

Prevalence and Characteristics of Intestinal Carriage of Multidrug-Resistant *Enterobacteriaceae* in Outpatients in Abidjan

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Abstract Background: The growing threat of antibiotic resistance poses a major challenge to global public health as it could lead to up to 10 million deaths annually by 2050, particularly in low-income countries. The COVID-19 pandemic has further worsened the issue of multidrug-resistant bacteria, particularly extended-spectrum β -lactamase-producing *Enterobacteriaceae* (ESBL-PE). In Africa, data on intestinal carriage on ESBL-PE are scarce. This study aimed to assess the prevalence and risk factors associated with ESBL-PE intestinal carriage among outpatients at Treichville University Hospital. **Method:** This study was conducted from July to December 2023 at Treichville University Hospital. Rectal swabs were collected from patients attending the general medical consultation ward selected by systematic random sampling. *Enterobacteriaceae* strains were identified by conventional methods and antibiotic susceptibility testing was carried out in accordance with the CA-SFM EUCAST 2022 guidelines. Data were analysed using R studio software version 4.0.3. **Results:** Rate of intestinal carriage with resistance *Enterobacteriaceae* was 54.55%. Prevalence of ESBL-PE in intestinal carriage was 30.90%. Among ESBL-PE carriers, the predominant age group was between 40 years and older; with a sex ratio of 1.26 (55.88% male). *Escherichia coli* and *Klebsiella pneumoniae* were the common ESBL producer species at 43.33% and 11.67% respectively. According to observed resistance patterns and predefined multidrug resistance categories, 94.60% of *Escherichia coli* strains and 100.00% of *Klebsiella pneumoniae* strains were identified as Multidrug-resistant. Only 5.40% of *Escherichia coli* strains were identified as Extensively drug-resistant. No isolates were classified as Pandrug-resistant. Risk factors like size of household living in a single room, presence of children under 15 years old, previous hospitalization (less than 6 months), antibiotic use (less than 3 months) and chronic medical diseases were significantly associated with ESBL-PE intestinal carriage ($p < 0.05$). **Conclusion:** High rate of ESBL-PE in intestinal carriage was observed. The knowledge of factors associated with Multi-resistant *Enterobacteriaceae* carriage helps to identify patients at risk to combat the spread of resistant bacteria within the healthcare system.

Keywords: intestinal carriage, antibiotic resistance, enterobacteriaceae, ESBL, Low-income contry, Côte d'Ivoire

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1. Introduction

Increasing antibiotic resistance is a growing threat to global public health, potentially leading to up to 10 million deaths per year by 2050, particularly in low-income countries [1]. In response to this threat, the World

Health Organization (WHO) identified multidrug-resistant *Enterobacteriaceae*, particularly those producing extended-spectrum beta-lactamases (ESBL), as priority bacteria that require immediate action [2,3]. ESBL-producing *Enterobacteriaceae* (ESBL-PE) are concerning because of their compromising effect on the efficacy of major antibiotics [2,4]. They have spread worldwide since their discovery in 1983 and often carry resistance genes

via mobile genetic elements such as plasmids [5,6]. Originating from human and animal intestines, these microorganisms are major reservoirs of resistance genes [5], facilitating their dissemination within communities and causing severe infections, both in healthcare establishments and in the community at large [7].

Since their initial observations in 2001 in Spain and 2002 in Poland [8], ESBL-PE have acquired a worldwide distribution, with prevalence levels varying from one community to another and from one healthcare establishment to another [7,9,10]. Over the past decade, the prevalence of intestinal carriage by these bacteria has been widely documented, with higher rates in Asia and lower rates in Europe and North America [10].

Although data on the intestinal carriage of these bacteria are limited in Sub-Saharan Africa, studies suggest a prevalence ranging from 6% in Mauritania to 66% in Cameroon among healthy volunteers and hospitalized patients [11,12]. The COVID-19 pandemic has also affected the prevalence of infections caused by multidrug-resistant bacteria, including ESBL-PE. The increased and often inappropriate use of antibiotics in patients with COVID-19 coupled with the disruption of healthcare systems and widespread use of antiseptics and biocides are likely to have contributed to this upsurge [13,14,15].

