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High Prevalence of ESBL-Producing *Escherichia coli* and Predominance of blaCTX-M genes among faecal carriage isolates from children in Kassala State, Sudan

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Abstract

The emergence of ESBL-producing Escherichia coli (E. coli) has raised concerns over paediatric health, especially in developing countries. The present study was conducted to determine the prevalence and molecular characteristics of ESBL producing E. coli isolated from stool samples of children under five years old in Kassala State, Sudan. A descriptive cross-sectional hospital-based study of 404 Diarrheal children 2021-2024 E. coli isolates from stool samples were identified and cultured on MacConkey agar by standard microbiological techniques. Antimicrobial susceptibility was assessed by MicroScan. We used multiplex PCR for detection of ESBL genes (blaCTX, blaTEM and blaSHV). E. coli was found in 123 (30.4%) of 404 stool samples. The majority of the participants were males (60.2%) and were less than 1 year of age (51.2%). The resistance rates were alarmingly high for cephalosporins cefepime (84.6%), cefixime (87.8%), cefotaxime (85.4%) and ceftazidime (84.6%) but cefoxitin was less resistant (56.9%) Molecular investigation showed blaCTX (72.4%), blaTEM (69.1%) and blaSHV (30.1%) as the most prevalent ESBL genes. Carriage of ESBL genes did not explain phenotypic cephalosporin resistance ($p > 0.05$). We found troubling rates of blaCTX-M-positive ESBL-producing E. coli among Kassala State youth. Our findings underscore the importance of improved antibiotic stewardship, surveillance and infection prevention in this region.

Keywords: SBL; *Escherichia coli*; Blactx-M; Antimicrobial Resistance; Children; Sudan; Fecal Carriage

1. Introduction

AMR, has emerged as one of the most prevalent global health challenges of the 21st Century, particularly via the emergence of ESBL-producing strains of Enterobacteriaceae [1]. ESBLs are hydrolytic enzymes responsible for the breakdown of various extended-spectrum cephalosporins and monobactams, making many of our most commonly prescribed antibiotics ineffective against bacteria producing ESBLs [2]. Of the numerous and diverse organisms that produce ESBLs, E. coli is the most frequently isolated pathogen and causes an extensive spectrum of infection types, including both uncomplicated urinary tract infections and life-threatening sepsis [3].

Transnational spread of CTX-M-type beta-lactamases, CTX-M-15 farthest among them, has led to an amplification of niche for extended-spectrum beta-lactamase-producing organisms amongst both community and hospital settings [4]. Plasmids propagate horizontally the transfer of beta-lactamase-encoding genes between bacterial species [5]. Though ESBL-producing E. coli are present all over the world, greater than half ESCB. E. coli occurs mainly in middle-to-low-income countries and the most developed regions [6].

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Diverse and numerous factors predispose children under 5 years of age to be especially susceptible to colonization and infection by ESBLs. This includes, but is not limited to, their immature immune systems, high levels of contamination related to consumption of foods and water, and frequent exposure to antibiotics [7]. Asymptomatic faecal carriage of ESBL-producing E. coli among children creates a reservoir of resistance genes that is transmitted throughout the community, making it difficult to treat future infections [8].

There is considerable variation in the rates of ESBL prevalence between pediatric populations in the African region, for example, rates reported were 17% for urban Ethiopia but >43% for rural Ethiopia [9], [10]. A study in Tanzania reported ESBL prevalence among infants <2 years of age to be 34% with blaCTX-M-15 as the prevalent ESBL genetic marker [11]. Recent studies on the prevalence of ESBL production among Enterobacteriaceae in Sub-Saharan Africa have reported rates of 8.6% to 23.3% in different geographic areas in different countries [12]. Wolde and colleagues [13] screened 2024 adults attending primary care in Ethiopia and found that 8.5% of these adults carried ESBL-producing E. coli, with blaCTX-M-15 being the predominant ESBL genetic marker (78.9%). Meta-analysis, Azzam et al. [14] found that 60% of all the bacteria in Egypt were ESBL-producing Enterobacteriaceae, with E. coli making up 64% of that total. There isn't a lot of information about the molecular distribution of ESBL-producing E. coli in children in Sudan. However, a study done at a school in Khartoum found that 38% of E. coli isolates were ESBL producers and that 78% of the isolates had the blaCTX-M genetic marker [15]. It is not well known how much ESBL is made in Kassala state in eastern Sudan.

