Research Square

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Phenotypes of antibiotic resistance in bacteria causing gastrointestinal infection isolated at

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Abstract

Background

Antibiotic resistance remains a major public health problem, particularly in developing countries where hygiene conditions are still precarious and the use of antibiotics is often abused and poorly controlled. In order to contribute to the development of strategies to combat antimicrobial resistance, we conducted a cross-sectional study with the general objective of determining the antibiotic resistance phenotypes of the bacteria responsible for gastrointestinal infections.

Method

Socio-demographic and clinical characteristics were obtained from the survey forms. Bacteria were identified using morpho-cultural characteristics and biochemical tests in the API 20E gallery. Susceptibility testing of isolated strains was carried out using the agar disk diffusion method. The synergy test and the algorithm were used to detect the phenotypes.

Results

In the course of the study, 101 stool samples were collected and examined, with 32 cases of gastrointestinal infections, representing a prevalence of 31.68%. Among the bacteria isolated, *E. coli* predominated (59.38%), followed by *Salmonella* (34.36%). Strain resistance to amoxicillin was very high, particularly in *E. coli* and *Salmonella*, at 78.95% and 54.55% respectively. Chloramphenicol, imipenem and amikacin were the most active molecules. Among the phenotypes identified, carbapenemases were the most common, with a rate of 25% in *E. coli*, followed by extended-spectrum beta-lactamases (ESBLs) at 15.60% in *Salmonella*.

Conclusion

Our results provide a data into the management of gastrointestinal diseases and guide the clinician in the fight against the emergence of future forms of bacterial resistance to antimicrobials through the resistance mechanism identified.

Introduction

Gastrointestinal infections lead to abdominal pain with nausea, vomiting, and diarrhea. These clinical signs can be accompanied by systemic manifestations including fever. Gastrointestinal disorders are divided into acute or chronic infections that can be caused by infectious pathogens including viruses, bacteria, and parasites (1). Resistance to antimicrobial agents has become a major source of morbidity and mortality worldwide. When antibiotics were first introduced in the 1900’s, it was thought that we had

won the war against microorganisms. It was soon discovered however, that the microorganisms were capable of developing resistance to any of the drugs that were used. Apparently most pathogenic microorganisms have the capability of developing resistance to at least some antimicrobial agents. The main mechanisms of resistance are: limiting uptake of a drug, modification of a drug target, inactivation of a drug, and active efflux of a drug (2). Today, it can be said with certainty that the mass production and use of antibiotics for purposes other than medical treatment has an impact on both the environment and human health (3).

Antimicrobial resistance (AMR) has now emerged as a chronic public health problem globally (4). Infections caused by antimicrobial-resistant pathogens are reported to result in approximately 700,000 deaths globally every year. Furthermore, if no intervention strategies are initiated, it is estimated that by 2050, mortalities attributed to AMR will have increased to 10 million annually, with Africa and South Asia bearing the highest burden of deaths (5). Equally, β-lactams are one of the three main groups of antibiotics that *Enterobacteriaceae* confer resistance to (6). Because of this resistance, carbapenems have been widely used in clinical treatment. However, their use has led to the emergence of carbapenemases, which inactivate these last-resort antibiotics (7).

A study conducted in hospitals in East, Central, and Southern Africa reported a high ESBL rate of 38%. The same study showed a very high prevalence in Congo (92%) and the lowest in Zimbabwe (8). In Cameroon, the level of resistance of bacteria isolated in hospital settings, animal and environment is high for typical empirical antibiotic treatment strategies. Common *Enterobacteriaceae* pathogens isolated in hospital settings such as *E. coli*, *Klebsiella spp.*, *Enterobacter spp* and *Proteus spp* showed high rates of AMR to ampicillin, amoxicillin, trimethoprim/Sulfamethoxazole, amoxicillin/ clavulanic acid, tetracycline, co-trimoxazole and nalidixic acid (9).