Given the clinical and epidemiological significance of the emergence and spread of ESBL-PE in healthcare settings and communities, it is imperative to identify any potential changes in the prevalence of intestinal carriage by these microorganisms following the COVID-19 pandemic.

This study aimed to assess the prevalence and risk factors associated with ESBL-PE intestinal carriage among outpatients at Treichville University Hospital.

2. Materials and Methods

2.1. Recruitment of Participants and Collection of Samples

Fecal swabs were collected from non-hospitalized volunteers aged over 15 years attending consultation services at Treichville University Hospital between July and December 2023. Patients were recruited from general consultation wards by systematic random sampling. The recruitment process consisted of approaching participants during their visits to these services. Inclusion criteria required participants to be outpatients aged over 15 years who had given permission in writing before enrolling in the study. Sociodemographic, clinical, and antibiotic use data were collected during face-to-face interviews using a structured form. The fecal swabs were then carefully transported to the laboratory in sterile containers to ensure sample integrity.

2.2. Microbiological Analysis

All microbiological analyses were performed in the Bacteriology and Virology laboratory of the University Hospital of Treichville.

2.2.1. Screening for ESBL-PE on Selective Medium

Collected fecal swabs were initially suspended in 2 mL of 0.9% sterile saline to prevent dehydration upon arrival at the laboratory. The suspensions were then cultured on Drigalski and EMB agar supplemented with 4 mg/L ceftazidime (Sigma, USA) and incubated at 37°C for 24 h to screen all strains susceptible to produce ESBL [16,17]. When fecal swabs could not be processed on the same day, they were stored at +4°C for less than 24 h and at -20 °C for more than 24 h to prevent dehydration and maintain sample integrity before analysis.

2.2.2. Bacterial Isolation and Identification

After 24 h of incubation, bacteria were preliminarily identified based on the characteristics of the colonies in the culture medium [17,18]. Identification of bacterial strains was carried out by phenotypic methods using Kligler Hajna agar (HiMedia), Urea-Indole broth (Bio-Rad), Simon's Citrate agar (Oxoid Ltd.), Lysine-Iron agar (Oxoid Ltd.) and Mannitol-Motility agar (HiMedia) [19].

2.2.3. Antibiotic Susceptibility Testing

Following bacterial identification, antibiotic susceptibility testing was performed using the Kirby-Bauer diffusion technique in accordance with the 2022 CASFM-EUCAST (European Committee of Antibiotic Susceptibility Testing) guidelines [20].

A panel of 18 different antibiotic disks (Bio-Rad) was placed on the medium 30 mm apart and 15 mm away from the edge of the plate, including amoxicillin (AMO 20 µg), ticarcillin (TIC 75 µg), amoxicillin/clavulanic acid (AMC 20/10 µg), cefuroxime (CXM 30 µg), cefoxitin (FOX 30 µg), ceftazidime (CAZ 30 µg), ceftriaxone (CRO 30 µg), cefotaxim (CTX 30 µg), cefixim (FIX 5 µg), cefepime (FEP 30 µg), imipenem (IMP 10 µg), meropenem (MEM 10 µg), aztreonam (ATM 30 µg), ciprofloxacin (CIP 5 µg), nalidixic acid (NAL 5 µg), gentamicin (GEN 10 µg), tetracycline (TET 30 µg), and trimethoprim-sulfamethoxazole (SXT 1.75/23.25 µg). The plates were incubated at 37 °C for 18-24 h. After incubation, the diameter of the inhibition zone was measured and interpreted according to the 2022 CASFM-EUCAST guidelines. The multidrug-resistance patterns of the isolates were identified using the criteria set by Magiorakos et al. [21]. ESBL production was qualitatively confirmed using the synergy method with cefotaxime, ceftazidime, and cefepime discs and the disc of amoxicillin combined with clavulanic acid. The presence of an ESBL is expressed by the appearance of a "champagne cork" synergy [20,22]. The reference strains *Escherichia coli* ATCC 25922 and *Klebsiella pneumoniae* ATCC 700603 were used for quality control.

