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Isolation and identification of pathogenic bacteria present in wastewater effluents discharged into Lake Victoria at Mukuuba landing site, Wakiso district, Uganda. A cross-sectional study.

Duluga Seldon[1], Kasozi James[1], Lujjibirwa Fortunate[1], Manowa Daniel[1], Wanambwa Wamono Herbert[1], Akena John Baptist[1], Situma Christopher[1], Oromocan Benjamin W[2], Ssentongo Vianney[1], Muzoora, Saphan[1], Kyosiimire Jacqueline[1], Sulwa Florence,[1] Nteziyaremye Jorome,[1] Akullo Mirriam,[2] Mabonga Habert[1,2,3*]
[1]Faculty of Health Sciences, University of Kisubi, Uganda
[2]School of Allied Health Sciences, Mengo Hospital Training Institute, Uganda
[3]Department of Allied Health Sciences, King College University, Uganda

Abstract

Background

Wastewater effluents discharged into Lake Victoria often contain pathogenic bacteria that threaten aquatic ecosystems and public health. This study aimed to isolate and identify the pathogenic bacteria present in wastewater effluents discharged into Lake Victoria at Mukuuba Landing Site, Wakiso District, Uganda.

Methodology

The study employed a descriptive, cross-sectional, laboratory-based design and quantitative methods. A total of 30 wastewater effluent samples, purposively selected, were described using standardized microbiological techniques. Microsoft Excel 2016 was used to analyze data.

Results

Citrobacter freundii was the most frequently isolated organism (75%), followed by Enterococcus faecalis (64.29%). Staphylococcus aureus and Escherichia coli accounted for 17.86%, while Klebsiella pneumoniae (10.71%) and Proteus mirabilis (7.14%) were the least amount isolated. 70% of isolates were Gram-negative rods consistent with enterics from fecal contaminant (pink bacilli in histological image). The remaining 30% were Gram-positive cocci (purple clusters or chains), suggestive of Staphylococcus and Enterococcus species, respectively.

Conclusion

Contamination of effluent water has the potential for serious public health risks, and there is a significant risk contribution from these bacteria in wastewater effluents.

Recommendation

There should be an ideal surveillance of environmental health programs at a national level, by the Ministry of Health, to put in place the appropriate action for public health in risk zones.

Keywords: Isolation and Identification, Pathogenic Bacteria, Wastewater Effluents, Lake Victoria, Mukuuba Landing Site, Wakiso District
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Corresponding Author: Mabonga Habert
Email: ***hmabonga@unik.ac.ug***
Faculty of Health Sciences, University of Kisubi, Uganda

Background of the study

Globally, wastewater treatment plants (WWTPs) are well known to be the real hotspots for microbial diversity, of which bacteria are dominant and reservoirs of many antimicrobial resistance genes (ARGs) (Zieliński et al., 2021). Antimicrobial resistance (AMR) is today a worldwide problem, which is caused by the excessive use of

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many different antibiotics in healthcare, agriculture, and also in veterinary practices. The One Health framework highlights the link between human, animal, and environmental health in tackling AMR (La Rosa et al., 2025).

In Africa, the growing population and also industrialization have resulted in a notable rise/increase in wastewater generation, which has an effect on Africa's water quality generally. The current wastewater treatment methods do fall reasonably short of these objectives, leading to significantly poor environmental and health outcomes as well as insufficient access to sanitary facilities and clean water needed for a healthy being (Omohwovo, 2024). The most affected are numerous vulnerable groups, such as women, children, and those with disabilities who reside in remote and rural areas without access to healthcare services within the African continent (Omohwovo, 2024). Approximately 319 million people in Sub-Saharan Africa do not have access to dependable drinking water sources, and 695 million lack access to improved sanitation facilities (Machado et al., 2022). The contamination of water sources mainly with bacterial pathogens is a vital public health challenge, which contributes substantially to the disease burden in the SSA regions (GBD 2021 Risk Factors Collaborators, 2024). Unsafe drinking water today is a key cause of diarrhoea, Bilharzia, Cholera, and so many of the water-borne diseases, which are so common in SSA, most of which are caused by pathogenic bacteria (Overgaard et al., 2021). Despite the existing efforts to enhance water access, 42% of the population in sub-Saharan Africa still do not have access to basic water supplies, which are defined as improved water sources within a 30-minute round trip (Kelly et al., 2021).

