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Patterns of infections, aetiological agents, and antimicrobial resistance at a tertiary care hospital in northern Tanzania

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Abstract

Objective: To determine the causative agents of infections and their antimicrobial susceptibility at a tertiary care hospital in Moshi, Tanzania, to guide optimal treatment.

Methods: A total of 590 specimens (stool (56), sputum (122), blood (126) and wound swabs (286)) were collected from 575 patients admitted in the medical and surgical departments. The bacterial species were determined by conventional methods and disk diffusion was used to determine the antimicrobial susceptibility pattern of the bacteria isolates.

Results: A total of 249 (42.2%) specimens were culture-positive yielding a total of 377 isolates. A wide range of bacteria was isolated, the most predominant being Gram-negative bacteria: *Proteus spp.* (n=48, 12.7%), *Escherichia coli* (n=44, 11.7%), *Pseudomonas spp.* (n=40, 10.6%), and *Klebsiella spp* (n=38, 10.1%). Wound infections were characterised by multiple isolates (n=293, 77.7%), with the most frequent being

Proteus spp. (n=44, 15%), *Pseudomonas* (n=37, 12.6%), *Staphylococcus* (n=29, 9.9%), and *Klebsiella spp.* (n=28, 9.6%). All *S. aureus* tested were resistant to penicillin (n=22, 100%) and susceptible to vancomycin. Significant resistance to cephalosporins such as cefazoline (n=62, 72.9%), ceftriaxone (n=44, 51.8%) and ceftazidime (n=40, 37.4%) was observed in Gram-negative bacteria; as well as resistance to cefoxitin (n=6, 27.3%) in *Staphylococcus aureus.*

Conclusion: The study has revealed a wide range of causative agents, with an alarming rate of resistance to the commonly used antimicrobial agents. Furthermore, the bacterial spectrum differs from those often observed in high-income countries. This highlights the imperative of regular generation of data on aetiological agents and their antimicrobial susceptibility patterns especially in infectious disease endemic settings. The key steps would be to ensure the diagnostic capacity at a sufficient number of sites and implement structures to routinely exchange, compare, analyse and report data. Sentinel sites (hospitals) across the country (and region) should report on a representative subset of bacterial species and their susceptibility to drugs at least annually. A central organizing body should collate the data and report to relevant national and international stakeholders.

Keywords: Bacterial infections; antimicrobial resistance; Africa; Western Europe; America

Introduction

Regular review of patterns of infections and their antibacteriogram is key for empirical treatment, which is common in resource-poor settings. Over the past 20 years the pattern of infections and their susceptibility to antimicrobial agents[1,2] has changed, likely due to factors such as increased use of antimicrobial agents[3] and rising prevalence of diabetes mellitus[4] which due to socio-demographic changes[5] is becoming a common comorbid condition for patients admitted due to infection[6]. Human immunodeficiency virus (HIV) has also changed the pattern of infections[2]; antiretroviral (ARV) therapies, which boost the immune status of the patients infected with HIV[7], may play a role in the susceptibility to both common and opportunistic infections[8], as well as other chronic conditions such as cancer and kidney disease.

In Africa, infectious diseases constitute a much higher burden in people of all age groups [9–14] than in Europe and North America. Active surveillance systems on infectious disease control are inadequate in most African countries[15–18], and the absence of data on disease causes and the lack of control measures add to the disease burden[7]. Obtaining adequate and timely data on infectious diseases in African countries is difficult, whereas much more data are available from developed countries. As a result empirical treatment in Africa regarding pathogenic bacteria might be based on data from clinical laboratories in developed countries[19]. The pattern of bacterial infections in Africa differs from those observed in Western Europe and

North America, hence empirical treatment should be adjusted to fit the different need. In Africa, as elsewhere, regular local data collection about patterns of infections, and their response to antimicrobial agents, coupled with a long-term commitment to providing adequate health information systems, is key to effective planning and policy formulation. The availability of data on disease patterns, etiological agents and their antimicrobial resistance is a prerequisite for the establishment of empirical treatment regimens and for avoiding escalation of the global trend of bacterial resistance to the current antimicrobial regimens[20–22].

This study was conducted to determine the most frequent bacterial species isolated from samples submitted for microbiological examinations at a tertiary care hospital in Moshi, Tanzania. We also determined antimicrobial susceptibility patterns of the isolates and associated comorbid conditions.

Materials and methods

Study design, location and sample collection

This study is a descriptive analysis of culture, bacterial identification and antimicrobial susceptibility testing conducted at Kilimanjaro Christian Medical Centre (KCMC), which hosts a tertiary health care facility for the northern zone of Tanzania. The study was conducted from August 2013 to August 2015. Clinical samples were collected from inpatients admitted to the medical or surgical wards of the hospital. Informed consent was obtained from all participants. Specimens including stool (56), sputum (122), blood (56) and wound/pus swabs (286) were collected from 575 patients. Twenty specimens were not included due to insufficient quantity. Blood, stool, or sputum samples were collected if the patient was diagnosed to have septicemia, diarrhoea, or upper respiratory infection, respectively. Blood samples were also collected from patients with fever of unknown cause. Wound or pus swabs were collected from wounds due to burns, surgical procedures, diabetes mellitus, animal bites, motor traffic accidents and other injuries.

Patient hospital files were used to obtain socio-demographics and clinical characteristics of the study participants admitted at KCMC wards. Data were recorded on designated case report forms (CRFs). All samples were transported immediately after collection to the Kilimanjaro Clinical Research Institute (KCRI), to be processed by the microbiology unit of the biotechnology laboratory department.