Kassala, a region in eastern Sudan, is facing many challenges. Some of these are poor sanitation, lack of access to health services and high rates of poverty. All of these factors can lead to the high levels of bacteria resistant to antimicrobials [16]. Understanding local epidemiology of ESBL producing E. coli is important for effective guidance on use of empirical therapy, appropriate implementation of infection control measures and development of effective public health programs.

Fecal samples were obtained from children under age 5 who presented for pediatric care at hospitals located in Kassala State, Sudan, and were screened for ESBL-producing E. coli. The objectives of this study were to evaluate these organisms' prevalence along with their molecular properties. In particular, we aimed to accomplish the following: (1) determine the incidence of ESBL-producing E. coli amongst children with diarrhea; (2) characterize the distribution of blaCTX, blaTEM and blaSHV gene sequences; and (3) evaluate the relationship between the presence of ESBL genes and phenotypic resistance to cephalosporins

2. Materials and methods

2.1. Study Design and Setting

The study was a descriptive cross-sectional hospital-based study conducted in the eastern Sudan state of Kassala between 2021 and 2024. The two main pediatric hospitals engaged in the research project were Kassala Teaching Hospital and Alqueity Pediatric Hospital. Kassala Teaching Hospital is a major referral hospital for the whole area and provides specialized paediatric services including inpatient services, emergency services and out-patient clinics.

2.2. Study Population and Sample Size

The study involved children under five years of age who presented with diarrhea to the participating hospitals. Children over five years and those whose parents refused participation were excluded. The sample size was designed utilizing the mathematical formula: $N = (Z^2 \times P(1-P)) / e^2$, where Z = 1.96 (95% confidence level), P = 0.5 (estimated prevalence), and e = 0.05 (margin of error). This yielded a minimum sample size of 384 participants, and accounting for a 5% non-response rate, the final sample size was 404.

2.3. Data Collection

Demographic and clinical data were obtained by means of a structured questionnaire submitted to the parents or guardians of the children under study. Data collected included age, sex, clinical signs (diarrhea, vomiting, abdominal pain, lack of appetite), history of antibiotic use, source of water and exposure to animals.

2.4. Sample Collection and Processing

Sterile swabs were used to collect fecal samples in order to perform a bacteriological study and the collected samples were sent to the laboratory for testing as quickly as possible. Samples were inoculated into primary cultures using MacConkey agar plates, following which the plates were incubated in an aerobic environment at 37 degrees Celsius for

one to four days. Incubation of the MacConkey agar plates was sufficient for identification of potential E. coli colonies based on colony morphology, Gram stains, biochemicals and other standard biochemical tests.

2.5. Antimicrobial Susceptibility Testing

The minimum inhibitory concentrations (MIC) of different antibiotics were determined by dehydrated broth dilution, using the MicroScan WalkAway System (Siemens Healthcare Diagnostics, USA) according to the manufacturer's instructions. The drugs tested included cefepime, ceftazidime, cefixime, cefotaxime, cefoxitin and cefuroxime, all fourth generation cephalosporins. The results were interpreted according to the recommendations of the Clinical Laboratory Standards Institute (CLSI) [17].

2.6. DNA Extraction: Genomic

DNA was isolated from pure bacterial cultures by Promega Wizard Genomic DNA Purification Kit (Promega, USA) according to manufacturer's instructions. In brief, 3–5 bacterial colonies were suspended in 600 µL nuclei lysis solution, incubated for 5 min at 80°C then room temperature. 3 µL RNAase solution was added and further incubated at 37°C for 30 min. 200 µL protein precipitation solution was added and centrifuged. The supernatant was moved to a fresh tube containing 600 µL isopropanol, again centrifuged and DNA pellet was washed with 70% ethanol and dried under vacuum. Rehydrated DNA in 100 µL of rehydration solution was kept overnight at 4°C and the purity and concentration of the DNA was determined spectrophotometrically

2.7. Molecular Detection of ESBL Genes

The ESBL genes (blaCTX, blaTEM and blaSHV) were detected by multiplex polymerase chain reaction (PCR) using specific primers as previously described [18]. Sequencing primers were as follows:

