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Prevalence of antibiotic-resistant bacteria among patients in two tertiary hospitals in Eastern Uganda

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ABSTRACT

Objective: The aim of this study was to determine the prevalence and antibiotic resistance patterns of bacterial isolates from inpatients and outpatients in Mbale and Soroti regional referral hospitals in Eastern Uganda.

Methods: A retrospective analysis of culture and antibiotic sensitivity test results from the microbiology laboratories of the two tertiary hospitals was conducted for a 3-year period (January 2016–December 2018).

Results: Microbiology records of 3092 patients were reviewed and analysed, with 1305 (42.1%) samples yielding clinical isolates. The most prevalent isolates were *Escherichia coli* (*n* = 442; 33.9%), *Staphylococcus aureus* (*n* = 376; 28.8%), *Klebsiella pneumoniae* (*n* = 237; 18.2%), and *Streptococcus pneumoniae* (*n* = 76; 5.8%). High rates of antimicrobial resistance were detected across both Gram-negative and Gram-positive bacteria. *Escherichia coli* and *K. pneumoniae* were resistant to several agents such as amoxicillin/clavulanate (83.5%; 64.6%), cefotaxime (74.2%; 52.7%), ciprofloxacin (92.1%; 27.8%), gentamicin (51.8%; 76%), imipenem (3.2%; 10.5%), tetracycline (98%; 74.5%), and trimethoprim-sulfamethoxazole (74.1%; 74.3%), respectively. *Staphylococcus aureus* and *S. pneumoniae* exhibited the following resistance profile: cefoxitin (44.4%; 40.9%), chloramphenicol (69.1%; 27.6%) clindamycin (21.5%; 24.4%), gentamicin (83.2%; 66.9%), penicillin (46.5%; -) tetracycline (85.6%; 97.6%), trimethoprim-sulfamethoxazole (88%; 91.3%), and vancomycin (41.2%; -).

Conclusion: We observed high resistance rates to antibiotics among the majority of microorganisms that were isolated from the samples collected from patients in Eastern Uganda. Furthermore, measures should be undertaken locally to improve microbiology diagnostics and to prevent the spread of antibiotic-resistant strains as this impedes the optimal treatment of bacterial infections and narrows the choice of effective therapeutic options.

1. Introduction

Antimicrobial resistance (AMR) has been recognized as a global public health problem of utmost importance that needs to be tackled urgently [1]. AMR not only impacts healthcare directly, causing numerous deaths in Europe and around the world, but also diminishes quality of life leading to substantial direct and indirect costs [2]. Unless action is taken, it is estimated that by 2050, up to 10 million people will die each year because of AMR [3]. AMR is a problem that concerns every country irrespective of its level of income and development as resistant pathogens do not respect borders [4]. Low-income countries, such as Uganda, have the greatest burden of severe and life-threatening infections and are most likely to suffer more from the spread of untreatable resistant bacteria.

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The 2014 WHO report identified Africa and South East Asia as the regions without established AMR surveillance systems. The lack of quality data is problematic and often leads to treatment guidelines that are not adequate for the local context. A report of low scores by diagnostic laboratories in southwestern Uganda reflects the need for improvement to reach certain minimum standards of quality in the country [5]. In Africa, lack of coordinated research on antibiotic resistance and consumption has made it difficult to tackle this problem at both local and regional levels [6]. The scientific literature on this topic is scarce with mostly case reports published, pertaining to certain regions of the African continent, and even less from East Africa and Uganda.

Lack of consistency in the measurement and reporting of susceptibility data from African countries hinders the comparison of findings among these countries and even between laboratories within each country [7]. Standardizing AMR methods could enable the comparability of results and improve collection of resistance surveillance data, which are currently either inconsistent or entirely missing [8]. Other studies [9,10] that have flagged high levels of resistance to commonly used antibiotics in some African countries show that there is a high level of resistance to chloramphenicol, as well as other first-line antibiotic regimens, such as amoxicillin and co-trimoxazole [11]. The aim of our study was to determine the prevalence and antimicrobial susceptibility patterns of bacteria isolated from various samples collected from patients at two tertiary hospitals in Eastern Uganda.