Culture and identification

Wound/pus swabs and sputum specimens were cultured onto Trypticase Soy Agar with 5% Sheep Blood (BD BBL™), chocolate agar and McConkey agar plate media (BD BBL™) and incubated at 37 °C with 5% CO_2 for 18-24 hours. Stool samples were cultured onto McConkey agar and incubated at 37 °C overnight. Blood samples were collected in 40 mL BD BACTEC standard 10 Aerobic/F, followed by incubation in BD BACTEC

for a maximum of 5 days. Gram stain was used to differentiate gram positive and negative bacteria from culture. Positive blood cultures were inoculated on blood agar, chocolate agar and McConkey agar and incubated for 18-24 hours at 37 °C with 5% CO_2. Bacteria were isolated from culture by picking single colonies and subculturing onto purity plate (Blood agar) overnight. From the purity plate, morphology determination and gram stain was done followed by microscopic examination.

Based on Gram staining results, Gram-negative bacteria were identified using API 20E and/or API NE 20 (bioMérieux) for *Enterobacteriacae* and other non-fastidious Gram-negatives. Catalase and coagulase tests were used to identify Gram-positive cocci. Optochin susceptibility testing (BD BBL Taxo™. Benex Limited, Shannon County Clare, Ireland) was used to confirm *Streptococcus pneumoniae*, and BD BBL Streptocard ® Enzyme Latex test was used to identify streptococcal group A, B, C, D, F and G.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing (AST) was done using disk diffusion on Müller Hinton II Agar (MHA) according to Clinical Laboratory Standards Institute (CLSI, 2013) guidelines. Gram negative bacterial isolates were tested for ampicillin 10 μg, amox-clavulanic acid 30 μg, cefazoline 30 μg, ceftazidime 30 μg, ceftriaxon 30 μg, chloramphenicol 30 μg, ciprofloxacin 5 μg, gentamicin 10 μg, nalidixic acid 30 μg and trimethoprim-sulfamethoxazole 23.75 μg/1.25 μg. Antimicrobials tested for Gram-positive bacterial isolates were chloramphenicol, trimethoprim-sulfamethoxazole (23.75 μg/1.25 μg), erythromycin 15 μg, vancomycin 30 μg, penicillin 10 μg, and cefoxitin 30 μg. Interpretation as susceptible, intermediate resistant and resistant was done according to CLSI 2013. Isolates with intermediate or resistant results were merged into a single group as resistant during data analysis. Considering intermediate group as resistance can be one of the ways of sidestepping uncertain therapeutic effects[23].

Data analysis

Data were double-entered in OpenClinica (OpenClinica LLC, Waltham MA, USA). Data extracts were exported to STATA 13 (StataCorp LP, Texas 77845 USA). This tool was used for all analyses. Proportions of comorbidities and bacteria isolates were calculated and presented as column or row percentages.

Results

Characteristics of the study participants

Table 1 summarizes characteristics of 575 patients with different medical conditions enrolled in the study from August 2013 to August 2015. Five patients were excluded during analysis due to incomplete patient information. The median age (IQR) was 43 (30-57) years. 61% (n=348) were males, 39% females (n=227).

Half of the participants were peasants (n=271, 47.3%), the predominant education level was primary education (n=339, 59%); few participants (n=34, 5.9%) had tertiary education. 71.9% participants (n=412) had a history of receiving antibiotic treatment prior to admission. 45.9% of patients were admitted due to wound infection (n=263), 14.4% due to pneumonia (n=81), 10.5% due to tuberculosis (n=60), 8.03 % due to septicemia (n=46), 3.5% due to diarrhoea (n=20) and 0.7% due to meningitis (n=4). Coexisting health conditions were diabetes mellitus (n=122, 21.3%), HIV (n=81, 14.1%), and cancer (n=52, 9.1%).

Culture results

A total of 590 specimens were cultured: 286 wound swabs, 126 blood, 122 sputum, and 56 stool samples. 42.2% of the cultured specimens had positive growth after overnight incubation: 72.3% of wound swabs (n=180), 14.1% of sputum samples (n=35), 7.6% of stools (n=19), and 6% of blood samples (n=15).

We obtained 377 bacterial isolates. 43.8%) of specimens (n=109) had more than one isolate. 77.7% of isolates (n=293) were obtained from wound swabs, 11% (n=4), from sputum, 6.1% (n=23) from stools, and 4.2% (n=16) from blood cultures (Table 2).

There was a wide range of bacterial isolates, the majority being Gram negative isolates, with *Proteus spp* (n=48, 12.7%), *E. coli* (n=44*,* 11.7%), *Pseudomonas spp* (n=40, 10.6%), and *Klebsiella spp* (n=38, 10.1%) being predominant, together accounting for 170 (45.1%) of all isolates. The Gram-positive bacteria were *Staphylococcus aureus* (n=35, 9.3%), coagulase negative *Staphylococcus spp* (n=25, 6.6%) and *Streptococcus spp* (n=17, 4.5%). Wound infections were characterised by multiple isolates (n=293, 77.7%), with the most frequent being *Proteus spp* (n=44, 15%), *Pseudomonas* (n=37, 12.6%), *Staphylococcus* (n=29, 9.9%), and *Klebsiella spp* (n=28, 9.6%). *Streptococcus spp* were the most common finding (n=9, 20%) in sputum samples, followed by *Klebsiella spp* (n=7, 15.6%). *E.coli* (n=11, 47.8%) was the predominant isolate in stool samples (Table 2).

Pattern of infections and aetiological agents

Table 3 outlines disease conditions found: wound infection (n=277, 45.8%), pneumonia (n=87, 14.4%), tuberculosis (n=64, 10.6%), septicemia (n=52, 8.6%), diarrhea (n=21, 3.5%) and %), and meningitis (n=4,

0.7%). *S.aureus, Klebsiella* spp*, Proteus* spp, *E.coli* and *Pseudomonas* spp were the most common bacterial pathogens isolated from patients with the above disease presentations. The distribution of these pathogens was diversified in wound infections. Septic wounds were dominated by *Pseudomonas spp* (n=31, 77.5%), *Proteus spp* (n=37, 75.5%), *E.coli* (n= 24, 54.5%), *S.aureus* (n=20, 57.1%) and *Klebsiella spp* (n= 21, 51.2%). Burn and diabetic wounds had more *Proteus* spp (n=10 (20.4%) and n=15 (30.6%), respectively). Motor traffic and post-surgical wounds had few bacterial isolates.