- blaTEM-F: 5'-AGTGCTGCCATAACCATGAGTG-3'
- blaTEM-R: 5'-CTGACTCCCCGTCGTGTAGATA-3' (product size: 431 bp)
- blaSHV-F: 5'-GATGAACGCTTTCCCATGATG-3'
- blaSHV-R: 5'-CGCTGTTATCGCTCATGGTAA-3' (product size: 214 bp)
- blaCTX-F: 5'-ATGTGCAGYACCAGTAARGT-3'
- blaCTX-R: 5'-TGGGTRAARTRAGTSACCAGA-3' (product size: 593 bp)

We performed PCR reactions in a total volume of 25µL containing 12.5µL Master Mix, 1µL of each primer(10µM) and 2µL template DNA.Amplification conditions were 94°C for 5min(initial denaturation)then 30 cycles of 94°C for 20sec(denaturation), 61°C for 30 sec(annealing)and 72°C for 1 min(extension) followed by a final extension step of 72°C for 5 min.PCR products were run on 1.5% agarose gels, stained with ethidium bromide and visualized under UV light

2.8. Statistical Analysis

The data were analyzed utilizing SPSS version 23.0 (IBM Corp., USA). Descriptive statistics were expressed as frequencies and percentages. Associations of ESBL gene carriage with cephalosporin resistance were determined by the use of χ^2 test, and statistical significance was defined as $p < 0.05$.

2.9. Ethical Considerations

The Institutional Review Board of the University of Kassala gave a go-ahead for the study to begin with the ethical considerations. Each kid who took part in the study, had their parent(s) or guardian(s) signing on a permission sheet after having been given sufficient information. All procedures were done accordingly with the Declaration of Helsinki.

3. Results

3.1. Distribution of Detected Pathogens

Out of the 404 stool samples obtained from children presenting with diarrhea, there were 123 (30.4%) producing E. coli isolates while 281 (69.6%) yielded other pathogenic pathogens (Fig1). The high frequency of this bacterium as a leading player in causing diarrheal illnesses among children is captured by its higher proportion within the isolated samples.

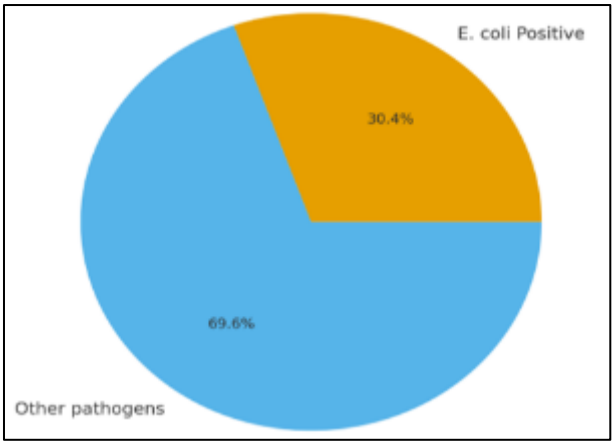

Figure 1 Distribution of Detected Pathogens in Stool Samples

3.2. Demographic Characteristics of Participants

Among the 123 youngsters who were found to have E. coli isolates, the bulk of them were male (74, 60.2%), while the number of females representing the cohort was 49 (39.8%). Over half of the children were below one year of age (63, 51.2%), while those aged 1-2 years made up 40 (32.5%). Children aged 2-3 years made up 8 (6.5%), 3-4 years 9 (7.3%), while those aged 4-5 years only made up 3 (2.4%) of the participants. Concerning maternal education, the majority had primary school education (67, 54.5%), followed by secondary education (47, 38.2%). Only 3 mothers (2.4%) had university education, while 6 (4.9%) had no education at all as shown on table 1.

Table 1 Sociodemographic Characteristics of Participants

Variable	Category	Frequency (n)	Percent (%)
Gender	Male	74	60.2%
	Female	49	39.8%
Age (years)	< 1 year	63	51.2%
	1-2 years	40	32.5%
	2-3 years	8	6.5%
	3-4 years	9	7.3%
	4-5 years	3	2.4%
Mother's Education	No education	6	4.9%
	Primary	67	54.5%
	Secondary	47	38.2%
	University	3	2.4%
Total Participants		123	100%

3.3. Behavioral and Environmental Factors

Analysis of behavioral and environmental factors showed that 52 (42.3%) children had history of recent antibiotic use against 71(57.7%) who did not receive any. Concerning water source, most households depended on municipal water (92 [74.8%]) whereas 31 (25.2%) used water from well. Only 18 (14.6%) children reported direct/indirect contacts with animals, compared to 105 (85.4%) without such contacts (Table 2).