2. Materials and methods

2.1. Study design

This is a retrospective study that was conducted over a 3-year period from January 2016 to December 2018. The antibiotic susceptibility test results of clinical specimens such as urine, blood, vaginal swabs, pus, samples from indwelling urinary catheters, pleural fluid, stool, wound swabs, abscesses, sputum, aspirates, eye swabs, ear swabs, and urethral swabs collected during the study period were included in the study. The laboratories received culture specimens from both inpatient and outpatient departments of Mbale Regional Referral Hospital (MRRH) and Soroti Regional Referral Hospital (SRRH).

2.2. Data collection and analysis

Data from culture (identification) and sensitivity results as well as patient demographics from the microbiology registers were captured. Data capturing was done using a Microsoft Excel 2010-based pre-designed data abstraction tool. The entered data were checked for completeness and accuracy, and a basic descriptive analysis of the resistance profiles of isolated organisms was performed.

3. Results

3.1. Clinical specimens and isolated pathogens

A total of 3092 records were reviewed in the two microbiology laboratories, of which 57.7% (n = 1783) were from MRRH and 42.3% (n = 1309) from SRRH. Urine specimens were the most frequently processed samples (n = 1211; 39.2%), followed by blood (n = 960; 31%), high vaginal swabs (n = 253; 8.2%), pus (n = 168; 5.3%), indwelling urinary catheters (n = 126; 4.1%), pleural fluid (n = 106; 3.4%), stool (n = 95; 3.1%), wound swabs (n = 70; 2.3%), abscess (n = 51; 1.6%), sputum (n = 40; 1.3%), aspirates (n = 7; 0.2%), eye swabs (n = 3; 0.1%), ear swabs (n = 1; 0.05%), and urethral swabs (n = 1; 0.05%). The most prevalent bacteria were *E. coli* (n = 442; 33.8%) isolated predominantly from blood specimens-187 (42.3%) and urine-184 (41.6%). *Staphylococcus aureus* was prevalent in 376 (22.8%) of the samples, more common in urine-200 (53.2%) and blood-97 (25.8%). *Klebsiella pneumoniae* was detected in 237 (18.2%) specimens, mostly from blood-147 (62%) and urine-76 (32%). *Streptococcus pneumoniae* was obtained from 5.4% of the samples (n = 76) predominantly from blood-42 (59.1%) and pus-19 (26.8%) (Tables 1 and 2).

3.2. Resistance profiles of the isolated microorganisms

The *E. coli* isolates exhibited high resistance rates to the extended spectrum penicillins such as ampicillin (n = 439; 99.3%) and amoxicillin/clavulanate (n = 369; 83.5%). The isolates showed a substantial degree of resistance to the oral cephalosporins cefotaxime (n = 328; 74.2%) and cefoxitin (n = 407; 92.1%). The resistance rates to other antibacterial agents were also high:

Table 1
Prevalence of clinical isolates from MRRH and SRRH between January 2016 and December 2018.

Isolates	Hospital		Total prevalence counts (%)
	N (%) MRRH	*N* (%) SRRH	
Escherichia coli	311 (23.8)	131 (10)	442 (33.8)
Staphylococcus aureus	198 (15.2)	178 (13.6)	376 (28.8)
Klebsiella pneumoniae	233 (17.9)	4 (0.3)	237 (18.2)
Streptococcus pneumoniae	38 (2.9)	38 (2.9)	76 (5.8)
Streptobacillus Spp.	38 (2.9)	34 (2.6)	72 (5.5)
Klebsiella aerogenes	2 (0.2)	16 (1.2)	18 (1.4)
Proteus Spp.	1 (0.1)	6 (0.5)	7 (0.5)
Enterobacter Spp.	0 (0)	2 (0.2)	2 (0.2)
Citrobacter Spp.	2 (0.2)	0 (0)	2 (0.2)
Salmonella Spp.	1 (0.1)	0 (0)	1 (0.1)
Coliforms[a]	37 (2.8)	0 (0)	37 (2.8)
Pseudomonas aeruginosa	10 (0.8)	4 (0.3)	14 (1.1)
Acinetobacter baumannii	2 (0.2)	0 (0)	2 (0.2)
Burkholderia gladioli	1 (0.1)	0 (0)	1 (0.1)
Enterococcus Spp.	0 (0)	10 (0.8)	10 (0.8)
Staphylococcus epidermidis	6 (0.5)	0 (0)	6 (0.5)
Haemophilus influenzae	6 (0.5)	0 (0)	6 (0.5)
Saccharomyces cerevisiae	2 (0.2)	0 (0)	2 (0.2)
Total isolates	882 (67.6)	423 (32.4)	1305 (100)