To our knowledge, there are few studies on antibiotic resistance phenotypes of bacteria causing gastrointestinal infections in Cameroon. To address this gap, we conducted this study and asked the following question: what is the phenotypic diversity of these bacteria in the city of Douala? We assume that self-medication and the uncontrolled sale of drugs outside legal systems may contribute to the emergence of multidrug-resistant bacteria, and that carbapenemase-producing bacteria are the most common phenotypes at Laquintinie Hospital in Douala. The general objective of this study is to determine the resistance phenotypes of bacteria responsible for gastrointestinal infections. Particularly, the isolation and identification of the bacteria causing gastrointestinal infections, the determination of their antibiotic resistance profiles and the identification of the resistance phenotypes they develop.

Methods

Patients, sampling and sample collection

This was a cross-sectional and prospective study conducted over a period of three months, from May 2024 to July 2024. The study was conducted at the Laquintinie Hospital, located in the Douala I

subdivision, Wouri Division, in the Littoral Region of Cameroon. To be included in the study, all patients signed an informed consent. A non-probability sampling method was used, and a total of 101 samples were collected. A few grams of freshly passed stool were collected in a sterile container at the laboratory, or brought by patients after prior explanation of the collection procedures, and were immediately handled in the laboratory. In infants and young children, rectal swabbing was performed. Samples were analysed within one hour of collection.

Isolation and purification of pathogens

Prior to inoculation, the different culture media were prepared and poured into Petri dishes under a biosafety cabinet. The plates were left to solidify and subsequently stored in a refrigerator (2-8^{o}C).

A portion of stool was first of all inoculated into Mueller–Kauffmann broth before inoculated in the Hektoen agar. EMB agar was inoculated for samples obtained from children. All inoculated media were incubated at 37°C for 18–24 hours. Colonies were subcultured onto Mueller–Hinton (MH) agar for further analysis.

Identification tests

For the catalase test, a 24-hour bacterial colony was collected using a sterile Pasteur pipette and placed into a drop of hydrogen peroxide. The presence of effervescence in the form of bubbles indicates catalase production by the bacterium.

For the oxidase test, organisms lacking cytochrome c as part of their respiratory chain do not oxidize the reagent, leaving it colourless within the limits of the test, and are oxidase-negative. The test was considered negative when the disc was remaining colourless indicating *Enterobacteriaceae*.

The morphological and cultural identification consisted of assessing specific cultural characteristics of the organisms based on colony size, colour, and margins. Typical colonies included small “S-type” greenish or bluish colonies, with or without a black center on Hektoen agar. Suspected colonies were subcultured onto Mueller–Hinton agar. We equally used the API 20E system for the identification of bacteria.

Antimicrobial susceptibility testing

The susceptibility of bacterial strains was assessed using the disk diffusion method on agar media, in accordance with the recommendations of CA-SFM/EUCAST (2024). From a pure culture, a bacterial suspension was prepared in a tube containing sterile distilled water to achieve a turbidity equivalent to the 0.5 McFarland standard, corresponding to an inoculum density of approximately 1×10^8 CFU/mL. In a sterile tube, 5 mL of sterile distilled or saline water was added, followed by 3–4 pure colonies using a

sterile swab, and the suspension was homogenized. The resulting bacterial inoculum was used within 15 minutes of preparation (10).

A sterile swab was immersed in the bacterial suspension and used to streak the entire surface of Mueller–Hinton agar in a confluent manner. After inoculation, antibiotic disks were placed on the agar surface using a flame-sterilized forceps. Disks were spaced at least 30 mm apart to prevent overlapping inhibition zones. The plates were then left at room temperature (21 ± 2°C) on the bench for approximately 15 minutes to allow pre-diffusion of antibiotics. Subsequently, the inoculated plates were incubated at 37°C for 18–24 hours.