Table 2 Behavioral and Environmental Factors

Variable	Category	Frequency (n)	Percent (%)
Antibiotic use	Yes	52	42.3%
	No	71	57.7%
Water source	Municipality	92	74.8%
	Wells	31	25.2%
Animal exposure	Yes	18	14.6%
	No	105	85.4%

3.4. Antimicrobial Susceptibility Patterns

Antimicrobial susceptibility testing showed a very high rate of resistance of the isolates of E. coli. Resistance to fourth generation cephalosporin cefepime was found in 104 isolates (84.6%). All third generation cephalosporins tested showed >85% resistance rates; cefixime (108 isolates, 87.8%), cefotaxime (105 isolates, 85.4%) and ceftazidime (104 isolates, 84.6%). Cefuroxime, a second-generation cephalosporin, had the highest resistance rate (89.4%) with 110 isolates. Cefoxitin another second generation cephalosporin showed relatively lower resistance (70 isolates, 56.9%) as shown in Table 3 and Fig 2.

Table 3 Antimicrobial Susceptibility of E. coli Isolates

Antibiotic	Sensitive (n)	Resistant (n)	Resistance Rate (%)
Cefepime	19	104	84.6%
Cefixime	15	108	87.8%
Cefotaxime	18	105	85.4%
Ceftazidime	19	104	84.6%
Cefuroxime	13	110	89.4%
Cefoxitin	53	70	56.9%

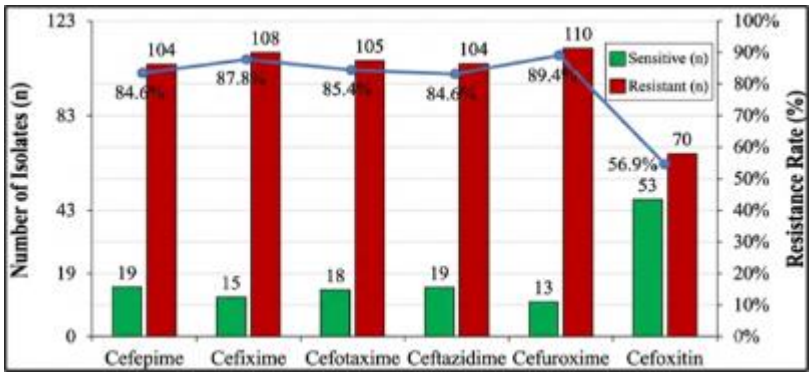

Figure 2 Antimicrobial Resistance Patterns of E. coli Isolates

3.5. Molecular Detection of ESBL Genes

Molecular analysis showed a high prevalence of ESBL genes among the isolates. The most frequently detected gene was blaCTX (in 89 isolates, 72.4%), followed by blaTEM (in 85 isolates, 69.1%). blaSHV gene was found in 37 isolates (30.1%) as shown in Table 4 and Fig 3. The predominance of blaCTX genes is in line with the global trend and suggests that CTX-M-type ESBLs are prevalent in this population.

Table 4 Distribution of ESBL Genes

Gene	Positive (+VE)	Negative (-VE)	Prevalence (%)
blaCTX	89	34	72.4%
blaTEM	85	38	69.1%
blaSHV	37	86	30.1%

