

## Original Research Article

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# Antimicrobial resistance in wastewater of Yangon Region, Myanmar from one health perspective

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## ABSTRACT

**Background:** Antibiotic resistance is an emerging concern both for public and animal health globally and also threatens the achievements of modern medicine. This study aimed to generate the baseline data of drug resistance pathogens in diversity of waste water of Yangon Region, Myanmar.

**Methods:** A cross-sectional descriptive study was conducted from January to July 2021. A total of forty samples of wastewater (two samples each from ten hospitals, one sample each from five poultry farms, five aquacultures and ten community drains) were aseptically collected, transported in ice box and processed following standard procedure for bacterial isolation and detection of antibiotic sensitivity pattern. Identification and antibiotic susceptibility testing of isolated colonies were done by VITEK 2 compact system.

**Results:** A total of 106 bacterial isolates were identified and 50% were from hospitals, 31.1% were from community drains and 9.4% each from poultry farms and aquacultures. The most frequently identified isolates were Enterobacteriaceae (65.1%) followed by Acinetobacter species (11.3%) and Pseudomonas species (8.5%). Among the isolated organisms, ESBL producers and Carbapenemase producer were 7.5% and 0.9% respectively. ESBL producers (62.5%) were resistant to cefuroxime, cefuroxime-axetil, cefotaxime, ceftriaxone and minocycline. Carbapenem resistant Enterobacteriaceae was multidrug resistant but sensitive to amikacin, tigecycline and cefaclor.

**Conclusions:** The proportion of antibiotic resistant bacteria are higher in hospital wastewater than other sites. Hence proper treatment plant for hospital wastewater should be installed and need to mitigate antibiotic resistance with a 'one-health' approach.

**Keywords:** Antimicrobial resistance, Wastewater, Hospitals

## INTRODUCTION

Antimicrobial resistance (AMR) is widely acknowledged as a serious global health problem that threatens not only human and animal health but also have an impact on public health and economic burden especially in low and middle income countries.<sup>1,2</sup> The World Health Organization (WHO) has included AMR as one of the top ten threats to global health in 2019.<sup>3</sup> Increasing threat of AMR requires to address a holistic and multisectoral (One Health)

approach as antimicrobials used to treat various infectious diseases in animals may be the same or be similar to those used in humans. Resistant bacteria arising either in humans, animals or the environment may spread from one to the other, and also from one country to another.<sup>4,5</sup> Enormous amount of antibiotics are used in agriculture, the food industry, and aquaculture.<sup>6,7</sup> Due to incomplete metabolism and the environmental spread of unused antibiotics, they enter the ecosystem, serving as a potent stimulus to elicit a bacterial adaptation response to develop antibiotic resistance and genes which is a major concern

facing modern medicine. Nowadays, AMR has been an increasing threat to the effectiveness of the treatment of infections caused by bacteria, parasites, viruses, and fungi. The magnitude of the problem and its impact on animal and human health and in wider society are still largely unknown.<sup>8</sup>

There are many common factors driving human health and animal health including overuse and misuse of antimicrobials, weak infection control and clinical practices, consumption of large volume of antimicrobials for non-therapeutic use in animals resulting in the widespread prevalence of antimicrobial resistant bacteria not only in humans and animals, but also in the natural environment through food chain and disposing of untreated or improperly treated wastewater. Hospital wastewater contain many kinds of pollutants such as radioactive, chemical and pharmaceutical wastes and also pathogenic microorganisms that can be hazardous to public health and contribute to the high rates of resistant bacteria that are being discharged in the natural environment.<sup>9</sup> There are multiple potential sources of antimicrobials entering the environment. Among the most important contributors to environmental pollution by antimicrobials are waste from hospitals, pharmaceutical manufacturing plants, wastewater treatment plants, untreated human wastes, waste and runoff from aquaculture, livestock, and plant-based food production and processing facilities. In agriculture sector of Myanmar, animal feed and veterinary medicinal products for animals must follow animal health and development law and there is no routine surveillance of AMR in animal and agricultural sectors.<sup>10</sup> Hence, there is an increased risk of getting exposed to AMR bacteria outside a health care setting through the preparation and consumption of contaminated food, ingestion of contaminated water, and recreational activities.<sup>11</sup> However, the attributable fraction of each source, and factors governing abundance and distribution of AMR organisms, antimicrobial resistant genes (ARGs), and residues in the environment from agricultural sources are unclear.<sup>12</sup>