Inhibition zone diameters were measured, and the results were interpreted to classify strains as Susceptible (S) or Resistant (R) in accordance with CA-SFM/EUCAST (2024) recommendations. A strain was considered susceptible when the measured diameter was greater than the critical diameter (D), and resistant when the diameter was lower than the critical breakpoint (d). The antibiotics that we tested are: Amoxicillin (AMX), Amoxicillin–clavulanic acid (AMC), Ticarcillin (TIC), Piperacillin (PRL), Piperacillin–tazobactam (PTZ), Temocillin (TEM), Cefixime (CXT), Cefoxitin (FOX), Ceftriaxone (CRO), Cefotaxime (CTX), Cefepime (FEP), Aztreonam (AZT), Imipenem (IPM), Gentamicin (GEN), Amikacin (AKN), Tobramycin (TOB), Ciprofloxacin (CIP), Chloramphenicol (C), Trimethoprim–sulfamethoxazole (SXT).

Detection of carbapenemases

Carbapenemases were investigated in all bacterial isolates that exhibited an ESBL phenotype, high-level cephalosporinase activity, or resistance to a carbapenem (imipenem). For the Class A carbapenemases, two 10 µg carbapenem disks were placed on the surface of Mueller–Hinton agar. Then, 6 µL of boronic acid solution (300 µg) was added to one of the carbapenem disks. The plates were incubated at 37°C for 18–24 hours. A difference in inhibition zone diameters of ≥ 5 mm between the disk with boronic acid and the disk without boronic acid was interpreted as positive for the production of class A carbapenemases. For the Class B carbapenemases or metallo-β-lactamases, two 10 µg imipenem disks were placed on Mueller–Hinton agar at a distance of 25 mm (center to center). One of the disks was supplemented with 10 µL of 0.1 M EDTA (292 µg). The plates were then incubated at 37°C for 18–24 hours. An increase in the inhibition zone diameter of ≥ 4 mm for the IPM+EDTA disk compared to the imipenem disk alone was considered indicative of the presence of a metallo-β-lactamase. Finally, for Class D carbapenemases or OXA-48, the detection is based on bacterial resistance to the temocillin disk or on the absence of inhibition by either boronic acid or EDTA.

Statistical analysis

Data were collected in Excel using a survey form designed on Sphinx software, then analysed using Epi Info version 7.0. An association between a variable and the studied outcome was considered significant when the odds ratio (OR) was greater than 1, with a 95% confidence interval (CI) excluding 1 at its lower bound, and a p-value less than 0.05.

Results

Distribution of patients according to sociodemographic characteristics

Table 1 shows that a total of 101 patients underwent stool culture testing, including 54.46% (n = 55) males and 45.54% (n = 46) females. Patients' ages ranged from 8 months to 87 years. The most represented age group was [23–33[, with a frequency of 22.77%, followed by the [43–53[age group, with a frequency of 14.85%. Equally, we notice that 59.41% of participants had abdominal pain while 63.37% had diarrhea as the most frequent reason for consultation and 62.38% were not having fever. Equally, 87.13% of participants were not vomiting at the time of consultation, 80.20% were not having nausea. In addition, outpatients represented 69.31% of the entire population.

Table 1
Distribution of the population according to the sociodemographic and clinical characteristics

Characteristics	Variables/categories	Number	Frequency
Sociodemographic	Sex		
	Female	46	45.54%
	Male	55	**54.46%**
	Age (years)		
	< 3	12	11.88%
	[3–13[	5	4.95%
	[13–23[	12	11.88%
	[23–33[	23	**22.77%**
	[33–43[	10	9.90%
	[43–53[	15	14.85%
	[53–63[	10	9.90%
	[63; above [	14	13.86%
Clinical	**Abdominal pain**		
	No	41	40.59%
	Yes	60	**59.41%**
	Diarrhea		
	No	37	36.63%
	Yes	64	**63.37%**
	Fever		
	No	63	**62.38%**
	Yes	38	37.62%
	Vomiting		
	No	88	**87.13%**
	Yes	13	12.87%
	Nausea		
	No	81	**80.20%**

Yes	20	19.80%
Loss of appetite		
No	58	**57.43%**
Yes	43	42.57%
Hospitalization status		
Outpatient	70	**69.31%**
Inpatient	31	30.69%

Distribution of bacterial strains isolated

Figure 1 shows that the isolates were predominantly *Escherichia coli* (59.38%) and *Salmonella* spp. (34.36%).

