



Monitoring of antimicrobial resistance in hospital, municipal, and treated wastewater in Mbarara, Uganda

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ABSTRACT

Objective: The aim of this study was to estimate the prevalence of antimicrobial resistance in the population of Mbarara through analysis of wastewater and determine the effectiveness of wastewater treatment in reducing discharge of antibiotic-resistant bacteria and antibiotic resistance genes into the environment.

Methods: Hospital, municipal, and treated wastewater (collected on 10 different dates) from Mbarara, Uganda, were analysed for extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli* using a culture-based method and selected clinically relevant antibiotic resistance genes using quantitative PCR.

Results: The finding of this study demonstrated that 30.6% of the total *E. coli* were ESBL producers, constituting a high proportion compared to studies in other countries. Furthermore, the investigation revealed the widespread distribution of the carbapenemase gene *bla*_{CMY-2} within the population. The comparative study of the inflow and outflow of the waste stabilisation pond system, which is used for wastewater treatment, demonstrated a log reduction of 1.9–2.4 for coliform bacteria and total as well as ESBL-producing *E. coli*. Conversely, the wastewater treatment was associated with an increase of the antibiotic resistance genes *sul1* and *tetC*.

Conclusions: The study shows that the waste stabilisation pond system is releasing significant amounts of coliform bacteria, *E. coli*, ESBL-producing *E. coli*, somatic bacteriophages, and antibiotic resistance genes into the Rwizi River. We also demonstrated that wastewater-based surveillance is a cost-effective method of obtaining information on the prevalence of AMR in the population, especially in countries where clinical surveillance is limited due to a lack of resources and infrastructure.

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1. Introduction

The extensive application of antibiotics in human and veterinary medicine, as well as in agriculture and animal husbandry, has led to the proliferation of antibiotic-resistant bacteria (ARB) and antibiotic-resistant genes (ARGs). The problem of AMR, which is inextricably linked to the use of antibiotics, compromises the effectiveness of available treatments for infectious diseases and poses a growing threat to human and animal health [1]. Furthermore, sub-Saharan Africa is expected to have the highest rates of AMR [2].

In 2015, the World Health Assembly adopted a resolution that committed to the development of (NAPs) for AMR in all UN member states [3]. Adoption of such action plans in sub-Saharan Africa has been slow [4]. A 2019 report to the Secretary General of the United Nations [5] emphasised the importance of better antibiotic stewardship in humans and animals in combating the rise of AMR, acknowledging the role of the environment. On the one hand, the environment can spread registered antibiotic-resistant pathogens; on the other, it can lead to the development and spread of resistance mechanisms [6].

The dissemination of ARB and ARGs in aquatic environments is predominantly attributed to wastewater from hospitals, municipal sewage treatment facilities, and wastewater from meat-producing and meat-processing industries [7]. The nutrient-rich wastewater is characterised by a high bacterial diversity and density, as well as therapeutic and sub-therapeutic concentrations of antibiotics and

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other environmental pollutants, such as biocides and heavy metals [7]. This combination is thought to promote the selection or co-selection of ARB and the transfer of genetic material between bacteria [8–10]. It has been shown that wastewater from health-care settings (e.g. hospital wastewater) contains a different spectrum of antibiotics and a higher level of AMR compared to municipal wastewater [11,12]. Conventional wastewater treatment (mechanical + biological treatment) has limited efficacy in removing micropollutants, hygienically relevant bacteria, ARB, and ARGs [7]. Consequently, wastewater treatment plants have been found to release these pollutants into the aquatic environment, thus being considered as hotspots for AMR development and spread [13,14].