2.3. Statistical Analysis

Data acquisition was performed using Excel 2019 and statistical analysis was performed using R software (R version 4.0.3). To assess statistical differences between carriers and non-carriers of ESBL-producing *Enterobacteriaceae*, the chi-square test (χ^2) or Fisher's exact test was used for categorical variables to reveal differences in ESBL-PE prevalence related to sociodemographic variables and antibiotic resistance profiles. Logistic regression analyses were performed to

investigate the risk factors associated with ESBL-PE carriage, including the calculation of odds ratios (OR) and 95% confidence intervals (CI). A p-value threshold < 0.05 was considered significant.

2.4. Ethical Approval

Ethical approval was obtained from the “Comité National d'Éthique pour les Sciences de la Vie et de la

Santé (n° 223-21/MSHPCMU/CNESVS-Km)” for the implementation of a research project on the circulation of multidrug-resistant enterobacteria in humans, animals, and the environment in rural, peri-urban, and urban areas of developing countries. Each study participant was informed of the objectives, collection methods, benefits, and risks of the study and informed consent was obtained from each study participant.

Table 1. Socio-Demographic and Clinical Characteristics of Participants in Association with Intestinal Carriage of *Enterobacteriaceae*

Characteristics	Modality	ESBL carriage		p-value
		No (n=76) n(%)	Yes (n=34) n(%)	
Age	16-24 years old	11(14.47)	7(20.59)	0.7
	25-30 years old	12(15.79)	3(8.82)	
	31-40 years old	17(22.37)	8(23.53)	
	>40 years old	36(47.37)	16(47.06)	
Sex	Female	35(46.05)	15(44.12)	0.9
	Male	41(53.95)	19(55.88)	
Profession	Administration	9(11.84)	9(26.47)	0.5
	Retailer	20(26.32)	6(17.65)	
	Student	14(18.42)	3(8.82)	
	Farmer	4(5.26)	1(2.94)	
	Housekeeper	22(28.95)	10(29.41)	
	Public transport personnel	2(2.63)	1(2.94)	
	Healthcare professionnel	2(2.63)	2(5.88)	
	Food industry	1(1.32)	0(0.00)	
	Sanitation worker	2(2.63)	2(5.88)	
Level of education	College	26(34.21)	9(26.47)	0.9
	Secondary school	15(19.74)	9(26.47)	
	Illetrate	6(7.89)	2(5.88)	
	Primary	11(14.47)	6(17.65)	
	University	18(23.68)	8(23.53)	
Household size in a room	Less than 2	1(1.32)	0(0.00)	0.015*
	Between 2 and 5	45(59.21)	11(32.35)	
	More than 5	30(39.47)	23(67.65)	
Presence of children (<15 years)	No	28(36.84)	6(17.65)	0.044*
	Yes	48(63.16)	28(82.35)	
Presence of elderly people (>65 years)	No	42(55.26)	12(35.29)	0.053
	Yes	34(44.74)	22(64.71)	
Living environment (proximity to livestock farm, field)	No	47(61.84)	15(44.12)	0.083
	Yes	29(38.16)	19(55.88)	
Presence of pets in the living space	No	48(63.16)	16(47.06)	0.11
	Yes	28(36.84)	18(52.94)	
Previous hospitalization in the last 6 month	No	26(34.21)	5(14.71)	0.036*
	Yes	50(65.79)	29(85.29)	
Chronic medical history	No	34(44.74)	7(20.59)	0.015*
	Yes	42(55.26)	27(79.41)	
Positive for COVID-19 this years	No	70(92.11)	27(79.41)	0.11
	Yes	6(7.89)	7(20.59)	
Recent use of antibiotics (less than 3 month)	No	50(65.79)	14(41.18)	0.016*
	Yes	26(34.21)	20(58.82)	

