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Occurrence and Antimicrobial Resistance of Extended-Spectrum Beta-Lactamase Producing Bacteria in Diabetic Foot Infections at Korle-Bu Teaching Hospital

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Abstract

Background: Common complications of diabetes mellitus include foot infections, which lead to increased healthcare cost and delayed wound healing. Diabetic foot infections (DFIs) can be caused by Gram-negative, Extended-Spectrum Beta-Lactamase (ESBL) producing bacteria which are resistant to a wide range of antibiotics used in clinical medicine. This presents a significant challenge to the treatment of DFIs. However, identifying the bacterial species involved can be critical for effective management and targeted therapy.

Objective: The study investigated the antimicrobial resistance and molecular characteristics of ESBL-producing bacteria from diabetic foot infections at Korle Bu Teaching Hospital (KBTH) using disk diffusion and Polymerase Chain Reaction (PCR).

Methods: From January to September 2018, tissue samples, aspirates, or pus were collected from diabetic patients from the ulcer room at the department of surgery, KBTH. Patients' demographics were gathered using a data collection tool. Bacterial culture, antimicrobial susceptibility testing and PCR detection of ESBL genes were performed.

Results: In total, 138 Gram-negative isolates were recovered from the 50 study participants enrolled. Majority of the isolates were resistant to ciprofloxacin (55.79%, n = 77/138) but susceptible to meropenem (97.82%, n = 135/138). Among the isolates, 41 (29.71%) were phenotypically positive for ESBL production using CHROMagar ESBL. The *CTX-M* gene was predominantly identified in *E. coli* (9/19) by PCR.

Conclusion: ESBL-producing Gram-negative bacteria continue to pose a major challenge in Ghana, with the *CTX-M* gene identified as the most prevalent among ESBL-positive isolates. Notably, a majority of the isolates remained susceptible to meropenem, suggesting its potential as an effective treatment option. Continued surveillance is crucial to monitor the emergence and dissemination of AMR pathogens in DFIs.

Keywords: Diabetic foot infection, ESBL, AMR, Ghana

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INTRODUCTION

Diabetic foot infection (DFI) is a major complication among diabetic patients which often leads to prolonged wound healing and hospitalization, amputations and in extreme cases death. Several factors including neuropathy, poor blood circulation, and a weakened immune system all of which are prevalent in diabetic patients contribute to these infections [1]. A crude estimate of diabetes in Ghana shows a prevalence of 6.30% with foot infections, gangrene, abscess, and cellulitis being the most common surgical complications [2,3]. DFIs can be either

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polymicrobial or monomicrobial, however, majority are complex polymicrobial infections commonly caused by *Escherichia coli, Klebsiella spp, Proteus spp, Pseudomonas aeruginosa* and obligate anaerobes such as *Bacteroides spp* [1,4,5,6].

Early and appropriate antibiotic treatment targeting the most likely etiological agent is vital in the management of these foot infections. However, the emergence of antimicrobial resistance particularly among Enterobacterales and *Pseudomonas spp* producing Extended-Spectrum Beta-Lactamase (ESBL) complicates the process [1,7,8,9]. In Ghana, a nationwide survey of ESBL prevalence showed a fast-growing silent pandemic with rates ranging from 41.50% to 50.50% [10-13]. This rise is compelling clinicians to prescribe second- and third-generation antimicrobials, which are typically in the reserve group for clinical use, especially in deep seated infections with poor healing history such as diabetic foot infections. The excessive reliance on these antibiotics accelerates the emergence of resistant bacterial strains, reducing therapeutic options and increasing treatment failures. Given these challenges, investigating resistance patterns and the genetic mechanisms underlying ESBL production is crucial. A deeper understanding of these factors can aid in optimizing antibiotic therapy, enhancing patient outcomes, controlling the spread of resistant bacteria, and informing public health strategies. This study investigated the antimicrobial resistance patterns and genetic determinants of resistance in ESBL-producing bacterial species recovered from diabetic foot infections.