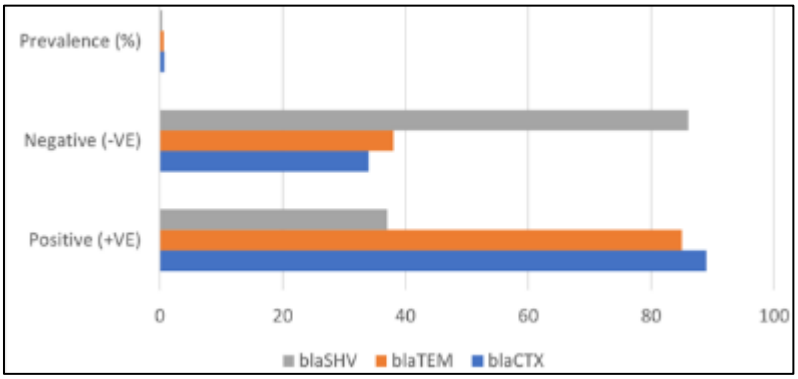

Figure 3 Distribution of ESBL Genes among E. coli Isolates

3.6. Association between ESBL Gene Carriage and Cephalosporin Resistance

The association between the presence of ESBL genes (blaCTX, blaTEM, blaSHV) and phenotypic cephalosporins (ceftazidime, ceftriaxone, cefotaxime, and cefepime) resistance was assessed by the chi-square test. There was no statistically significant association found for any of the tested gene-antibiotic combinations. The $\chi 2$ values ranged from 0.000 to 0.563 and p-values from 0.453 to 1.000, all above the significance level ($p > 0.05$) as described in table 5.

Table 5 Association of ESBL Genes with Cephalosporin Resistance

Antibiotic	blaCTX gene (χ^2, p-value)	blaTEM (χ^2, p-value)	blaSHV (χ^2, p-value)	Interpretation
Ceftazidime (CAZ)	0.299, 0.584	0.389, 0.533	0.030, 0.861	No significant association
Ceftriaxone (CRO)	0.082, 0.774	0.006, 0.941	0.217, 0.641	No significant association
Cefotaxime (CTX)	0.000, 1.000	0.000, 1.000	0.043, 0.836	No significant association
Cefepime (FEP)	0.004, 0.953	0.563, 0.453	0.144, 0.704	No significant association

4. Discussion

Chi-square tests were performed to determine whether or not any correlation existed between the presence of ESBL genes (blaCTX, blaTEM, blaSHV) with resistant phenotypic forms of the cephalosporin antibiotics tested (ceftazidime, ceftriaxone, cefotaxime, cefepime). None of the gene-antibiotic combinations showed significant results, as demonstrated by the $\chi 2$ values of 0.000 to 0.563 and their associated p-values of 0.453 to 1.000, all above the $p > 0.05$ significance cutoff seen in table 5.

4.1. High Prevalence of ESBL-Producing E. coli

In this investigation, we found that the frequency of determined blaCTX gene (72.4%) is one of the highest levels determined to date in this area of the world. The burden of ESBL-producing E. coli is significantly greater than any previously published studies, for example 17.1% in urban Ethiopia [9] or 43% [10] in rural Ethiopia. In addition, there was a higher prevalence than was reported in Tanzanian children (34.3%) [11], and close to the upper range of the

pooled prevalence from Egypt (60%) [14]. In the most recent systematic review on ESBL-producing Enterobacteriaceae from sub-Saharan Africa, the range of the included studies was 8.6%-23.3% with South Africa having the highest prevalence at 23.3%, Kenya at 23.0%, Nigeria at 11.1%, and Tanzania at 8.1%[12]. Thus, the observation that there is 72.4% carriage of blaCTX among our E. coli isolates is significantly greater than the other regional studies indicate a particularly high level of circulation in eastern Sudan.

There are several reasons why we think the ESBLs carriage rate in Kassala is so high. One might be that our study population had high prior use of antibiotics (42.3%). Other studies showed that using previous antibiotics is an important predictor for ESBL colonization [19]. A second reason might be that the majority of people (74.8%) use municipal water, providing opportunities for resistant bacteria to transmit through contaminated water. Finally, a third possibility might be because due to the fact that most mothers have very little formal education (54.5% attended only primary) they may not have knowledge of hygiene or how to use antibiotics properly.

The dominance of blaCTX genes (72.4%) over blaTEM (69.1%) and blaSHV (30.1%) in this study concurs with the world's epidemiology as CTX-M-type ESBLs has replaced the TEM and SHV types [4]. Also, recent studies from Ethiopia indicate that blaCTX-M-15 was the most prevalent ESBL gene found in 78.9% of ESBL producing isolate of bacteria [13]. CTX-M frequently associates with mobile genetic element, spreading quickly [20]. Finally, CTX-M-15 was the most common ESBL variant identified worldwide especially those people with community acquired infection [8].