While 75% and 71% of household wastewater is treated safely in North America and Europe, respectively, less than 30% is treated safely in Africa [15]. In Uganda, for example, only 4% of domestic wastewater is treated safely [15]. Uganda is a country facing significant challenges, including a low Gross Domestic Product and a substantial influx of refugees, leading to population growth and conflicts over land and resources. The management of water resources and the implementation of affordable and effective water treatment systems are crucial for African low- and middle-income countries (LMICs) to improve water quality and access to clean water. Waste stabilisation ponds (WSPs) play an important role in this context as they are the simplest form of wastewater treatment and a cost-effective biological treatment method [16]. Although studies have demonstrated the wide distribution of clinically relevant ARB and ARGs in wastewater and surface water in Africa [17,18], information on removal by treatment in WSPs is lacking. A WSP system in eastern Ethiopia achieved removal rates of 1.74–2.57 log levels of faecal indicator bacteria, and isolated indicator bacteria were resistant to several antibiotics, but the removal of these ARB by the treatment was not quantified [19].

On the other hand, wastewater can also provide a relatively unbiased estimate of AMR circulating in the population [20]. Wastewater-based surveillance is therefore a cost-effective tool for monitoring the spatio-temporal AMR patterns. One major advantage is that it circumvents the practical and legal problems associated with public health surveillance based on testing of patient samples [21]. AMR surveillance is essential to monitor trends and identify targeted interventions. There is evidence that LMICs, such as Uganda, are disproportionately affected by the burden of AMR-related morbidity and mortality [1]. However, the data situation in these countries is relatively patchy, highlighting the need to improve surveillance systems in LMICs.

This study examined wastewater and a wastewater treatment system in Mbarara, Uganda, to understand the occurrence of AMR determinants and their removal. It focused on the River Rwizi, a major water source used for drinking water production, and analysed extended-beta-lactamase-producing *Escherichia coli* and selected ARGs as indicators. It is anticipated that the work presented will inform future efforts to treat wastewater and monitor the treatment efficiency as a human and animal health risk associated with the introduction of resistance determinants into the environment.

2. Materials and methods

2.1. Sampling points and sampling campaigns

The study was carried out in Mbarara city, in the south-western part of Uganda. The city is situated in hilly terrain separated by short, small, and shallow valleys, with a total area of about 52 km² [22]. The region experiences two rainy seasons (March to May and September to November), with November and April being the months with the highest precipitation [23]. The Rwizi River, with a length of approximately 55 km, originates in the hilly regions and

traverses districts and the city of Mbarara before discharging into Lake Victoria. The river catchment area covers an area of approximately 8000 km².

Mbarara is a densely populated city with a population of about 200 000. Pollution along Rwizi's banks comes from farming, brick-laying, open defecation, and littering, with the most significant sources being industries, hotels, and educational institutions [24].

Mbarara Regional Referral Hospital is a government-owned referral and teaching hospital serving as a referral centre for south-western Uganda. It provides medical services to a population of over 6.5 million and has over 600 beds. Wastewater from the hospital is directed into the Katete WSPs, and effluent from these is discharged into the Rwizi River at a rate of 200 m³/d.

A total of 10 sampling campaigns were conducted in Mbarara between June 2022 and July 2023. Wastewater samples were obtained from the Mbarara Regional Referral Hospital and a WSP Katete. Samples were transferred to sterile 1 L bottles and transported to the laboratory on ice. Coliforms, *E. coli*, and extended-spectrum beta-lactamase (ESBL) *E. coli* were detected within 24 h, and somatic coliphages within 48 h.

The 10 sampling campaigns were distributed over a 1-y period, with samples collected approximately every 2 months. Additional campaigns were conducted during visits by German collaborators in June and November 2022 and July 2023, when laboratory training and quality assurance activities took place. Weather data from Mbarara on sampling days showed average temperatures between 18.9°C and 24.3°C and rainfall between 0 and 2.6 mm (0–5.3 mm on the previous day, see Table S1). A Kruskal–Wallis test revealed no significant differences in temperature or rainfall across sampling dates or seasons ($P \approx 0.43$), supporting the decision to analyse all data collectively.

2.2. Culture-based detection methods

2.2.1. Detection of faecal indicators

The quantification of total coliforms and *E. coli* was performed using the Colilert-18 and the Quanti-Tray 2000 (ISO 9308-2:2012) from IDEXX Laboratories, according to the manufacturer's instructions.