MATERIALS AND METHODS

Study Site, Study Design and Sampling

In this prospective cross-sectional study, 50 diabetic patients with inframalleolar foot infections including ulcer, cellulitis, gangrene, plantar fasciitis and necrotising fasciitis were enrolled at the ulcer room of the department of surgery at the Korle-Bu Teaching Hospital (KBTH). The Perfusion, Extent, Depth, Infection and Sensation (PEDIS) index as described by the Infectious Diseases Society of America and International Working Group on the Diabetic Foot was used to establish colonisation, contamination and infection, ensuring careful selection of participants for the study [14].

After obtaining informed consent, tissue biopsies were collected during debridement by a qualified surgeon. Localised anaesthesia was administered using a subcutaneous injection of 2% w/v lidocaine by a qualified nurse anaesthetic before collection. For patients with deep-seated pus, aspirates or fluid from fluctuant areas were collected using sterile syringes. Patients' treatment histories were collected for the period between January and October 2018. Additionally, demographic data, including age, gender, and empirical antibiotic treatment were also obtained. Patients' blood sugar and blood pressure were also checked and recorded.

Sample Preparation and Transport

Tissue samples, pus and aspirates collected were quickly dispensed into a glass bottle containing thioglycolate broth, capped, sealed with parafilm and transported (within 4 hours of sampling) to the Bacteriology Department of the Noguchi Memorial Institute for Medical Research, for analysis.

Bacterial identification

The broth sample mixture was incubated aerobically for 18-24 hours at 37 ºC prior to subculture. The samples were then plated on Blood agar and MacConkey agar and incubated aerobically for 18-24 hours at 37 ºC. Preliminary identification of bacteria was done by colonial morphology and Gram staining. Bacterial identification was confirmed using the Matrix-Assisted Laser Desorption/Ionization Time of Flight Mass Spectrometry (MALDI-TOF-MS) (Bruker Daltonics, Germany). Briefly, colonies from fresh overnight cultures were spotted on the target plate. One microliter of formic acid was then added and allowed to dry for 15 minutes. One microliter of matrix preparation was then placed on each sample and left to dry for about 15 minutes. The target plate was then introduced into the machine. Within the machine, the ionization peaks (spectra) generated were matched against the integrated reference library of the MALDI system for confirmation of bacteria species.

Antibiotic Susceptibility Testing and ESBL phenotypic screening

Antibiotic susceptibility testing was performed by the Kirby-Bauer disk diffusion method and interpreted according to the Clinical Laboratory Standards Institute (CLSI 2018) guidelines [15]. Gram-negative organisms recovered were screened for production of ESBL using CHROMagar ESBL (Biomerieux, France). The isolates were inoculated on the agar and incubated aerobically for 18 - 24 hours at 37ºC. The plates were observed for growth and colony appearance after incubation. ESBL-positive strain *K. pneumoniae* NCTC 13368 (ATCC 700603) and ESBL-negative strain *E. coli* ATCC 25922 were used as Controls.

Polymerase Chain Reaction (PCR) Detection of ESBL genes (*CTX-M, SHV and TEM-1*)

Multiplex PCR was performed on presumptive ESBL-producing isolates to determine ESBL genes (*CTX-M, SHV and TEM-1*) as described by Sharma et al., (2013) [16]. Briefly, crude DNA was obtained by transferring three freshly prepared colonies of bacteria into 200µl of molecular-grade nuclease-free water and boiled for 5 minutes at 98 °C. The resulting mixture was frozen in -20 ºC for 10 minutes. The mixture was then centrifuged for 5 minutes at 4 °C and the supernatant was transferred into Eppendorf® tubes and used as DNA template for the PCR. For PCR amplification, each reaction-mix of 25 µL consisted of 12.5 uL of Green PCR Master Mix (2×) (DreamTaq, Thermo Scientific, Waltham, MA, USA), 4.5 µL of primer mix, 6 µL of molecular-grade nuclease-free

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water and 2 µL of crude DNA template, as previously demonstrated by Khurana et al., 2018. [17]. Table 1 shows the primers used for the PCR. The cycling conditions included initial denaturation at 95 °C for 5 minutes, followed by denaturation at 95 °C for additional 30 seconds and template annealing for 30 seconds and elongation at 72 °C for 2 minutes and final elongation for 10 minutes. All PCR amplicons were analyzed with gel-electrophoresis in a 2% (weight/volume) agarose gel (SeaKem®GTG®Agarose, Lonza, Basel, Switzerland) using Tris/Acetate/EDTA buffer.

