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# High Prevalence of Antimicrobial Resistance Among Common Bacterial Isolates in a Tertiary Healthcare Facility in Rwanda

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*Abstract.* Antimicrobial resistance (AMR) is a serious public health threat in both developed and developing countries. Many developing countries, including Rwanda, lack adequate surveillance systems, and therefore, the prevalence of AMR is not well-known. We conducted a prospective observational study to assess the prevalence of AMR among common bacterial isolates from clinical specimens obtained from patients on the medical wards of Kigali University Teaching Hospital (KUTH). We evaluated the antibiotic sensitivity patterns of bacterial pathogens cultured from urine, blood, sputum, and wound swab specimens obtained over a 6-month period (July 1 to December 30, 2013). There were 154 positive cultures from specimens obtained from 141 unique patients over the study period. Urine, blood, wound swab, and sputum cultures comprised 55.2%, 25.3%, 16.2%, and 3.3% of the total specimens evaluated; 31.4% and 58.7% of *Escherichia coli* and *Klebsiella* isolates, respectively, were resistant to at least one of the third generation cephalosporins. Eight percent of *E. coli* isolates were resistant to imipenem; 82% and 6% of *Staphylococcus aureus* strains were oxacillin- and vancomycin-resistant respectively. Antimicrobial resistance rates are high in Rwanda and pose a serious therapeutic challenge to the management of common infections.

## INTRODUCTION

Antimicrobial resistance (AMR) is an emerging and serious public health threat in both developed and developing countries.[1] Monitoring and controlling AMR is particularly challenging in developing countries because of multiple factors including lack of surveillance systems, limited resources, poor adherence to infection control measures, injudicious use of antibiotics, and limited antimicrobial formulary.

Multidrug-resistant (MDR) pathogens have rendered common infections either more difficult to treat or in some instances, untreatable, with resultant devastating consequences to patients. Recently, extended-spectrum β-lactamase (ESBL) -producing organisms, including those elaborating metallo-β-lactamases, have become the poster child of this emerging threat.[2–4] The advent of MDR pathogens (MDRPs) has necessitated the development of new antibiotics; however, in developing countries, the limited availability and affordability of these new antimicrobial agents remain a significant barrier to the effective treatment of MDRP infections.

Although there is a paucity of data on AMR from Africa, some studies have shown that the prevalence of MDRPs is both high and increasing over time. A systematic review of studies from a group of African countries, including Tunisia, Ivory Coast, South Africa, Ethiopia, Botswana, Libya, Nigeria, Algeria, Morocco, Eritrea, and Egypt, conducted in 2013, showed that the prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) was between 25% and 50% in most countries and had increased compared with rates before the year 2000.[5] Similarly, a study performed at Mulago Hospital in Uganda between September of 2011 and April of 2012 assessing AMR rates among bacterial isolates from surgical wound infections showed that more than 75% of the Enterobacteriaceae were ESBL producers and that 37.5% of *Staphylococcus aureus* isolates were methicillin-resistant. Furthermore, the observed rates were higher than what had been previously reported.[6]

A recent study conducted in two large referral hospitals in Kigali, Rwanda specifically assessing the antimicrobial susceptibility pattern of uropathogens showed a high prevalence of AMR, with broad resistance to commonly used oral antibiotics, including quinolones.[7] However, there is very limited information from Rwanda on the prevalence of AMR among gram-positive bacteria as well as gram-negative bacteria causing non-urinary tract infections. We conducted this study to determine and describe the prevalence of AMR among bacterial pathogens associated with common infections in patients on the medical wards of the largest tertiary hospital in Rwanda.

## MATERIAL AND METHODS

**Study design.** The prospective and descriptive study involved collection of data on the spectrum, frequency, and antimicrobial sensitivity patterns of bacterial organisms isolated in cultures of clinical specimens collected from patients on the internal medicine wards of the Kigali University Teaching Hospital (KUTH) over a 6-month period (July 1, 2013 to December 31, 2013). We excluded samples with improper labeling and those lacking adequate patient and specimen identifiers or clinical information. For patients with persistently positive cultures, data were collected only on bacterial isolates from the first positive specimen.