[a] Other Gram-negative rods not identified to genus/species level.

Table 2
Distribution of the most prevalent microorganisms isolated across different clinical specimens.

Type of specimen[a]	Bacterial isolates			
	Escherichia coli	*Staphylococcus aureus*	*Klebsiella pneumoniae*	*Streptococcus pneumoniae*
Urine (*N* = 576)	184 (41.6)	200 (53.2)	76 (32)	0
Blood (*N* = 488)	187 (42.3)	97 (25.8)	147 (62)	42 (59.1)
Pus (*N* = 72)	29 (6.6)	24 (6.4)	3 (1.3)	19 (26.8)
High vaginal swab (*N* = 59)	19 (4.3)	16 (4.3)	7 (3)	0
Stool (*N* = 48)	13 (2.9)	15 (4)	0	0
Indwelling urinary catheter (*N* = 24)	0	12 (3.2)	1 (0.4)	0
Pleural fluid (*N* = 18)	4 (0.9)	6 (1.6)	3 (1.3)	10 (14.1)
Sputum (*N* = 7)	1 (0.2)	3 (0.8)	0	3 (3.9)
Aspirate (*N* = 7)	3 (0.7)	0	0	1 (1.3)
Eye swab (*N* = 3)	1 (0.2)	1 (0.3)	0	1 (1.3)
Ear swab (*N* = 1)	0	1 (0.3)	0	0
Urethral swab (*N* = 1)	0	1 (0.3)	0	0
Abscess (*N* = 1)	1 (0.2)	0	0	0
Total number[b] (%; *N* = 1305, [100])	442 (37.4)	376 (31.8)	237 (20)	76 (5.4)

[a] Number and proportion of isolates from a specified sample *N* (%).
[b] Percentages represent frequencies of bacterial species across all specimens.

ciprofloxacin-49.3% (*n* = 218), gentamicin-51.8% (*n* = 229), trimethoprim-sulfamethoxazole-74.1% (*n* = 331), imipenem-3.2% (*n* = 14). *Klebsiella pneumoniae* isolates showed lower rates of resistance compared with *E. coli*: amoxicillin/clavulanate-64.6% (*n* = 153), cefotaxime-52.7% (*n* = 125), cefoxitin-55.3% (*n* = 131), ciprofloxacin-27.8% (*n* = 66), gentamicin-76% (*n* = 189), tetracycline-74.5% (*n* = 187), trimethoprim-sulfamethoxazole-74.3% (*n* = 176). However, carbapenem resistance was slightly higher compared with that of *E. coli*-imipenem 10.5% (*n* = 25) (Table 3). The Gram-positive bacteria also showed resistance to commonly used antibacterial drugs. *Staphylococcus aureus*: amoxicillin/clavulanate-98.4% (*n* = 125), ampicillin-88% (*n* = 331), cefotaxime-39.8% (*n* = 150), cefoxitin-44.4% (*n* = 167), ciprofloxacin-62.2% (*n* = 234), trimethoprim-sulfamethoxazole-88% (*n* = 331). In total, 41.2% (*n* = 155) of the isolates were vancomycin-resistant. *Streptococcus pneumoniae* exhibited high rates of resistance, as well: amoxicillin/clavulanate-49.7% (*n* = 187), cefotaxime-32.3% (*n* = 41), cefoxitin-40.9% (*n* = 52), ciprofloxacin-94.5% (*n* = 120), tetracycline-97.6% (*n* = 124), trimethoprim-sulfamethoxazole-91.3% (*n* = 116) (Table 3).