Data Analysis

Data collected were entered into Microsoft excel version 2016. The data were checked for consistency and then transferred into Epi Info Version 7.2.6 software for statistical analysis. This was presented as frequencies and percentages in tables.

RESULTS

In total, 50 patients comprising nine (9) in-patients and 41 out-patients were recruited in this study. There was a gender balance of (50.00%, n = 25) males and (50.00%, n = 25) females. Majority of the participants (38.00%, n = 19) fell in the 60 years to 70 years age group. The nature of infections seen included ulcers (80.00%, n = 40), abscess (6.00%, n = 3), cellulitis (10.00%, n = 5) and plantar fasciitis (2.00%, n = 1). Table 2 shows the demographic characteristics of patients involved in the study. Random blood sugar was

Table 1. List of primer sets showing the oligonucleotides

Gene	Primer set	Expected amplicon size (bp)
TEM-1	F:5′-GAGACAATAACCCTGGTAAAT-3′	459
	R:5′-AGAAGTAAGTTGGCAGCAGTG-3′	
CTX-M	F:5′-GAAGGTCATCAAGAAGGTGCG-3’	560
	R:5′-AGAAGTAAGTTGGCAGCAGTG-3′	
SHV	F:5’-GTCAGCGAAAAACACCTTGCC-3’	383
	R:5’-GTCTTATCGGCGATAAACCAG-3’	

Table 2. Demographic table (showing distribution of age, sex and infection type)

Characteristics	Group	Frequency (%)
Sex	Female	25(50.00%)
	Male	25(50.00%)
Department	IPD	9(18.00%)
	OPD	41(82.00%)
Age	≤60	25(50.00%)
	≥60	25(50.00%)
Type of infection	Ulcers	40(80.00%)
	Abscess	3(6.00%)
	Cellulitis	5(10.00%)
	Plantar fasciitis	1(2.00%)

Table 3. Empirical Antibiotic Treatment of Various Infections with Associated ESBL Genes

ESBL bacteria	Patient ID	Sex	Infection	Empirical antibiotic given	Phenotypic antibiotype	ESBL gene
Escherichia coli	1G	M	Ulcer	CLN	AMC/MEM/GEN/PIP	*TEM/CTX/SHV*
	2A	M	Ulcer	NI	AMC/MEM/GEN/PIP	*CTX*
	3N	M	Ulcer	NI	AMC/MEM/GEN/PIP	*CTX*
	4J	F	Ulcer	NI	AMC/MEM/GEN/PIP	*CTX*
	6B	F	Abscess	FLU	MEM/CHL/GEN/CFT/PIP	*TEM*
	9B	F	Cellulitis	AMC	MEM/GEN/PIP	*CTX*
	11B	M	Ulcer	CLN	AMC/MEM/GEN/CIP	*SHV*
	17D	M	Ulcer	CLN	MEM/GEN/PIP	*TEM/CTX*
	18B	M	Ulcer	CLN	MEM/GEN/PIP	*SHV/CTX*
	21C	M	Ulcer		MEM/GEN/CIP/CFT	*CTX*
	27A	M	Ulcer	CLN	CFX/AMC/MEM/CTM/CFP/GEN/PIP	*CTX*
Enterobacter kobei	7C	F	Ulcer	CLN	MEM/CHL/CEF/GEN/CIP	*TEM/CTX*
Klebsiella pneumoniae	4K	F	Ulcer	NI	MEM/CHL/CFT	*TEM/CTX/SHV*
	5G	F	Ulcer	NI	TET/CHL/GEN	*TEM/CTX/SHV*
Morganella morganii	14B	F	Cellulitis	CLN/CIP	CTM/MEM/CFP/GEN/PIP	*SHV/TEM*
Proteus mirabilis	5D	F	Ulcer	NI	AMC/MEM/CTM/CFP/GEN/CFT/PIP	*CTX*
	40A	F	Ulcer	CLN/CIP	MEM/GEN/CFT/PIP	*TEM/CTX*
Providencia stuartii	27I	M	Ulcer	CLN	MEM/CFP/GEN/PIP	*SHV/CTX*
P. aeruginosa	10J	F	Plantar fasciitis	AMC	MEM/TET/CFT/CFP/GEN/CIP/PIP	*TEM/CTX/SHV*
	27C	M	Ulcer	CLN	MEM/TET/CHL/CFP/GEN/CIP/CFT/PIP	*TEM/CTX/SHV*
	47A	M	Ulcer	CIP/CLN	MEM/CFP/GEN/CIP	*CTX*