**Sample collection and processing.** Clinical specimens were typically sent to the microbiology laboratory by the clinicians managing the patients and included urine, blood, sputum, and pus swab specimens from adult patients on internal medicine wards. Blood samples were collected and incubated into Brain Heart Infusion (BHI) bottles with 25 mL solution. Urine, wound, and sputum cultures were collected in sterile containers. Laboratory materials, including sterile containers, antibiotic disks, and culture media, were obtained from Becton, Dickinson and Company (Franklin Lakes, NJ).

Blood cultures were directly incubated at 37°C and observed daily for 7 days for turbidity or hemolysis that would suggest

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growth and/or presence of pathogens. Samples found with bacterial growth were subcultured on appropriate media guided by gram stain results as follows: gram-positive cocci were plated on mannitol salt agar (MSA) and blood agar, whereas MacConkey agar and Xylose Lysine Deoxycholate agar (XLD) media were used for isolation of gram-negative bacilli. Additional identification of gram-positive cocci species was performed using catalase and coagulase tests. Identification of genus and species of gram-negative bacilli was done by colony morphology. In addition, biochemical tests were performed, including triple sugar iron (TSI), motility indole urea (MIU), and citrate tests to identify and differentiate Enterobacteriaceae species.

Urine samples, after wet mount examination, were cultured on blood agar, chocolate agar, cysteine lactose electrolyte-deficient (CLED), and MacConkey agar. The number of colonies were counted after 18–24 hours of incubation at 37°C. Urinary specimens with $> 10^4$ colony-forming units (CFUs)/mL urine were considered significant. Maximum duration of incubation was 48 hours. For wound swabs and sputum specimens, the gram stain morphology of principal pathogens dictated the selection of appropriate media for culture, which were then incubated at 37°C for 24 hours. As with other specimens, identification of bacterial genus and/or species was done using a combination of colony morphology, growth characteristics on selective media, and confirmatory biochemical tests.

Antibiotic susceptibility testing was performed by the Kirby Bauer disk diffusion method. The following antibiotic disks were used: ampicillin, 10 μg; ceftazidime, 30 μg; cefotaxime, 30 μg; ceftriaxone, 30 μg; cefalothin, 30 μg; cefuroxime, 30 μg; ciprofloxacin, 5 μg; trimethoprim/sulfamethoxazole (TMP/SMX), 1.25/23.75 μg; amikacin, 30 μg; amoxicillin/clavulanic acid (amox/clav), 20/10 μg; clindamycin, 2 μg; cloxacillin, 1 μg; erythromycin, 10 μg; gentamicin, 10 μg; imipenem, 10 μg; norfloxacin, 10 μg; penicillin, 10 units; ofloxacin, 5 μg; oxacillin, 1 μg; piperacillin, 100 μg; vancomycin, 30 μg; and tetracycline, 30 μg.

A suspension from growth on a solid media plate was prepared by adding bacterial colonies into sterile distilled water until it approximated the same turbidity as the MacFarland turbidity standard 0.5. The resulting suspension was inoculated on Muller Hinton agar by using a sterile cotton swab. After this procedure, the antibiotic disks were added to the plate with at least 20 mm between each disk and subsequently incubated at 37°C for 18–24 hours; thereafter, interpretation of the diameter of inhibition was done according to 2012 Clinical and Laboratory Standards Institute (CLSI) guidelines. Quality control for the Kirby Bauer disk diffusion test was performed using three American Type Culture Collection (ATCC) strains: *Escherichia coli* ATCC 25922, *S. aureus* ATCC 25923, and *Pseudomonas* spp. ATCC 27853. Suspensions of the organisms were prepared as described above, and the inhibition diameter obtained was compared with the standard range expected for the ATCC strains.

**Data analysis.** Data were captured, recorded, and analyzed using a Microsoft Excel database. The frequency of individual bacterial species isolated was reported as a percentage or a fraction of total samples within and across sample types. The frequency of microbes resistant to antibiotics was reported as a simple percentage of the total number of same-species microbes against which the antibiotic was tested for susceptibility.

**Approval.** We received approval from the ethics committee of KUTH and the research committee of the Faculty of Medicine, University of Rwanda to conduct the study.

