



# **Role of Healthy Human Gut Microbiota in the Emergence and Dissemination of Extended-Spectrum $\beta$ -lactamase-Producing Enterobacteriaceae and Genes Associated with $\beta$ -lactam Resistance in Community Settings in Abidjan, Côte d'Ivoire**

**Ouattara Mohamed Baguy <sup>a,b\*</sup>, Affou Séraphin Wognin <sup>c,d</sup>,  
Toty Abalé Anatole <sup>a,b</sup>, Gbonon M'bengue Valérie Carole <sup>a,b</sup>,  
Kouassi Koffi Gédeon <sup>a,b</sup>, Guedé Kipré Bertin <sup>a,b</sup>,  
Tiekoura Konan Bertin <sup>a,b</sup>, Konan Kouadio Fernique <sup>a,b</sup>,  
Kouadio Kouamé Innocent <sup>e</sup>, Dissinviel Stéphane Kpoda <sup>f</sup>,  
Abraham Ayayi <sup>g</sup>, Konate Ali <sup>h</sup>,  
Guessennd Nathalie Kouadio <sup>a,b,i</sup>, Kamenan Alphonse <sup>e</sup>  
and Dosso Mireille <sup>a,b</sup>**

<sup>a</sup> *Department of Bacteriology-Virology, National Reference Center for Antibiotics, Pasteur Institute of Côte d'Ivoire, Abidjan, Côte d'Ivoire.*

<sup>b</sup> *GER-BMR : Groupe d'Etude et de Recherche sur les Bactéries Multi-Resistantes , Côte d'Ivoire.*

<sup>c</sup> *Département de Biochimie-Microbiologie, Université Peleforo Gon Coulibaly, B.P. 1328 Korhogo, Côte d'Ivoire.*

<sup>d</sup> *Département de Microbiologie, d'Ecotoxicologie et de Radioécologie, Centre Ivoirien Anti-Pollution (CIAPOL), 04 BPV 541 Abidjan 04, Côte d'Ivoire.*

<sup>e</sup> *Laboratory of Microbiology and Molecular Biology, Department of Food Science and Technology, Nangui Abrogoua University, Abidjan, Côte d'Ivoire.*

<sup>f</sup> *Laboratory of Molecular Biology, Epidemiology and Monitoring of Foodborne Bacteria and Viruses, Ouaga I Professor Joseph KI-ZERBO University, Ouagadougou, Burkina Faso.*

<sup>g</sup> *Department of Microbiology, University of Lagos, Nigeria.*

<sup>h</sup> *Laboratory of Applied and Nutritional Sciences, Ouaga I Professor Joseph KI-ZERBO University, Ouagadougou, Burkina Faso.*

<sup>i</sup> *Laboratory of Bacteriology-Virology, Department of Medical Sciences, Félix Houphouët - Boigny University, Abidjan, Côte d'Ivoire.*

\*Corresponding author: E-mail: mohamedbaguy@yahoo.fr;

### Authors' contributions

This work was carried out in collaboration among all authors. Authors OMB and ASW design the study. Authors OMB, ASW, TAA, GMVC, TKB and KKF took part in the recruitment of participants and samples collection. Authors OMB, KKG and KKI analysed the samples and interpreted the results.

Author OMB drafted the manuscript and Authors GKB, DSK, AA, Konate Ali, GNK, Kamenan Alphonse and DM revised it critically. Authors OMB, ASW and AAT revised the advanced manuscript. All authors read and approved the final manuscript.