Tables 4a and b summarize the association between co-existing health conditions such as diabetes, cancer and HIV and the burden of commonly isolated bacteria. The prevalence of *Proteus spp, Escherichia coli, and Pseudomonas spp* infections was higher among people with diabetes and cancer, although the associations were not statistically significant (P>0.05). A statistically significant independent association was observed between the prevalence of *Pseudomonas spp* among HIV-negative patients (11%) and HIV-positive patients (3%) (P=0.03). The prevalence of both *Proteus spp* (16%) and *Pseudomonas spp* (13%) among patients with wound infection was higher than in patients without (P=0.03).

Pattern of resistance to antimicrobial agents

About three-quarters of the patients (n=412, 71.9%) had a history of antibiotic/antimicrobial treatment before arriving to the hospital (Table 1). Drugs that were commonly used were ceftriaxone (n=173, 46.2%), metronidazole (n=147, 39.4%), cloxacillin (n=64, 17.1%), ciprofloxacin (n=25, 6.6%) and co-trimoxazole (n=21, 5.5%).

Generally, there was high antimicrobial resistance in bacterial isolates in this study; *Proteus spp*, *Klebsiella spp,* and *E.coli* exhibited relatively high resistance to all drugs tested among Gram-negative isolates. Ampicillin resistance was frequent among *Klebsiella spp* (n=24, 92.3%), *Proteus spp* (n=21, 75%), and *E. coli* (n=13, 68.4%). Other bacterial spp such as *Enterobacter cloacae*, *Acinetobacter baumannii*, *Serratia spp, Morganella morganii* and *Providentia spp* were resistant by 100% to ampicillin. Resistance of *Proteus spp*, *Klebsiella spp* and *E.coli* to cefazolin was (n=23, 82.1%), (n=16, 61.5%), and (n=11, 57.9%) respectively with all other spp at 100% resistance. Resistance to third generation cephalosporins (ceftriaxone and ceftazidime) was as well observed for *Klebsiella spp* (n=14, 53.8% and n=12, 46.2%) and *E. coli* (n=8, 42.1% and n=7, 36.8%). Table 5a. Among the Gram-positive isolates, *S. aureus* was the only species, which demonstrated detectable resistance to penicillin (n=22, 100%), erythromycin (n=11, 50%), trimethoprim/sulpha (n=10, 45.5%), as well as cefoxitin (n=6, 27.3%). All *S. aureus* in this study were sensitive to vancomycin. Refer to table 5b. Table 5c summarizes the susceptibility pattern of the six cefoxitin-resistant *S. aureus* and 16 cefoxitin-susceptible *S. aureus*. Resistance of cefoxitin-resistant *S. aureus* to other drugs such as erythromycin, penicillin and trimethoprim sulpha was 100%, while none were resistant to vancomycin and chloramphenicol. All cefoxitin-susceptible *S. aureus* isolates were resistant to penicillin (100%), 6 (37.5%) to erythromycin, 5 (31.3%) to trimethoprim sulpha and 1 (6.3%) to chloramphenicol. None were resistant to vancomycin.

Discussion

Culture results

KCMC is a referral hospital serving approximately 11 million people in the northern zone of Tanzania. We conducted a two-year study from August 2013 to August 2015 to determine the pattern of bacterial pathogens associated with different health conditions among patients who were admitted at medical and surgical departments in this hospital.

The culture results revealed a higher positive growth rate on wound swab specimens (n=180, 72.3%), compared to others. Both Gram-negative and positive species were observed. Our findings are in agreement with other studies in Africa where wound infections tend to manifest with a variety of bacterial pathogens [24,25]. This is explained by the complexity of wound specimens that will tend to have a variety of bacterial pathogens, depending on the way wounds were acquired. Wounds acquired from a community environment will have more diverse organisms than hospital-acquired wounds [26,27]. In our study there were few positive blood specimens (n=15, 6%) on culture, a finding which is in agreement with other studies that showed a low positive growth of blood cultures [28]. Possibly this is because most septicemia cases we tested were not due to bacterial infections, a finding that has been reported from other studies in Tanzania[29]. The use of antibiotic prior to coming to the hospital, which hinders the detection of susceptible organisms[30], may be another reason. This is a practice which is very common in Tanzania and other developing countries [31–33]. KCMC being a tertiary care hospital receives patients referred from health facilities in Kilimanjaro region and other parts of Tanzania. The majority of these patients have been treated with antibiotics in the referring hospital. However, the patients could also have self-medicated since antibiotics are easily available and policies to control improper use of antibiotics are non-existent in Tanzania, as in other developing countries [31,33–36].

Bacterial spectrum

The bacterial spectrum observed from this study showed a high diversity of Gram-negative bacilli such as *Proteus spp* (12.7%), *E.coli* (11.7%), *Pseudomonas spp* (10.6%) and *Klebsiella spp* (10.1%), with *Staphylococcus aureus* (9.3%) being the predominant Gram-positive isolate. The majority of these Gram-negative bacilli were from wound infections rather than from other disease conditions. This predominantly Gram-negative infection pattern, as also observed in other studies,[25,37,38] is different from that most commonly reported from Western Europe and North America[39,40]. The reasons for this are not entirely known, but recent studies have also shown that higher temperatures are correlated with increased numbers of infections caused by Gram-negative bacterial species [41]. Our results do however emphasize that we cannot use knowledge obtained in Western Europe and North America directly for clinical care and empirical treatment in Sub-

Saharan Africa.