3. Results

3.1. Demographics and Clinical Characteristics of Study Participants

This study included 110 participants and analyzed their

demographic profiles, living conditions, and medical history. Demographic and clinical characteristics of the participants are presented in Table 1. In this study, the mean age was 45.82% years, with a sex ratio of 1.2. The participants came from various professions, predominantly traders and homemakers. Regarding household composition, most had two to five members, with frequent presence of children under 15 years of age (69.09%) and

individuals over 65 years of age (50.90%). Approximately 43.63% of the participants lived near farms or fields and 42.00% owned pets. Regarding COVID-19, 11.81% of the participants were infected. Concerning medical history, 62.72% had chronic illnesses and 71.81% had been hospitalized in the last 6 months. With regard to antibiotics, 29.09% were undergoing treatment, and 41.81% had recently used antibiotics, primarily under medical prescription, with most adhering to the recommended dosages [Table 1](#).

3.2. Intestinal Carriage Rate of Resistant *Enterobacteriaceae* Isolates

All suspect colonies isolated were *Enterobacteriaceae* after identification. The intestinal carriage rate of 3rd generation cephalosporin-resistant *Enterobacteriaceae* isolates was 54.55%. Among these, the intestinal carriage rate of ESBL-PE was 30.90%.

[Table 2](#) shows the different bacterial species identified and intestinal carriage rate of *Enterobacteriaceae* isolates.

Table 2. Rate of carriage of resistant *Enterobacteriaceae* isolates

Culture	n	Isolates	Number of isolates n(%)	Number of ESBL-PE isolates n(%)
Positive	60	<i>E. coli</i>	37 (61.67)	26 (43.33)
		<i>K. pneumoniae</i>	17 (28.33)	7 (11.67)
		<i>E. cloacae</i>	6 (10.00)	1 (1.66)
Negative	50	-	-	-

Table 3. Levels of antibiotic resistance in isolated strains

Antibiotics	Dosage (µg)	Bacteria		
		<i>Escherichia coli</i> (n=37)	<i>Klebsiella pneumoniae</i> (n=17)	<i>Enterobacter cloacae</i> (n=6)
AMO	20	37 (100.00)	-	-
TIC	75	37 (100.00)	-	6 (100.00)
AMC	30	14 (37.84)	-	-
CXM	30	37 (100.00)	17 (100.00)	-
FOX	30	7 (18.92)	7 (41.18)	-
CAZ	10	37 (100.00)	17 (100.00)	6 (100.00)
CRO	30	37 (100.00)	17 (100.00)	6 (100.00)
CTX	30	37 (100.00)	17 (100.00)	6 (100.00)
FIX	5	37 (100.00)	17 (100.00)	6 (100.00)
FEP	30	34 (91.89)	17 (100.00)	6 (100.00)
IMP	10	2 (5.41)	0 (0.00)	0 (0.00)
MEM	10	2 (5.41)	0 (0.00)	0 (0.00)
ATM	30	34 (91.89)	16 (94.12)	6 (100.00)
CIP	5	27 (72.97)	10 (58.82)	6 (100.00)
NAL	5	35 (94.59)	16 (94.12)	6 (100.00)
GMN	10	12 (32.43)	8 (47.06)	2 (33.33)
TET	15	31 (83.78)	15 (88.24)	5 (83.33)
SXT	1.25-23.75	30 (81.08)	14 (82.35)	5 (83.33)

3.3. Antimicrobial Resistance Profiles

A total of 18 antibiotics belonging to 8 classes of antimicrobial agents were used to assess the rate of resistance in the isolated strains. Significantly high rates of resistance were observed for amoxicillin, ticarcillin, cefuroxime, 3rd generation cephalosporins, cefepime, nalidixic acid, aztreonam, tetracycline, sulfamethoxazole-trimethoprim, and ciprofloxacin. In contrast, amoxicillin-clavulanic acid, gentamicin, ceftazidime, imipenem, and meropenem showed relatively low levels of resistance [Table 3](#).