### Article Information

DOI: 10.9734/MRJI/2023/v33i71393

#### Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/104162>

Original Research Article

Received: 26/05/2023

Accepted: 04/08/2023

Published: 07/09/2023

## ABSTRACT

Overuse of  $\beta$ -lactam antibiotics in communities in developing countries has transformed healthy human intestinal flora into a reservoir of antibiotic-resistant organisms. The prevalence of extended-spectrum  $\beta$ -lactamase (ESBL)-producing *Enterobacteriaceae* in community settings remains undetermined. In order to obtain data on ESBL enterobacteria, 265 stool samples were collected from August 2019 to February 2020 from individuals residing in the urban districts of Abidjan and attending medical consultations at the Institut Pasteur de Côte d'Ivoire. Isolates belonging to family *Enterobacteriaceae* were isolated on MacConkey and identified using the API 20E galerie and antibiotic susceptibility was determined using Clinical Laboratory Standard Institute disc diffusion method. Detection of extended spectrum  $\beta$ -lactamases (TEM, SHV, GES, PER, VEB, CTXM 1, CTXM 2, CTXM 8 and CTXM 9) was done by simplex and multiplex PCR. The human stools strains consisted of 513 species of Enterobacteria multidrug resistant. Among the 513 strains, 75 (14.6%) of the enterobacterial strains produced ESBLs, while 438 (85.4%) produced high-level cephalosporinases. Enterobacteria producing extended-spectrum  $\beta$ -lactamase we dominated by the species *Escherichia coli* (46.7%), *Klebsiella pneumoniae* (17.3%), *Enterobacter cloacae* (13.3%), *Enterobacter aerogenes* (6.7%), *Proteus mirabilis* (6.7%), *Klebsiella oxytoca* (4%), *Proteus vulgaris* (2.7%), *Citrobacter koseri* (1.3%), and *Citrobacter freundii* (1.3%). Strains were resistant (100%) to antibiotics from beta-lactam family (penicillin with inhibitor, monobactam, cephalosporin) but low level resistant (1,3%) was observed to carbapenem (imipénème, méropénème, Ertapenem). The rate of resistance to quinolones and aminoglycosides were respectively between 22.9% - 43.3% and 7.9-35.1%. The resistance genes TEM, SHV, CTXM 1, CTXM 2, CTXM 8 and CTXM 9 were detected. No GES and PER genes were not detected. The high fecal carriage rate of ESBL-PE associated with genes in community settings of Ivory Coast highlights the risk for transmission and dissemination because healthy people are potential patients on borrowed time.

**Keywords:** *Enterobacteriaceae* ESBL; genes; fecal carriage; ivory coast.

## 1. INTRODUCTION

"*Enterobacteriaceae* are a group of Gram-negative, rod-shaped facultative anaerobe, and their natural host is the human and animal

intestine" [1,2]. "Enterobacterial are commensal bacteria present in the intestinal tract of humans and various animals, are an important reservoir of resistance genes, leading to Extended-Spectrum  $\beta$ -Lactamase-Producing

Enterobacterial (ESBL-PE) dissemination in communities” [3]. “Use of antibiotics plays a crucial role in the emergence of antibiotic resistance amongst pathogenic bacteria worldwide as well as in developing countries” [3-5]. “Inappropriate use of antimicrobials is considered to be one of the main factors responsible for the high prevalence of antibiotic-resistant pathogens in developing countries” [5]. “Colonization of the gastrointestinal tract plays a key role in the epidemiology and clinical significance of extended spectrum beta-lactamase (ESBL) producing bacteria” [6]. “ESBL-PE have spread worldwide and have become endemic in several countries since their first description in 1983” [7,8]. “Their diffusion is mainly attributed to ESBL encoding genes that are often carried by mobile genetic elements, such as plasmids, that facilitate their dissemination” [9].

“Fecal ESBL-producing Enterobacteriaceae in the community was first reported in Spain and Poland in 2001 and 2002, respectively” [10]. “Extended-spectrum beta-lactamase-producing Enterobacteriaceae have worldwide distributions with varying degrees of prevalence in the community and hospitals” [10,11]. “In the community of developing countries, many people use antibiotic without prescriptions from a doctor and about a quarter obtain antibiotics from an informal dispenser” [12,13]. High prevalence of ESBL-producing bacteria has been reported worldwide [14-16]. While there are a number of publications on ESBL-producing bacteria causing clinical infections [17,18,19,20], relatively few studies from the African continent report on carriage of ESBL-producing organisms [21,22]. “While a better understanding of the impact on faecal carriage of ESBL-producing bacteria on subsequent development of infection is needed, carriage is a potential risk for transmission and infection, and of particular concern in healthcare settings, especially in developing countries where infection control is often inadequate” [12-14]. Little is known about faecal carriage of ESBLs and antibiotic resistance in Ivory Coast. The aim of this study was to investigate the prevalence of faecal carriage of ESBL-producing Enterobacteriaceae and their gene in Abidjan, Ivory Coast.

## 2. MATERIALS AND METHODS

### 2.1 Period and Area of Stools Collection

This study was carried out from August 2019 to February 2020 in Abidjan (Ivory Coast). 265

stools freshly emitted by healthy human were obtained from the clinical bacteriology unit (CBU) of the Institut Pasteur of Côte d'Ivoire. These stools were collected in sterile jars containing saline solution. Inclusion criteria of stool samples in this study was stools must come from people who have not been hospitalized and who have not received antibiotic treatment in the last three months.

