Patterns of Antimicrobial Resistance and ESBL Carriage in Enterobacteriaceae Isolates from Broiler Chicken in the West Region of Cameroon: A Cross-sectional Study

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Abstract

Background: The emergence of multidrug-resistant foodborne pathogens of animal origin is a growing concern. In particular, antibiotic resistance in *Enterobacteriaceae* of clinical importance has been on the rise. Identifying and monitoring resistance patterns in residual intestinal microflora in poultry are of great significance in the containment of antimicrobial resistance. The current study aimed to detect *Enterobacteriaceae* among broiler chicken and determine key antibiotic resistance patterns in isolates from poultry chicken in the West Region of Cameroon.

Results: 275 cloacal swabs were collected from 28 poultry farms in 11 locations in 5 out of the 8 Divisions in the West Region. All samples tested positive for *Enterobacteriaceae* with an average of 3 different colonies per sample. 394 isolates were obtained belonging to 12 different Genera of *Enterobacteriaceae* distributed as 81 (20.56 %) *Escherichia* spp, 74 (18.78 %) *Salmonella* spp, 39 (9.90 %) *Klebsiella* spp, 38 (9.64 %) *Proteus* spp, 34 (8.63 %) *Citrobacter* spp, 31 (7.87 %) *Enterobacter* spp, 28 (7.87%) *Providencia* spp, 19 (4.82%) *Hafnia* spp, 15 (3.30 %) *Shigella* spp, 14 (3.55 %) *Raoultella* spp, 13 (3.30 %) *Yersinia* spp and 8 (1.78 %) *Morgenella* spp. Antibiotic susceptibility testing on isolates showed the following overall resistance to the various antibiotics tested: amoxicillin 345 (87.8%), amoxicillin/clavulanic acid 227 (57.8%), ceftriaxone 79 (20.1%), cefotaxime 65 (16.5%), imipenem 16 (4.1%), gentamicin 58 (14.5%), amikacin 12 (3.1%), ciprofloxacin 142 (37.1%), levofloxacin 124 (33.1%) and doxycycline 380 (96.7). 217 (55.1 %) were resistant to at least one antibiotic class of choice against *Enterobacteriaceae*, 80 (20.3 %) resistant to at least one cephalosporin, 164 (41.62 %) resistant to at least one quinolone and 66 (16.75 %) resistant to at least one aminoglycoside. 173 (44.0%) showed MDR and 84 (21.32 %) were ESBL producers. Poor sanitation increased *Enterobacteriaceae* carriage, antibiotic misuse and long periods of rearing increased the risk of developing antimicrobial resistance, MDR and ESBL production.

Conclusion: Poor sanitation in poultries caused high *Enterobacteriaceae* carriage in subjects. This high co-infection coupled with antibiotic abuse caused high prevalence of resistance, MDR and ESBL production. These outcomes showed relatively uniform distribution across the area of study.

Background

Enterobacteriaceae are a Family of gram negative non-spore forming rod shaped bacteria. They are found everywhere; in soil, water, and decaying matter and also in guts of animals and humans where they can be pathogens or members of the normal intestinal microflora^{1,2}. Antimicrobial resistance in *Enterobacteriaceae* is a serious threat to public health due to the association of different resistance mechanisms and the insufficient development of new drugs which make these microorganisms resistant to almost all available antibiotics³. Animal husbandry, mainly poultry and pig farming which provide food and jobs to a great number of people in this Region, are highly linked to zoonosis^{4,5}. Chicken are an important source of contamination with clinically important human pathogens⁶, they tend to harbour extensive numbers and diverse types of enteric bacteria both commensal and pathogenic⁷. Such co-occurrence coupled with abuse of antibiotics in Cameroonian poultries⁸ give opportunity for sharing of resistance genes among species and chromosomal recombinations due to stress from antibiotics leading to emergence of resistant strains, multidrug resistance and emergent