4. Discussion

Escherichia coli (33.8%), *S. aureus* (28.8%), *K. pneumoniae* (18.2%), and *S. pneumoniae* (5.8%) were the most prevalent bacteria, with high rates of antimicrobial resistance to cephalosporins (cefotaxime) and penicillins (ampicillin), gentamicin and co-trimoxazole and a relatively lower resistance to imipenem, vancomycin (for *S. aureus*) and piperacillin. A study conducted in central Uganda also detected high resistance rates of *E. coli* and *K. pneumoniae* isolates combined: trimethoprim/sulfamethoxazole 70%, amoxicillin/clavulanate 36%, piperacillin/tazobactam 27%, cefoxitin 22%, cefepime 15%, chloramphenicol 20%, ciprofloxacin 11%, and gentamicin 11% [12]. Another similar study from the region, reported resistance to at least one third-generation cephalosporin in isolates from sputum and wound swab specimens from patients attending a tertiary healthcare facility in Kigali, Rwanda [13]. Eight per cent of *E. coli* isolates demonstrated resistance to imipenem, whereas in our study the rate was lower-3.2%.

Besides being resistant to several beta-lactam antibiotics, the Enterobacterales isolates recovered in Mbale and Soroti regional hospitals between January 2016 and December 2018 showed high resistance rates to the commonly used oral antibiotics such as ciprofloxacin, cotrimoxazole, and tetracycline. The resistance exhibited by the microorganism to some of these antibiotics can be associated with certain factors in our environmental settings, for example, the prophylactic use of co-trimoxazole in patients with HIV could be one of the driving factors in the increasing resistance to trimethoprim-sulfamethoxazole [14].

Table 3
Resistance profile of isolated microorganisms.

Antibiotics	*Escherichia coli* *n* (%)	*Klebsiella pneumoniae* *n* (%)	*Staphylococcus aureus* *n* (%)	*Streptococcus pneumoniae* *n* (%)
Amoxicillin/clavulanate	369 (83.5)	153 (64.6)	187 (49.7)	125 (98.4)
Ampicillin	439 (99.3)	*	331 (88)	*
Cefotaxime	328 (74.2)	125 (52.7)	150 (39.8)	41 (32.3)
Cefoxitin	407 (92.1)	131 (55.3)	167 (44.4)	52 (40.9)
Ciprofloxacin	218 (49.3)	66 (27.8)	234 (62.2)	120 (94.5)
Chloramphenicol	*	*	260 (69.1)	35 (27.6)
Clindamycin	*	*	81 (21.5)	31 (24.4)
Gentamicin	229 (51.8)	89 (76)	313 (83.2)	85 (66.9)
Imipenem	14 (3.2)	25 (10.5)	15 (3.9)	5 (3.9)
Ofloxacin	441 (99.8)	*	268 (71.3)	*
Penicillin	385 (87.10)	*	175 (46.5)	*
Piperacillin	103 (23.3)	173 (73)	137 (36.4)	40 (31.5)
Tetracycline	433 (98)	187 (74.5)	322 (85.6)	124 (97.6)
Trimethoprim-sulfamethoxazole	331 (74.1)	176 (74.3)	331 (88)	116 (91.3)
Vancomycin	*	*	155 (41.2)	*

Antibiotic not tested is indicated by *.
Numbers represent total number of isolates tested and (percentage of resistant isolates).

Heidary et al. [15] reported drug-resistant *K. pneumoniae* strains to ceftazidime and imipenem-55.7% and 3.2%, respectively. A high rate of resistance in *K. pneumoniae* isolates was seen towards ampicillin (82.2%), aztreonam (55.4%), and nitrofurantoin (54.5%). Several studies have reported high rates of MDR strains in different regions of Africa and the world at large [16–18]. The increase in resistance has a great impact on the economy of both developed and developing countries as it is most likely to affect the labour force through mortality and morbidity [19,20]. Our study also detected a substantially high resistant rate of *K. pneumoniae* to imipenem (10.5%). Numerous reports on carbapenem-resistant *K. pneumoniae* have been published around the world [21–23]. The emergence of carbapenem-resistant *K. pneumoniae* has been associated with the wide spread of carbapenemases and the increasing unrestricted use of carbapenem as a last resort for the treatment of multidrug-resistant infections [24–26].