Distribution of bacterial isolates according to their origins

Table 2 shows that bacteria were more frequently isolated from outpatients with a percentage of 62.50%. Equally, we observe that *E. coli* and *Salmonella spp* were significantly higher on the outpatients compared to the inpatients with p = 0.002 and p = 0.01 respectively.

Table 2
Distribution of bacterial isolates according to their origins

Bacteria	Outpatient	Inpatient	p-value
E. coli	10 (31.25%)	9 (28.13%)	0.002
Salmonella spp	8 (25.00%)	3 (9.38%)	0.01
shigella spp	2 (6.25%)	0 (0.00%)	0.28
Total	20 (62.50%)	12 (37.51%)	

Distribution of E. coli according to age range

Table 3 illustrates that *E. coli* were predominantly isolated on infants with a frequency of 36.00%.

Table 3
distribution of *E. coli* according to age range

Age (year)	Number	Frequency (%)
< 3	9	36.00%
[3–13[	3	12.00%
[13–23[	2	8.00%
[23–33[	4	16.00%
[33–43[	1	4.00%
[43–53[	3	12.00%
[53–63[	1	4.00%
≥ 63	2	8.00%

Resistance profile of bacteria to antibiotics

Table 4 shows that *E. coli* was resistant to Amoxicillin (78.95%), Amoxicillin-clavulanic acid (59.38%), Piperacillin-tazobactam (78.95%), Cefotaxime (57.89%), Aztreonam (52.63%). Also, we notice that *Salmonella spp* was resistant to cefoxitin (54.55%), ceftriaxone (26.20%), cefepime (54.55%). Finally, *Shigella spp* was susceptible to Amoxicillin (50.00%), Amoxicillin-clavulanic acid (100.00%), Piperacillin-tazobactam (50.00%), cefoxitin (100.00%), cefotaxime (100.00%), Aztreonam (100.00%), ceftriaxone (100.00%), cefepime (100.00%), Imipenem (100.00%).

This table equally shows that *E. coli* exhibited high resistance to gentamicin (94.74%), tobramycin (94.74%), ciprofloxacin (57.89%), chloramphenicol (23.53%) and Trimethoprim–sulfamethoxazole (66.67%). Also, *Salmonella* demonstrates resistance to amikacin (36.36%), gentamicin (87.50%) but was highly susceptible to chloramphenicol (90.00%) while *Shigella* is found susceptible at 100.00% to amikacin, tobramycin, ciprofloxacin, chloramphenicol and Trimethoprim–sulfamethoxazole.

Table 4
Resistance profile of bacteria to antibiotics

Class of antibiotics	Antibiotic/identified organism	*E. coli*	*Salmonella* spp.	*Shigella* spp.
Beta-lactams	**Amoxicillin**	-	-	-
	R	**78.95%**	54.55%	50.00%
	S	21.05%	45.45%	**50.00%**
	Amoxicillin-clavulanic acid	-	-	-
	R	**59.38%**	34.38%	0.00%
	S	40.62%	65.62%	**100.00%**
	PTZ	-	-	-
	R	**78.95%**	54.55%	50.00%
	S	21.05%	45.45%	**50.00%**
	Cefoxitin (FOX)	-	-	-
	R	31.58%	**54.55%**	0.00%
	S	68.42%	45.45%	**100.00%**
	Cefotaxime (CTX)	-	-	-
	R	**57.89%**	18.80%	0.00%
	S	42.11%	81.82%	**100.00%**
	Aztreonam (AZT)	-	-	-
	R	**52.63%**	27.27%	0.00%
	S	47.37%	72.73%	**100.00%**
	Ceftriaxone (CRO)	-	-	-
	R	23.10%	**26.20%**	0.00%
	S	76.90%	73.80%	**100.00%**
	Cefepime (FEP)	-	-	-
	R	47.37%	**54.55%**	0.00%
	S	52.63%	45.45%	**100.00%**
	Imipenem (IPM)	-	-	-