Infection pattern

Like any other resource-constrained countries, Tanzania is still experiencing the burden of infectious diseases. In the current study we observed presence of wound infections (n=263, 45.9%), septicemia (n=46, 8.03%), diarrhoea (n=20, 3.5%), HIV (n=81, 14.1%), and tuberculosis (n=60, 10.5%) and many other respiratory infections. As also indicated in other studies [14,42] , these diseases are still health challenges in low-income countries. We also recognized the presence of non-communicable diseases such as cancer (n=52, 9.1%) and diabetes (n=122, 21.3%). This suggests co-existence of communicable and non-communicable diseases in low-income countries as has been indicated in other studies [43,44]. The increase of diabetes in Tanzania may be the effect of little knowledge about the risk factors associated with the disease[4], which may be related to the majority (n=339, 59.2%) of the participants having only primary level education. There was no relationship between the most frequently isolated bacteria and conditions like diabetes and cancer. However, a non-statistically significant association between diabetes and *Proteus spp* (19%) *and E. coli* (14%) (P=0.07) was observed. The finding was more or less the same with HIV status. It was noted that prevalence of *Proteus spp* (16%)*, and Pseudomonas spp* (13%) were higher in wound infections than in those with no wound infection (9% and 6%, respectively), and the difference was statistically significant (P =00.3). This is in agreement with other studies[26] despite the fact that the design of the studies was different. Again we can generally attest that aetiology of a wound infection is broad, depending on environment and nature of the wound.

Antimicrobial susceptibility testing

Proper identification and determination of antimicrobial resistance of the bacterial pathogens is crucial in order to help physicians to provide proper treatment promptly. The advancement in pharmaceutical industries has lead to discoveries of many antibiotics, which has facilitated physicians' efforts into providing quality effective medical care. Despite of this increase, prudent use is essential in controlling antimicrobial resistance, which has now become one of the major challenges for medical progress. The current study demonstrated that a majority (n=412, 71.9%) of patients had sought treatment prior to coming to the hospital. It is likely these patients received antibiotics during their previous treatment. The most frequently used drugs were ceftriaxone (46.2%), metronidazole (39.4%), cloxacillin (17.1%), ciprofloxacin (6.6%) and co-trimoxazole (5.5%). Along with this, the observed resistance patterns of Gram negative bacterial isolates tested on drugs such as amoxicillin, ampicillin, gentamicin, trimethoprim sulpha and chloramphenicol was relatively high in ampicillin (82.4%) and trimethoprim-sulpha (60%), and below 50% in the rest. This is probably due to the fact that these drugs are used in Tanzania as first-line antibiotics in treatment of gas-

trointestinal diseases, respiratory diseases, obstetrical/gynaecological, cardiovascular and nervous system diseases [45]. Their easy availability from hospitals causes these drugs to be commonly used for treatment by medical practitioners as well as for self-medication, factors which play a great role in drug resistance [34,35,46]. The finding is in agreement with other two studies in Tanzania which indicated resistance of *E.coli* and *Klebsiella* to trimethoprim-sulfamethoxazole, ampicillin, amoxicillin-clavulanic acid and gentamicin (100%, 96%, 88%, 60%) and (85%, 95%, 70%, 70%) respectively [47,48]. Resistance ranging from 9.1% to 78% also has been noted to ciprofloxacin and nalidixic acid. These are categorized as second line drugs in Tanzania yet they show a high frequency of resistance. As ceftriaxone is a third-generation cephalosporin, we expected its use to be controlled, yet it was the most used. Moreover, convincing percentages of resistant strains of *E. coli* and *Klebsiella* to first and third-generations of cephalosporins have been broadly noted, ranging from 36.8 to 61.5%. This finding suggests existence of extended spectrum beta lactamase (ESBL) bacteria, as has been addressed in other studies in Tanzania[49] where 64.3% of *E. coli* and 80% of *Klebsiella pneumoniae* were ESBL producers. The presence of ESBL producers reduces treatment options, resulting in higher morbidity and mortality due to severe infections and sepsis.

S. aureus was the predominant spp among Gram-positive isolates. It accounted for 6 (27.3%) of the observed resistances to cefoxitin and other antibiotics such as erythromycin, trimethoprim and penicillin G, a characteristic that we would postulate to indicate methicillin-resistant *Staphylococcus* (MRSA) clones, as has been suggested in other studies[50].

Conclusion

The study has revealed a wide range of causative agents, with an alarming rate of resistance to the commonly used antimicrobial agents. Furthermore, the bacterial spectrum differs from those observed in high-income countries. This highlights the imperative of regular generation of data on aetiological agents and their antimicrobial susceptibility patterns especially in infectious disease endemic settings. The key steps would be to ensure the diagnostic capacity at a sufficient number of sites and routine exchange, comparison, analysis and reporting of data. As the minimum, sentinel sites (hospitals) across the country and region should report on a representative subset of bacterial species and their susceptibility to drugs at least once a year. A central organizing body should collate the data and report to all relevant national and international stakeholders. [51]