*AMC-Amoxicillin/Clavulanate, CLN- Clindamycin, CIP-Ciprofloxacin, FLU- Flucloxacin, NI-not indicated MEM-Meropenems, CFX-Cefuroxime, CTM-Cefotaxime, CFP-Cefepime, CFT- Ceftazidime GEN-Gentamicin, PIP-Pipercillin-tazobactam, CHL-Chloramphenicol, M-Male, F-Female

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Table 4. Distribution of bacteria isolates among wound types sampled from diabetic patients

Bacterial Isolate	Ulcers 40(80%)	Abscess 3(6%)	Plantar Fasciitis 1(2%)	Cellulitis 5(10%)	CHROMagar ESBL Positive
Proteus mirabilis (n=31)	24(22.22)	2(18.18)	2(33.33)	3(23.07)	2(6.45)
Proteus vulgaris (n=13)	10(9.25)	0	1(16.66)	2(15.38)	0
Klebsiella pneumoniae (n=14)	10(9.25)	2(18.18)	0	2(15.38)	4(28.57)
Klebsiella oxytoca (n=8)	4(3.70)	2(18.18)	1(16.66)	1(7.69)	1(12.50)
Escherichia coli (n=38)	32(29.62)	2(18.18)	2(33.33)	2(15.38)	19(50.00)
Enterobacter cloacae (n=4)	4(3.70)	0	0	0	0
Pseudomonas aeruginosa(n=24)	19(17.59)	3(27.27)	0	2(15.38)	9(37.50)
Morganella morganii (n=2)	1(0.92)	0	0	1(7.69)	2(100)
Providencia stuartii (n=3)	3(2.77)	0	0	0	3(100)
Enterobacter kobei (n=1)	1(0.92)	0	0	0	1(100)
Total	108	11	6	13	41

Table 5. Distribution of ESBL genes among ESBL-positive isolates

Isolates	*SHV*(%)	*TEM-1*(%)	*CTX-M*(%)	Total No. of genes detected
Escherichia coli(n=19)	3(33.33)	3(30.00)	9(50.00)	15
Pseudomonas aeruginosa(n=9)	2(22.22)	2(20.00)	3(16.66)	7
Klebsiella pneumoniae(n=4)	2(22.22)	2(20.00)	2(11.11)	6
Proteus mirabilis(n=2)	0	1(10.00)	2(11.11)	3
Enterobacter kobei(n=1)	0	1(10.00)	1(5.55)	2
Morganella morganii(n=2)	1(11.11)	1(10.00)	0	2
Providencia stuartii(n=3)	1(11.11)	0	1(5.55)	2
Total	9	10	18	37

No gene was detected in *Klebsiella oxytoca* (n=1)

tested using a One-touch select glucometer, with the median blood sugar in the study being 9.85 mmol/L. Out of the 50 patients, 88.0% (n = 44) were already receiving antibiotic treatment. Four patients were on B-lactam/β-lactamase inhibitors, nine (9) were on aminoglycoside/fluoroquinolones combination therapy, and three (3) on aminoglycosides/ fluoroquinolone/β-lactamase triple therapy. Three patients received quinolone monotherapy, while aminoglycoside monotherapy was administered to 21 patients. Table 3 shows antibiotics administered to patients with ESBL-producing bacteria.