In addition, somatic coliphages as viral indicators were detected using double-layer plaque technique according to ISO 10705:2.

2.2.2. Antibiotic-resistant bacteria

In this study, the focus was on the analysis of ESBL-producing *E. coli* as a model for ARB. These bacteria are a target for One Health AMR surveillance due to their long-standing use in environmental monitoring and the function of *E. coli* as an indicator of faecal contamination in water and food [25].

ESBL *E. coli* was detected using a clinical method based on a selective antibiotics-containing chromogenic medium adapted for environmental use [26]. Depending on the expected bacterial concentration, different sample volumes were concentrated by vacuum filtration on a cellulose nitrate filter with a pore size of 0.45 μm (Millipore). After filtration, the membrane was applied to a selective and differential CHROMagar ESBL medium (MAST Diagnostica) and incubated at 42°C ± 1°C for 24 ± 3 h. Pink colonies classified as ESBL *E. coli* were verified by typical growth at 37°C ± 1°C overnight on Chromocult Coliform agar (Merck). Positive (ESBL *E. coli* CIP 103982) and negative (*E. coli* ATCC25922) controls were performed prior to the use of each new batch of culture media.

2.3. PCR-based detection of antibiotic resistance genes

2.3.1. Sample concentration and DNA extraction

For PCR-based analysis, water samples were filtered through a cellulose ester membrane filter with a diameter of 45 mm and a

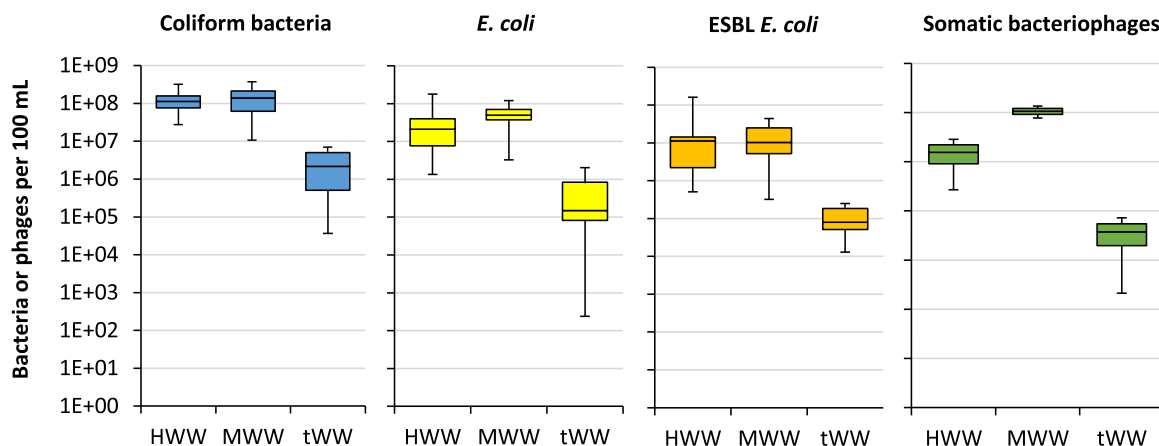


Fig. 1. Coliform bacteria, *Escherichia coli*, extended-spectrum-beta-lactamase-producing *E. coli*, and somatic bacteriophages in hospital wastewater (HWW), municipal wastewater (MWW), and treated wastewater (tWW) in Mbarara.

pore size of 0.45 μm (SO-PAK, Millipore) using a vacuum filtration unit. The volume filtered varied between 20 and 100 mL. The filters were placed in 5 mL tubes containing 0.5 mL GITC buffer (5 M guanidine thiocyanate, 100 mM EDTA [pH 8.0], and 0.5% sarkosyl) and stored at -20°C until DNA extraction. Subsequent DNA extraction was performed using the QIAamp DNA Blood Mini Kit (QIAGEN) according to the manufacturer's instructions with modifications as previously reported [27]. The modifications include the addition of 700 μL QIAGEN AL buffer to the filter membranes and the omission of the proteinase K step. DNA extracts were transferred to Germany and stored at -20°C until PCR analysis.