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References

1. Cohen ML. Changing patterns of infectious disease. Nature. 2000;406(August).
2. Lobber B. Changing Patterns of Infectious Disease. Am J Med. 1988;84(3):569–78.
3. Blomberg B. [Antimicrobial resistance in developing countries]. Tidsskr den Nor lægeforening Tidsskr Prakt Med ny række. 2008;128(21):2462–6.
4. Ruhembe CC, Mosha TCE, Nyaruhucha CNM. Prevalence and awareness of type 2 diabetes mellitus among adult population in Mwanza city , Tanzania. 2014. p. 1–11.
5. Cohen ML. Changing patterns of infectious disease. Nature. 406(6797):762–7.
6. Kibirige D, Ssekitoleko R, Mutebi E, Worodria W. Overt diabetes mellitus among newly diagnosed Ugandan tuberculosis patients : a cross sectional study. BMC Infect Dis. BMC Infectious Diseases; 2013;13(1):1.
7. Africa S, Cohen C, Moyes J, Tempia S, Groom M, Walaza S, et al. Severe Influenza-associated Respiratory Infection in High HIV Prevalence Setting ,. Emerg Infect Dis. 2013;19(11):2009–11.
8. Masur H, Read SW. Opportunistic Infections and Mortality : Still Room for Improvement. 2015;212:1348–50.
9. Mhada T V, Fredrick F, Matee MI, Massawe A. Neonatal sepsis at Muhimbili National Hospital , Dar es Salaam , Tanzania ; aetiology , antimicrobial sensitivity pattern and clinical outcome. BMC Public Health. BMC Public Health; 2012;12(1):1.
10. Moyo SJ, Steinbakk M, Aboud S, Mkopi N, Kasubi M, Blomberg B, et al. Penicillin resistance and serotype distribution of Streptococcus pneumoniae in nasopharyngeal carrier children under 5 years of age in Dar es Salaam , Tanzania. J Med Microbiol. 2012;61:952–9.
11. Blomberg B, Jureen R, Manji KP, Bushir S, Mwakagile DSM, Urassa WK, et al. High Rate of Fatal Cases of Pediatric Septicemia Caused by Gram-Negative Bacteria with Extended-Spectrum Beta-Lactamases in Dar es Salaam , Tanzania High Rate of Fatal Cases of Pediatric Septicemia Caused by Gram-Negative Bacteria with Extended-Spectrum B. J Clin Microbiol. 2005;43(2):745–9.
12. Ad M, Kigonya E. Bacteriuria among adult non-pregnant women attending Mulago hospital assessment centre in Uganda. Afr Health Sci. 2011;11(2):182–9.
13. Feikin DR, Olack B, Bigogo GM, Audi A, Cosmas L, Aura B, et al. The burden of common infectious dis-

ease syndromes at the clinic and household level from population-based surveillance in rural and urban Kenya. PLoS One. 2011 Jan;6(1):e16085.

14. Mattioli MC, Pickering AJ, Gilsdorf RJ, Davis J, Boehm AB. Hands and Water as Vectors of Diarrheal Pathogens in Bagamoyo, Tanzania. Am Chem Soc. 2013;47:355–63.
15. Tambo E, Ai L, Zhou X, Chen J-H, Hu W, Bergquist R, et al. Surveillance-response systems: the key to elimination of tropical diseases. Infect Dis poverty. 2014 Jan;3(1):17.
16. de Kadt E. Making health policy management intersectoral: Issues of information analysis and use in less developed countries. Soc Sci Med. 1989;29(4):503–14.
17. Harries AD, Jensen PM, Zachariah R, Rusen ID, Enarson DA. How health systems in sub-Saharan Africa can benefi t from tuberculosis and other infectious disease programmes. Int J Tuberc Lung Dis. 2009;13(10):1194–9.
18. Tambo E, Ugwu EC, Ngogang JY. Need of surveillance response systems to combat Ebola outbreaks and other emerging infectious diseases in African countries. Infect Dis poverty. 2014 Jan;3(1):29.
19. Baron EJ, Miller JM, Weinstein MP, Richter SS, Gilligan PH, Thomson RB, et al. A guide to utilization of the microbiology laboratory for diagnosis of infectious diseases: 2013 recommendations by the Infectious Diseases Society of America (IDSA) and the American Society for Microbiology (ASM)(a). Clin Infect Dis. 2013 Aug;57(4):e22–121.
20. Zumla A, Abubakar I, Raviglione M, Hoelscher M, Ditiu L, McHugh TD, et al. Drug-resistant tuberculosis--current dilemmas, unanswered questions, challenges, and priority needs. J Infect Dis. 2012 May 15;205 Suppl(suppl_2):S228-40.
21. Falagas ME, Karageorgopoulos DE, Leptidis J, Korbila IP. MRSA in Africa: filling the global map of antimicrobial resistance. PLoS One. 2013 Jan;8(7):e68024.
22. Ndihokubwayo JB, Yahaya AA, Desta AT, Ki-zerbo G. Antimicrobial resistance in the African Region : Issues , challenges and actions proposed. African Heal Monit. 2013;(16).
23. Turnidge J, Paterson DL. Setting and Revising Antibacterial Susceptibility Breakpoints. Clin Microbiol Rev. 2007;20(3):391–408.
24. Mawalla B, Mshana SE, Chalya PL, Imirzalioglu C, Mahalu W. Predictors of surgical site infections among patients undergoing major surgery at Bugando Medical Centre in Northwestern Tanzania. BMC Surg. BioMed Central Ltd; 2011;11(1):21.
25. Pondei K, Fente BG, Oladapo O. Current microbial isolates from wound swabs, their culture and sensi-

tivity pattern at the niger delta university teaching hospital, okolobiri, Nigeria. Trop Med Health. Jun;41(2):49–53.

26. Källman O, Lundberg C, Wretlind B, Ortqvist A. Gram-negative bacteria from patients seeking medical advice in Stockholm after the tsunami catastrophe. Scand J Infect Dis. 2006 Jan;38(6–7):448–50.

27. Ran Y-C, Ao X-X, Liu L, Fu Y-L, Tuo H, Xu F. Microbiological study of pathogenic bacteria isolated from paediatric wound infections following the 2008 Wenchuan earthquake. Scand J Infect Dis. 2010 May;42(5):347–50.

28. Dong B, Liang D, Lin M, Wang M, Zeng J, Liao H, et al. Bacterial etiologies of five core syndromes: laboratory-based syndromic surveillance conducted in Guangxi, China. PLoS One. 2014;9(10):e110876.

29. Mahende C, Ngasala B, Lusingu J, Butichi A, Lushino P, Lemnge M, et al. Bloodstream bacterial infection among outpatient children with acute febrile illness in north-eastern Tanzania. BMC Res Notes. BioMed Central; 2015;8(1):289.

30. Blomberg B, Manji KP, Urassa WK, Tamim BS, Mwakagile DSM, Jureen R, et al. Antimicrobial resistance predicts death in Tanzanian children with bloodstream infections: a prospective cohort study. BMC Infect Dis. 2007;7:43.