3.4. Risk Factors Associated with ESBL-PE Carriage

The results of the chi-square (χ^2) or Fisher's exact test to determine the association between patient characteristics and ESBL-PE carriage are presented first in [Table 1](#).

Significant associations ($p < 0.05$) were found for the following factors: size of household living in a single room, presence of children under 15 years old, previous hospitalization in the last six months, chronic medical history and recent use of antibiotics.

The significant factors identified by the univariate analysis were included in the logistic regression model. The results of the multivariate analysis are summarized in the [Table 4](#).

Table 4. Logistic Regression of Factors Associated with Intestinal Carriage of ESBL-PE

Characteristics	Modality	Odds-ratio	IC 95%	p-value
Household size in one room	Less than 2	3,14	[1,36-7,59]	0,009
	Between 2 and 5			
	More than 5			
Presence of children (<15years)	No	3,04	[1,19-8,92]	0,028
	Yes			
Previous hospitalization (< 6 month)	No	3,78	[1,41-12,1]	0,013
	Yes			
Chronic medical history	No	3,12	[1,26-8,58]	0,018
	Yes			
Recent use of antibiotics (>3 month)	No	2,75	[1,21-6,42]	0,017
	Yes			

3.5. Resistance Pattern of Isolates and Resistance Profile of ESBL Producing Strains

The resistance patterns of these isolates are presented in [Table 5](#). Multidrug-resistant (MDR) bacteria are defined as isolates that are resistant to at least one agent in three or more antimicrobial categories. Extensively drug-resistant (XDR) bacteria are those that are resistant to at least one agent in all but two or fewer antimicrobial categories. Pandrug-resistant (PDR) bacteria are resistant to all agents in all antimicrobial categories. Based on the observed resistance patterns and predefined multidrug resistance classes, 94.60% of *Escherichia coli* strains and 100.00% of *Klebsiella pneumoniae* and *Enterobacter cloacae* strains were classified as MDR. Only 5.40% of *Escherichia coli* strains were classified as XDR. No isolates were classified as PDR.

Table 5. Resistance pattern of isolates

Bacterial	No-MDR	MDR	XDR	PDR	Total
<i>Escherichia coli</i>	0 (0.00)	35 (94.60)	2 (5.40)	0 (0.00)	37 (100.00)
<i>Klebsiella pneumoniae</i>	0 (0.00)	17 (100.00)	0 (0.00)	0 (0.00)	17 (100.00)
<i>Enterobacter cloacae</i>	2 (33.33)	4 (66.67)	0 (0.00)	0 (0.00)	6 (100.00)

Figure 1 shows a significant level of resistance to most of the antibiotics tested among the commonly isolated ESBL producers. Variable levels of resistance were observed for commonly used antibiotics such as amoxicillin/clavulanic acid (AMC), with 26.92% resistance in *Escherichia coli*. Cefoxitin (FOX) showed resistance rates of 7.69% and 42.86% in *Escherichia coli* and *Klebsiella pneumoniae*, respectively. Ciprofloxacin (CIP) showed resistance rates of 76.92% and 42.86% against *Escherichia coli* and *Klebsiella pneumoniae*, respectively. With regard to carbapenems (Imipenem, Meropenem), only 5.41% of ESBL-producing *Escherichia coli* strains were resistant, and no resistance was observed in ESBL-producing *Klebsiella pneumoniae* strains for these antibiotics.