Multiple waterborne pathogens connected to human gastrointestinal diseases were found in the investigation. These pathogens were mostly linked to leaks at two locations along the wastewater channel that drains into Lake Victoria's natural waters in Uganda. According to the findings, at the time of sampling, the local wastewater treatment facility's capability for microbiological decontamination was really very insufficient. Concerns regarding the wetlands' suitability for urban agriculture were also being raised by the discovery of human pathogen contamination in a number of sites being studied (Schneeberger et al., 2019). However, the increasing discharge of untreated or inadequately treated wastewater into lakes such as Lake Victoria poses risks to public health and the ecosystem. This study aimed to isolate and identify the pathogenic bacteria present in wastewater effluents discharged into Lake Victoria at Mukuuba Landing Site, Wakiso District, Uganda.

Methodology

Study design

A cross-sectional study design using a quantitative technique was used to carry out this research study. The quantitative aspect of the study was conducted through the laboratory-based analysis of wastewater effluent samples collected from discharge points at Mukuuba Landing Site.

Study area

The selected location is around the Ugandan shores of Lake Victoria, particularly at the Mukuuba landing site in Katabi sub-county, Wakiso District, where wastewater effluents from various sources were dumped, and therefore, was the study's site.

Study population

This study consisted of the samples of Wastewater effluents that were being discharged into Lake Victoria at Mukuuba Landing Site, in Katabi sub-county, Wakiso District, from which the Pathogenic bacteria were isolated.

Sample size determination

A sample size of 30 for this study was chosen using the Central Limit Theorem (CLT), which states that the distribution of the sample means approximates a normal distribution as the sample size gets larger, regardless of the population's distribution.

Sampling technique

Convenient sampling was done during the selection of the water samples. A convenient sampling technique involves choosing samples that are easy for the researcher to reach and obtain the desired results.

Sampling procedure

Specific sampling points were chosen based on conveniently accessible wastewater discharge points at Mukuuba Landing Site. This site provided good representativeness of the effluent. Wastewater samples were collected in the morning, afternoon, and evening; therefore, the analysis reflected temporal changes in contamination. The sampling technique was a convenience technique, and 500 mL sterile bottles were used; the samples were drawn directly from the

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effluent discharge points into Lake Victoria. All specimens obtained were stored in a cool box at 4°C as soon as they were obtained and were transported to the laboratory within six hours post-collection for timely analysis. All sampling procedures were standardized to improve consistency and dependability, and allowed for a reliable assessment of patterns of antimicrobial susceptibility of the wastewater samples collected.

Data collection method

The wastewater effluent samples were collected directly from selected discharge points using sterile 500 mL bottles. From the laboratory, standard microbiological techniques were used to isolate and identify pathogenic bacteria from the samples. The antimicrobial susceptibility of the isolated and identified pathogenic bacteria was tested using the Kirby-Bauer disk diffusion method to determine resistance patterns. The feasibility and functionality of the wastewater treatment strategies were noted based on the lab findings of the sample collected on different sites, with the Mukuuba landing site. Data on bacterial growth, inhibition zones, and resistance profiles were recorded and analyzed to assess antimicrobial susceptibility trends in wastewater effluents at Mukuuba Landing Site.

Data collection tools

Samples were collected in sterile bottles from discharge points at Mukuuba landing site and processed in the lab using standard microbiological tools. Bacterial isolation and identification were performed, and antimicrobial susceptibility testing (AST) was conducted using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar. Inocula turbidity was standardized to 0.5 McFarland, and antibiotic-impregnated disks were applied to seeded plates, which were then incubated at 37 °C for 24 hours. Data on bacterial growth, inhibition zones, and resistance patterns were recorded for analysis.

Data collection procedure

Gathering of the water samples at various times of the day, where sterile 500 mL bottles were utilized to collect wastewater effluent samples from the specific discharge locations identified.

Regarding transportation as well as the preservation of the samples so as to preserve integrity, samples were kept in a cool box at 4°C and brought to the lab within six hours.

The isolation and identification of pathogenic bacterial colonies was acknowledged by their physical as well as their biochemical traits after the samples were cultured on different selective media within the lab.