WHO global report on AMR surveillance mentioned that resistance of common bacteria has reached alarming levels in many parts of the world with high level resistance of *Escherichia coli* and *Klebsiella* species (spp.) to third-generation cephalosporins and carbapenems. The high proportions of resistance to 3rd generation cephalosporins reported for *Escherichia coli* and *Klebsiella pneumoniae* in many settings must rely on carbapenems, the last resort to treat severe community and hospital acquired infections. These drugs are expensive and may not be available in resource limited settings and are likely to further accelerate the development of resistance. Carbapenem-resistant *Klebsiella pneumoniae* has been identified in most countries with proportion of resistance up to 54% is of great concern.<sup>13</sup> Myanmar Laboratory surveillance in human and animals (2016) revealed that WHO critical priority bacteria in Myanmar are carbapenem resistant bacteria such as *Pseudomonas* spp. (27%), *Acinetobacter*

spp. (21%) and *Enterobacteriaceae* (14%) and extended spectrum beta-lactamase (ESBL) producing *Enterobacteriaceae* (47%) which is one of the high priority pathogens.<sup>10</sup> High resistance rates have been described in bacteria isolated from food-producing animals, vegetables and environment.<sup>14</sup> One study in Myanmar mentioned that multidrug resistant *Acinetobacter* species were identified among isolates of various clinical specimens and the majority of *Acinetobacter* species were *Acinetobacter baumannii* (60%) and highly resistant to cefotaxime (77.5%), followed by ceftazidime, gentamicin and levofloxacin (67.5%).<sup>15</sup>

Myanmar National AMR situational analysis is an ongoing process and propose a single comprehensive implementable multisectoral governance mechanism in line with WHO National Action Plan guideline.<sup>10</sup> Currently there are very few proper functioning wastewater treatment plants in the community as well as in the hospital setting of Myanmar. Majority of wastewater from hospitals, agriculture and aquaculture run off and community directly dispose to nearby water body via community drains leading to contamination of both surface and ground water. There is a limited data concerning resistance profiles of microorganisms isolated from wastewater from one health perspective that is from hospitals, agricultural sectors and community. This study aimed to generate the baseline data of the magnitude of drug resistance pathogens in diversity of waste water of Yangon Region by determining the antibiotic sensitivity pattern and detecting ESBL producing organisms and carbapenem resistant organisms from isolated bacteria. In Myanmar, there is no National Residue Monitoring Plan and also a total One Health AMR plan. Therefore, the information from this study could provide a baseline assessment for the development of the National AMR monitoring plan on One Health perspective and prevention and control of AMR in Myanmar.

## METHODS

### Study setting and sampling

A cross-sectional descriptive study was conducted from January to July 2021 in Yangon Region, Myanmar. A total of forty samples of wastewater (two samples each from ten hospitals, one sample each from five poultry farms, five aquacultures and ten community drains) were collected. There are 10 General Hospitals and 13 Specialist Hospitals in Yangon Region. Ten Hospitals (5 General Hospitals and 5 Specialist Hospitals) were randomly selected among hospitals of Yangon Region. From each hospital, two samples of wastewater were collected. For ten samples from community wastewater, five samples were collected from community drains within the same township of the selected hospitals and another five samples from five different townships of non-hospital drainage site. Five samples each from poultry farms and aquaculture were collected purposely.

### Sample collection

Background information of source of wastewater was taken with checklist and face to face interview. Since this study was carried out during COVID pandemic situation, the researchers were committed to follow the COVID 19 prevention and control guidelines from MOHS.

The superficial wastewater samples were collected at the open surface from hospitals, community, poultry farms and aquaculture sites. Hospital wastewater samples were taken within 5m from the outlet of the hospital prior to dispose into the community drain. Each sample was collected 500 ml in a sterile bottle. All samples were brought to the National Health Laboratory and private lab within one hour for bacterial isolation and detection of antibiotic sensitivity pattern. Wastewater was aseptically collected, transported in ice box and processed following standard procedure for further analysis.<sup>16</sup>