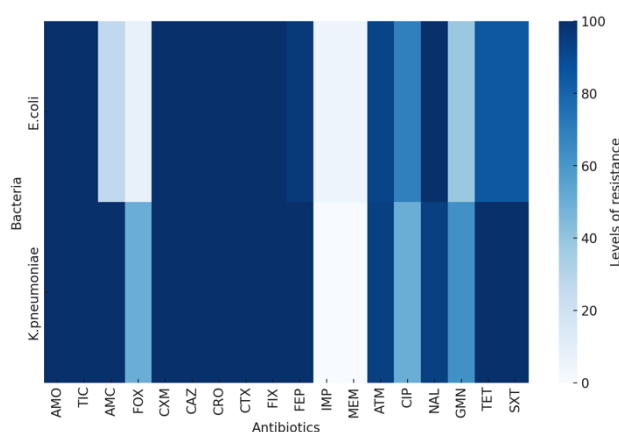


Figure 1. Resistance profiles of ESBL-producing strains

4. Discussion

The extensive use of antibiotics during the COVID-19 pandemic has accelerated the selection of multidrug-resistant bacteria [23,24]. Microorganisms exposed to antibiotics may develop survival techniques like resistance mechanisms that can be transferred to other bacteria and propagate quickly. The process of intestinal carriage mediated by ESBL-PE is a significant factor in the global dissemination of bacteria in healthcare and community settings across the world [8]. In fact, selection pressure due to antimicrobial treatment in hospitals and communities has created a major problem, leading to increased morbidity, mortality, and healthcare costs [25]. In our investigation, we assessed the ESBL-PE carriage rate, analyzed the ESBL-PE profile of outpatients attending consultation services at Treichville University Hospital, and identified associated risk factors.

The global prevalence of intestinal carriage by ESBL-PE in outpatients at Treichville University Hospital was

30.90%. This prevalence is higher than the rate observed (14.6%) before the COVID-19 pandemic reported in Côte d'Ivoire among outpatients by Ouattara et al. [26] but is close to those reported in Botswana (31%) and in Nepal (30.92%) on individuals attending routine control clinics [27,28]. In addition, our results were lower than those in West Africa, such as Nigeria (58%), Ghana (50.4%), and Burkina Faso (54.5%) [29,30,31]. The prevalence reported in this study was somewhat higher than that reported in recent studies, including a systematic review of sub-Saharan African data published by Lewis et al. in 2020, which reported a prevalence of 23% in outpatients [32]. This suggests the possibility of a local outbreak, most probably due to the inappropriate use of antibiotics, the lack of strict infection control measures and poor hygiene practices. In addition, selection pressure may have been intensified during the COVID-19 outbreak because of the use of antibiotics in self-medication, and it is possible that individuals are consuming antibiotics in the absence of knowledge due to their presence in the meat of farm animals.

The fact that ESBL-PE carriage is a significant risk factor for subsequent infections suggests that patients with these bacteria are at high risk of contracting ESBL-PE infections [5,9]. Moreover, their presence poses a threat to other individuals by increasing the likelihood of human-to-human transmission of resistant bacteria or environmental contamination [33,34].

Escherichia coli (43.33%) was the most commonly identified ESBL producer, followed by *Klebsiella pneumoniae* (11.67%), and *Enterobacter cloacae* (1.66%). These results are similar to those of previous studies that reported *E. coli* as the predominant ESBL producer in Côte d'Ivoire [26,35], Burkina Faso [36], Chad [37], and Ghana [29]. The predominance of *Escherichia coli* as the main producer of ESBL can be attributed to several factors. It is a common commensal bacteria among aero-anaerobic bacteria in the human gut, which gives it many opportunities to acquire and disseminate resistance genes through horizontal gene transfer [4]. Moreover, the high prevalence of *Escherichia coli* could be linked to its ability to survive and proliferate in various environments, including hospitals, which are hot spots for antibiotic resistance [8,11].

The average resistance rates to second-generation cephalosporins (FOX), third- and fourth-generation cephalosporins (CAZ, CRO, FEP, and CTX), monobactam (ATM), and penicillin with beta-lactamases' inhibitors (AMC) among all the strains ranged from 26% to 100%.