There are various studies reporting methicillin-resistant *S. aureus* (MRSA) isolates [27]. Ld et al. [28] reported the average prevalence of *S. aureus* in 122 patients as 53.9% for both inpatients and outpatients at Lacor hospital in Uganda. The average antibiotic susceptibility patterns for the eight antibiotics tested were: ampicillin (75.0%), chloramphenicol (34.4%), ciprofloxacin (1.6%), erythromycin (7.8%), gentamycin (0%), oxacillin (1.6%), tetracycline (45.3%), and co-trimoxazole (50%). To the contrary, the *S. aureus* isolates in our study were largely resistant to cefoxitin (44.4%), gentamicin (83.2%), and tetracycline (85.6%). With limited treatment options, MRSA infections could complicate clinical treatment of the infections and are associated with higher mortality and increased treatment costs [29].

Pneumococcal resistance to commonly used antimicrobial agents has been reported and is becoming a public health concern. Infections by this pathogen have been associated with a million of deaths globally [30]. Findings from our study similarly show a relatively high resistance exhibited by these bacteria to cefotaxime (32.3%), ciprofloxacin (94.6%), amoxicillin/clavulanate (98.4%), tetracycline (97.6%), and trimethoprim-sulfamethoxazole (91.3%). These antibiotics are part of empirical therapy that has been previously effective against *S. pneumoniae* infection. However, the emerging increase in the resistance to each of these agents creates significant barriers to the effective treatment of pneumococcal infections.

Our study has several limitations. It is a retrospective observational study that was performed in tertiary hospitals, where patients usually have many comorbidities often requiring multiple exposures to healthcare settings. All of these are known risk factors for AMR; therefore, the rates of resistance described in our study might not be a true estimate of the actual burden in the country. We have not assessed the quality and reliability of data generated at the two sites, as well as the methods and procedures for culture and susceptibility testing used at the microbiology laboratories of the two hospitals. The clinical significance of specimen culture results could not be ascertained as the link of the microbiology and clinical patient data could not be retrieved. Furthermore, it was challenging to reconstruct the gaps in the raw data (handwritten records, missing data regarding ward/department, diagnosis, symptoms of the patient). Lack of in-depth data on clonality of the isolates from molecular typing methods puts a limitation to the analysis and interpretation of the local spread of certain clones and types, crucial for surveillance and subsequent measures that need to be implemented to prevent that spread.

In conclusion, we reviewed a relatively large number of isolates from two hospitals in Uganda and there is limited information from this part of the world, therefore establishing a baseline is important in allowing future trends to be tracked. We also report a high prevalence of antibiotic resistance exhibited by *E. coli*, *S. aureus*, *K pneumoniae*, and *S. pneumoniae* to antibiotics commonly prescribed in two tertiary hospitals in Eastern Uganda. The high levels of antimicrobial resistance reported in this study could be attributed to unnecessary antibiotic use or misuse, poorly trained healthcare personnel with motives of cutting treatment costs, hasty treatment of suspected bacterial infections without a conclusive laboratory investigation, under treatment of severe bacterial infections; lack of strong government drug regulation policies on use, importation and sale of substandard drugs by unlicensed drug shops and pharmacies in low-income countries such as Uganda [21–23]. Irrational drug practices such as over-the-counter use of antibiotics and self-medication may result in patients taking antibiotics for non-infectious causes, and inadequate dosing may result in suboptimal plasma and tissue drug concentrations, which can promote generation of bacterial strains that are drug-resistant [24,25]. We, therefore, recommend that accurate and reliable microbiology diagnostics is conducted before prescription to guide clinicians in prescribing the most appropriate targeted treatment for infectious diseases.

