonam

3.1.4 Molecular Identification and Distribution of Beta-Lactam Resistance Genes (Bla Genes)

Table 4 highlights a diversity of genotypic profiles of bla genes in *Escherichia coli* and *Klebsiella pneumoniae*, with a total of 40 isolates analysed. In E. coli, the most common profile is P1 (22.5%), characterised by the

combination of TEM and CTX-M-8 genes, followed by P3 (17.5%) with TEM and CTX-M-1, and then P2 (12.5%) combining SHV and CTX-M-8. Less common profiles include P4 (7.5%) carrying only CTX-M-2 and P8 (2.5%) combining TEM, SHV, and CTX-M-1. In *K. pneumoniae*, the dominant profiles are P6 (15%) and P7 (15%), corresponding respectively to the combinations TEM + CTX-M-1 and SHV + CTX-M-1, followed by P5 (7.5%) with TEM + SHV. Overall, the most prevalent genes are CTX-M-1 (50%), CTX-M-8 (35%), and TEM (32.5%), while CTX-M-2 (7.5%) is rare and CTX-M-9 is completely absent.

Table 4. Genotypic profiles of beta-lactam resistance in human isolates

Profile	Gènes *bla*							
génotypic	***TEM***	***SHV***	***CTX-M-1***	***CTX-M-2***	***CTX-M-8***	***CTX-M-9***	**Espèces**	**N (%)**
P1	+	-	-	-	+	-	*E. coli*	9 (22.5)
P2	-	+	-	-	+	-	*E. coli*	5 (12.5)
P3	+	-	+	-	-	-	*E. coli*	7 (17.5)
P4	-	-	-	+	-	-	*E. coli*	3 (7.5)
P5	+	+	-	-	-	-	*K.pneumoniae*	3 (7.5)
P6	+	-	+	-	-	-	*K.pneumoniae*	6 (15)
P7	-	+	+	-	-	-	*K.pneumoniae*	6 (15)
P8	+	+	+	-	-	-	*E. coli*	1 (2.5)
Total (%)	60	32,5	50	7,5	35	0	40 (100)	

E. coli: Escherichia coli; K. pneumoniae: Klebsiella pneumoniae; N : number

3.2 Discussion

Antibiotic resistance in Enterobacteriaceae is becoming increasingly widespread, making it a major public health concern. This resistance is believed to be due to its ability to render antibiotic treatments ineffective, leading to infections that are increasingly difficult to treat, higher treatment costs, prolonged hospital stays, and rising mortality rates. According to Thakur et al. (2025), this resistance is the result of the excessive use of antibiotics in humans and animals.

3.2.1 Enterobacteriaceae Strains Identified by MALDI-TOF

Identification by MALDI-TOF mass spectrometry confirmed the presence of 25 strains of Escherichia coli (62.5%) and 15 strains of Klebsiella pneumoniae (37.5%). The predominance of E. coli is consistent with numerous studies reporting that this species is one of the main causative agents of human infections. The high proportion of K. pneumoniae observed in our study also confirms its major role in community-acquired and nosocomial infections. These results underscore the importance of these two species among Enterobacterales of clinical interest. Furthermore, the use of MALDI-TOF enabled rapid and reliable identification of bacterial isolates, consistent with the work of Seng et al. (2009) and Patel (2015), who demonstrated the excellent performance of this technique for the identification of Gram-negative bacilli.

3.2.2 Prevalence of Extended-Spectrum Beta-Lactamase (ESBL)-Producing Enterobacteriaceae

In this study, the prevalence of extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae was 75%. This resistance is believed to be due to the production of extended-spectrum beta-lactamases (ESBLs) by these bacteria, which makes treating infections caused by them more difficult and potentially more complex (Belbel, 2014). According to Muller (2017), one reason for the increase in this resistance may lie in the preventive and therapeutic use of antibiotics in animals whose products are consumed by humans. Taking antibiotics that have been improperly stored and failing to follow the prescribed regimen (dose and duration of treatment) can lead to bacterial resistance (Maïworé et al., 2021). The results of this study are significantly higher than those reported by Gadou (2019). In a study conducted in the city of Abidjan, Ivory Coast, this author reported a rate of 58.8%. This higher rate may be due to the misuse of antibiotics and their unregulated sale outside established standards. The results of this study differ from those reported by Guessennd et al. (2008a), who found a rate of 9%. The high rate observed in our various samples is likely due to the overuse of antibiotics and self-medication. The results of this study are also higher than those reported by Toty et al. (2016) and Ouedraogo et al. (2016). In a study conducted in Ivory Coast and Burkina Faso, these authors reported resistance rates of 56.2% and 58%, respectively, among ESBL-producing Enterobacteriaceae. In this study, the resistance rate of ESBL-producing Enterobacteriaceae to fluoroquinolones was 78.95% for pefloxacin and