31. Chipwaza B, Mugasa JP, Mayumana I, Amuri M, Makungu C, Gwakisa PS. Self-medication with antimalarials is a common practice in rural communities of Kilosa district in Tanzania despite the reported decline of malaria. Malar J. 2014;13(1):252.

32. Ocan M, Obuku EA, Bwanga F, Akena D, Richard S, Ogwal-Okeng J, et al. Household antimicrobial self-medication: a systematic review and meta-analysis of the burden, risk factors and outcomes in developing countries. BMC Public Health. BMC Public Health; 2015;15(1):742.

33. Biswas M, Roy MN, Manik MIN, Hossain MS, Tapu SMTA, Moniruzzaman M, et al. Self medicated antibiotics in Bangladesh: a cross-sectional health survey conducted in the Rajshahi City. BMC Public Health. 2014;14(1):847.

34. Ocan M, Bwanga F, Bbosa GS, Bagenda D, Waako P, Ogwal-Okeng J, et al. Patterns and predictors of self-medication in northern Uganda. PLoS One. 2014;9(3):e92323.

35. Abasiubong F, Bassey EA, Udobang JA, Akinbami OS, Udoh SB, Idung AU. Self-Medication: potential risks and hazards among pregnant women in Uyo, Nigeria. Pan Afr Med J. 2012;13:15.

36. Shehnaz SI, Khan N, Sreedharan J, Issa KJ, Arifulla M. Self-medication and related health complaints among expatriate high school students in the United Arab Emirates. Pharm Pract (Granada). 2013;11(4):211–8.

37. Abraham Y, Wamisho BL. Microbial susceptibility of bacteria isolated from open fracture wounds presenting to the err of black-lion. African J Microbiol Res. 2009;3(12):939–51.

38. Mshana SE, Kamugisha E, Mirambo M, Chakraborty T, Lyamuya EF. Prevalenpce of multiresistant gram-negative organisms in a tertiary hospital in Mwanza, Tanzania. BMC Res Notes. 2009;6:1–6.

39. Giacometti A, Cirioni O, Schimizzi AM, Prete MS Del, Errico MMD, Petrelli E, et al. Epidemiology and Microbiology of Surgical Wound Infections Epidemiology and Microbiology of Surgical Wound Infections. J Clin Microbiol. 2000;38(2):918–22.

40. Reilly GD, Reilly CA, Smith EG. Vibrio alginolyticus -associated wound infection acquired in British waters , Guernsey , July 2011. Eurosurveillance. 2011;(July):3–4.

41. Schwab F, Gastmeier P, Meyer E. The warmer the weather, the more gram-negative bacteria - impact of temperature on clinical isolates in intensive care units. PLoS One. 2014;9(3):e91105.

42. Crump JA, Ramadhani HO, Morrissey AB, Saganda W, Mwako MS, Yang L, et al. Invasive Bacterial and Fungal Infections Among Hospitalized HIV-Infected and HIV-Uninfected Adults and Adolescents in Northern Tanzania. 2011;52:341–8.

43. Mayige M, Kagaruki G, Ramaiya K, Swai A. Non communicable diseases in Tanzania : a call for urgent action. Tanzanian J Heal Res. 2012;14(2):1–12.

44. Young F, Critchley J a, Johnstone LK, Unwin NC. A review of co-morbidity between infectious and chronic disease in Sub Saharan Africa: TB and diabetes mellitus, HIV and metabolic syndrome, and the impact of globalization. Global Health. 2009 Jan;5:9.

45. Massele A MJ et al. Standard treatment guidelines and the national essential medicines list for mainland Tanzania. 2007.

46. Eticha T, Mesfin K. Self-Medication Practices in Mekelle, Ethiopia. PLoS One. 2014;9(5):e97464.

47. Fredrick F, Francis JM, Fataki M, Maselle SY. Aetiology , antimicrobial susceptibility and predictors of urinary tract infection among febrile under-fives at Muhimbili National Hospital , Dar es Salaam-Tanzania. Academicjournals. 2013;7(12):1029–34.

48. Mshana SE, Matee M, Rweyemamu M. Antimicrobial resistance in human and animal pathogens in Zambia, Democratic Republic of Congo, Mozambique and Tanzania: an urgent need of a sustainable surveillance system. Ann Clin Microbiol Antimicrob. Annals of Clinical Microbiology and Antimicrobials; 2013;12(1):28.

49. Mawalla B, Mshana SE, Chalya PL, Imirzalioglu C, Mahalu W. Predictors of surgical site infections

among patients undergoing major surgery at Bugando Medical Centre in Northwestern Tanzania. BMC Surg. 2011 Jan;11:21.

50. Lelièvre H, Lina G, Jones ME, Olive C, Forey F, Roussel-Delvallez M, et al. Emergence and spread in French hospitals of methicillin-resistant Staphylococcus aureus with increasing susceptibility to gentamicin and other antibiotics. J Clin Microbiol. 1999;37(11):3452–7.

51. Frank A, Marion K. Sharing Data for Global Infectious Disease Surveillance and Outbreak Detection. Trends Microbiol. 2016;24(4):241–245.