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Conflict of interest

None declared.

Ethical approval

Ethical approval to conduct the study was obtained from CURE – Children's Hospital Uganda Research and Ethics Committee (reference no. CCHU-REC/10/019) and Uganda National Council of Science and Technology (reference no. HS2686). Administrative clearance was given by both Mbale and Soroti regional referral hospitals. A waiver of consent was granted by the relevant approving authorities.

Author contributions

PW, TK, SA, JSI, HG, PVR conceived the idea, designed the study, supervised the study, and participated in manuscript writing. SBO, KK, GP, and AN contributed to data collection, analysis, and writing of the manuscript. All authors read and approved the final version to be published.

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References

[1] Brinkac L, Voorhies A, Gomez A, Nelson KE. The threat of antimicrobial resistance on the human microbiome. Microb Ecol 2017;74:1001–8.
[2] Naylor NR, Atun R, Zhu N, Kulasabanathan K, Silva S, Chatterjee A, et al. Estimating the burden of antimicrobial resistance: a systematic literature review. Antimicrob Resist Infect Control 2018;7:58–75.
[3] O'Neill J. The review on antimicrobial resistance 2016;vol. 7:. . [Accessed 9 February 2020] amr-review.org.
[4] Hay SI, Rao PC, Dolecek C, Day NPJ, Stergachis A, Lopez AD, et al. Measuring and mapping the global burden of antimicrobial resistance. BMC Med 2018;16:78–80.
[5] Taremwa IM, Ampaire L, Iramiot J, Muhwezi O, Matte A, Itabangi H, et al. Assessment of three medical and research laboratories using WHO