Testing for the antimicrobial susceptibility inhibition zone diameters was measured using the Kirby-Bauer disk diffusion method, commonly done to identify patterns of bacterial resistance.

The recording of data was done using a recording sheet as well as computed using Microsoft Excel 2016 software to analyze the findings on bacterial growth and patterns of antibiotic susceptibility for additional examination.

Study variables

Independent Variables. Referring to this topic, these include wastewater effluent features, e.g, sampling location and time of collection, as well as bacterial species present.

Dependent Variables. Referring to this topic, these variables include antimicrobial susceptibility patterns, which were measured by the size of inhibition zones in the Kirby-Bauer disk diffusion test, and the presence or absence of bacterial resistance to specific antibiotics.

Quality control

Pre-Analytical Stage

There was pretesting of the research tools to refine sampling protocols as well as data collection instruments. There was training on proper sample handling to ensure accuracy and consistency by the research assistant. The samples were collected using sterile containers as well, and they shall be transported under controlled conditions, specifically using a cool box at 4 °C. Inclusion criteria, which include sites where wastewater effluents are being discharged, and exclusion criteria, which include sites where wastewater effluents are not discharged, will be strictly applied to maintain data reliability.

Analytical Stage

There were very strict SOPs to guide the researcher on bacterial isolation and identification, as well as susceptibility testing, when in the lab. The QC strains validated the antimicrobial susceptibility test results obtained by the researcher during the research process. The duplicate testing ensured the reproducibility and reliability of the findings of this study. There was adequate incubation time allowed for accurate bacterial growth and testing during this stage of the study.

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Post-Analytical Stage

The data validation was done to check for any errors before reporting. The study's results were understood based on Clinical and Laboratory Standards Institute (CLSI) European Committee on Antimicrobial Susceptibility Testing(/EUCAST) guidelines for the accuracy of the findings. The study's results were documented clearly and systematically in a structured report with the guidance of the supervisors. The respective stakeholders reviewed findings for verification and feedback on the results. Strict ethical and regulatory guidelines were followed by the researcher to ensure research integrity throughout the research process.

Data Analysis

There was use of descriptive statistics, e.g, frequencies and percentages, among others as needed. The inferential statistics are used with the use of Microsoft Excel for proper data analysis. The findings were presented with the use of narratives and tables as well as charts and figures.

Ethical consideration

There was ethical clearance, which was obtained from an Institutional Review Board (IRB) of the UniK Faculty of Health Sciences, following Uganda National Council for Science and Technology (UNCST) guidelines. An authorization was pursued from the relevant authorities on the grounds before data collection. The data obtained was securely stored and used only for research purposes. The sample handling as well as the lab proceedings followed strict ethical and safety standards, with holistic support from the research supervisors.

Results

Isolation and identification of pathogenic bacteria present in wastewater effluents at Mukuuba Landing Site, Wakiso District, Uganda.

Primary Cultures Results

Three selective and differential media, MacConkey Agar (MAC), Mannitol Salt Agar (MSA), and Bile Esculin Agar (BEA) were used for the primary culture. The media selected promoted the selective growth of Enteric Gram-negative bacteria (MAC), Staphylococcus species (MSA), and Enterococcus species (BEA). After incubating the inoculated plates at 37 degrees Celsius for 24 hours, most of the water samples exhibited visible microbial growth on one or more of the media.

On MacConkey agar, colonies were easily differentiated between lactose fermenters (pink to red colonies suggestive of Enterobacterae such as E. coli) or non-lactose fermenters (colorless or pale colonies, suggestive of Salmonella, Proteus, or Pseudomonas spp). On Mannitol Salt Agar, which would grow salt-tolerant organisms like Staphylococcus spp, there were colonies showing yellow growth with a yellow surrounding zone, which would be predictive of mannitol fermentation characteristic of Staphylococcus aureus. The BEA is used for identification of Enterococcus spp, and either blackening of the medium would suggest positive for hydrolysis of esculin in the presence of bile, commonly seen in Enterococcus faecalis.