2.3.2. Quantification of antibiotic resistance genes by real-time PCR analysis

In total, 6 different genes were selected and analysed by real-time quantitative PCR: sulphonamide resistance gene *sul1*, beta-lactamase genes *bla*_{TEM}, *bla*_{CMY-2}, and *bla*_{OXA-48}, tetracycline resistance gene *tetC*, colistin resistance gene *mcr-1*, and the bacterial 16S rRNA gene. With *sul1* and *tetC*, two resistances were selected that are ubiquitous and occur in high abundance, which is advantageous for measuring the removal capacity in the WSP system. On the other hand, the beta-lactamase genes and the colistin resistance gene *mcr-1* are of more interest in terms of wastewater-based epidemiology.

The specific primer sequences and annealing temperatures used in this study are listed in the Supplementary Material. The qPCR assays were performed using Rotor-Gene Q instruments (Qiagen) and SsoAdvanced SYBR Green Supermix (BioRad). Each reaction mixture had a final volume of 10 μL and included 400 nM of forward and reverse primer, 5 μL of 2 \times Sso Supermix, and 1 μL of sample DNA or standard with known target concentration. The temperature profile was as follows: (1) initial denaturation and enzyme activation at 95°C for 2 min, (2) 45 cycles of 98°C for 20 s, 60°C – 68°C (see Table S2, Supplementary Material) for 20 s, and 72°C for 20 s at primer, and (3) melting curve analysis.

All samples were measured in both undiluted and diluted (1:10) form to detect inhibitory effects. All reactions were performed in technical duplicates, along with negative and positive controls. Standard curves were generated using serial dilutions of known amounts of linearised plasmid containing the target genes (positive control). Data obtained from each of the above assays were analysed using Rotor-Gene Q series software (Qiagen), with the following parameter settings: Dynamic tube normalisation was set to 'on'; noise slope correction was set to 'on'; the first cycle was set to 'ignore'; and outlier removal was set to 10%. For quality assur-

ance reasons, only runs with R_2 values >0.990 and efficiencies between 90% and 105% were considered, and amplicon length was confirmed by automated capillary gel electrophoresis using the QIAxcel system (Qiagen). The limit of quantification for the different assays was 10 gene copies per μL DNA extract.

2.4. Statistical methods

Statistical analyses were performed using Python (version 3.12.4), with the SciPy module (version 0.9.0) for statistical testing and Seaborn (version 0.13.2) for data visualisation. Normality of the measurement datasets was assessed using the Shapiro-Wilk test, which indicated that most datasets were not normally distributed ($P < 0.05$). Consequently, non-parametric methods were applied to evaluate statistically significant differences between sample groups. The Kruskal–Wallis test was used to assess overall differences between sample groups. Where statistically significant differences were observed ($P < 0.05$), Dunn's post hoc test was applied to identify pairwise differences between sample types. Statistical significance was defined as $P < 0.05$.

3. Results

3.1. Indicator bacteria, ARB, and bacteriophages

Faecal indicator counts were similar in hospital and municipal wastewaters and ranged from 1.0×10^7 to 4.8×10^8 coliforms and 1.4×10^6 to 1.8×10^8 *E. coli* per 100 mL (Fig. 1). Counts in the effluent of the WSPs were lower ranging between 3.7×10^4 and 6.4×10^6 coliforms and 2.4×10^2 and 2.1×10^6 *E. coli*/100 mL (Fig. 1). The concentration of somatic bacteriophages was found to be 1.6×10^5 , 1.1×10^6 and 3.8×10^3 median values per 100 mL for hospital wastewater, municipal wastewater, and treated wastewater, respectively. These values are approximately 2–3 log levels lower than the median values of faecal indicator bacteria. The culture methods also demonstrate the presence of active ESBL-producing *E. coli* bacteria in both raw wastewater (hospital and municipal, 3.2×10^5 – 1.6×10^8 per 100 mL) and treated wastewater (1.3×10^4 – 2.5×10^6 per 100 mL). Statistical analysis revealed significant differences in the levels of coliform bacteria, *E. coli*, and ESBL-producing *E. coli* between hospital wastewater and treated wastewater, as well as between municipal wastewater and treated wastewater (Fig. S1).