R: *Resistant;* **S**: *Susceptible;* **PTZ**: *Piperacillin-tazobactam;* **AKN**: *Amikacin;* **GEN**: *Gentamicin;* **TOB**: *Tobramycin;* **CIP**: *Ciprofloxacin;* **C**: *Chloramphenicol;* **SXT**: *Trimethoprim–sulfamethoxazole*

Class of antibiotics	Antibiotic/identified organism	*E. coli*	*Salmonella* spp.	*Shigella* spp.
	R	**42.11%**	27.27%	0.00%
	S	57.89%	72.73%	**100.00%**
Aminoglycosides	**AKN**	-	-	-
	R	21.05%	**36.36%**	0.00%
	S	78.95%	63.50%	**100.00%**
	GEN	-	-	-
	R	**94.74%**	**87.50%**	**100.00%**
	S	5.26%	**12.50%**	0.00%
	TOB	-	-	-
	R	**94.74%**	57.00%	0.00%
	S	5.26%	43.00%	**100.00%**
Quinolones	**CIP**	-	-	**-**
	R	**57.89%**	50.00%	0.00%
	S	42.11%	50.00%	**100.00%**
	C	-	-	-
Other antibiotics	R	**23.53%**	10.00%	0.00%
	S	76.47%	90.00%	**100.00%**
	SXT	-	-	-
	R	**66.67%**	63.64%	0.00%
	S	33.33%	36.36%	**100.00%**

R: *Resistant;* **S**: *Susceptible;* **PTZ**: *Piperacillin-tazobactam;* **AKN**: *Amikacin;* **GEN**: *Gentamicin;* **TOB**: *Tobramycin;* **CIP**: *Ciprofloxacin;* **C**: *Chloramphenicol;* **SXT**: *Trimethoprim–sulfamethoxazole*

Distribution of bacterial strains according to phenotype and classes of carbapenemase

Figure 2a demonstrates that the carbapenemase phenotype was the most frequently expressed by *E. coli*, with an expression rate of 25.00%, while ESBL was expressed by *Salmonella* at 12.60%. Penicillinase was expressed by *Shigella* at 15.60%. Also, Fig. 2.b shows a high frequency (12.50%) of class D carbapenemase observed in *E. coli*. This predominance was followed by class A (9.40%) in the same

species. *Salmonella* showed class D carbapenemase with a prevalence of 6.30%. *Shigella* did not exhibit any carbapenemase.

Discussion

In order to contribute to better management of gastrointestinal infections, we conducted this study, whose general objective was to determine the resistance phenotypes of bacteria isolated from patients and responsible for these enteric infections.

From a sociodemographic perspective, we registered 59.40% of gastrointestinal infections cases among male patients compared with 40.60% among female patients, corresponding to a male-to-female sex ratio of 1.46 (Table 1). This may be explained by the fact that men sometimes have less rigorous personal hygiene and dietary habits than women. Alcohol abuse is a significant contributor to the global burden of disease and can lead to tissue damage and organ dysfunction in a subset of alcoholics (12).

Diarrhea was the most frequent reason for consultation, accounting for 63.37% (n = 64), followed by abdominal pain at 59.41% (n = 60)(Table 1). This can be explained by the fact that water used in most households in developing countries are unsafe for consumption, as it is also evident that, each year, contaminated drinking-water contributes to the death of millions of the poorest people of the world from preventable diseases with vulnerable groups, such as children, women, and the elderly who are the main victims (13). Our findings are consistent with those of a study carried out in Bangladesh where diarrhea remains one of the main reasons for seeking acute medical care despite the significant progress that has been made in reducing the burden of diarrhea through introducing interventions such as oral rehydration salts (ORS), increasing access to safe water, sanitation and hygiene, and promoting breastfeeding and nutritional education (14).