Table 1: Primary-Culture Results on Selective Media

Site ID	MSA	BEA	MacConkey
Site 1	+	+	+
Site 2	–	+	+
Site 3	–	–	+
Site 4	+	+	+
Site 5	–	+	+
Site 6	–	+	+
Site 7	–	–	+
Site 8	–	+	+
Site 9	–	+	+
Site 10	+	_	+
Site 11	–	+	+
Site 12	–	+	+
Site 13	+	+	+

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Site 14	–	+	+
Site 15	–	+	+
Site 16	+	+	+
Site 17	–	_	+
Site 18	–	+	+
Site 19	–	–	+
Site 20	–	+	+
Site 21	–	–	+
Site 22	–	–	+
Site 23	–	–	+
Site 24	–	–	–
Site25	–	–	–
Site 26	–	–	+
Site 27	–	–	+
Site 28	–	–	+
Site 29	–	+	+
Site 30	–	+	+

Notes: (+ = growth; – = no growth),

Table 1 shows that MSA had 5/30 positive, suggestive of S. aureus, BEA had 18/30 positive, suggestive of E. faecalis, and MacConkey had 28/30 positive (various Gram-negatives), and finally, Sites 24 and 25 showed no growth on any medium.

Figure 1: Showing the distribution of growth on the different primary media

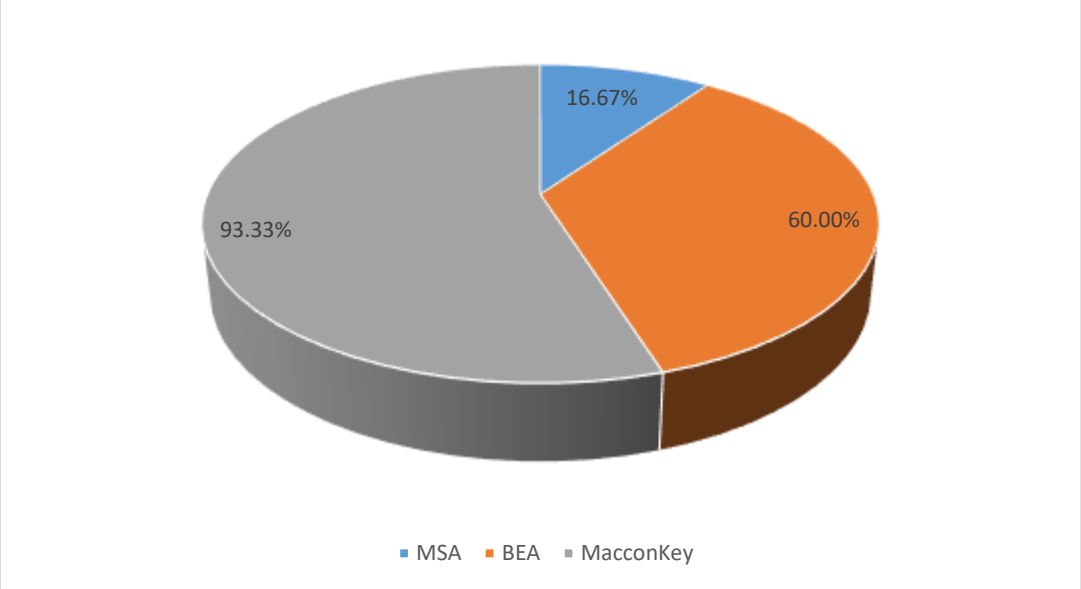

Figure 1 shows that the results on the three different selective and differential media indicated that MacConkey agar supported the highest level of bacterial growth, where 93.33% of the water samples grew bacteria, indicating the presence of Gram-negative enteric bacteria, specifically coliforms. The high level of growth, especially on MacConkey agar, is an indication of fecal contamination, since this medium is meant to isolate and differentiate

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lactose-fermenting Gram-negative bacilli (E. coli, Citrobacter, and Klebsiella).

On Bile Esculin Agar (BEA), 60.00% of the samples grew bacteria. This medium is selective for enterococci and group D streptococci, with Enterococcus faecalis being the principal organism. The growth rate indicates that a majority (60%) of the water sources contained enterococci, a strong indicator of fecal pollution, and enterococci are often more resistant in the environment than coliforms.

Mannitol Salt Agar (MSA) showed the least growth at 16.67%. MSA is selective for Staphylococcus species, since it contains a high concentration of salt, and differential for Staphylococcus aureus based on mannitol fermentation.