Several factors may contribute to this situation. For example, the extensive use of broad spectrum antibiotics may contribute significantly. Broad spectrum antibiotics increase the possibility of selection of antibiotic resistant strains not only within those antibiotics used, but also to other classes of antibiotics, through co-selection mechanisms [38]. In addition, enzymes such as beta-lactamases, produced by bacteria to inactivate these antibiotics, could also explain the large variety of antibiotics affected. These enzymes, in particular extended spectrum beta-lactamases (ESBLs), are capable of hydrolysis of penicillins, cephalosporins and monobactams [5]. Most ESBL-PE isolates were resistant to three or more classes of antibiotics, mainly quinolones (ciprofloxacin and

nalidixic acid), aminoglycosides (gentamicin), tetracyclines, and sulfonamides (trimethoprim-sulfamethoxazole). We noted high rates of resistance in *E. coli* isolates to trimethoprim-sulfamethoxazole, tetracycline (84.62%), and ciprofloxacin (76.92%) but low rates of resistance to gentamicin (38.46%) and cefoxitin (7.69%). Co-resistance of ESBL to other classes of drugs, such as aminoglycosides and fluoroquinolones, has been documented in Côte d'Ivoire [35,39,40,41]. The results of our study are similar to those of Chad [30], which reported a high level of co-resistance to antibiotic classes in all isolates tested. This situation explains the acquisition of resistance genes via the horizontal transfer of mobile genetic elements such as plasmids across different bacterial species [42]. This leads to the rapid spread of resistance through different bacterial populations, increasing the diversity of antibiotics affected by resistance [43].

In this study, we observed a carbapenem resistance rate of 5.41%, in contrast to the study by Ouattara et al. [26], which did not report any carbapenem-resistant strains. The emergence of this resistance among carriers could be explained by the increased use of these last-resort antimicrobials for the treatment of infections caused by ESBL-PE, particularly in cases of therapeutic impasse [44]. Indeed, the rise in resistance to third-generation cephalosporins leads to more frequent use of carbapenems, thereby exerting additional selective pressure that favors the emergence of resistant strains [44].

Carbapenemase-producing *Enterobacteriaceae* (CPE) infections are difficult to manage and are associated with high mortality rates [45]. The results of our study provide the necessary baseline data for future efforts to better contain ESBL-PE in healthcare and to limit its clinical impact.

With regard to associated risk factors, our study revealed that several factors were significantly associated with the carriage of ESBL-PE in the studied population ($p < 0.05$). In particular, the size of the household living in a single room, the presence of children under the age of 15, a history of hospitalization in the last six months, the recent use of antibiotics and a chronic medical history were identified as factors associated with the carriage of ESBL-PE.

These results are in accordance with many previous studies that have demonstrated the impact of these factors on ESBL-PE carriage. For example, two studies in developing countries, where ESBL carriage is relatively low in outpatients, have reported similar associations between the presence of pre-school children, household size and MDR bacteria carriage [46,47]. Similarly, research in Africa [48,49,50] has highlighted the importance of a history of hospitalization, antibiotic use and the presence of pets in the home for the spread of ESBL-PE. These results highlight the importance of considering these risk factors in strategies to prevent and control the spread of ESBL-PE. Actions to reduce exposure to antibiotics, to improve environmental hygiene and to intensify surveillance of hospital-acquired infections could help to reduce the prevalence of ESBL-PE in the studied population.

5. Conclusion

In summary, the COVID-19 pandemic's has notably accelerated the spread of multidrug-resistant bacteria. Our study at Treichville University Hospital revealed a high prevalence of ESBL-PE (30.90%), surpassing the pre-pandemic rates in Côte d'Ivoire. ESBL-PE, mainly *Escherichia coli*, exhibits resistance to multiple antibiotics, including last-resort options such as carbapenems. This highlights the urgent need for antimicrobial stewardship and infection control. We identified various risk factors associated with ESBL-PE carriage, emphasizing the need for multifaceted interventions targeting antibiotic prescription practices, environmental hygiene, and hospital infection surveillance to control the spread and clinical impact of ESBL-PE.

Declaration of Conflicting Interests

The authors declare no potential conflicts of interest in the research, writing, and/or publication of this article.

Authors' Consent

After several readings and corrections of the manuscript, the authors approved the publication of this article.

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