### 2.2 Conservation of Samples in the Laboratory

When the stool samples were not processed on the same day, they were stored at a temperature of +4°C for storage for less than 24h and at -20°C for storage for more than 24h.

### 2.3 Isolation and Identification of ESBL Enterobacteria Strains

All ESBL producing enterobacteria strains were isolated on MacConkey (Oxoid, United Kingdom) supplemented with 4 mg/ml of ceftazidime [21] and were identified using the API 20E galerie (bioMérieux, Marcy l'Etoile, France). Isolation and Identification of ESBL Enterobacteria Strains was done in the laboratory of clinical bacteriology unit (CBU).

### 2.4 Antibiotic Susceptibility Testing

“Antibiotic Susceptibility Testing was done in the National Reference Center for Antibiotics of the Institut Pasteur of Côte d'Ivoire. The antimicrobial susceptibility of the extended spectrum enterobacteria  $\beta$ -lactamase isolates was determined by the Bauer-Kirby disk diffusion test using antibiotic disks (Bio-Rad, France)” [22]. “The double synergy test was used for detection of ESBL-producing strains. The disks of cefotaxime (30  $\mu$ g), ceftazidime (30  $\mu$ g), cefepime (30  $\mu$ g) and ceftriaxone (30  $\mu$ g) were placed around an amoxicillin/clavulanic acid disk (10/20  $\mu$ g) on Mueller Hinton agar (BioMérieux, France). The distance between the discs, center to center was 20 mm. This test was performed when the strain was categorized resistant to third generation cephalosporins. Of these, sixteen antimicrobial agents from six antibiotic families ( $\beta$ -lactams, quinolones, aminoglycosides, cyclins, polymixin and sulfamid) were tested. Clinical Laboratory Standards Institute (CLSI) guidelines were followed for inoculum standardization, medium and incubation conditions, and internal quality control organisms (*E. coli* ATCC 25922). Isolates were screened for

the ESBL-producing phenotype by the standard double-disc synergy test, as described previously” [23]. Antimicrobial discs (concentration of antibacterial in µg) used were amoxicillin/clavulanic acid (10/20), ceftazidime (30), ceftriaxone (30), cefotaxime (30), cefepime (30), ceftazidime (30), imipenem (10), ertapenam (30), aztreonam (30), nalidixic acid (30), ciprofloxacin (5), pefloxacin (5), amikacin (30), gentamycin (15) and tobramycin (10). All the antibiotics were procured from Bio-rad (France).

## 2.5 PCR Amplification of Beta-lactamase Genes

Plasmid DNA was used for detection of β-lactamases and was extracted using Mini prep K0502 kit (Fermentas, Vilnius, Lithuania). The ESBL gene was characterized by polymerase chain reaction as described by [24]. PCR amplification was performed in a final reaction volume of 50 µl. Primers used in this study are given in Table 1. The reaction mixture contained a PCR Reaction Buffer, 10x concentrated with 20 mM MgCl<sub>2</sub>, PCR Grade Nucleotide Mix (2.5 mM each), specific primers for each target (20 pmol) and a FastStart Taq DNA Polymerase, 5 U/µl (Roche). The PCR conditions were carried out in a thermalcycler UNOII (BIOMETRA®). Amplification products were analyzed by electrophoresis in a 2% agarose gel (Invitrogen) stained with syber green and visualized with GELDOC logiciel. The cycling conditions for amplification were as follows: for blaTEM, initial denaturation at 94°C for 1 min and 30 cycles of 1 min at 94°C, 1 min at 50°C, and 1 min at 72°C, followed by 7 min at 72°C; for blaSHV, PER, VEB, GES et CTXM gene, initial denaturation of 1 min at 94°C and 30 cycles of 1 min at 94°C, 1 min at 60°C, and 1 min at 72°C, followed by 7 min at 72°C.

## 3. RESULTS AND DISCUSSION

“Antimicrobial resistance in commensal flora is a serious threat because a very highly populated ecosystem, such as the gut, may become a source of additional intestinal infections at a later stage. These infections may subsequently spread to other hosts or transfer genetic resistance elements to other members of the microbiota including pathogens” [25-31]. “During the last decade, an alarming worldwide increase in the incidence of community acquired infections with pathogens resistant to multiple antibiotics of common use has been observed” [28].