4.2. Antimicrobial Resistance Patterns

Resistance levels found in this study are of concern, with >85% of isolates being resistant to every 3rd/4th gen cephalosporin tested. This is far higher than has been reported previously in many different studies throughout Africa e.g., ceftriaxone resistance among ESBL producing E. coli in Ethiopia was reported at 48% [9]; approximately 50–60% of E.coli isolated from Tanzania had ceftriaxone resistance [11]; and 52.7% of all E. coli isolated in Ethiopia in 2024 were resistant to ampicillin, and 8.5% were ESBL producers [13]. The significantly higher rates of resistance seen in Kassala might be due to over utilization of antibiotics without indication, lack of access to quality assured antibiotics, and circulation of highly resistant clones. Interestingly, the lower level of resistance to cefoxitin (56.9%) suggests that cephamycins still have activity against E. coli in this region. Consistent with previous studies finding cefoxitin (a second-generation cephalosporin which is stable to most ESBL's) having more activity than 3rd generation cephalosporins [21]; nonetheless, because of the high proportion of cefoxitin resistant isolates, there is also a high degree of MDR in this population.

4.3. Discordance between ESBL Gene Carriage and Phenotypic Resistance

Throughout our study, we also found that there was no statistically significant relationship between the presence of ESBL gene (blaCTX, blaTEM and blaSHV) and phenotypic cephalosporin resistance, which was one of the exciting discoveries we made. Our team's previous studies [22], [23] produced similar results. The major reasons for this difference are numerous

Firstly, gene carriage does not necessarily mean that genes will be expressed because promotor mutations, insertional elements or even epigenetic modification might be able to silence gene expression [24]. Secondly, other resistance mechanisms such as AmpC β-lactamases, porin mutations or efflux pumps may cause phenotypic resistance independent of ESBL gene carriage [25]. Thirdly, discrepancies could also be explained by technical difficulties in phenotypic testing such as inoculum effects and interpretive criteria [26]. Recently, genomic studies revealed that there were multiple β-lactamase genes often detected among ESBL producers. A research project in Ethiopia published in the year 2024 showed that more than half (57.9%) of all E.coli isolates producing extended-spectrum beta-lactamase (ESBL) had multiple β-lactamase genes coexisted with genes encoding both ctx-m-15 and tem-1B at a very high rate (52.6% for all isolates tested wide) and is possibly responsible for the lack of correlation between phenotypic resistance to antibiotics exhibited by those isolates who did have either of the above β-lactams and carriage of those β-lactams. [13].

This research has major implications for clinicians. Sherry et al. [27] indicated that these will continue to support that phenotypically susceptible testing must be a primary component of the approach used to determine antibiotic use. Molecular detection of resistance genes does not always predict susceptibility when used alone. Furthermore, detecting resistant organisms from phenotypically susceptible isolates may identify a reservoir of resistance that could be produced in the right selection environment, indicating the need to continue monitoring [28]. Therefore, ongoing monitoring is necessary to address this issue.

4.4. Clinical and Public Health Implications

High levels of ESBL-producing E. coli found among these young people has profound implications for healthcare and public health. “Children who are colonized by ESBL producing organisms have a greater risk of developing infections which are resistant to almost all antibiotics because there are only very few antibiotics left that work,” said Flokas et al. [19]. “Because of this limited number of effective drugs, carbapenems are commonly used to treat such patients, however they are expensive and rarely accessible in low resource settings” [29].

Also, children act as reservoirs of ESBL-producing bacteria from families and communities [7]. This is well known. The high rates of carriage suggest the possibility of widespread community diffusion that might cause outbreaks of disease and further spread of these bugs even without contact with healthcare [30].

Public health implications go far beyond caring for the patient. The fact that the transfer of the ESBL gene (and in particular the BlaCTX_A) shows us that there are mobile genetic elements able to transfer genes from species to species [20] means that they can cause multidrug resistant infections that become much harder to treat [20]. One recent “one-health” surveillance initiative carried out in 13 countries showed just how widespread this problem was already: showing that ESBL producing E.coli ranges as low as 17.4% in Ethiopia to a terrifyingly high 98.2% in DRC, showing just how big an issue we already have on our hands [31].