### Microbiological examination of wastewater

Water sample of 10 ml was mixed with double strength MacConkey broth and incubated for 48 hours. If there was bacteria growth, the colour was changed into yellow. Then, these culture positive samples were subcultured onto Blood Agar and MacConkey agar. All the plates were incubated aerobically overnight at 37 °C. After overnight incubation, both Blood agar and MacConkey agar plates were examined macroscopically for colonial morphology. Then, a representative discrete colony was taken from the culture plate and subjected to automated culture. Identification and antibiotic susceptibility testing of isolated colonies was done by VITEK 2 compact system (bioMerieux, France). For detailed identification of genus and species of organisms was carried out by GN and GP cards, and their antibiotics susceptibility pattern by AST card (GN-363 and GP card). If ESBL positive was

identified by VITEK 2 compact, phenotypic confirmatory test of ESBL production was done by Cephalosporin/clavulanate combined disc diffusion method. Carbapenem resistant organisms among culture positive bacteria was also detected.

### Detection of ESBL and phenotypic confirmatory test for ESBL production

Isolates that indicate the zone diameter of ceftazidime ( $\leq 22$  mm), cefotaxime ( $\leq 27$  mm) and ceftriaxone ( $\leq 25$  mm) would be presumably ESBL producers, and testing of ESBL production was done by phenotypic screening and confirmed by Cephalosporin/clavulanate combination disc method. Mueller Hinton agar plate was seeded with standardized inoculum of the test organism (corresponding to 0.5 McFarland tube). Discs containing ceftazidime, ceftazidime plus clavulanic acid and cefotaxime, cefotaxime plus clavulanic acid was placed on Mueller Hinton agar, center to center at least 25 mm apart. After 16-18 hours incubation at 37°C, a difference of  $\geq 5$  mm between the zone diameter of either of the cephalosporin discs and their respective cephalosporin/clavulanic disc was taken to be phenotypic confirmation of ESBL production.

### Confirmatory test for Carbapenemase production

According to CLSI guideline, Modified Hodge test was conducted to determine the carbapenemase production in the isolates of Enterobacteriaceae using standard control organisms.

## RESULTS

Out of 40 wastewater samples, all samples were positive to one or more isolates.

**Table 1: Bacterial isolates according to study sites (n=106).**

Bacteria isolates	Hospital No. (%)	Community drain No. (%)	Poultry farms No. (%)	Aquaculture No. (%)	Total No. (%)
<i>Enterobacter cloacae</i> complex	4 (7.5)	0 (0)	1 (10.0)	0 (0)	5 (4.7)
<i>Escherichia coli</i>	13 (24.5)	7 (21.2)	1 (10.0)	1 (10.0)	22 (20.8)
<i>Klebsiella</i> spp.	10 (18.9)	9 (27.3)	1 (10.0)	2 (20.0)	22 (20.8)
<i>Aeromonas</i> spp.	8 (15.1)	6 (18.2)	2 (20.0)	3 (30.0)	19 (17.9)
<i>Serratia</i> ficaria	1 (1.9)	0 (0)	0 (0)	0 (0)	1 (0.9)
<i>Acinetobacter</i> spp.	5 (9.4)	5 (15.2)	2 (20.0)	0 (0)	12 (11.3)
<i>Pseudomonas</i> spp.	7 (13.2)	0 (0)	0 (0)	2 (20.0)	9 (8.5)
Others*	5 (9.4)	6 (18.2)	3 (30.0)	2 (20.0)	16 (15.1)
<b>Total</b>	<b>53 (100.0)</b>	<b>33 (100.0)</b>	<b>10 (100.0)</b>	<b>10 (100.0)</b>	<b>106 (100.0)</b>

Others\*: Aneurinibacillus-1, Comamonas spp.-4, Spingomonas spp.-4, Staphylococcus spp.2, Achromobacter spp.2, Cupriavidus spp.-1, Alcaligenes spp.-1, Ralstonia spp.-1

The most frequently identified isolates were *Enterobacteriaceae* (65.1%) followed by *Acinetobacter*

spp. (11.3%) and *Pseudomonas* spp. (8.5%). Among the *Enterobacteriaceae* group, *Escherichia coli* and *Klebsiella*

spp. were highest percentage (20.8%) followed by *Aeromonas* spp. (17.9%), *Enterobacter cloacae* complex (4.7%) and *Serratia ficaria* (0.9%). The frequency of isolates from the hospital sites was high compared to other sites (Table 1). The hospitals without proper treatment plant were found to be 60%. Antibiotic sensitivity pattern of isolated bacteria to commonly used antibiotics revealed

that the overall resistance of *Enterobacteriaceae* to cefuroxime was 20.3%, followed by ceftriaxone (18.8%), amoxicillin/clavulanic acid (15.9%) and cefotaxime (14.5%) while they showed highest sensitivity to amikacin (98.6%), gentamicin (88.4%), imipenem (84.1%) and tetracycline (81.2%) (Table 2).