Bacterial Isolates, Antimicrobial Resistance and ESBL Production

A number of patients (20.00%, n = 10/50) had polymicrobial infections. A total of 138 Gram-negative bacteria species were recovered and 29.71% (n = 41) showed positivity for ESBL production using CHROM agar. Among them were *Escherichia coli* (46.34%, n = 19/41), *Pseudomonas aeruginosa* (21.95%, n = 9/41) and *Klebsiella pneumoniae* (9.75%, n = 4/41). Isolates recovered were resistant to ciprofloxacin (55.79%, n = 77/138), cefepime (44.20%, n =61/138), but susceptible to meropenem (97.82%, n = 135/138), gentamicin (97.82%, n = 135/138) and piperacillin-tazobactam (95.65%, n = 132/138). Table 4 shows the distribution of isolates recovered, type of infections as well as the proportions of ESBL positive isolates.

Distribution of ESBL Genes Among ESBL Positive Isolates

All three ESBL genes (*TEM-1*, *SHV*, *CTX-M*) were detected in one *E. coli*, two *K. pneumoniae*, and two *P. aeruginosa* isolates. Six isolates had both *TEM* and *SHV* genes. *TEM* and *CTX-M* genes were both present in 8 of the isolates. Both *SHV* and *CTX-M* were found in 7 isolates. Phenotypic ESBL detection indicated ESBL production in *Klebsiella oxytoca*, however, none of the genes associated with ESBL production was found in the isolate. Table 5.0 shows the distribution of ESBL genes among the ESBL-positive isolates.

DISCUSSION

In this study, the presence of ESBL among bacterial isolates obtained from diabetic foot infections and their accompanying antimicrobial resistance patterns was investigated. DFIs present a significant and challenging complication for individuals with diabetes, often leading to severe outcomes. Ulcers were observed as being the most common diabetic foot infections. Gram-negative bacteria were isolated from the DFIs and many of the infections were polymicrobial which probably contributed to poor wound healing [4-6]. This study presents an overall ESBL-producing percentage positivity of 29.70% with *E. coli* having the highest level of ESBL positivity. Other studies in Ghana

have reported rates of 57.80% (Kumasi), 50.50% and 43.70% (Accra) as well as 41.50% (Ho) [10-13]. In Africa, studies have recorded prevalence rates of 50.00% (Lagos, Nigeria) and 36.10% (South Africa) [18,19]. Several other African studies have also reported relatively high levels of ESBL- producing *E. coli* [20-23]. ESBL percentage positivity among *Proteus mirablilis*, *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* were 6.45%, 28.57%, and 37.50%, respectively, which is not unexpected. The prevalence of ESBL-producing organisms observed in this study, along with findings from previous research in the country, is concerning as it significantly limits available treatment options and contributes to increased rates of therapeutic failure [13]. In light of these challenges, urgent intervention is needed, particularly the strengthening of laboratory capacity as most clinical microbiology laboratories in Ghana do not routinely test for ESBLs. The widespread practice of self-medication without prior laboratory diagnosis, coupled with the limited capacity to detect and report ESBLs at the community level, may further drive the emergence of antibiotic resistance. If not addressed, this growing threat could have serious implications, especially for patients with diabetic foot infections, where treatment options are already limited. Isolates recovered frequently demonstrated resistance to amoxicillin and ciprofloxacin, which are preferred antibiotics for managing patients with diabetic foot infections in the hospital setting. The high proportion of resistance could be as a result of indiscriminate use of these antimicrobials [24]. The low resistance to meropenem and gentamicin reflects their less frequent usage among patients. Meropenem has emerged as the antimicrobial agent of choice in the treatment of serious infections caused by ESBL-producers based on in vitro testing [11,25,26]. Preserving the efficacy of this drug is an essential measure as they belong to the category of critically needed antibiotics used to treat life-threatening infections caused by *E. coli* and other pathogens in humans. Significantly, the second and third-generation cephalosporins exhibited a resistance percentage ranging from 70% to 75%. Fortunately, they were not observed to be frequently prescribed to patients in this study. Some strains also exhibited co-resistance to aminoglycosides, quinolones, and third-generation cephalosporins. This is a significant concern, as these strains may lead to therapeutic challenges [27,28]. Among the three genes detected (*SHV, TEM-1, CTX-M*), *CTX-M* was prevalent among ESBL-producing *E. coli*, similar to the observation made among the isolates recovered in Komfo Anokye Teaching Hospital, Ghana [11]. Although *Klebsiella oxytoca* tested positive for ESBL on Chromagar, none of the ESBL genes (*CTX-M, TEM-1 and SHV*) were detected. The mode of resistance may involve efflux pumps or the utilization of cell wall transpeptidases that are insensitive to β-lactam antimicrobials [29].