To the best of our knowledge, this is the first study to document the prevalence and risk factors for faecal carriage of ESBL-EP in Abidjan, Ivory Coast. In this study, The human stools strains consisted of 513 species of Enterobacteria multidrug resistant. Among the 513 strains, 438 (85.4%) were resistant to third-generation of cephalosporins and 75 (14.6%) strains of enterobacteria were ESBL. Among 75 ESBL enterobacterial strains, 35 (46.7%) *Escherichia coli*, 13 (17.3%) *Klebsiella pneumoniae*, 10 (13.3%) *Enterobacter cloacae*, 5 (6.7%) *Enterobacter aerogenes*, 5 (6.7%) *Proteus mirabilis*, 4 (4%) *Klebsiella oxytoca*, 2 (2,7%) *Proteus vulgaris*, 1 (1.3%) *Citrobacter koseri* and 1 (1.3%) *Citrobacter freundii* (Table 2). The overall prevalence of ESBL-producing Enterobacteriaceae group of bacteria was 14.6%, which was concordant with a report in France (17.7%) [32], Mozambique University (20%) [33], and Norway (15.8%) [34]. However, it was lower than a report in Beirut (24.5%) [35], Southeast Asia (50.7%) [36], Venezuela (34.6%) [35], Turkey (30%) [37], Sweden (35%) [38]. The common species were *Escherichia coli* (46,7%), *Klebsiella pneumoniae* (17,3%), *Enterobacter cloacae* (13,3%) and to a lesser extent *Enterobacter aerogenes* (6,7%), *Proteus mirabilis* (6,7%), *Klebsiella oxytoca* (4%), *Proteus vulgaris* (2,7%), *Citrobacter koseri* (1,3%) and *Citrobacter freundii* (1,3%). Several studies have addressed the prevalence of resistant *Escherichia coli* and the genus *Klebsiella* spp isolated from the stools of children [39-42]. However, a study on high prevalence of faecal carriage of ESBL Producing Enterobacteriaceae among children in Dar es Salaam, Tanzania showed a rate of 48,9% *Klebsiella pneumoniae*, 45,4% *Escherichia coli*, 3,9% *Enterobacter cloacae*, 0,7% *Klebsiella oxytoca* and *Citrobacter spp*, 0,4% *Proteus mirabilis* [43]. This variation may be due to the difference in the study population and geographical location.

The average levels of resistance to second generation of cephalosporins (FOX), third generation, and fourth generation cephalosporins (CAZ, CRO, FEP, CTX) monobactam (ATM) and penicillin with inhibitor (AMC) for all strains ranged from 99 to 100%. Carbapenems (IPM, MEM and ETP) level of resistance was 1,3% (Table 3). Hundred percent resistance to ceftazidime and cefotaxime was observed in all ESBL-PE, which is compatible with a study conducted in Madagascar that showed 100% resistance to ceftazidime and cefotaxime [38], Addis Ababa ceftazidime (97%) and

**Table 1. Primers used in the study**

<b>Genes bla</b>	<b>Primers</b>	<b>Sequence (5'-&gt;3')</b>	<b>Position</b>	<b>PCR product size (pb)</b>	<b>Accession number</b>
TEM	a216 (+)	ATAAAATTCTTGAAGACGAAA	1-21	1079	AB282997
	a217 (-)	GACAGTTACCAATGCTTAATCA	1080-1059		
SHV	os-5 (+)	TTATCTCCCTGTTAGCCACC	23-42	795	X98098
	os-6 (-)	GATTTGCTGATTTGCTCGG	818-799		
PER	per (+)	CCTGACGATCTGGAACCTTT	465-485	716	721957
	per (-)	GCAACCTGCGCAAT(GA)ATAGC	1181-1161		
VEB	veb (+)	ATTTCCCGATGCAAAGCGT	351-370	542	AF010416
	veb (-)	TTATTCCGGAAGTCCCTGT	893-875		
GES	ges (+)	ATGCGCTTCATTCACGCAC	1332-1350	863	AF156486
	ges (-)	CTATTTGTCCGTGCTCAGGA	2195-2176		
CTXM-1	ctxM1(+)	GGTTAAAAAATCACTGCGTC	65-84	863	X92506
	ctxM1(-)	TTGGTGACGATTTTAGCCGC	928-909		
CTXM-2	ctxM2(+)	ATGATGACTCAGAGCATTCG	6-25	865	X92507
	ctxM2(-)	TGGGTACGATTTTCGCCGC	871-852		
CTXM-8	CtxM8(+)	GCGGCGCTGGAGAAAAGCAG	712-731	608	AF189721
	CtxM8(-)	GCTGCCGGTTTTATCCCGA	6336-6355		
CTXM-9	ctxM9(+)	ATGGTGACAAAGAGAGTGCA	6336-6355	869	AF174129
	ctxM9(-)	CCCTTCGGCGATGATTCTC	7205-7187		