**Table 2: Antimicrobial sensitivity pattern of Enterobacteriaceae (n=69).**

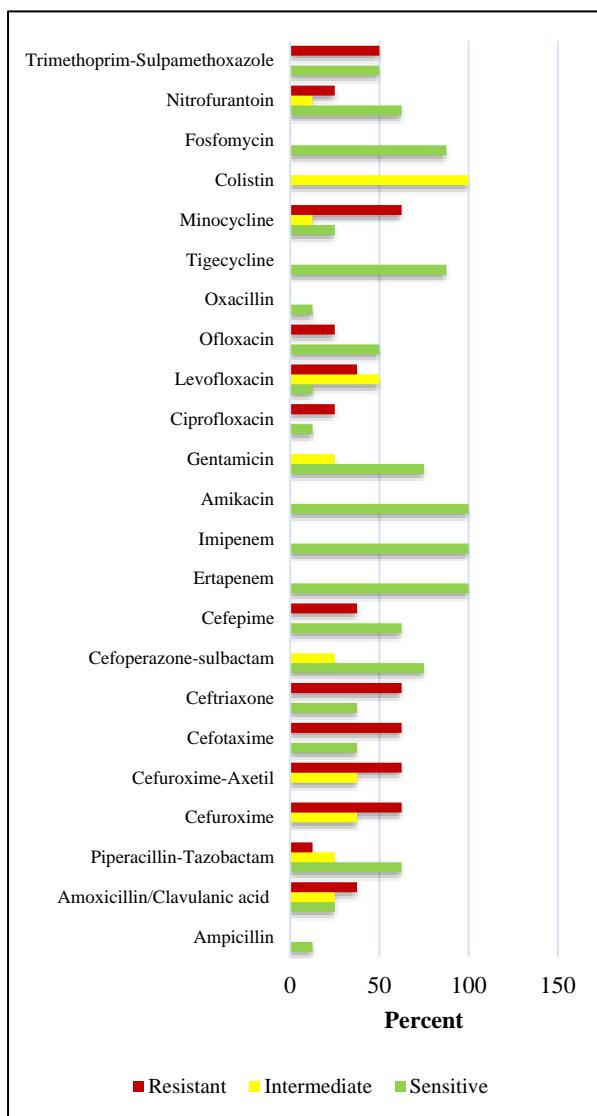
Drugs	Sensitive No. (%)	Intermediate No. (%)	Resistant No. (%)
<b>Ampicillin</b>	2 (2.9)	0 (0)	6 (8.7)
<b>Amoxicillin/Clavulanic acid</b>	25 (36.2)	13 (18.8)	11 (15.9)
<b>Ampicillin/Sulbactam</b>	2 (2.9)	3 (4.3)	5 (7.2)
<b>Piperacillin-Tazobactam</b>	56 (81.2)	4 (5.8)	6 (8.7)
<b>Cefazolin</b>	4 (5.8)	1 (1.4)	10 (14.5)
<b>Cefuroxime</b>	40 (58.0)	6 (8.7)	14 (20.3)
<b>Cefuroxime-Axetil</b>	26 (37.7)	6 (8.7)	8 (11.6)
<b>Cefixime</b>	29 (42.0)	0 (0)	0 (0)
<b>Cefotaxime</b>	39 (56.5)	1 (1.4)	10 (14.5)
<b>Ceftazidime</b>	9 (13.0)	0 (0)	0 (0)
<b>Ceftriaxone</b>	52 (75.4)	3 (4.3)	13 (18.8)
<b>Cefoperazone-sulbactam</b>	54 (78.3)	2 (2.9)	1 (1.4)
<b>Cefepime</b>	60 (87.0)	0 (0)	6 (8.7)
<b>Aztreonam</b>	34 (49.3)	1 (1.4)	4 (5.8)
<b>Ertapenem</b>	50 (72.5)	0 (0)	1 (1.4)
<b>Imipenem</b>	58 (84.1)	2 (2.9)	3 (4.3)
<b>Meropenem</b>	15 (21.7)	0 (0)	0 (0)
<b>Amikacin</b>	68 (98.6)	0 (0)	0 (0)
<b>Gentamicin</b>	61 (88.4)	1 (1.4)	6 (8.7)
<b>Ciprofloxacin</b>	30 (43.5)	1 (1.4)	5 (7.2)
<b>Levofloxacin</b>	47 (68.1)	16 (23.2)	5 (7.2)
<b>Oflloxacin</b>	31 (44.9)	0 (0)	4 (5.8)
<b>Tetracycline</b>	7 (10.1)	1 (1.4)	4 (5.8)
<b>Oxacillin</b>	4 (5.8)	0 (0)	0 (0)
<b>Moxifloxacin</b>	4 (5.8)	0 (0)	0 (0)
<b>Tigecycline</b>	56 (81.2)	0 (0)	0 (0)
<b>Minocycline</b>	16 (23.2)	13 (18.8)	10 (14.5)
<b>Colistin</b>	0 (0)	39 (56.5)	1 (1.4)
<b>Fosfomycin</b>	35 (50.7)	0 (0)	3 (4.3)
<b>Cefaclor</b>	0 (0)	0 (0)	5 (7.2)
<b>Nitrofurantoin</b>	28 (40.6)	15 (21.7)	7 (10.1)
<b>Ticarcillin clavulanic</b>	0 (0)	0 (0)	1 (1.4)
<b>Norfloxacin</b>	4 (5.8)	0 (0)	0 (0)
<b>Tobramycin</b>	4 (5.8)	0 (0)	0 (0)
<b>Doxycycline</b>	0 (0)	0 (0)	2 (2.9)
<b>Trimethoprim-Sulpamethoxazole</b>	52 (75.4)	0 (0)	16 (23.2)