zoonoses^{7,9,10}. When antimicrobial resistance develops in commensal intestinal microflora it tends to go unchecked making these commensals to act as reservoir of antimicrobial resistance⁷. Thus the development of antimicrobial resistance in commensal *Enterobacteriaceae* of animal origin is a measure for early detection of antimicrobial resistance in the community¹¹. Within the West Region, there are regular reports of gastrointestinal infections among patients, most of these infections are linked to *Enterobacteriaceae*^{12,13}. Treatment of these diseases has been proving difficult at times due to the development of antibiotic resistance in these bacteria¹⁴. Chicken being one of the main meat types in Cameroon¹⁵ and an important source of *Enterobacteriaceae* infection for humans⁶, and bearing in mind that the development of antibiotic resistance in commensal *Enterobacteriaceae* of animal origin is a measure for early detection of antibiotic resistance in the community¹¹, our quest for patterns of antibiotic resistance in *Enterobacteriaceae* in the West Region of Cameroon prompted us to use chicken as our sample source. This research aimed to bring out information that can attract the attention of stakeholders, including veterinarians, physicians, microbiologists, livestock producers, public health workers and relevant government agencies to the need for basic salvaging measures to curb chicken spread zoonosis. We supposed that due to the inadequacy of published works in this area, there is the development of antibiotic resistance, multidrug resistance (MDR) and extended spectrum beta lactamase (ESBL) production among animal hosts which go unreported.

Results

1. Evaluation of risks in farms

Samples were collected from 28 farms in 11 locations in 5 out of the 8 Divisions in the West Region. Evaluating risks, 25 farms out of 28 regularly used antibiotics on their chicken, 138 subjects sampled were more than 30 days old and fell on the category “old” while 137 were 30 days old or less and fell in the category “young”, 7 farms out of 28 regularly cleaned feeders and drinkers for the chicken, 12 farms out of 28 gave unsure water to their chicken and 18 out of 28 farms had dirty environment with or without stagnant sewage. Bacterial carriage in terms of different colony types present in culture correlated significantly with the 3 environmental risk factors evaluated.

Table 1

Information on the locations of farms, number of samples and isolates and the risk factors to which chicken subjects were exposed

Location	Number of farms	Samples (1 per subject)	Isolates	Evaluated risks at farms				
				Use of antibiotics	Age of subject	Poor feeding hygiene	Unsure water	Poor sanitation
Bafoussam Rural	4	40	66	4	18, 22	3 / 4	1/4	2 / 4
Bafoussam Urban	5	50	72	5	22, 27	2 / 5	0	2 / 4
Batcham	1	10	16	0	5, 5	1	1	1
Balesseng	2	15	22	2	8, 7	2	2	1 / 2
Banjoun	3	30	44	3	18, 12	2 / 3	2/3	1 / 3
Dschang	3	30	40	3	16, 14	2/ 3	2 / 3	3
Foumbot	2	20	26	1 / 2	11, 9	2	1/2	2
Mbouda	2	20	24	2	11, 9	2	1 / 2	1 / 2
Nkong-Ni	2	20	27	2	10, 10	2	2	2
Penka Michel	2	20	27	2	10, 10	1 / 2	2	1 / 2
Santchou	2	20	30	2	10, 10	1 / 2	2	2
Total	28	275	394	26 / 28	138, 137	20/ 28	16 / 28	18 / 28
Percentage exposure to risk				92.86	50.18, 49.81	71.43	57.14	64.29

Evaluated risk	Description
Unsure water	Using any other source of water apart from pipe-borne water without prior treatment.
Use of antibiotics	Regular use of antibiotics in feed for chicken subjects or have used on the subject.
Sanitation	Conditions of the environment such as litter, stagnant sewage, rearing of animals around poultry, state of workers' restroom.
Feeding hygiene	Cleaning of feeders and drinkers.
Age	≤30 days for category "young" and ≥30 days for category "old" chicken.

Table 2

Relationship between bacterial carriage in samples and environmental risk factors

	Bacteria carriage (number of colonies) of ≥ 3 per sample	
	Odds ratio (95% CI)	p value
Poor feeding hygiene	2.55 (1.67, 3.89)	0.000
Unsure water	1.75 (1.16, 2.64)	0.011
Poor sanitation	1.97 (1.31, 2.96)	0.009

2. Prevalence of members of the *Enterobacteriaceae*

A total of 275 cloacal swabs were collected. All these samples tested positive for *Enterobacteriaceae* with a carriage of at least 2 different colony types and a mean of 3 different colony types per sample. In total, 394 isolates were obtained and characterised belonging to 12 different Genera of *Enterobacteriaceae*. The 394 isolates were distributed as 81 (20.56 %) *Escherichia* spp, 74 (18.78 %) *Salmonella* spp, 39 (9.90 %) *Klebsiella* spp, 38 (9.64 %) *Proteus* spp, 34 (8.63 %) *Citrobacter* spp, 31 (7.87 %) *Enterobacter* spp, 28 (7.87 %) *Providencia* spp, 19 (4.82 %) *Hafnia* spp, 15 (3.30 %) *Shigella* spp, 14 (3.55 %) *Raoultella* spp, 13 (3.30 %) *Yersinia* spp and 8 (1.78 %) *Morgenella* spp.