Conclusion

This study found that several organisms causing diabetic foot infections (DFIs) were ESBL producers. Among these, ESBL-positive *E. coli* had a high prevalence, with *CTX-M* and *TEM-1* identified as the predominant resistance genes. Although few in number, some ESBL isolates also exhibited resistance to meropenem, a reserve antibiotic. These findings highlight the urgent need for continuous surveillance and preventive measures to curb the spread of resistant bacteria.

DECLARATIONS

Ethical consideration

This work received clearance from the Ethical and Protocol Review Committee of the University of Ghana Medical School. Patients were provided with written consent before enrolment into the study. All specimen were labelled using a unique coding system to ensure confidentiality. Written consent was obtained from each patient before enrolling into the study.

Consent to publish

All authors agreed to the content of the final paper.

Funding

None

Competing Interest

The authors have no conflict of interest to declare.

Author contribution

BE, KS, and PF conceptualized the study. KS, JB, SS, and BE designed the methodology. BE, KS, JB, and SS conducted the investigation and performed formal analysis. BE, KS, NO-N, PF, JB, and SS contributed to validation. KS, BE, JB and SS handled data curation. KS and BE drafted the original manuscript. BE, KS, SS, JB, NO-N, and PF reviewed and revised the manuscript. KS, BE, JB and PF contributed to visualization. BE and PF supervised the study. BE managed the project and acquired funding. All authors read and approved the final manuscript.

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Availability of data

Data is available upon request to the corresponding author

REFERENCES

1. Uckay I, Garani K, Pataky Z, Lipsky BA (2014) Diabetic foot infections: state-of-the-art. Diabetes Obes Metab 16:305–316

2. Amoah GB, Owusu KS, Adjei S (2002) Diabetes in Ghana: a community-based prevalence study in Greater Accra. Diabetes Res Clin Pract 56:197–205

3. Asumanu E, Ametepi R, Koney CT (2010) Audit of diabetic soft tissue infection and foot disease in Accra. West Afr J Med 29:86–90

4. Majcher-Peszynska J, Haase G, Sab M (2008) Pharmacokinetics and penetration of linezolid into inflamed soft tissue in diabetic foot infections. Eur J Clin Pharmacol 64:1093–1100

5. Vardakas KZ, Maria H, Matthew EF (2008) Factors associated with treatment failure in patients with diabetic foot infections: an analysis of data from randomized controlled trials. Diabetes Res Clin Pract 80:344–351

6. Yates C, May K, Hale T, Allard B (2009) Wound chronicity, inpatient care, and chronic kidney disease predispose to MRSA infection in diabetic foot ulcers. Diabetes Care 32:1907–1909

7. Armstrong DG (2011) An overview of foot infections in diabetes. Diabetes Technol Ther 13:951–957

8. Iraj B, Fariborz K, Alireza E, Gholamreza A (2013) Prevention of diabetic foot ulcer. Int J Prev Med 4:373–376

9. Pucci MJ, Bush K (2013) Investigational antimicrobial agents of 2013. Clin Microbiol Rev 26:792–821

10. Agyepong N, Usha G, Alex O, Sabiha YE (2018) Multidrug-resistant Gram-negative bacterial infections in a teaching hospital in Ghana. Antimicrob Resist Infect Control 7:1

11. Feglo PK, Adu-Sarkodie Y (2016) Antimicrobial resistance patterns of extended spectrum β-lactamase producing Klebsiellae and E. coli isolates from a tertiary hospital in Ghana. Eur Sci J 12:1857–7881