**Table 3: Antimicrobial sensitivity pattern of *Acinetobacter* species (n=12).**

Drugs	Sensitive No. (%)	Intermediate No. (%)	Resistant No. (%)
<b>Ampicillin/Sulbactam</b>	2 (16.7%)	0 (0)	0 (0)
<b>Piperacillin-Tazobactam</b>	9 (75.0)	0 (0)	1 (8.3)
<b>Cefazolin</b>	0 (0)	0 (0)	4 (33.3)
<b>Cefuroxime</b>	0 (0)	0 (0)	2 (16.7)
<b>Ceftriaxone</b>	7 (58.3)	3 (25.0)	1 (8.3)
<b>Cefoperazone-sulbactam</b>	9 (75.0)	0 (0)	0 (0)
<b>Cefepime</b>	8 (66.7)	1 (8.3)	0 (0)
<b>Aztreonam</b>	0 (0)	0 (0)	2 (16.7)
<b>Ertapenem</b>	1 (8.3)	0 (0)	0 (0)
<b>Imipenem</b>	10 (83.3)	0 (0)	0 (0)
<b>Meropenem</b>	2 (16.7)	0 (0)	0 (0)
<b>Amikacin</b>	7 (58.3)	0 (0)	0 (0)
<b>Gentamicin</b>	12 (100)	0 (0)	0 (0)
<b>Ciprofloxacin</b>	4 (33.3)	1 (8.3)	0 (0)
<b>Levofloxacin</b>	10 (83.3)	0 (0)	0 (0)
<b>Tetracycline</b>	1 (8.3)	0 (0)	1 (8.3)
<b>Tigecycline</b>	7 (58.3)	0 (0)	0 (0)
<b>Minocycline</b>	7 (58.3)	0 (0)	0 (0)
<b>Colistin</b>	0 (0)	2 (16.7)	0 (0)
<b>Cefaclor</b>	0 (0)	0 (0)	2 (16.7)
<b>Trimethoprim-Sulpamethoxazole</b>	9 (75.0)	0 (0)	2 (16.7)