The proportion of ESBL-producing bacteria in the total *E. coli* bacteria was found to range from 26% to 37% across all samples (see Fig. 2).

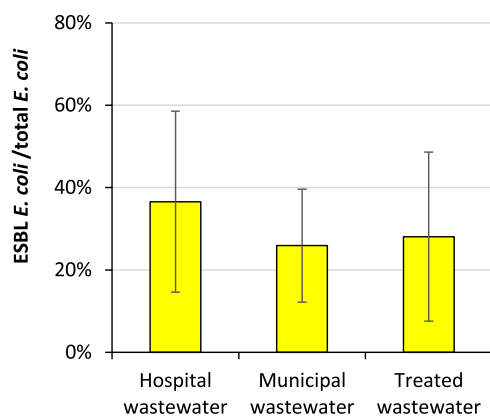


Fig. 2. Ratio of extended-spectrum-beta-lactamase-producing *Escherichia coli* to total *E. coli* in hospital wastewater, municipal wastewater, and treated wastewater.

3.2. Antibiotic resistance genes

In addition to the presence of ESBL-producing *E. coli*, the study also examined the presence of selected ARGs in the samples. The four ARGs *sul1*, *bla_{TEM}*, *bla_{CMY-2}*, and *tetC* were detected in all samples examined, whereby the sulphonamide resistance gene *sul1* was present in the highest copy numbers in the raw wastewater samples, followed by the beta-lactamase/carbapenemase gene *bla_{CMY-2}* and the tetracycline resistance gene *tetC* (see Fig. 3 upper part). In addition, sporadic detections (above the limit of quantification) for the carbapenemase gene *bla_{OXA-48}* and the colistin resistance gene *mcr-1* were found in both the wastewater and the treated wastewater. The relative abundance of the selected ARGs was determined by detecting conserved regions of the bacterial 16S rRNA gene (see Fig. 3, bottom) and calculating the ARG to 16S ratio. Gene copy numbers for the 16S rRNA gene were on average 6.1×10^6 per mL for the hospital wastewater, 3.1×10^7 per mL for the municipal wastewater, and 8.2×10^7 per mL for the treated wastewater. The determination of relative abundances shows a higher ratio for the beta-lactamase genes *bla_{TEM}* and *bla_{CMY-2}* in clinical wastewater compared to municipal wastewater. In addition, a decrease in relative abundance was also observed for these two genes due to the wastewater treatment process in the WSPs. This was not the case for the *sul1* and *tetC* genes.

Statistical analysis revealed a significant difference in the absolute abundance of the resistance gene *sul1* between untreated (hospital and municipal) and treated wastewater (Fig. S2). For *bla_{TEM}*, a significant difference in absolute abundance was observed only between hospital wastewater and treated wastewater. In the case of *bla_{CMY-2}*, a significant difference between these two groups was found only in terms of relative abundance. No significant differences were observed for *tetC* across the three wastewater types. Overall, these results indicate that for three out of the four investigated genes, statistically meaningful differences between sample groups were detected.

3.3. Reduction by wastewater treatment

Log reduction values were determined to better assess the removal performance of the WSP system for various microbiological parameters (see Table 1). The highest log reduction was observed for somatic coliphages (2.92). The log reduction values for bacteria detected by culture methods ranged from 1.88 (coliforms) to 2.42 (*E. coli*). In contrast, the log reduction values for the beta-lactamase genes *bla_{TEM}* and *bla_{CMY-2}* were 0.57 and 0.01, respectively. For the *sul1* and *tetC* resistance genes, negative log reduction values of -1.57 and -1.64 were found.