12. Obeng-Nkrumah N, Twum-Danso K, Krogfelt AK, Newman MJ (2013) High levels of extended-spectrum beta-lactamases in a major teaching hospital in Ghana: the need for regular monitoring and evaluation of antibiotic resistance. Am J Trop Med Hyg 89

13. Deku JG, Duedu KO, Ativi E, Kpene GE, Feglo PK (2021) Occurrence and distribution of extended-spectrum β-lactamase in clinical Escherichia coli isolates at Ho Teaching Hospital in Ghana. Ghana Med J 55:298–307

14. Institute of Clinical and Laboratory Standards (2018) CLSI. Methods for dilution antimicrobial susceptibility tests for bacteria that grow aerobically; approved standard — ninth edition. CLSI 32

15. Senneville E, Zaina A, Suzzanne AA, Zulfigarali GA, Allisson G (2018) Guidelines on the diagnosis and treatment of diabetes-related foot infections (IWGDF/IDSA 2018). Clin Infect Dis 2018

16. Sharma M, Sati P, Preeti S (2013) Prevalence and antibiogram of extended spectrum β-lactamase (ESBL) producing gram negative bacilli and further molecular characterization of ESBL producing Escherichia coli and Klebsiella spp. J Clin Diagn Res 7:2173–2177

17. Khurana S, Mathur P, Kapil A, Valsan C, Behera B (2017) Molecular epidemiology of beta-lactamase producing nosocomial Gram-negative pathogens from North and South Indian hospitals. J Med Microbiol 66:999–1004

18. Aibinu IT, Odugbemi WK, Ghebremedhin B (2012) Sequence type ST131 and ST10 complex (ST617) predominant among CTX-M-15-producing Escherichia coli isolates from Nigeria. Clin Microbiol Infect 18:49–51

19. Tau NP, Smith AM, Sooka A, Keddy KH (2012) Molecular characterization of extended-spectrum β-lactamase-producing Shigella isolates from humans in South Africa, 2003–2009. J Med Microbiol 61:162–164

20. Ako-Nai IC, Ikem OO, Akinloye OA (2006) Characterization of bacterial isolates from diabetic foot infections in Ile-Ife, southwestern Nigeria. Foot 16:158–164

21. Kabli SA, Alaa ED, Abdelbasit H, Mohammed Nabih NB (2012) An epidemiological survey of extended-spectrum β-lactamases producing bacteria genotypes and the evaluation of the antimicrobial effect of Rhazya stricta leaf extract. Microbiol Res 32:66

22. Mengesha RE, Kasa BG (2014) Aerobic bacteria in post-surgical wound infections and pattern of their antimicrobial susceptibility in Ayder Teaching and Referral Hospital, Mekelle, Ethiopia. BMC Res Notes 7:575

23. Tansarli GS, Panagiotis P, Anastasios K, Matthew EF (2014) Proportion of extended-spectrum β-lactamase (ESBL)-producing isolates among Enterobacteriaceae in Africa: evaluation of the evidence-systematic review. J Antimicrob Chemother 69

24. Newman MJ, Frimpong E, Donkor ES (2011) Resistance to antimicrobial drugs in Ghana. Infect Drug Resist 4:215–220

25. Acquah M, Samuel EK, Appiah KL (2013) Susceptibility of bacterial etiological agents to commonly-used antimicrobial agents in children with sepsis at the Tamale Teaching Hospital. BMC Infect Dis 13:89

26. Ayisi LA, Adu-Sarkodie Y (2015) Extended-spectrum-beta-lactamase (ESBL) production among Escherichia coli and Klebsiella species in Kumasi, Ghana. J Nat Sci Res 5:81–86

27. Walsh TR (2008) Clinically significant carbapenemases: an update. Curr Opin Infect Dis 21:367–371

28. Zarrilli R, Vitale D, Di Popolo A (2008) A plasmid-borne blaOXA-58 gene confers imipenem resistance to Acinetobacter baumannii isolates from a Lebanese hospital. Antimicrob Agents Chemother 52:4115–4120

29. Nedbalcova K, Nechvatalova K, Pokludov M (2014) Resistance to selected beta-lactam antibiotics. Vet Microbiol 171:328–336