The results revealed a predominance of *Escherichia coli* and *Salmonella* spp., which accounted for 59.38% and 34.38% of isolates, respectively (Fig. 1). This may be explained by its ubiquitous nature, being present both in humans and in the environment. Under certain environmental conditions, it may become pathogenic and infect humans. Likewise, it was reported a predominance of the same species, with a frequency of 48.50% in a study conducted between 2005 and 2012 at the Laquintinie Hospital in Douala (15). *E. coli* is the *enterobacterium* most frequently isolated in the laboratory and one of the most widespread in bacterial infections. The age group under 3 years was the most affected, with a prevalence of 36.00% (Table 3). This could be explained by the fact that this age group remains particularly vulnerable to enteric infections, since during this period the child's immune system is still developing while food diversification is also taking place. This finding is similar to findings from previous studies by Mbuthia and Guindo (16, 17).

Also, *E. coli* was resistant to Amoxicillin (78.95%), Amoxicillin-clavulanic acid (59.38%), Piperacillin-tazobactam (78.95%), Cefotaxime (57.89%), Aztreonam (52.63%). This could be connected to changes in the way patients are exposed to antibiotics, which is a key contributor to the development of antibiotic resistance (18). Likewise, we noticed that *Salmonella spp* was resistant to cefoxitin (54.55%), cefepime

(54.55%). *Shigella spp* exhibited resistance to amoxicillin (50.00%) and Piperacillin-tazobactam (50.00%) (Table 4). These high resistance rates to beta-lactams may be explained by the widespread empirical prescription of these antibiotics, their frequent over-the-counter availability, and their relatively low cost according to (19). This resistance may also result from the fact that Extended-Spectrum-Beta-Lactamase producing *Enterobacteriaceae* confer resistance to several significant antimicrobials (20). In Algeria, it was also reported a 100.00% resistance rate to both amoxicillin and amoxicillin-clavulanic acid (21). Variation in bacterial resistance to third-generation cephalosporins was observed, with *Salmonella* showing 26.20% resistance to ceftriaxone (Table 4). This proportion is similar to what was reported as they found bacterial resistance to third-generation cephalosporins ranging from 29.10% to 51.60% (15).

A high level of resistance to gentamicin was observed, with rates of 100.00% in *Shigella*, 87.50% in *Salmonella*, and 94.74% in *E. coli* (Table 4). In contrast, *Shigella* remained 100.00% susceptible to imipenem. Amikacin was effective against the bacterial isolates, with susceptibility rates ranging from 87.00% to 100.00%. Furthermore, we observed a high proportion of resistance of *Salmonella* to ciprofloxacin, at 50.00% (Table 4). This could be explained by the widespread self-medication use of ciprofloxacin in the treatment of salmonellosis, which may have promoted the development of bacterial resistance. It was equally reported at the University Hospital of Mahdia 50.00% resistance to the same molecule (22). Also, in Togo they reported an increase in enterobacterial resistance to ciprofloxacin from 37.94% in 2010 to 59.85% in 2017 (23). Resistance of *E.coli* to chloramphenicol was 23.53% (Table 4). This suggests that despite the toxicity associated with this molecule, it remains effective against this bacterium. In contrast, trimethoprim-sulfamethoxazole showed markedly reduced activity with high resistance rates against *E.coli* (66.67%) and *Salmonella* (63.64%).

The most frequently detected beta-lactamases were carbapenemases, with a frequency of 34.40%, followed by extended-spectrum beta-lactamases (ESBLs), at 28.10% (Fig. 2a). The highest proportions of carbapenemase production were observed in *Escherichia coli* (25.00%), while ESBL production was highest in *Salmonella* (15.60%) (Fig. 2a). This could be explained by the fact that the increased consumption of antibiotics in clinical settings could also increase the selection pressure of antibiotic resistance genes and may lead to high antimicrobial resistance rates (18). Also, it can be justified by the fact that carbapenemases vary in their prevalence and geographic distribution, depending on the bacterial species and their resistance mechanisms (24). It was reported that carbapenemase-producing *Enterobacteriaceae* was 6.45% in Central Ethiopia (25), and in Cameroon a prevalence of 16.00%(26). ESBLs ranked second in our study, with a frequency of 15.60% in *Salmonella.* A high frequency (12.50%) of class D carbapenemase was observed in *E. coli* (Fig. 2b). This can be justified by the fact that a city like Douala has high temperature that can trigger the production of class D carbapenemase in *E. coli*.