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Socio-demographics and clinical characteristics of the study participants admitted at KCMC (n=575) **n (%)**	
Median age in years (IQR)	43 (30-57)
Male gender	348 (61%)
Female gender	227 (39%)
Department	
Surgical ward	232 (40.5)
Medical ward	277 (48.3)
ICU	49 (8.6)
Paediatric	15 (2.6)
Occupation	
Farming	271 (47.3)
Employed	56 (9.8)
Business	121 (20.7)
Other	132 (21.8)
Education	
None	130 (22.7)
Primary	339 (59.2)
Secondary	70 (12.2)
Tertiary	34 (5.9)
Marital	
Single	179 (31.2)
Married	325 (56.7)
*Widowed	69 (12)
Disease conditions	
***Wound**	263 (45.9)
Pneumonia	87 (14.4)
Tuberculosis	64 (10.6)
Septicemia	52 (8.6)
Diarrhea	21(3.5)
Meningitis	4(0.7)
Comorbidities	
Diabetes	122 (21.3)
HIV	81 (14.1)
Cancer	52 (9.1%)
Treatment prior to admission	
Yes	412 (71.9%)

IQR (Interquartile range) ICU, intensive care unit TB, Tuberculosis HIV, Human Immunodeficiency Virus
* Widowed: widowed and divorced, Gender n=574, age n=559, the rest n=573, 2 patients had no information, *wound (includes abscess)

Table 1

Table 2

Bacteria isolates obtained from culture positive specimens

		Specimen N (%)			
Isolates	**Total (N)**	**Wound swab**	**Sputum**	**Stool**	**Blood**
Gram neg rods	61	52 (85.2)	6 (9.8)	2 (3.3)	1 (1.6)
Proteus spp	48	44 (91.7)	0 (0)	2 (4.2)	2 (4.2)
Escherichia spp	44	24 (54.5)	5 (11.4)	11 (25)	4 (9.1)
Pseudomonas spp	40	37 (92.5)	3 (7.5)	0 (0)	0 (0)
Klebsiella spp	38	28 (73)	7 (18.4)	3 (7.9)	0 (0)
Staphylococcus aureus	35	29 (82.9)	2 (5.7)	0 (0)	4 (11.4)
CoN Staphylococcus	25	18 (72)	2 (8)	2 (8)	3 (12)
Unknown	22	17 (77.3)	4 (18.2)	1 (4.5)	0 (0)
Streptococcus spp	17	7 (41.2)	9 (52.9)	0 (0)	1 (5.9)
Enterobacter spp	15	12 (80)	2 (13.3)	1 (6.7)	0 (0)
Bacillus spp	8	7 (87.5)	0 (0)	0 (0)	1 (0)
Acinetobacter spp	5	3 (60)	2 (40)	0 (0)	0 (0)
Serratia spp	4	2 (50)	1 (25)	1 (25)	0 (0)
Providentia spp	4	4 (100)	0 (0)	0 (0)	0 (0)
Enterococcus spp	3	3 (100)	0 (0)	0 (0)	0 (0)
Gram positive cocci	2	1 (50)	1 (50)	0 (0)	0 (0)
Dipthroids spp	2	1 (50)	1 (50)	0 (0)	0 (0)
Stenotrophomonas spp	1	1 (100)	0 (0)	0 (0)	0 (0)
Morganella spp	1	1 (100)	0 (0)	0 (0)	0 (0)
Cytrobacter spp	1	1 (100)	0 (0)	0 (0)	0 (0)
Aeromonas spp	1	1 (100)	0 (0)	0 (0)	0 (0)
Total	**377**	**293 (77.7)**	**45 (11.9)**	**23 (6.1)**	**16 (4.2)**

Table 1 summarizes bacterial pathogens identified in this study. Where more than one subtypes identified, collectively they were named as species (spp) of that genus in order to accommodate all groups of bacteria in a single table.

Table 3

Health conditions and commonly isolated bacterial species

Health condition	**S.aureus,** n (%)	**Klebsiella spp,** n (%)	**Proteus spp,** n (%)	**E.coli,** n (%)	**Pseudomonas spp,** n (%)
Burn wound	6 (17.1)	6(14.6)	10(20.4)	2(4.5)	8(20)
Motor traffic wound	3 (8.6)	1(2.4)	6(12.2)	1(2.3)	1(2.5)
Post surgical wound	2 (5.7)	6(14.6)	2(4.1)	3(6.8)	2(5)
Diabetic wound	5 (14.3)	7(17.1)	15(30.6)	8(18.2)	8(20)
Septic wound	20 (57.1)	21(51.2)	37(75.5)	24(54.5)	31(77.5)
[a] Other wound	11(31.4)	6(14.6)	13(26.5)	9(20.5)	17(42.5)
Diarrhea	1 (2.9)	1(2.4)	1(2)	5(11.4)	0(0)
Pneumonia	1 (2.9)	3(7.3)	0(0)	4(9.1)	0(0)
Septicemia	0 (0)	2(4.9)	3(6.1)	1(2.3)	2(5)
Malaria	1 (2.9)	0(0)	1(2)	0(0)	1(2.5)
Cancer	4 (11.4)	4(9.8)	2(4.1)	4(9.1)	5(12.5)
Diabetes	9 (25.7)	10(24.4)	18(36.7)	13(29.5)	8(20)
HIV	3 (8.6)	4(9.8)	3(6.1)	6(13.6)	1(2.5)
TB	1 (2.9)	1(2.4)	0(0)	3(6.8)	1(2.5)

[a] wound due to animal bite, gunshot
TB tuberculosis
HIV-Human Immunodeficiency Virus
NB: Percentages were obtained by cross tabulation of each comorbidity and isolate
S.aureus N=35, *Klebsiella spp* N=41, *Proteus spp* N=49, *E.coli N*=44, *Pseudomonas spp* N=40