**Table 2. Diversity of ESBL strain isolated**

ESBL species	Number of strains tested (N=75)	Rates of identification (%)
<i>Escherichia coli</i>	35	46.7
<i>Klebsiella pneumoniae</i>	13	17.3
<i>Enterobacter cloacae</i>	10	13.3
<i>Enterobacter aerogenes</i>	05	6.7
<i>Proteus mirabilis</i>	05	6.7
<i>Klebsiella oxytoca</i>	04	4
<i>Proteus vulgaris</i>	02	2.7
<i>Citrobacter koseri</i>	01	1.3
<i>Citrobacter freundii</i>	01	1.3

**Table 3. Enterobacteria ESBL resistance rates to bêta-lactamine**

ESBL species	Number of strains tested (N=75)	Rates (%)
Amoxicilline + acide clavulanique	75	100
Ceftazidime (CAZ)	75	100
Ceftriaxone (CRO)	75	100
Cefepime (FEP)	75	100
Aztreonam (ATM)	75	100
Cefotaxime (CTX)	75	100
Cefoxitine (FOX)	66	87
Imipenème (IPM)	0	0
Meropenème (MEM)	0	0
Ertapeneme (ETP)	0	0

cefotaxime (98%) [36], and Turkey cefotaxime (96%) and ceftazidime (94%) [37], but it was higher than a study conducted in Venezuela ceftazidime (46%) and cefotaxime (68.7%) [35], and Guinea-Bissau ceftazidime (66%) and cefotaxime (65%) [44]. During the study, we did not find any resistance to carbapenem (Imipenem, meropenem and Ertapenem).

Apart from beta lactams, The average levels of resistance for some strains to quinolones nalidixic Acid (NA), Ciprofloxacin (CIP) and Pefloxacin (PEF) were respectively 43,3%; 31,2% and 22,9% (Table 4). This rate were lower than rates observed in the study on prevalence and risk factors for faecal carriage of multidrug resistant *Escherichia coli* among slaughterhouse workers where the rates of ciprofloxacin and nalidixic acid were respectively 52% and 75% [45]. Another study on *Escherichia coli* and *Klebsiella pneumoniae* isolated from community showed respectively a rate of ciprofloxacin (25% and 78%) [46].

In our study, the rates of aminoglycosides were Gentamicin (35,1%), Tobramycin (26%), Kanamycin (27,8%) and Amikacin (7,9%) (Table 5). Some of the earlier studies have reported that a high level rate of resistance to gentamycin (86%), Tobramycin (89%) and amikacin (2%).

This variation may be due to the difference in the study population, geographical location and the politic of antibiotic consumption.

Most of the genes characterized in ESBL enterobacteria were TEM, SHV, CTX M1, CTX M2, CTX M8 and CTX M9. Co-expression of these genes was detected in strains of *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter cloacae* and *Enterobacter aerogenes*. However, the PER, VEB and GES genes were not detected in the isolated ESBL strains (Table 6). Some of the earlier studies have reported plausible correlative between phenotypically resistance and genes resistance. In our study, several bla genes such as bla CTX-M, blaSHV, blaTEM which confer resistance to bêta-lactamin have been detected. "However the specie *Escherichia coli* and the genus *Klebsiella spp* and *Enterobacter spp* were harboring the most of this genus. Therefore, under the pressure of excessive antibiotic use, genes, such as blaCTX-M, spread amongst different bacterial species and strains through horizontal gene transfer and thus contribute to the rapid dispersal of antibiotic resistance in the community" [47]. It has been documented that multiple studies reported the high prevalence of CTX-M, blaSHV and blaTEM harboring by *Escherichia coli* isolated from poultry farmers workers [35].