**Table 4: Antimicrobial sensitivity pattern of *Pseudomonas* species (n=9).**

Drugs	Sensitive No. (%)	Intermediate No. (%)	Resistant No. (%)
<b>Ampicillin/Sulbactam</b>	0 (0)	0 (0)	4 (44.4)
<b>Cefazolin</b>	0 (0)	1 (11.1)	5 (55.6)
<b>Cefotaxime</b>	0 (0)	0 (0)	4 (44.4)
<b>Ceftriaxone</b>	4 (44.4)	0 (0)	1 (11.1)
<b>Cefoperazone-sulbactam</b>	6 (66.7)	0 (0)	1 (11.1)
<b>Cefepime</b>	9 (100)	0 (0)	0 (0)
<b>Imipenem</b>	9 (100)	0 (0)	0 (0)
<b>Meropenem</b>	2 (22.2)	0 (0)	0 (0)
<b>Amikacin</b>	8 (88.9)	1 (11.1)	0 (0)
<b>Gentamicin</b>	8 (88.9)	1 (11.1)	0 (0)
<b>Ciprofloxacin</b>	6 (66.7)	1 (11.1)	0 (0)
<b>Levofloxacin</b>	7 (77.8)	0 (0)	1 (11.1)
<b>Ofloxacin</b>	4 (44.4)	0 (0)	0 (0)
<b>Tetracycline</b>	2 (22.2)	0 (0)	0 (0)
<b>Tigecycline</b>	1 (11.1)	0 (0)	6 (66.7)
<b>Minocycline</b>	1 (11.1)	0 (0)	2 (22.2)
<b>Colistin</b>	0 (0)	4 (44.4)	0 (0)
<b>Cefaclor</b>	0 (0)	0(0)	4 (44.4)
<b>Trimethoprim-Sulpamethoxazole</b>	3 (33.3)	0(0)	2 (22.2)



**Figure 1: Antimicrobial sensitivity pattern of ESBL producing organisms (n=8).**

Isolates of *Acinetobacter* spp. were resistant to cefazolin (33.3%), cefuroxime (16.7%), trimethoprim (16.7%), cefaclor (16.7%), and aztreonam (16.7%). However, all isolates of *Acinetobacter* spp. were sensitive to gentamycin (100%) followed by levofloxacin (83.3%) and imipenem (83.3%) (Table 3). Regarding *Pseudomonas* spp., they were resistant to tetracycline (66.7%), cefazolin (55.6%), cefaclor (44.4%), cefotaxime (44.4%) and ampicillin/sulbactam (44.4%) whereas 100% of them showed sensitivity to cefepime and imipenem (Table 4).

Out of 106 isolates, 17 isolates (16%) were found to be indicative of presumably ESBL producers and testing of ESBL production was done by phenotypic confirmatory test. Eight isolates (7.5%), 6 isolates from hospitals and 2 isolates from community drains, were identified as confirmed ESBL producers which were 4 *Escherichia coli* and 4 *Klebsiella pneumoniae* isolates. Among ESBL producers, 62.5% of them were resistant to cefuroxime, cefuroxime-axetil, cefotaxime, ceftriaxone and

minocycline while 100% of them were sensitive to ertapenem, imipenem and amikacin (Figure 1). No ESBL producer was detected from poultry farms and aquacultures.

Among the isolated organisms, one carbapenem resistant *Enterobacteriaceae* (*Escherichia coli*) was detected from one hospital site where there was no proper treatment plant. It was resistant to many antibiotics tested but sensitive to amikacin, tigecycline and cefaclor. All poultry farms used to add antibiotics and vitamin supplements to animal feed according to the prescription of veterinarian. Wastewater from all poultry farms and aquacultures disposed into nearby water body.

## DISCUSSION

Among 106 isolates identified in this study, antibiotic resistant isolates of hospital environment origin were higher than non-hospital environment origin such as community drains, poultry farms and aquacultures. Similar trend was reported by Moges et al as hospital wastewater can contain many kinds of pollutants such as radioactive, chemical and pharmaceutical wastes and also pathogenic microorganisms and can be hazardous to public health and ecological balance.<sup>17,18</sup> Isolates of *Enterobacteriaceae* (*Escherichia coli* and *Klebsiella* spp.) were most frequently identified and followed by *Acinetobacter* spp. and *Pseudomonas* spp. More gram-negative organisms were isolated than gram positive organisms in this study. Many studies supported this finding.<sup>9,17,19</sup> Gram negative bacteria are the most common causes of hospital and community acquired infections and of particular concern because these organisms are inherently resistant to many antibiotics.