Conclusion

This study investigated the antibiotic resistance phenotypes of bacteria responsible for gastrointestinal infections at Laquintinie Hospital in Douala, with the aim of contributing to the development of effective strategies for the prevention and control of bacterial resistance. The findings revealed that *Escherichia*

coli (59.38%) was the predominant pathogen, particularly among children. Other identified pathogens included *Salmonella* spp. (34.36%) and *Shigella* spp. (6.25%) (Table 2). Antimicrobial susceptibility testing showed that chloramphenicol, amikacin, imipenem, and cefoxitin were the most active agents against the isolated strains; so, they could be used for empirical therapies. However, varying levels of resistance were observed, leading to the identification of multiple resistance phenotypes. Carbapenemase production was detected in 25.00% of *E. coli* isolates, while extended-spectrum beta-lactamase (ESBL) production was observed in 15.60% of *Salmonella* isolates. Other beta-lactamase phenotypes included penicillinases (12.50%) and cephalosporinases (15.63%).

Despite ongoing efforts for the good management of antimicrobial agents, the emergence of novel resistance mechanisms continues to outpace therapeutic advances. This trend contributes to increased treatment failure, prolonged hospitalization, and higher healthcare costs. In light of these findings, the implementation of effective control measures is imperative. Such strategies should adopt an integrated approach targeting policymakers, healthcare providers, and the general population to limit the emergence and spread of antimicrobial resistance.

Nonetheless, this study has some limitations as the sample size was not representative enough and the study period too short to draw literal conclusions. The sample size does not represent the true population because random variation can have a larger effect on the small samples. Equally, a short study period which reduces the representativeness as collected data may only reflect a temporary situation rather than the usual pattern in the population.

Declarations

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Authors' contributions

Talom Tangue Benjamin and Waffo Tekam Joel contributed equally to the work as co-first authors: Conceptualization; designing; revision; Formal analysis of data; Analyses and interpretation of data; Writing - original draft.

Caroline Mangwi: Conceptualization; Writing - original draft

Albert Doumsou Nakassou : designing, analyses and interpretation of data

Christiane Ingrid Medi Sike : analyses and interpretation of data

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Availability of data and materials

All the data generated and/or analysed during the current study are available from the corresponding author upon request.

Ethics approval and consent to participate

An ethical approval was obtained from clearance committee of Laquintinie Hospital, Cameroon (N°316/AR/MINSANTE/DHL of May 13,2024). Informed written consent was obtained from the study participants. Participants were given a full right to continue or withdraw from study. For participants under the age of 18 years old, written informed was obtained from their parents or legal guardian

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Clinical trial number:

Not applicable.’