The computed coefficient of variation of the prevalence of each organism in the various locations showed relatively uniform prevalence across locations of sampling

3. Prevalence of antibiotic resistance

Antibiotic susceptibility testing on isolates showed the following overall resistance to the various antibiotics tested: amoxicillin 345 (87.8%), amoxicillin/clavulanic acid 227 (57.8%), ceftriaxone 79 (20.1%), cefotaxime 65 (16.5%), imipenem 16 (4.1%), gentamicin 58 (14.5%), amikacin 12 (3.1%), ciprofloxacin 142 (37.1%), levofloxacin 124 (33.1%), doxycycline 380 (96.7).

173 (44.0%) of the isolates showed multi drug resistance phenotype and 84 (21.32) were ESBL producers. 217 (55.1 %) of isolates were resistant to at least one antibiotic class of choice against *Enterobacteriaceae* (cephalosporins, carbapenems, quinolones or aminoglycosides). 80 (20.3 %) of the isolates were resistant to at least one of the cephalosporins tested, 164 (41.62 %) were resistant to at least one of the quinolones tested and 66 (16.75 %) were resistant to at least one of the aminoglycosides tested. 232 (58.88 %) of the isolates showed penicillinase production but ESBL production was much lower with 84 (21.32 %) and 173 (43.91 %) showed MDR when considering only beta lactamins, quinolones and aminoglycosides, but adding the contribution of tetracyclines MDR rose to 85.53 % (337 isolates). (See Table 5 Complementary tables for details of the prevalence of antibiotic resistance in various isolates)

The association of resistance to the various antibiotic classes is shown in the following diagram.

The diagram shows that the number of ESBL producing isolates that were quinolone resistant was significantly lower than the number of isolates that were not quinolone resistant (32/84 against 52/84 respectively) while the number of aminoglycoside isolates that were resistant to quinolones was significantly higher than the number of isolates that were not quinolone resistant (43/66 against 23/66).

4. Association of risk factors among chickens with antibiotic resistance

The outcome “resistance” indicates isolates showing resistance to at least one antibiotic from one class of choice. The development of resistance to at least one antibiotic class correlated significantly to the age of the chicken and food hygiene. Isolates had higher risk of developing resistance on exposure to all risks except unsure water. ESBL production correlated significantly to age of chicken and isolates had higher risk of developing ESBL on exposure to all risks except use of antibiotics. MDR correlated significantly to the age of the chicken and isolates had a higher risk of developing MDR on exposure to all risks except unsure water. The risk “use of antibiotics” was quasi constant thus did not correlate with outcomes.

Table 5

Association of risks to resistance outcomes

N=394					
Factor	Outcome	Risk estimate		Correlation	
		Odds ratios (<i>increased risk</i> ≠ 1)	95% confidence interval		<i>(significant correlation ≤ 0.01)</i>
			Lower	Upper	
Use of antibiotics	Resistance	1.394	0.852	2.280	0.186
Age of chicken	Resistance	13.491	8.274	21.997	0.000
Feeding hygiene	Resistance	1.783	1.172	2.714	0.007
Sanitation	Resistance	1.495	1.000	2.234	0.049
Unsure water	Resistance	0.709	0.471	1.065	0.098
Use of antibiotics	ESBL	0.669	0.356	1.259	0.212
Age of chicken	ESBL	4.505	2.352	8.626	0.000
Feeding hygiene	ESBL	1.182	0.657	2.125	0.578
Sanitation	ESBL	1.322	0.754	2.316	0.330
Unsure water	ESBL	2.589	1.372	4.885	0.003
Use of antibiotics	MDR	1.490	0.897	2.473	0.123
Age of chicken	MDR	7.980	5.054	12.600	0.000
Feeding hygiene	MDR	1.538	1.004	2.354	0.047
Sanitation	MDR	1.348	0.900	2.018	0.148
Unsure water	MDR	0.544	0.362	0.818	0.003