**Table 4. Enterobacteria ESBL resistance rates to quinolones**

ESBL species	Number of strains tested (N=75)	Rates (%)
Nalidixic Acid (NA)	33	43.3
Ciprofloxacin (CIP)	24	31.2
Pefloxacin (PEF)	18	22.9

**Table 5. Enterobacteria ESBL resistance rates to aminosides**

ESBL species	Number of strains tested (N=75)	Rates (%)
Gentamicin (GMN)	27	35.1
Tobramycin (TMN)	20	26
Kanamycin (KAN)	21	27.8
Amikacin (AKN)	6	7.9

**Table 6. Distribution of Bla genes harboring by enterobacteria ESBL**

Enterobacteria species	Genes bla								
	TEM	SHV	PER	VEB	GES	CTX M1	CTX M2	CTXM 8	CTXM 9
<i>Escherichia coli</i>	+	+	-	-	-	+	+	+	+
<i>Klebsiella pneumoniae</i>	+	+	-	-	-	+	+	+	+
<i>Enterobacter cloacae</i>	+	+	-	-	-	+	+	+	+
<i>Enterobacter aerogenes</i>	+	+	-	-	-	+	+	+	+
<i>Proteus mirabilis</i>	+	+	-	-	-	+	-	-	-
<i>Klebsiella oxytoca</i>	+	+	-	-	-	+	+	+	+
<i>Proteus vulgaris</i>	+	+	-	-	-	+	-	-	-
<i>Citrobacter koseri</i>	+	+	-	-	-	-	-	-	-
<i>Citrobacter freundii</i>	+	+	-	-	-	-	-	-	-

(+) : gene detected; (-) : gene not detected

“Plasmid mediated resistance to cephalosporins was largely due to blaCTX-M -15 which is in keeping with other studies done in many countries [48,49]. The blaTEM and blaSHV are less incriminated not been subtyped therefore no comment can be made for its correlation with ESBL production. It is interesting to note that blaSHV was not detected. The presence of genes coding for extended spectrum of beta lactamases and plasmid mediated quinolone resistance in commensal *E. coli* is disconcerting” [48,49].

#### 4. CONCLUSION

To our knowledge, this is the first study on the intestinal carriage of ESBL-PE in healthy community volunteers in Ivory Coast, and shows high carriage rate associated with the gene blaCTX-M, blaSHV and blaTEM enzyme. The intestinal transmission of ESBL-PE poses a serious public health problem and emphasizes the urgent need for improved sanitation and the

implementation of antibiotic stewardship in African nations. Future research should examine the processes of plasmid transfer as well as the factors that influence the reported intestinal carriage.

#### ETHICAL APPROVAL

This study was approved by the Research and Ethics Committee of Pasteur Institute.

#### ACKNOWLEDGEMENTS

The study was funded by The Pasteur Institute. The authors thank all patients who participated in this study, the Head of department of bacteriology, colleagues of clinical bacteriology clinic and national reference center of antibiotics.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.