94.74% for moxifloxacin. The high resistance rate could be explained by the fact that fluoroquinolones are the most commonly prescribed antibiotics after β-lactams in Africa, and particularly in Ivory Coast (Abay et al., 2025). Aminoglycoside resistance in ESBL-producing Enterobacteriaceae is a significant public health problem affecting several countries (Gadou, 2019). In this study, the resistance rates of ESBL-producing Enterobacteriaceae to aminoglycosides were 73.68% for gentamicin and 42.10% for amikacin. The results of this study are lower than those reported by Anago et al. (2015). In a study conducted in Benin, these authors demonstrated that 82.7% of BLSE-producing strains were resistant to gentamicin and 72.4% of the strains were resistant to amikacin. These rates may be due to the excessive or inappropriate use of aminoglycosides, which would promote the emergence and persistence of resistant strains. Previous studies also confirm high resistance to aminoglycosides. For example, Abdoulaye et al. (2023) reported high rates of resistance among Enterobacteriaceae to gentamicin (52%) and amikacin (38%), particularly among ESBL-producing strains. These findings are consistent with national resistance trends observed in the region, according to recent clinical data (Niger, 2022).

3.2.3 Molecular Identification of Beta-Lactamase Resistance Genes (Bla Genes)

Genotypic analysis of bla genes in Enterobacteriaceae reveals significant diversity among extended-spectrum β-lactamases (ESBLs), with species-specific profiles that reflect distinct resistance mechanisms and have important clinical implications. In *Escherichia coli*, the blaTEM and blaCTX-M genes predominate, whereas in *Klebsiella pneumoniae*, the blaTEM and blaSHV genes are the most common (Feizabadi et al., 2010; Martinez et al., 2012). The profiles (blaTEM, blaCTX-M-8) and (blaTEM, blaCTX-M-1) in *E. coli* accounted for 22.5% and 14% of the strains, respectively, while the combined profiles (blaTEM, blaSHV, and blaCTX-M-1) remained rare (2.5%) (Kim et al., 2023), as demonstrated by our study. In *K. pneumoniae*, the blaTEM and blaSHV genes are predominant, with prevalence rates ranging from 7.5% to 15% among strains, often in association with blaCTX-M-1. These genes are frequently co-localised on plasmids, which facilitates their spread between strains and species (Sidjabat et al., 2015). A study found that 96% of K. pneumoniae strains carried the blaCTX-M gene, 69% carried the blaTEM gene, and 42% carried the blaSHV gene. This distribution suggests parallel evolution of the blaTEM and blaCTX-M genes within *K. pneumoniae* strains (Lubwama et al., 2024). The species-specific distribution of bla genes underscores the importance of regular genetic surveillance to guide treatment decisions and limit the spread of ESBL-producing bacteria. The coexistence of multiple resistance genes on plasmids facilitates rapid dissemination within bacterial populations, posing a major challenge to public health. In this study, human-derived ESBL-producing Enterobacteriaceae strains were found to harbour several resistance genes. In addition, several gene combinations were identified bla_{TEM} / $bla_{CTX\text{-}M\text{-}8}$ (22.5 %), bla_{SHV}/ $bla_{CTX\text{-}M\text{-}8}$ (12.5 %), bla_{TEM} / $bla_{CTX\text{-}M\text{-}1}$ (17.5 %), bla_{SHV} / $bla_{CTX\text{-}M\text{-}1}$ (15 %), bla_{TEM}/ bla_{SHV} (7.5 %) and bla_{TEM} / bla_{SHV} / $bla_{CTX\text{-}M\text{-}1}$ (2.5 %). These proportions are lower than those reported by Bamba et al. (2024) in Abidjan, who observed frequencies of 22%, 64%, and 30 % for $bla_{CTX\text{-}M\text{-}1}$, bla_{TEM} and bla_{SHV}, respectively. This difference could be explained by variations in the clinical sources of the strains studied (hospitalised patients and community settings), the detection methods used, the diversity of plasmids harbouring resistance genes, as well as local antibiotic prescribing practices that influence the selection pressure on resistance genes.

4. Conclusion

Antibiotic resistance has become a major public health problem worldwide, and particularly in the Ivory Coast, with the emergence and spread of multidrug-resistant bacteria in hospital settings. The study of multidrug-resistant bacteria (BMR) isolated from human biological products has revealed the presence of resistance genes that have been present in Enterobacteriaceae for several years. Resistance genes such as $bla_{CTX\text{-}M}$, bla_{SHV} and bla_{TEM} have been identified. The presence of these resistance genes in ESBL-producing strains underscores their public health significance, as they are responsible for outbreaks. The emergence of new mechanisms of resistance to beta-lactams, combined with resistance to quinolones and aminoglycosides, is a cause for concern in Ivory Coast, particularly in hospital settings.

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Disclaimer (Artificial Intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

Competing Interests

Authors have declared that no competing interests exist.

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