Discussion

Prevalence

The sanitary conditions in the various poultries visited were average, not up to standard conditions mainly due to the nature of construction and materials used which promoted poor hygiene around the poultries. Some areas did not have pipe borne water thus farmers used well water with doubtful cleanliness. These conditions favoured extensive infection of the animals^{16,17}. The chicken harboured a myriad of *Enterobacteriaceae*

observed by the co-occurrence of an average of 3 different colony types in each sample. This is telling of the possibility of new antibiotic resistance and multidrug resistance to develop by horizontal gene transfer by means of mobile genetic materials such as plasmids or transposons^{7,18}. There was a high prevalence of *Escherichia* (20.56 %) and *Salmonella* (18.78 %) among the isolates followed by *Klebsiella* (9.90 %). These are clinically important genera with several species causing various diseases in human¹⁹. The isolation of members like *Shigella* even in few numbers is already a cause for concern given the virulence of the bacterium. However, their prevalence is similar to what is found elsewhere in several studies^{20,21}. The fairly uniform prevalence of the organisms in locations studied can be explained by the uniform socio-demographic and geographical nature (grass field highlands) of the area²².

Antibiotic susceptibility testing

All the isolated *Enterobacteriaceae* genera tested showed a high level of resistance to amoxicillin (87.8 %) of the group of Penicillins and doxycycline (96.7 %) of the class of Tetracyclines. These results were concordant with results obtained by Tago K. G., *et al* 2013²³ and further confirmed that these are no more drug classes of choice against *Enterobacteriaceae*. Generally, among the drug classes of choice prescribed against *Enterobacteriaceae*, isolates showed a higher resistance to Quinolones (37.1 % in ciprofloxacin and 31.1 % in levofloxacin) compared to third generation Cephalosporins (20.1 in ceftriaxone % and 16.5 in cefotaxime), imipenem and Aminoglycosides (3.1 % in amikacin and 14.5 % in gentamicin). Compared to early reports such as J Robert *et al*, 2001²¹, resistance to quinolones is on the rise with for example ciprofloxacin 10 % (90 % susceptibility) in 1998 to 37.1 % in the present study. The high resistance to ciprofloxacin should be monitored closely because it is one of the highest self-medications taken in simple *Enterobacteriaceae* related diseases and gastroenteritis in the West Region and most of parts of Cameroon owing to rampant drug misuse and self-medication in Cameroon which is not only in clinical settings but also in poultry farms⁸. However, the bacteria showed high susceptibilities to third generation Cephalosporins and Aminoglycosides compared to those observed elsewhere in Jamal F *et al*. 2011²⁴ and Sebastien B. *et al*. 2016²⁵.

There was observed a generally high MDR in all the genera with a general prevalence of 85.53 %. This is similar to the trend seen elsewhere as reported in Leski *et al*. 2016²⁶. However considering that tetracyclines are not drugs of choice against *Enterobacteriaceae*²⁷, ignoring the contribution of doxycycline this value falls considerably to 43.91 %. This high MDR prevalence in mostly commensal organisms like *Escherichia* and *Proteus* may go unchecked but in the face of an opportunistic infection, the treatment becomes difficult due to the developed MDR²⁸. ESBL production was observed at fairly moderate levels but the co-development of MDR and ESBL further compounds the failure of antibiotics in disease treatment²⁹.

Traditionally *Enterobacteriaceae* have developed high resistance to Penicillins via production of penicillinase³⁰ this explains high resistance to amoxicillin. *E coli* and *Klebsiella* maintained their known high production of ESBLs³¹ with 24.69 % and 30.77 % respectively compared to the general 21.32 %.

This research showed from the analysis of the odds ratios of risks that poor sanitation at poultry site from environment to feeding predisposed chicken first to high bacterial carriage and secondly predisposed these

bacteria to developing resistance, MDR and ESBLs. Though antibiotic use did not correlate as risk to these outcomes, it was because almost all poultries samples used antibiotics regularly making it a statistical constant. This is confirmed by Guetiya *et al.* 2016³². Correlation of these outcomes with “old age” of the chicken could be explained by the long duration of exposure to the risks³³, the time to get infected or for co-infection to allow horizontal gene transfers.

This researched also showed that ESBL producing isolates that were quinolone resistant were significantly lower than those that were not quinolone resistant (32/84 against 52/84 respectively) while aminoglycoside isolates that were resistant to quinolones were significantly higher than those that were not quinolone resistant (43/66 against 23/66). This suggests that quinolone resistance could not be largely plasmid mediated because plasmid-carried quinolone resistance genes tend to occur with ESBL producing genes creating the opposite scenario²⁹. This observation thus suggests a chromosomal DNA based quinolone resistance developed due to antibiotic misuse as noted in this study. Elena López *et al.* showed that ciprofloxacin induced chromosomal recombinations in *E coli* enabled the bacterium to resist the drug¹⁰. However given the high association of aminoglycoside resistance to quinolone resistance, it suggests a shared rather than intrinsic mechanism such as plasmid mediated resistance but the lower overall prevalence of resistance to aminoglycosides shows a smaller contribution of this mechanism in the resistance observed^{34,35}.