Table 1

Log reduction values for different microbiological parameters by wastewater treatment in Mbarara.

Parameter	Log reduction value
Coliform bacteria	1.88 ± 0.68
<i>Escherichia coli</i>	2.42 ± 1.11
ESBL <i>E. coli</i>	1.97 ± 0.76
Somatic phages	2.92 ± 0.64
Bacterial 16S rRNA gene	-0.51 ± 0.58
Sulphonamide resistance gene <i>sul1</i>	-1.57 ± 0.46
Tetracycline resistance gene <i>tetC</i>	-0.64 ± 0.98
Beta-lactamase gene <i>bla_{TEM}</i>	0.57 ± 0.73
Beta-lactamase gene <i>bla_{CMY-2}</i>	-0.01 ± 0.60

4. Discussion

Our results indicate that ESBL-producing *E. coli* are present in the wastewater of Mbarara, and therefore in the local population of this town, at much higher levels than is the case in high-income countries. Median concentration of ESBL-producing *E. coli* is 7.3 log CFU per 100 mL compared to 4.0–5.5 log CFU per 100 mL found in Germany [28], Switzerland [29], the Netherlands [13], Spain [30], or Northern CO, USA [31]. Furthermore, the median proportion of ESBL-producing *E. coli* relative to total *E. coli* in Mbarara at 30.6% was considerably higher than the range from 1.2% to 5.2% found in Denmark, Finland, Norway, Belgium, France, Germany, Greece, Italy, Spain [32], the Netherlands [13], and Switzerland [29].

Although our results are higher than those reported in Europe, they are consistent with findings from other African countries [33,34]. Gumede et al. [34] analysed wastewater from a district in South Africa and found resistance rates to first- and second-generation cephalosporins (cephalexin, cephalothin and cefuroxime), third- and fourth-generation cephalosporins (ceftazidime, cefepime, cefixime, and cefotaxime), and carbapenems (imipenem and meropenem) of 63%–68%, 20%–56%, and 15%, respectively. Similarly, Gomi et al. [33] detected resistance to cefotaxime and the combination of cefotaxime, ciprofloxacin, and gentamicin in 39.2% and 5.1% of 90 *E. coli* isolated from wastewater in Kampala, Uganda.

The presence of ESBL genes, which can also confer resistance to carbapenems, and the colistin resistance gene *mcr-1* are of particular importance, as both carbapenems and colistin are last resort antibiotics reserved for use in difficult-to-control infections. While the *bla_{CMY-2}* gene was present in all raw wastewater samples in a concentration range of 3.7–6.3 log gene copies per mL, *bla_{OXA-48}* and *mcr-1* were only detected in a few samples (30% and 10% respectively). This study indicates that the *bla_{CMY-2}* beta-lactamase gene is widespread in the Ugandan population, consistent with a previous study on the prevalence of plasmid-mediated AmpC beta-lactamases in *Enterobacteriaceae* isolated from urban and rural populations in Uganda [35].

Although the fact that only one representative of ARB and a very limited spectrum of ARG were examined in this study, important findings on the spread of AMR in the population of Mbarara were obtained. This is particularly significant given the lack of data on AMR in LMICs like Uganda. Our results confirm the value of wastewater monitoring in settings where clinical surveillance of AMR may not be practical. Despite concerns that AMR bacteria could be selected for in the environment, the balance of evidence is that AMR presence in the environment is largely due to human faecal pollution [36].