## RESULTS

**Study subject characteristics.** There were 154 positive bacterial cultures during the study period obtained from 141 unique individuals comprised of 78 females (55.3%) and 63 males (44.7%). All patients had requisite laboratory test labeling and clinical information found in the medical records to meet inclusion criteria for the study. The median age was 45 years old, with an interquartile range (IQR) of 30–66 years old and a range of 15–89 years old. Elderly patients (> 65 years old) made up 26.2% of the cohort (Table 1); 30% of the patients had human immunodeficiency virus (HIV) infection. Other significant comorbidities, including diabetes mellitus, liver cirrhosis, malignancy, and severe malnutrition, were reported in 17%, 5%, 7.8%, and 1.4% of source patients, respectively; 23.4% of patients had no underlying medical condition. Indwelling urinary catheters were present in 14.2% of patients with positive urine cultures.

**Clinical specimens and bacterial isolates.** Urine culture specimens yielded 55.2% of bacterial isolates. Blood, wound, and sputum culture isolates made up 25.3%, 16.2%, and 3.3% of bacteria identified; 91% of specimens yielded monomicrobial growth. *E. coli* was the most frequent pathogen isolated from urine specimens followed by *Klebsiella* spp., comprising 56.4% and 32.9% of uropathogens, respectively. *Klebsiella* spp. was the predominant pathogen among isolates from blood (28.2%), sputum (60%), and wound swabs (28%). *S. aureus* was isolated at a similar frequency as *Klebsiella* from wound cultures (28%) and was the second most common isolate in blood cultures (23%). Coagulase-negative *Staphylococci* (CoNS) comprised 15.4% of bacteria cultured from blood. Remarkably, *Klebsiella* spp. featured prominently across all types of clinical specimens (Table 2).

**Resistance profile of organisms.** Among gram-negative isolates, *E. coli* isolates showed high resistance rates to penicillins (ampicillin, 96%; amox/clav, 88%), TMP/SMX (76%), and quinolones (ofloxacin, 63%; ciprofloxacin, 66%; norfloxacin, 39%). *E. coli* isolates also showed significant rates of resistance

TABLE 1
Key demographic and clinical characteristics of source patients

| Variables | *N* (% or IQR) |
|---|---|
| Age (years; *N* = 141) | |
| Median age | 45 (30–66) |
| Mean age | 47.65 (30–66) |
| Age < 25 | 26 (18.4) |
| Age > 65 | 37 (26.2) |
| Underlying medical condition predisposing to infection (*N* = 141) | |
| Elderly | 37 (26.2) |
| HIV | 42 (29.8) |
| Indwelling urinary catheter | 20 (14.2) |
| Diabetes mellitus | 25 (17) |
| Cirrhosis | 7 (5) |
| Severe malnutrition | 2 (1.4) |
| Malignancy | 11 (7.8) |
| No comorbidity | 33 (23.4) |
| At least one comorbidity | 108 (76.6) |
| Two or more comorbidities | 46 (32.6) |

TABLE 2
Distribution of microbes isolated across clinical specimens

| Bacterial isolates | Type of sample | | | | |
|---|---|---|---|---|---|
| | Urine* ($N = 85$) | Blood* ($N = 39$) | Wound* (pus; $N = 25$) | Sputum* ($N = 5$) | Total number† (%; $N = 154$ [100]) |
| *E. coli* | 48 (56.4) | 5 (12.8) | 2 (8) | 0 (0) | 55 (35.7) |
| *Klebsiella* spp. | 28 (32.9) | 11 (28.2) | 7 (28) | 3 (60) | 49 (31.8) |
| *S. aureus* | 4 (4.7) | 9 (23) | 7 (28) | 2 (40) | 22 (14.3) |
| CoNS | 0 (0.0) | 6 (15.4) | 1 (4) | 0 (0) | 7 (4.5) |
| *Proteus* spp. | 2 (2.4) | 1 (2.6) | 4 (16) | 0 (0) | 7 (4.5) |
| *Acinetobacter* spp. | 1 (1.2) | 3 (7.7) | 2 (8) | 0 (0) | 6 (3.9) |
| *Pseudomonas* spp. | 1 (1.2) | 2 (5.1) | 1 (4) | 0 (0) | 4 (2.6) |
| *Citrobacter* spp. | 1 (1.2) | 0 (0.0) | 1 (4) | 0 (0) | 2 (1.3) |
| *Enterobacter* spp. | 0 (0.0) | 1 (2.6) | 0 (0) | 0 (0) | 1 (0.7) |
| *Salmonella* spp. | 0 (0.0) | 1 (2.6) | 0 (0) | 0 (0) | 1 (0.7) |

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

to the third generation cephalosporins, with 30% resistant to ceftriaxone and 33% resistant to ceftazidime; 37% and 8% of *E. coli* isolates also showed resistance to gentamicin and imipenem, respectively.