Conclusion

This research showed that sub-standard hygienic conditions at poultries caused heavy *Enterobacteriaceae* carriage in chicken in the West Region of Cameroon with a fairly uniform distribution of organisms across the area of study. *Enterobacteriaceae* in this Region show high resistance to Penicillins and Tetracyclines. 3rd generation Cephalosporins and Aminoglycosides proved to be drug classes of choice against *Enterobacteriaceae* with low resistance rates. The high resistance observed against quinolones calls for close monitoring of the use of these antibiotics in the community. The high prevalence of MDR and ESBL production especially in clinically important genera like *Salmonella*, *Escherichia* and *Klebsiella* indicate the necessity for stakeholders to put efforts and resources to combat misuse of antibiotics especially in animal farms. Further studies need to be conducted in this area on human subjects to evaluate same risk factors and consequences on the prevalence of resistance, MDR and ESBL production so as to do comparative studies and make more implication of this study on human populations.

Methods

Aim

The aim of this study was to contribute towards ameliorating the management and treatment of diseases linked to *Enterobacteriaceae* in Cameroon; providing epidemiological data on prevailing *Enterobacteriaceae* and their resistance patterns and risk factors.

Design

The design used was a cross-section design.

Study site

The West Region with an area of 13,892 km² is a territory located in the central-western portion of the Republic of Cameroon located at 5°30'N 10°30'E. It borders the North West Region to the northwest, the Adamawa Region to the northeast, the Centre Region to the southeast, the Littoral Region to the southwest, and the Southwest Region to the west. The West Region is the smallest of Cameroon's ten regions in area, yet it has the highest population density; a population of 1,865,394 (2013) with density of 134/km². Its Capital is Bafoussam in the Mifi Division. It has 8 Divisions: Bamboutos, Upper-Nkam, Upper-Plateau, Koung-Khi, Ménoua, Mifi, Ndé and Noun³⁶. The Region is found in the Grass field plateaus of the Western highlands with a cold climate and the main ethnic groups are the Bameliké and Bamoum²².

Laboratory work was carried out in the Research Unit of Microbiology and Antimicrobial Substances (RUMAS) in the University of Dschang.

Sample collection

In Cameroon, research on livestock is under the supervision of the Ministry of Livestock, Fisheries and Animal Industries (MINEPIA). Poultry and other livestock farms are registered under this Ministry which follows the health of the animals while still in the farm and before sales. A research authorisation (reference number 68/18/L/DREPIA-O/SRAG of 04/06/2018) addressed to the Divisional Delegates was obtained from the Regional Delegation of this Ministry. With the authorisation, the Divisional Delegates connected us to registered farms in the various Divisions. Consent from the farmers was verbal upon presentation of research authorisation and researchers' credentials and affiliations. The study was performed on cloacal swabs from healthy broiler chicken of any age from 28 farms in 11 locations in 5 out of the 8 Divisions of the West Region of Cameroon. We used stratified sampling with Divisions as the strata.

Cloacal swabs were collected by rubbing a 50 cm² area of the cloaca with a sterile swab pre-wetted with physiological water. Each swab was immersed in 5 ml of a sterile physiological solution in swab sampling tubes. The samples were transported in cool thermos flasks to the laboratory for analysis³⁷.

Sample enrichment and culture

The swabs were dissolved in buffered peptone water and incubated for 24hrs at 38°C³⁸. The enriched samples were cultured on EMB agar by plate streaking¹ and incubated for 48 hours.

Isolation of isolates and preservation

Isolated colonies on the EMB agar were identified based on colony characteristics, picked and conserved in a conservation medium; a mixture of glycerol and Muller Hilton broth at 1 part : 3 parts and stored in a refrigerator^{39,40}.

Phenotypic characterisation of isolates

A total of nine (9) rapid screening biochemical tests^{1,18} were performed on the isolates including: glucose and lactose fermentation, and hydrogen sulphide (H₂S) and gas production using Kligler Iron Agar (KIA), urease activity and indole production using urea broth and Kovacs’ reagent, mannitol fermentation and motility using mannitol agar, and citrate fermentation using citrate agar.