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Figures

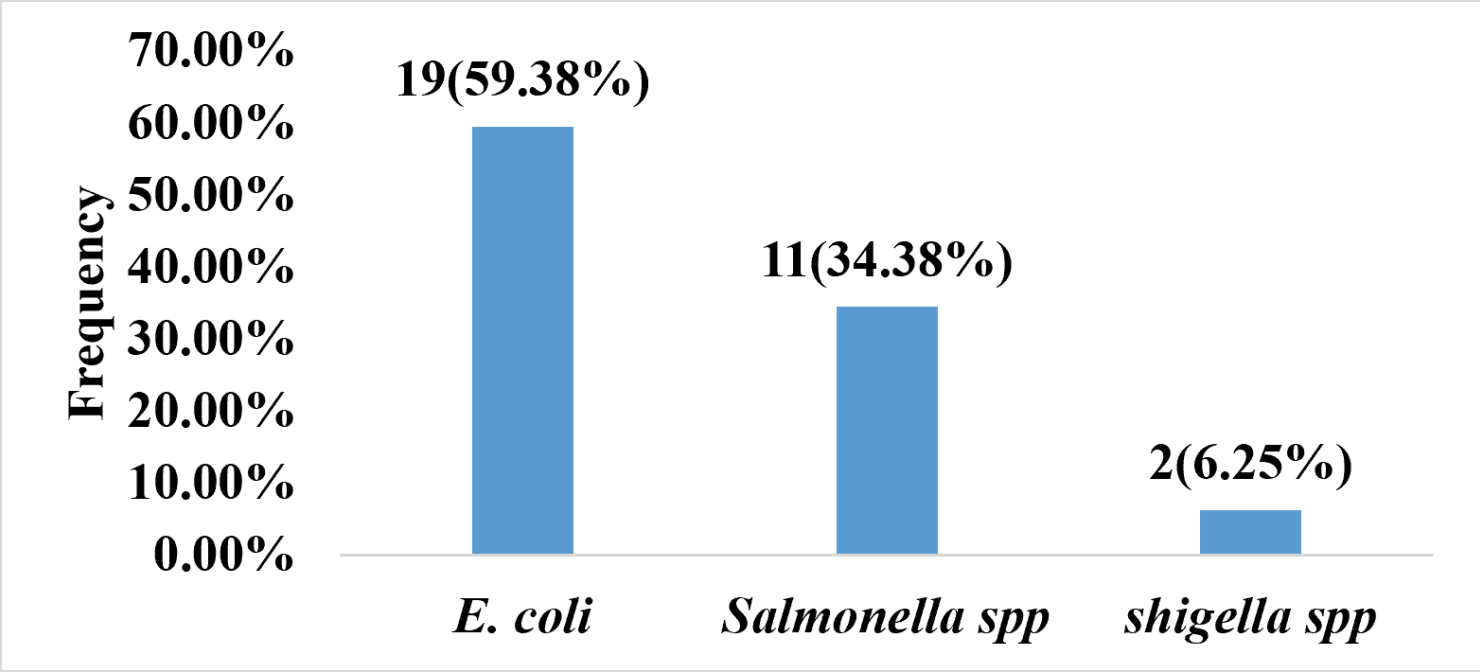


Figure 1

distribution of bacterial strains isolated

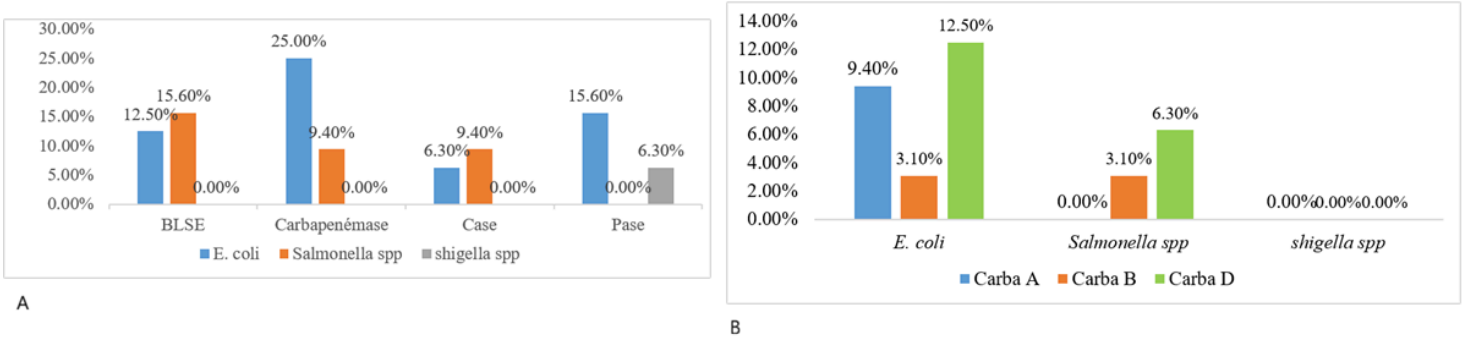


Figure 2

distribution bacterial strains according to phenotype and classes of carbapenemase

BLSE = ESBL: *Extended-Spectrum Beta-Lactamase,* ***Pase***: *Penicillinase,* ***Case***: *Cephalosporinase*

Carba *: carbapenemase ;* ***A, B, C and D*** *: different classes of carbapenemase*