*Klebsiella* spp., compared with *E. coli* spp., showed higher rates of resistance to most antibiotics tested, including third generation cephalosporins (ceftazidime, 58%; ceftriaxone, 55%; cefotaxime, 44%; gentamicin, 53%). There were no carbapenem-resistant isolates. *Acinetobacter* species were mostly susceptible to piperacillin, cephalosporins, gentamicin, and ciprofloxacin, whereas *Proteus* species were predominantly susceptible to the third generation cephalosporins; 33% and 25% of *Pseudomonas* species showed resistance to antipseudomonal β-lactams (piperacillin and ceftazidime) and gentamicin, respectively. Amikacin showed broad activity against all isolated gram-negative bacteria, with only one *Klebsiella* isolate resistant to the drug (Table 3).

Among *S. aureus* isolates, 82% were resistant to oxacillin. The isolates were also resistant to commonly used oral antibiotics—penicillin (88%), TMP/SMX (70%), tetracycline (62%), and erythromycin (33%) (Table 4). There was vancomycin resistance among 6% of *S. aureus* isolates; 100% of CoNS were resistant to oxacillin, and 50% and 29% of isolates remained susceptible to erythromycin and tetracycline, respectively.

TABLE 3
Resistance profile of gram-negative microbes

| Antimicrobial drug | Resistance rate (%)* | | | | |
|---|---|---|---|---|---|
| | *E. coli* | *Klebsiella* spp. | *Acinetobacter* spp. | *Pseudomonas* spp. | *Proteus* spp. |
| Ampicillin | 96 | 100 | – | – | 71 |
| Piperacillin | – | – | 33 | 33 | – |
| Amox/clav | 93 | 95 | – | – | 71 |
| Cefalothin | – | 67 | – | – | – |
| Cefuroxime | 35 | 68 | 50 | – | 57 |
| Ceftazidime | 33 | 58 | 33 | 33 | 50 |
| Cefotaxime | 31 | 44 | – | – | – |
| Ceftriaxone | 30 | 55 | 40 | – | 17 |
| Ciprofloxacin | 66 | 65 | 25 | 67 | 67 |
| Norfloxacin | 39 | 46 | 0 | 0 | 0 |
| Ofloxacin | 63 | 17 | 33 | – | 67 |
| Amikacin | 0 | 2 | 0 | 0 | 0 |
| Gentamicin | 37 | 53 | 33 | 25 | 83 |
| Imipenem | 8 | 0 | – | – | – |
| Tetracycline | – | – | 80 | – | – |
| TMP/SMX | 76 | 84 | 67 | – | – |

Resistance not tested is indicated by –.
*Percentages represent resistant isolates/total number of isolates tested.

## DISCUSSION

Multiple studies have shown that AMR is a significant problem in sub-Saharan Africa and that there is also a paucity of data on prevalence rates.[8,9] Factors contributing to the paucity of data include limited or absent antimicrobial surveillance systems and poor resources for antimicrobial susceptibility testing.[8] However, available evidence suggests that multidrug resistance is widespread among gram-negative and gram-positive bacterial pathogens causing common infections, such as urinary and respiratory tract infections, regardless of whether they are community- or hospital-acquired.[9–11]

Our survey of AMR among bacterial isolates from common clinical specimens obtained from patients in Kigali, Rwanda showed rather alarming rates of drug resistance among both gram-negative and gram-positive organisms, consistent with other studies from the sub-Saharan African region.[12–14] Using the definition of ESBL producers as being resistant to third generation cephalosporins,[15,16] 31.4% and 58.7% of *E. coli* and *Klebsiella* organisms, respectively, met the criteria. There were also high rates of coresistance to commonly used antibiotics—amox/clav, TMP/SMX, quinolones, and aminoglycosides—and a few isolates (8% of *E. coli*) showed resistance to imipenem. The majority (82%) of *S. aureus* isolates was resistant to oxacillin, and 6% were also resistant to vancomycin.