Antibiotic susceptibility testing

Fresh colonies were used to prepare 0.5 McFarland solution inoculums using sterile physiological water. Antibiotic susceptibility testing was carried out on Mueller Hilton Agar by the Kirby-Bauer disc diffusion method^{2,18}. Screening for antibiotic resistance in the isolates was done using following antibiotics⁴¹:

Class	Antibiotics
Beta lactamins	Amoxicillin, amoxicillin/clavulanic acid, ceftriaxone, cefotaxime and imipenem
Aminoglycosides	Gentamicin and amikacin
Quinolones	Ciprofloxacin and levofloxacin
Tetracycline	Doxycycline

Phenotypic determination of resistance by penicillinase production was tested by combination disc test with amoxicillin/clavulanic acid with comparison to amoxicillin. Extended spectrum beta-lactamase production was tested by observing resistance to amoxicillin followed by resistance to ceftriaxone or cefotaxime⁴², and then the double disc synergy test was conducted by placing the ceftriaxone or cefotaxime 3 cm from amoxicillin/clavulanic acid giving a clear zone of intersection between the two discs⁴³.

DATA ANALYSIS

Interpretation of phenotypic reactions

This research work generated information on *Enterobacteriaceae* carriage in broilers, identity of *Enterobacteriaceae* organisms, their prevalence, their antibiotic susceptibility profiles (susceptible, resistant, multidrug resistant and ESBL producing) and, odds ratios and correlations between outcomes (*Enterobacteriaceae* carriage, prevalence, resistance, MDR and ESBL production) and risks.

Enterobacteriaceae carriage was determined by the count of the different colonies on the *Enterobacteriaceae*-specific growth medium (EMB agar) based on colony aspect and morphology. The identity of the organism was gotten by interpreting the colony aspect and the results of the phenotypic reactions using a KIA user guide alongside the identification software: *Feuille de calcul pour l'identification microbienne* developed by J-Noël JOFFIN (8 Dec 2007 version). Susceptibility to antibiotics was evaluated using standard values as given by Sigma Aldrich®⁴⁴. MDR was assessed as resistance of an isolate to two or more antibiotics belonging antibiotic classes of choice used against *Enterobacteriaceae* (cephalosporins, carbapenems, quinolones or aminoglycosides). ESBL production was interpreted from double disc synergy test between amoxicillin/clavulanic acid disc and ceftriaxone or cefotaxime disc.

Simple arithmetic operations and conversions were done using Microsoft Excel sheets while frequencies, prevalence, odds ratios, correlations and diagrams were done using IBM SPSS Statistics 20.

Abbreviations

CI: confidence interval

EMB: eosin methylene blue

ESBL: extended spectrum beta lactamase

KIA: Kligler Iron Agar

MDR: multidrug resistance

MINEPIA: French acronym for Ministry of Livestock, Fisheries and Animal Industries

RUMAS: Research Unit of Microbiology and Antimicrobial Substances

Declarations

Ethical consideration

This study did not involve active participation of the fowls and sampling by cloacal swabs was a non-invasive procedure.

Working with poultry farms falls under the authorities of the Ministry of Livestock, Fisheries and Animal Industries (MINEPIA), thus an authorisation (authorisation reference number 68/18/L/DREPIA-O/SRAG of 04/06/2018) to sample chicken within the West Region was obtained from the Regional Delegation of MINEPIA which also helped to enable collaboration with its Divisional Delegates and farmers.

Consent for publication

Not applicable

Availability of data

The datasets generated during the present study are presented in this manuscript. Any other raw data are available from the corresponding author upon a reasonable request.

Conflicting interest

The authors declare that they have no conflicting interests.

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Authors' contribution

Leinyuy Jude Fonbah: Field work and laboratory analysis, data analysis and writing of the article.

Innocent Mbulli Ali: Study conception, designed protocols for laboratory analysis, supervised field and laboratory analysis, interpreted data and reviewed the manuscript.

Ousenu Karimo: Performed laboratory analysis, data analysis interpretation and drafting section of the manuscript.

Christopher B. Tume: Study conception, supervision and manuscript review.

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Tables

Due to technical limitations, table 3 and table 4 are only available as a download in the Supplemental Files section.

Figures

Figure 1

Prevalence of isolates of different Enterobacteriaceae species

Figure 2

Association of various resistance phenotypes among isolates

Figure 3

General prevalence of resistance of isolates to various antibiotics tested

Figure 4

General prevalence of MDR amongst the isolates

Figure 5

General prevalence of ESBL production among the isolates

Figure 6

Localisation of the study area

Figure 7

Antibiogram disc showing penicillinase and ESBL production

Supplementary Files

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