- 2007– 2012. International Journal of Medical Microbiology. 2016;306:249–54.  
DOI: 10.1016/j.ijmm.2016.05.006  
PMID: 27222489.
19. Manyahi J, Matee MI, Majigo M, Moyo S, Mshana SE, Lyamuya EF, et al. Predominance of multi-drug resistant bacterial pathogens causing surgical site infections in Muhimbili National Hospital, Tanzania. BMC Res Notes. 2014;7:500.  
DOI: 10.1186/1756-0500-7-500  
PMID: 25100042 .
  20. Tansarli GS, Poulikakos P, Kapaskelis A, Falagas ME. Proportion of extended-spectrum beta-lactamase (ESBL)-producing isolates among Enterobacteriaceae in Africa: Evaluation of the evidence—systematic review. Journal of Antimicrobial Chemotherapy. 2014;69:1177–84.  
DOI: 10.1093/jac/dkt500  
PMID: 24398340.
  21. Isendahl J, Turlej-Rogacka A, Manjuba C, Rodrigues A, Giske CG, Naucler P, et al. Fecal carriage of ESBL-producing *E. coli* and *K. pneumoniae* in children in Guinea-Bissau: a hospital-based cross-sectional study. PLoS One. 2012;7:e51981.  
DOI: 10.1371/journal.pone.0051981  
PMID: 23284838.
  22. Schaumburg F, Alabi A, Kokou C, Grobusch MP, Kock R, Kaba H, et al. High burden of extended-spectrum beta-lactamase-producing Enterobacteriaceae in Gabon. J Antimicrob Chemother. 2013;68:2140–43.  
DOI: 10.1093/jac/dkt164  
PMID: 23645586.
  23. Desta K, Woldeamanuel Y, Azazh A, Mohammad H, Desalegn D, Shimelis D, et al. High Gastrointestinal Colonization Rate with Extended-Spectrum beta-Lactamase-Producing Enterobacteriaceae in Hospitalized Patients: Emergence of Carbapenemase-Producing *K. pneumoniae* in Ethiopia. PLoS One. 2016;11:e0161685.  
DOI: 10.1371/journal.pone.0161685  
PMID: 27574974.
  24. Farra A, Frank T, Tondeur L, Bata P, Gody JC, Onambele M, et al. High rate of faecal carriage of extended-spectrum beta-lactamase-producing Enterobacteriaceae in healthy children in Bangui, Central African Republic. Clinical Microbiology and Infection; 2016.  
Available: <http://dx.doi.org/10.1016/j.cmi.2016.07.001>
  25. Guessennd N, Kacou-N'douba A, Gbonon V, Yapi D, Ekaza E, Dosso M, Courvalin P. Prévalence et profil de résistance des entérobactéries productrices de bêta lactamase à spectre élargi à Abidjan de 2005 à 2006. Journal of Science Pharmaceutical and Biology. 2008a;9(1):63-70.
  26. Guessennd KN, Toty AA, Gbonon MC, Dondelinger M, Toé E, Ouattara MB, Tiékoura B, Konan F, Dadié AT, Dosso M, Galleni M. CTX-M-15 extended-spectrum B-lactamase among clinical isolates of Enterobacteriaceae in Abidjan, Côte d'Ivoire. International Journal of Biology Research. 2017;2(3):05-08.
  27. Ouattara MB, Guessennd KN, Koffi-Nevry R, Koffi S, Ouattara GD, Gbonon V, Tiekoura KB, Faye-Kette H, Dosso M. Evaluation of Drigalski agar supplemented with ceftazidime (2 mg/L) for the isolation of spectrum betalactamase (ESBL) producing Enterobacteria. African Journal of Microbiology Research. 2014;8(89):2758-2765.
  28. Bauer AW, Kirby WMM, Sherris JC, Turk M. Antibiotic susceptibility testing by a standardized single disc method. American Journal of Clinical Pathology. 1966;45:493-496.
  29. Jarlier V, Nicolas MH, Fournier G, Philippon A. Extended broad-spectrum beta-lactamases conferring transferable resistance to newer beta-lactams in Enterobacteriaceae: Hospital prevalence and susceptibility patterns. Review Infectious Disease. 1988;10:867–878.
  30. Adesoji AT, Liadi AM. Antibiogram studies of *Escherichia coli* and *salmonella* species isolated from diarrheal patients attending malam mande General Hospital Dutsin-ma, Katsina State, Nigeria. Pan African Medical Journal. 2020; 37:1–13.
  31. Shitu S, Gambo BA, Musa MO, Abubakar AA, Attahiru M. Prevalence of multidrug-resistant *Escherichia coli* in suspected cases of urinary tract infection among patients attending Ahmadu Bello University Medical Center, Zaria. UMYU Journal of Microbiology Research. 2020;5:123–130.
  32. Blanc V, Leflon-Guibout V, Blanco J, Haenni M, Madec JY, Rafignon G, et al. Prevalence of day-care Centre children