The use, misuse and underuse of antibiotics are responsible for resistance development to antimicrobials worldwide. Although high proportions of resistance to 3rd generation cephalosporins have been reported for *Escherichia coli* and *Klebsiella pneumoniae* in all WHO regions, few percentages of isolated *Enterobacteriaceae* in this study were resistant to 3rd generation cephalosporins however they were still highly sensitive to gentamycin, tetracycline and imipenem.<sup>9</sup> Isolates of *Acinetobacter* spp., mostly recovered from hospital sites and common drains, were resistant to cefazolin, cefuroxime and trimethoprim. Nevertheless, all isolates of *Acinetobacter* spp. were sensitive to gentamycin followed by levofloxacin and imipenem. *Acinetobacter* species are now emerging as important nosocomial pathogens and the emergence of carbapenamase and metallo beta lactamases producing *Acinetobacter* species is becoming a therapeutic challenge.<sup>15</sup> The resistant pattern of *Pseudomonas* species, frequently isolated from hospital origin, for ciprofloxacin and gentamycin was lower in the present study, 11.1%. This was contradicting from other study done in Nigeria where the resistance to ciprofloxacin and gentamycin were 80% and 70% respectively.<sup>20</sup>

Out of 40 wastewater samples, 8 isolates (4 *Escherichia coli* and 4 *Klebsiella pneumoniae*) recovered from hospital sites and community drains were confirmed as ESBL producers. This finding is consistent with a study undertaken in Brazil mentioned that the most common ESBL producers in hospital wastewater were *Klebsiella pneumoniae*, *Enterobacter cloacae* and *Escherichia coli*.<sup>21</sup> ESBL producing organisms in this study were 100% sensitive to Carbapenems. Carbapenems are regarded as the drugs of choice in the treatment of severe infections caused by ESBL-producing organisms. However, carbapenem resistance has been increasingly reported in many countries recently.<sup>22</sup> One carbapenem resistant *Enterobacteriaceae* (*Escherichia coli*) was also detected from one hospital site where there was no proper treatment plant. Carbapenem resistant *Enterobacteriaceae* are a serious public health threat since infections due to these organisms are associated with significant morbidity and mortality.

WHO recommend that hospitals have onsite facilities for the pre-treatment of hospital effluent prior to its release into the general wastewater stream in order to eliminate the presence of hazardous components including microbiological pathogens, radioactive drugs, toxic chemicals and antibiotic residue.<sup>23</sup> Unfortunately, due to high-cost and operational challenges associated with onsite treatment of hospital effluent, progress on this issue has been slow in many countries.<sup>24</sup> Not all hospitals in this study have proper treatment plant and hospital effluent is generally released untreated into the urban wastewater stream for treatment at an urban wastewater treatment plant prior to discharge into the environment. The prime focus of urban wastewater treatment is to eliminate organic and inorganic contaminants; however, it is not designed to eliminate antibiotic residues or antimicrobial resistant bacteria. Hence, drug resistance to commonly used antibiotics was higher in hospital environment and community drains than other sites. On the top of that like other developing countries, antibiotics are available to the public as over a counter in Myanmar and thus people may practice self-medication and further increase the prevalence of drug resistant strains.

Neither ESBL producers nor Carbapenemase producers was detected from samples collected from poultry farms and aquacultures, this may be due to usage of antibiotics at these sites were according to the prescription of veterinarian avoiding misuse and overuse. The results of present study evidenced that the clinically important pathogens are present in hospital wastewater which is likely to dispose into the public drains either treated properly or untreated. The proportion of antibiotic resistant bacteria are higher in hospital wastewater than other sites. Hence proper treatment plant for hospital wastewater should be installed and sustainability of the treatment facilities should be maintained. To address the AMR phenomenon effectively, One Health approach has been taking into account through multidisciplinary collaboration between human health, animal health and the

environment. The findings of recent study could provide the baseline data of the magnitude of drug resistance pathogens in diversity of waste water in Yangon Region for the development of the national AMR monitoring plan on One Health perspective and prevention and control of AMR in Myanmar.

## CONCLUSION

The proportion of antibiotic resistant bacteria are higher in hospital wastewater than other sites. Hence proper treatment plant for hospital wastewater should be installed and need to mitigate antibiotic resistance with a 'one-health' approach.

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*Ethical approval: The study was approved by the University of Public Health-Institutional Review Board*

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