TABLE 4
Resistance profile of gram-positive microbes

| Antimicrobial drug | Resistance rate (%)* | |
|---|---|---|
| | *S. aureus* | CoNS |
| Penicillin | 88 | 67 |
| Oxacillin | 82 | 100 |
| Cefalothin | – | 71 |
| Cefuroxime | – | 60 |
| Erythromycin | 33 | 50 |
| Ciprofloxacin | 33 | – |
| Norfloxacin | 33 | 67 |
| Ofloxacin | 27 | 40 |
| Vancomycin | 6 | – |
| Tetracycline | 62 | 71 |
| TMP/SMX | 70 | – |

Resistance not tested is indicated by –.
*Percentages represent resistant isolates/total number of isolates tested.

The distribution of the cultured bacterial species in our study is representative of typical flora expected to cause common infections in patients on an internal medicine ward. Urine samples yielded the most positive bacterial cultures across specimens at 55.2%. *E. coli* was the most prevalent pathogen isolated in urine samples in our study (56.4%) followed by *Klebsiella* spp. (32.9%). This finding is similar to that of other studies, where *E. coli* is typically the predominant uropathogen, which was seen in previous reports from Rwanda (60.7%)[7] and across other sites in Africa.[17–19]

Our study found that 31.4% of all *E. coli* exhibited an ESBL phenotype resistance pattern. The frequency of presumed ESBL-producing *E. coli* reported in our study is similar to that previously reported by other studies. Muvunyi and others[7] showed that ESBL phenotypes made up 38% of urinary bacterial isolates (13.8% of *E. coli*) among hospitalized patients in two large tertiary facilities in Rwanda. Other studies from Africa have shown similar rates. Kariuki and others[20] reported that 36% of community-acquired urinary *E. coli* isolates in Ghana showed multidrug resistance and that 12 of 17 studied isolates were ESBL producers. A single-center study describing the resistance profile of urinary tract infection pathogens among pregnant women in Tanzania showed that 29.4% of *E. coli* isolates were resistant to ceftriaxone.[19]

We also found that 58.7% of all *Klebsiella* spp. isolates were resistant to at least one third generation cephalosporin and probable ESBL producers. The observed resistance to third generation cephalosporins by *Klebsiella* spp. is alarming; 44.4%, 58%, and 55% of isolates were resistant to cefotaxime, ceftazidime, and ceftriaxone, respectively. This finding is also in concordance with studies from other African settings. Obeng-Nkrumah and others[21] reported a 61.5% prevalence of ESBL phenotypes among *K. pneumoniae* isolates from a large referral teaching hospital. As expected, there are large variations in reports on AMR over time, across geographical locations, and across study populations (inpatients versus outpatients). A higher prevalence of AMR is generally noted among samples from inpatients compared with samples from outpatients as well as samples from patients with certain comorbidities, such as HIV infection, diabetes mellitus, and end-stage renal disease, who are more likely to have previous contact with healthcare settings.[15]

Other than third generation cephalosporins, we noted very high rates of coresistance by Enterobacteriaceae—*E. coli* and *Klebsiella*—to the commonly used oral antibiotics amox/clav, TMP/SMX, and ciprofloxacin as well as the injectable aminoglycoside gentamycin. There were too few isolates of *Pseudomonas*, *Proteus*, and *Acinetobacter* to make any meaningful generalizations. The phenomenon of multidrug resistance among Enterobacteriaceae is not unique to our study.[7,22–24] A study done in Sudan by Ibrahim and others[25] showed that 92.2% of *E. coli* isolates were MDR and that resistance rates were high to most antibiotics tested, including amox (97.7%), cefuroxime (92.5%), TMP/SMX (88.3%), tetracycline (77.1%), ciprofloxacin (58.4%), ofloxacin (55.1%), and amox/clav (50.4%). Ibrahim and others[25] also reported discordant sensitivity patterns of *E. coli* to aminoglycoside drugs, which we also observed in our study. Although there were high rates of resistance to gentamicin (35%), resistance to amikacin was low (1.9%).[25] Our study showed that resistance rates of *E. coli* to amikacin and gentamicin were 2% and 37%, respectively. Imipenem showed activity against the vast majority of gram-negative isolates, although one *E. coli* isolate was resistant to it. Indeed, carbapenem resistance has been reported in Africa, despite limited availability of this class of antibiotics. Infections with *Klebsiella*-producing carbapenemase-2 (KPC-2), New Delhi Metalloproteinase-1 (NDM-1) -producing *K. pneumoniae* and KPC-2–producing *Enterobacter* strains were reported in two patients from South Africa, both of whom died.[26]