There was little difference between concentrations of coliforms, *E. coli*, and ESBL *E. coli* in untreated hospital and municipal wastewater. Somatic bacteriophages were detected in higher concentrations in municipal wastewater. Even though there was little difference in the concentration of ESBL *E. coli* between hospital and

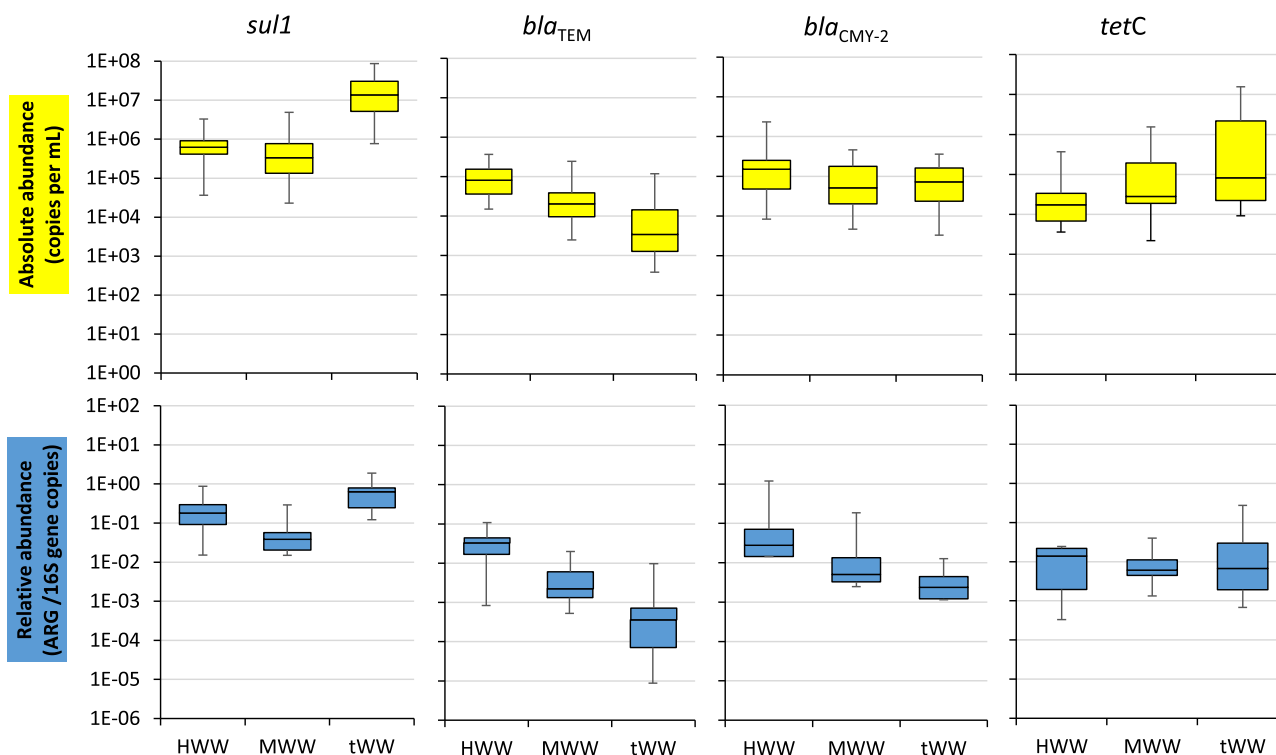


Fig. 3. Absolute and relative abundance of antibiotic resistance genes in hospital wastewater (HWW), municipal wastewater (MWW), and treated wastewater (tWW).

municipal wastewaters, both the absolute and relative presence of ARGs tended to be a little higher in hospital wastewaters.

Wastewater treatment by WSPs in Mbarara reduced the concentration of coliforms, *E. coli*, and ESBL *E. coli* by 1.9–2.4 log and somatic bacteriophages by 2.9 log. However, the proportion of *E. coli* producing ESBL did not change significantly with treatment. In other studies of full-scale WSP systems in Africa, Asia, America and Europe, significantly higher removal efficiencies could be determined [37,38]. For systems consisting of anaerobic, facultative, and maturation ponds, log removal efficiencies of 3–6 for bacteria and 2–4 for viruses are generally assumed [16]. The analysis revealed suboptimal bacterial removal efficiency, with decreased pathogen elimination rates indicating compromised treatment system performance. This reduction in efficiency can be attributed to inadequate maintenance procedures, stemming from insufficient operational oversight and monitoring protocols.