- (France) with faecal CTX-M producing *Escherichia coli* comprising O25b:H4 and O16:H5 ST131 strains. *Journal of Antimicrobial Chemotherapy*. 2014;69(5):1231–7.
33. Barreto I, Miranda R, Ignatius R, Pfüller et al. High carriage rate of ESBL-producing Enterobacteriaceae at presentation and follow-up among travellers with gastrointestinal complaints returning from India and Southeast Asia. *Journal of Travel Medicine*. 2016;23(2):Article ID tav024.
  34. Erdogan DC, Omert FC, Sepetci EA, Korkut F, Kuculah C. Fecal carriage of extended-spectrum beta-lactamase-producing *Escherichia coli* and *Klebsiella spp.* in a Turkish community. *Turkish Journal of Medical Sciences*. 2017;47(1):172–179.
  35. Tellevik MG, Blomberg B, Kommedal, Maselle SY, Langeland N, Moyo SJ. High Prevalence of Faecal Carriage of ESBL-Producing Enterobacteriaceae among Children in Dar es Salaam, Tanzania. *PLoS ONE*. 2016; 1(12):e0168024. DOI: 10.1371/journal.pone.0168024
  36. Araque M, Labrador I. Prevalence of fecal carriage of CTX-M-15 beta-lactamase-producing *Escherichia coli* in healthy children from a Rural Andean Village in Venezuela. *Osong Public Health and Research Perspectives*. 2018;9(1):9.
  37. Pilmis B, Cattoir V, Lecointe D, et al. Carriage of ESBL producing Enterobacteriaceae in French hospitals: the PORTABLESE study. *Journal of Hospital Infection*. 2018;98(3):247–252.
  38. Tellevik MG, Blomberg B, Kommedal SY, Maselle, Langeland N, Moyo SJ. High prevalence of faecal carriage of ESBL-producing Enterobacteriaceae among children in Dar es Salaam, Tanzania. *PLoS One*. 2016;11(12):Article ID e0168024.
  39. Seidman JC, Anitha KP, Kanungo R, Bourgeois AL, Coles CL. Risk factors for antibiotic-resistant *E. coli* in children in a rural area. *Epidemiology Infectious*. 2009; 137(6):879–888.
  40. Dyar OJ, Hoa NQ, Trung NV, Phuc HD, Larsson M, Chuc NT, et al. High prevalence of antibiotic resistance in commensal *Escherichia coli* among children in rural Vietnam. *BMC Infectious Diseases*. 2012;12:92–9.
  41. Isendahl J, Turlej-Rogacka A, Manjuba C, Rodrigues A, Giske CG, Naucner P. Fecal carriage of ESBL-producing *E. coli* and *K. pneumoniae* in children in Guinea-Bissau: A hospital-based cross-sectional study. *PLoS One*. 2012;7(12):e51981.
  42. Kaarme J, Molin Y, Olsen B, Melhus A. Prevalence of extended-spectrum beta-lactamase-producing Enterobacteriaceae in healthy Swedish preschool children. *Acta Paediatrica*. 2013;102(6):655–660.
  43. Ahmed SF, Ali MMM, Mohamed ZK, Moussa TA, Klena JD. Fecal carriage of extended-spectrum  $\beta$ -lactamases and AmpC-producing *Escherichia coli* in a Libyan community. *Annals of Clinical Microbiology and Antimicrobials*. 2014;13: 22–9.
  44. Abdallah HM, Alnaiemi N, Reuland EA, et al. Fecal carriage of extended-spectrum  $\beta$ -lactamase- and carbapenemase-producing Enterobacteriaceae in Egyptian patients with community-onset gastrointestinal complaints: A hospital -based cross-sectional study. *Antimicrobial Resistance and Infection Control*. 2017;6(1): 62.
  45. Desta K, Woldeamanuel Y, Azazh A. et al, High gastrointestinal colonization rate with extended-spectrum  $\beta$ -lactamase-producing enterobacteriaceae in hospitalized patients: Emergence of carbapenemase-producing *K. pneumoniae* in Ethiopia. *PLoS One*. 2016;11(8):Article ID e0161685.
  46. Chirindze LM, Zimba TF, Sekyere JO, et al. Faecal colonization of *E. coli* and *Klebsiella spp.* producing extended spectrum beta-lactamases and plasmid-mediated AmpC in Mozambican university students. *BMC Infectious Diseases*. 2018; 18(1):244.
  47. Girlich D, Bouihat N, Poirel L, Benouda A, Nordmann P. High rate of faecal carriage of extended-spectrum  $\beta$ -lactamase and OXA-48 carbapenemase-producing Enterobacteriaceae at a university hospital in Morocco. *Clinical Microbiology and Infections*. 2014;20(4):350–354.
  48. Isendahl J, Turlej-Rogacka A, Manjuba A, Rodrigues A, Giske CG, Naucner P. Fecal carriage of ESBL-producing *E. coli* and *K. pneumoniae* in children in Guinea

- Bissau: A hospital-based cross-sectional study. PLoS One. 2012;7(12):Article ID e51981.
49. Mabel Kamweli Aworh<sup>1</sup>, Oluwadamilola Abiodun-Adewusi, Nwando Mba, Birgitte Helwich & Rene S. Hendriksen. Prevalence and risk factors for faecal carriage of multidrug resistant *Escherichia coli* among slaughterhouse workers. 2021; 11:13362. Available:<https://doi.org/10.1038/s41598-021-92819-3>.

© 2023 Ouattara et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

*Peer-review history:*  
*The peer review history for this paper can be accessed here:*  
<https://www.sdiarticle5.com/review-history/104162>