4.5. Comparison with Regional and Global Data

The results of the present study confirm that the prevalence of blaCTX is representative, as a measure of resistance to antibiotics, in Ethiopia compared with other countries in Africa and confirms previous reports of CTX-M type ESBLs in particular CTX-M-15 as the predominant type of ESBL isolated from laboratory specimens in Ethiopia (78.9% of all ESBL positive specimens) [13]. A blaCTX-M-15-like gene was found to be present in 94.7% of all ESBL-producing isolates in Tanzania [11]. Moreover, CTX-M has been identified as the most frequently identified ESBL gene (73%) in E. coli control specimens in a meta-analysis of literature in Egypt [14]. Collectively, these similar findings further support that CTX-M type ESBLs are the predominant ESBL found in Africa and mirror the global findings of CTX-M type ESBL*s* [4].

At the same time, the prevalence ratio for Kassala (72.4%) exceeds that of each of the references considered above, indicating that the ESBL producing strains circulate in eastern Sudan at an exceptionally high level of intensity. Due to the variation in prevalence, it is also important to have ongoing local surveillance to guide empirical treatment and control of infections in different regions [32]. In a systematic evaluation of ESBL-producing Klebsiella pneumoniae isolates from clinical, veterinary and environmental sources from 2009-2021, CTX-M-15 was identified as the most common ESBL gene detected [12]. This study further supports that this diversity is the product of widespread establishment.

4.6. Limitations

This study has a number of critical shortcomings. First of all, the study design is cross-sectional, which does not allow for evaluation of causality or change over time. Second, the study was performed in a hospital setting, so the carriage rates in the community may differ from those in hospitals. Lastly, the study did not perform sequencing to identify specific CTX-M variants (e.g., CTX-M-15 vs CTX-M-14), which could have provided better epidemiologic data, but this was not considered. Furthermore, we did not evaluate for other forms of resistance such as AmpC β-lactamases, carbapenems or plasmid-mediated colistin resistance. Finally, although the sample size is acceptable; it is possible that the sample will not adequately represent the variety of ESBL-producing strains in the geographic area.

4.7. Recommendations

The data supports our recommendation that ongoing monitoring of ESBL-producing Ecoli and other resistant pathogens in children is necessary for tracking changes over time and guiding interventions. In addition, strengthen antibiotic prescribing, as this will reduce the pressure that creates favourable conditions for resistance. This can be accomplished by (1) adopting guidelines for empirical therapy and limiting the use of broad-spectrum antibiotics (2) adopting appropriate infectious prevention and control measures such as improving the quality of water and sanitation in homes and healthcare facilities so that resistant pathogens are not transmitted from these locations (3) providing health education for the public that promotes appropriate antibiotic use, hand hygiene, and safe drinking water to assist with long-term sustainable control of AMR (4) conducting molecular surveillance with molecular methods (e.g. PCR, sequencing) for routine surveillance, which will provide valuable data about resistance genes that circulate and emerging threats (5) there is a need for greater research/longitudinal studies to help define the dynamics of ESBL colonization /transmission for this population including environmental/animal reservoirs.

5. Conclusion

This study has shown a high number of children <5 years old living in Kassala State, Sudan infected with ESBL genes carrying E. coli. The predominant blaCTX gene was found in an astounding 72.4% of isolates. Our findings reveal the high level of cephalosporin resistance as well as the discordance between ESBL gene carriage and phenotypic resistance. As a result, the authors call for further attention to antimicrobial stewardship, monitoring and improved infection control in order to fight back against the rise of MDR infections amongst this vulnerable population.

The heightened blaCTX presence and the ACSSuT resistance pattern linked with cephalosporins represent formidable barriers for both patient care and public health management in the country of Sudan. Achieving a better balance of laboratories capable of molecular typing, implementing an antibiotic stewardship program, and improving water/sanitation facilities are all vital components of stemming this rising tide. If not tackled promptly, the occurrence of ESBL-associated E. coli infections among children will continue unabated, ultimately yielding disastrous consequences for the health of children living within this region.

Compliance with ethical standards

Acknowledgments

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Disclosure of conflict of interest

No conflict of interest to be disclosed.

Statement of informed consent

Informed consent was obtained from all individual participants included in the study.

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