Comparing the bacterial removal rates with those of the ARGs shows that these genes are hardly reduced (*bla*_{TEM}) or even increase during the treatment process (*bla*_{CMY-2}, *tetC*, and *sul1*). Quantitative analyses of the 16S rRNA gene show that the total number of bacteria also increases by 0.4 log during the treatment process. While PCR data do not differentiate whether ARGs originate from viable or non-viable bacteria, nor whether they are present as free DNA or within bacteriophages, it is important to note that DNA extracts were obtained following bacterial enrichment via membrane filtration. Therefore, the detected ARGs are unlikely to be present as extracellular or phage-associated DNA. The differing behaviours of the ARGs in the Mbarara wastewater treatment are probably due to the bacteria in whose genomes the ARGs are present. For instance, the prevalence of lactamase-producing *Enterobacteriaceae* carrying genes such as *bla*_{TEM} is reduced by 2–3 log in WSPs. In contrast, *sul1* and *tetC* are among the most prevalent ARGs in wastewater and environmental samples and are frequently associated with environmental bacteria such as *Pseudomonas* spp. These bacteria are known for their resilience and ability to proliferate in nutrient-rich conditions, such as those

found in WSPs [39]. Furthermore, these genes are frequently located on mobile genetic elements, such as plasmids, integrons, and transposons. These mechanisms facilitate horizontal gene transfer between bacteria [40]. To date, there has been a paucity of research on the behaviour and removal of ARGs in WSP systems. A recent study using a metagenomic approach to compare the occurrence and fate of ARGs between a pond system in Namibia and a wastewater treatment plant in Germany also showed an increase in the relative abundance of the *tet* group in the Namibian treatment plant [17]. Overall, the findings of the present study demonstrate that the discharge of WSPs results in the release of elevated concentrations of coliform bacteria, total *E. coli*, ESBL-producing *E. coli*, ARGs, and somatic coliphages into the Rwizi River.

The risk to public health posed by the presence of high levels of ESBL *E. coli* and ARGs in wastewater, as found in our study, is uncertain. There is evidence to suggest that swimming in polluted waters may increase risk of carrying AMR bacteria [41,42]. It is highly probable that the ingestion of water or swimming in the rivers surrounding Mbarara that have been impacted by wastewater would pose a significant risk to human health. More generally, however, the relative contribution of environmental exposure to the burden of AMR disease is not yet well understood, and there are significant knowledge gaps in this area. A recent modelling study based on data from Thailand suggested that controlling human antibiotic use would be the most effective intervention [43]. As we have shown, the WSP system reduced bacterial contamination, including ARB, by a factor of 1–3 log levels and thus reduced the risk of infection, with or without ARB, for bathers in wastewater-impacted surface waters. Nevertheless, ARB, ARGs, and antibiotic residues are released to the aquatic environment with treated wastewater [13,14].

5. Conclusions

Monitoring the removal efficiency of AMR determinants by wastewater treatment can indicate whether the system is oper-

ating optimally or whether steps should be taken to improve removal performance. This is particularly important because the release of AMR to the environment should be minimised to avoid adverse health effects to humans and animals that have contact with the waters into which the effluent is discharged.

The present study has demonstrated the widespread distribution of ESBL and ARGs in the Mbarara population of Uganda. Our results suggest that AMR is much more common in Uganda, and probably much of Africa, than would be the case in higher-income countries. Such high levels of resistance pose a significant threat to public health in Africa. Reducing the burden of AMR in Africa should be a top priority. As reported here, wastewater monitoring could be an important component of national strategic plans for AMR in African settings.

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Declaration of competing interests: None declared.

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Ethical approval: Not required.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.jgar.2025.09.002](https://doi.org/10.1016/j.jgar.2025.09.002).

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