The high prevalence and pattern of AMR among gram-negative bacteria closely reflect antibiotic use patterns in Rwanda; ciprofloxacin, amox/clav, and TMP/SMX are oral antibiotics widely prescribed by healthcare providers for many infections without guidance of culture and sensitivity results. Quinolone usage in Rwanda skyrocketed in the past decade based on treatment guidelines recommending its use for urinary tract infections when resistant rates to the drug class were lower (Nkurikiyinfura JL and others, unpublished data). TMP/SMX is widely used for prophylaxis against opportunistic pathogens and other infections, including malaria, for patients with HIV disease. In hospital settings in Rwanda, cefotaxime and gentamicin are the most frequently prescribed antibiotics in their drug class. Furthermore, prior exposure of patients to antibiotics before referral to tertiary facilities also contributes to the selection of drug-resistant isolates. Chromosomal resistance mechanisms, such as 3-*N*-aminoglycoside acetyltransferases I, II, and IV as well as aminoglycoside 2″-*O*-nucleotidyltransferase, may also explain variability in susceptibility to different aminoglycosides.[27]

Among gram-positive microbes, *S. aureus* also showed high resistance to antibiotics commonly used in treating staphylococcal infections, including penicillin, cloxacillin, tetracycline, and TMP/SMX; 82% were resistant to oxacillin. The observed resistance profile suggests that most *S. aureus* strains are hospital-acquired strains, which is not unexpected in patients in a tertiary-level healthcare facility, the majority of whom were exposed to antibiotics during prior hospitalizations at lower-tier health facilities and/or acquired the organism from prolonged hospital stays.

Studies from other African countries have shown similar antibiotic profiles for *S. aureus* isolates, with 100% resistance to penicillin[5,17] and high rates of methicillin resistance.[28] However, lower rates of MRSA have also been reported from some sub-Saharan African countries (e.g., Nigeria).[29] Concerning among the observed antimicrobial sensitivity patterns of our gram-positive isolates was the finding of one strain of *S. aureus* that was resistant to vancomycin. To our knowledge, this is the first report in the published literature of vancomycin resistance among *S. aureus* strains in Rwanda. Other African countries, including South Africa and Algeria, have also reported emergence of these strains.[30,31]

Our study has several limitations. It was performed in a tertiary hospital, which serves as a national referral center. In addition, our patients had high rates of comorbidities and resultant multiple exposures to healthcare settings. All of these are known risk factors for AMR; therefore, the rates of resistance described in our study are higher than would be expected for community-acquired infections in otherwise healthy individuals. We were unable to perform confirmatory testing or genotyping of ESBL isolates because of limited resources. However, most Enterobacteriaceae (especially *E. coli* and *K. pneumoniae*), which are resistant to third generation cephalosporins, will be found to be true ESBL producers

on subsequent genetic testing.[32,33] We were also unable to perform the cefoxitin disk diffusion test, the phenotypic test that is more sensitive than the oxacillin disk diffusion test for detection of MRSA.[34] It is plausible that AMR rates on internal medicine wards may not be similar to those of other sites in our facility—intensive care unit, orthopedics, or surgical wards- where there is more frequent use of intravascular devices and mechanical ventilation which promotes exposure to, and/or colonization with, drug-resistant pathogens. Also, we did not ascertain the clinical significance of specimen culture results (i.e., assess for contaminants), perform strain typing to assess for possible strain-specific nosocomial outbreaks, or distinguish between community- and hospital-acquired infections with regards to AMR rates.

## CONCLUSION

The magnitude of AMR in the KUTH is worrisome and poses a serious threat to the successful treatment of common infections with available antibiotics. Our study has shown that MDR *E. coli, Klebsiella*, *Proteus*, and MRSA are prevalent in Rwanda; therefore, antibiotics with broad antibacterial spectrums that retain activity against ESBL-producing organisms and MRSA should be part of the antibiotic formulary of local hospitals. Low resistance rates of Enterobacteriaceae to imipenem and amikacin suggest that they remain valuable drugs for the treatment of resistant gram-negative infections.

It is clear that more judicious use of antibiotics, institution of antimicrobial surveillance programs, and appropriate infection control measures are essential to stem the tide of drug-resistant bacteria. More studies are needed to further explore trends of AMR, which will also be important to guide recommendations for empiric antibiotic therapy for common infections by national and regional guideline-issuing bodies.

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