Table 4

A. Commonly isolated bacteria and disease comorbidity status

Bacterial Isolates	Diabetes		P Value	HIV		P Value	Cancer		P Value
	No	Yes		No	Yes		No	Yes	
Proteus spp	0.11 (0.85 - 0.92)	0.19 (0.12 - 0.28)	0.07	0.13 (0.10 - 0.17)	0.10 (0.03 - 0.26)	0.53	0 .14 (0.10 - 0.18)	0.06 (0.02 - 0.22)	0.10
E.coli	0.11 (0.08 - 0.15)	0.14 (0.08 - 0.22)	0.50	0.11 (0.08 - 0.15)	0.19 (0.09 - 0.37)	0.26	0.12 (0.09 - 0.15)	0.12 (0.05 - 0.29)	0.93
Klebsiella spp	0.11 (0.07 - 0.15)	0.11 (0.06 - 0.18)	0.89	0.11 (0.08 - 0.14)	0.13 (0.05 - 0.30)	0.73	0.11 (0.08 - 0.15)	0.12 (0.05 - 0.29)	0.82
S.aureus	0.09 (0.06 - 0.13)	0.09 (0.05 - 0.17)	0.94	0.09 (0.07 - 0.13)	0.10 (0.03 - 0.27)	0.94	0.09 (0.06 - 0.13)	0.12 (0.05 - 0.29)	0.60
Pseudomonas spp	0.11 (0.08 - 0.16)	0.08 (0.04 - 0.16)	0.39	0.11 (0.08 - 0.15)	0.03 (0.00 - 0.20)	0.03	0.10 (0.07 - 0.14)	0.15 (0.06 - 0.32)	0.45

B. Commonly isolated bacteria and wound infections status

Bacterial iso-lates	Wound infection		P-value
	No	Yes	
Proteus spp	0.09 (0.05 - 0.14)	0.16 (0.12 - 0.21)	0.03
E.coli	0.14 (0.08 - 0.15)	0.10 (0.07 - 0.15)	0.26

Klebsiella spp	0.14 (0.09 - 0.21)	0.09 (0.06 - 0.13)	0.13
S.aureus	0.11 (0.06 - 0.17)	0.08 (0.06 - 0.13)	0.50
Pseudomonas spp	0.06 (0.03 - 0.12)	0.13 (0.09 - 0.18)	0.03

Table 4a summarizes the association between commonly isolated groups of bacteria and absence or presence of three health conditions Diabetes, HIV and Cancer as common co-morbidities identified in patients participated in this study. While table 4b summarizes association between common bacteria isolates and presence or absence of wound infection since most of the patients were diagnosed to have wound infections.

NB: Numbers described as; Proportion (95% Confidence interval).

Table 5

Antimicrobial resistance* pattern of bacterial isolated from patients admitted at KCMC tertiary care hospital (N=130)

A: Gram-negative bacterial isolates (n=106)

		AM	**CZ**	**SXT**	**NA**	**C**	**CRO**	**CAZ**	**AMC**	**CIP**	**GM**
Organisms	**N**	**R (%)**	**R (%)**	**R (%)**	**R (%)**	**R (%)**	**R (%)**	**R (%)**	**R (%)**	**R (%)**	**R (%)**
Proteus spp	**28**	21(75)	23(82.1)	18(64.)	22(78.6)	19(67.9)	15(53.6)	12(42.9)	4(14.3)	11(39.3)	8(28.6)
Klebsiella spp	**26**	24(92.3)	16(61.5)	18(69.2)	12(46.2)	6(23.1)	14(53.8)	12(46.2)	15(57.7)	11(43.2)	10(38.5)
Pseudomonas spp	**22**	ND	DN	ND	ND	14(66.7)	ND	4(18.2)	ND	2(9.1)	3(13.6)
E.coli	**19**	13(68.4)	11(57.9)	12(63.2)	10(52.6)	3(15.8)	8(42.1)	7(36.8)	8(42.1)	9(47.4)	7(36.8)
E.cloacae	**5**	5(100)	5(100)	2(40)	2(40)	2(40)	4(80)	3(60)	5(100)	2(40)	3(60)
A.baumanii	**3**	3(100)	3(100)	1(33.3)	2(66.7)	2(66.7)	3(100)	2(66.7)	3(100)	1(33.3)	1(33.3)
Serratia spp	**2**	2(100)	2(100)	0	0	0	0	0	2(100)	0	0
Morganella morganii	**1**	1(100)	1(100)	0	0	0	0	0	1(100)	0	0
Providentia spp	**1**	1(100)	1(100)	0	0	1(100)	0	0	1(100)	0	0
Total	**106**	**70(82.4)**	**62(72.9)**	**51(60)**	**48(56.5)**	**47(44.3)**	**44(51.8)**	**40(37.4)**	**39(45.9)**	**36(33.6)**	**32(29.9)**

B. Gram positive bacteria (n=24)

		P	**E**	**SXT**	**CTX**	**C**	**VA**
Organisms	**N**	**R (%)**	**R (%)**	**R (%)**	**R (%)**	**R (%)**	**R (%)**
S.aureus	22	22(100)	11(50)	10(45.5)	6(27.3)	1(4.5)	0(0)
S.pneumoniae	2	1(50)	1(50)	1(50)	0(0)	0(0)	ND
Total	24	23/24(95.8)	12/24(50)	11/24(45.8)	6/24(25)	1/24(4.2)	0(0)

C: Susceptibility pattern of CXT resistant and CXT sensitive S.aureus to other drugs (N=22)

		CTX	C	E	P	SXT	VA
	N	**R (%)**	**R (%)**	**R (%)**	**R (%)**	**R (%)**	**R (%)**
Organism							
CXT resistant *S.aureus*	6	6 (100)	0 (0)	6 (100)	6 (100)	6 (100)	0 (0)
CXT susceptible *S.aureus*	16	0 (0)	1 (6.3)	6 (37.5)	16 (100)	5 (31.3)	0 (0)

AMC: Amoxicillin-Clavilunic acid, AM: Ampicillin, CZ: Cefazoline, CAZ: Ceftazidime, CRO: Ceftriaxone, C: Chloramphenical, CIP: Ciprofloxacin, GM: Gentamycin, NA: Nalidixic acid, SXT: Trimeth/sulpha. ND =not determined, CXT: Cefoxitin, E: Erythromycin, P: Penicillin G, VA: Vancomycin, *Resistance represent intermediate and resistance ND =not determined
N= Total number tested, 0= No resistance.

NB: Part C of the table shows susceptibility pattern of the six cefoxitin resistant *S.aureus* (probably MRSA) and sixteen cefoxitin susceptible *S.aureus*