AFRO_SLIPTA quality standards in Southwestern Uganda: a long way to go. Pan Afr Med J 2017;28:1–7.
[6] World Health Organization (WHO). Antimicrobial resistance global report on surveillance, vol. 1. WHO Library Cataloguing-in-Publication Data; 2014. . [Accessed 8 February 2020] https://www.who.int/drugresistance/documents/surveillancereport/en/.
[7] Williams PCM, Isaacs D, Berkley JA. Antimicrobial resistance among children in Sub-Saharan Africa. Lancet Infect Dis 2018;18:e33–44.
[8] Ombelet S, Ronat J-B, Walsh T, Yansouni CP, Cox J, Vlieghe E, et al. Clinical bacteriology in low-resource settings: today's solutions. Lancet Infect Dis 2018;18:e248–58.
[9] Ndihokubwayo JB, Yahaya AA, Desta A Tamer, Ki-Zerbo G, Odei E Assamoah, Keita B, Antimicrobial resistance in the African region: issues, challenges and actions proposed, vol. 16. WHO, Regional Office for Africa; 2013. . [Accessed 8 February 2020] http://www.who.int/bulletin/%0Ahttps://www.aho.afro.who.int/en/ahm/issue/16/reports/antimicrobial-resistance-african-region-issues-challenges-and-actions-proposed.
[10] Ekwanzala MD, Dewar JB, Kamika I, Momba MNB. Systematic review in South Africa reveals antibiotic resistance genes shared between clinical and environmental settings. Infect Drug Resist 2018;11:1907–20.
[11] Kariuki S, Dougan G. Antibacterial resistance in Sub-Saharan Africa: an underestimated emergency. Ann N Y Acad Sci 2014;1323:43–55.
[12] Najjuka CF, Kateete DP, Kajumbula HM, Joloba ML, Essack SY. Antimicrobial susceptibility profiles of *Escherichia coli* and *Klebsiella pneumoniae* isolated from outpatients in urban and rural districts of Uganda. BMC Res Notes 2016;9:1–14.
[13] Ntirenganya C, Manzi O, Muvunyi CM, Ogbuagu O. High prevalence of antimicrobial resistance among common bacterial isolates in a tertiary healthcare facility in Rwanda. Am J Trop Med Hyg 2015;92:865–70.
[14] Odongo CO, Anywar DA, Luryamamoi K, Odongo P. Antibiograms from community-acquired uropathogens in Gulu, northern Uganda — a cross-sectional study. BMC Infect Dis 2013;13:1471–2334.
[15] Heidary M, Nasiri MJ, Dabiri H. Prevalence of drug-resistant *Klebsiella pneumoniae* in Iran: a review article. Iran J Public Health 2018;47:317–26.
[16] Adenipekun EO, Jackson CR, Ramadan H, Iwalokun BA, Oyedeji KS, Frye JG, et al. Prevalence and multidrug resistance of *Escherichia coli* from community-acquired infections in Lagos, Nigeria. J Infect Dev Ctries 2016;10:920–31.
[17] Rutebemberwa E, Mpeka B, Pariyo G, Peterson S, Mworozi E, Bwanga F, et al. High prevalence of antibiotic resistance in nasopharyngeal bacterial isolates from healthy children in rural Uganda: a cross-sectional study. Ups J Med Sci 2015;120:249–56.
[18] Alemayehu T, Ali M, Mitiku E, Hailemariam M. The burden of antimicrobial resistance at tertiary care hospital, southern Ethiopia: a three years' retrospective study. BMC Infect Dis 2019;19:585.
[19] Shrestha P, Cooper BS, Coast J, Oppong R, Do Thi Thuy N, Phodha T, et al. Enumerating the economic cost of antimicrobial resistance per antibiotic consumed to inform the evaluation of interventions affecting their use. Antimicrob Resist Infect Control 2018;7:98.
[20] O'Neill J. Antimicrobial resistance: tackling a crisis for the health and wealth of nations. 2014. amr-review.org.
[21] Lee CR, Lee JH, Park KS, Kim YB, Jeong BC, Lee SH. Global dissemination of carbapenemase-producing *Klebsiella pneumoniae*: epidemiology, genetic context, treatment options, and detection methods. Front Microbiol 2016;7:895.
[22] Paczosa MK, Mecsas J. *Klebsiella pneumoniae*: going on the offense with a strong defense. Abstr Gen Meet Am Soc Microbiol 2016;80:629–61.
[23] Reyes J, Aguilar AC, Caicedo A. Carbapenem-resistant *Klebsiella pneumoniae*: microbiology key points for clinical practice. Int J Gen Med 2019;12:437–46.
[24] Zhang D, Cui K, Lu W, Bai H, Zhai Y, Hu S, et al. Evaluation of carbapenem use in a tertiary hospital: antimicrobial stewardship urgently needed. Antimicrob Resist Infect Control 2019;8:5.
[25] Li Y, Sun Q-L, Shen Y, Zhang Y, Yang J-W, Shu L-B, et al. Rapid increase in prevalence of carbapenem-resistant Enterobacteriaceae (CRE) and emergence of colistin resistance gene *mcr-1* in CRE in a hospital in Henan, China. J Clin Microbiol 2018;56:e01932–17.
[26] Park SO, Liu J, Furuya EY, Larson EL. Carbapenem-resistant *Klebsiella pneumoniae* infection in three New York city hospitals trended downwards from 2006 to 2014. Open Forum Infect Dis 2016;3: ofw222.
[27] Morgenstern M, Erichsen C, Hackl S, Mily J, Militz M, Friederichs J, et al. Antibiotic resistance of commensal *Staphylococcus aureus* and coagulase-negative staphylococci in an international cohort of surgeons: a prospective point-prevalence study. PLoS One 2016;11:e0148437.
[28] Ld K, Ad A, Acullu D, Aloyo J, Fendu M. Antibiotic susceptibility of *Staphylococcus aureus* in suppurative lesions in Lacor Hospital, Uganda. Afr Health Sci 2011;11:S34–9.
[29] Chen K, Lin S, Li P, Song Q, Luo D, Liu T, et al. Characterization of *Staphylococcus aureus* isolated from patients with burns in a regional burn center, Southeastern China. BMC Infect Dis 2018;18:51.
[30] Brooks LRK, Mias GI. *Streptococcus pneumoniae*'s virulence and host immunity: aging, diagnostics, and prevention. Front Immunol 2018;9:1366.