Subcultures on Nutrient Agar (NA)

Pure colonies must be obtained for biochemical testing; therefore, they were sub-cultured in peptone water, a non-selective enrichment medium suitable for the growth of both Gram-negative and Gram-positive bacteria. Use of peptone water facilitated growth by not suppressing the growth of either the Gram-negative or Gram-positive bacteria, while allowing standardized inocula for biochemical tests. Use of peptone water ultimately determined that these were living, well-preserved isolates prepared for metabolic characterizations under these planned activities.

Gram Stain Results

Gram staining was useful for baseline classification of isolates. Roughly 70% of isolates were Gram-negative rods consistent with enterics from fecal contaminant (pink bacilli in histological image). The remaining 30% were Gram-positive cocci purple clusters or chains) suggestive of Staphylococcus and Enterococcus species, respectively. These early differentiations were useful to scaffold the proper choice of biochemical tests for confirmatory identification.

Biochemical Identification of Isolates

The bacterial isolates were confirmed with biochemical testing using standard biochemical reactions for each suspected group. Each reaction was interpreted based on a color change or the formation of a reaction product by an organism following inoculation and incubation. The biochemical profiling of the Gram-negative isolates included citrate, urease, Sulphur indole motility (SIM), and triple sugar iron (TSI) tests. Utilizing the reaction patterns of the biochemical tests and reference identification keys, six species of Gram-negative bacteria were identified. Escherichia coli. Negative for citrate, urease, and H_2S production, positive for indole, with TSI reaction showing an acid slant and an acid butt (A/A). Citrobacter freundii. Positive for citrate and H_2S production, mostly indole negative, with motility. TSI reaction showed both acid (A) and alkaline slants with H_2S. Klebsiella pneumonia. Positive for citrate and urease, non-motile and non-indole producers, TSI A/A. Proteus mirabilis. Positive for citrate and urease, positive for indole, motile, and positive for H_2S, and the TSI reaction was K/A with H_2S production.

For the Gram-positive cocci, we confirmed Staphylococcus aureus with Catalase and Coagulase tests. The isolates that showed vigorous bubbling with the Catalase test and yielded clot formation with the Coagulase test were confirmed. The °isolation colonies also fermented mannitol on MSA, which resulted in yellow colonies and a yellow halo due to the pH change, which served as another confirmation. In contrast, the identification of the Enterococcus faecalis was determined by the negative Catalase test, organism growth at 6.5% NaCl, and organism hydrolysis of esculin in the presence of bile, which resulted in the black color formed when the BEA medium was assessed for complete growth. There were 5 isolates of Staphylococcus aureus and 18 isolates of Enterococcus faecalis.

The biochemical profiles confirmed the presence of several bacterial species, which were demonstrated to be significant with respect to public health concerns. The laboratory results were congruent with WHO´s concern about the presence of antibiotic-resistant organisms in environments that had been polluted by wastewater.

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Table 2: Biochemical Identification from MacConkey Subcultures (only MacConkey-positive sites)

Site ID	Citrate	Urease	Sulphur Indole Motility (SIM)			Triple Sugar Iron (TSI)			Identified Organism
			Indole	Motility	H_2S	Butt	Slant	H_2S	
Site 1	–	–	+	+	–	A	A	–	Escherichia coli
Site 2	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 3	+	+	_	_	_	A	A	_	Klebsiella pneumoniae
Site 4	+	–	_	+	–	K	A	+	Citrobacter freundii
Site 5	–	–	_	–	–	K	A	+	Citrobacter freundii
Site 6	–	–	_	–	–	K	A	+	Citrobacter freundii
Site 7	–	–	+	+	–	A	A	–	Escherichia coli
	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 8	+	+	_	_	_	A	A	_	Klebsiella pneumoniae
Site 9	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 10	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 11	–	–	+	+	–	A	A	–	Escherichia coli
Site 12	+	+	_	+	+	K	A	+	Proteus mirabilis
	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 13	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 14	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 15	–	–	_	+	+	A	A	+	Citrobacter freundii
Site 16	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 17	+	–	_	+	–	K	A	+	Citrobacter freundii
Site 18	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 19	–	–	+	+	–	A	A	–	Escherichia coli
Site 20	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 21	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 22	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 23	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 26	–	–	+	+	–	A	A	–	Escherichia coli
Site 27	+	+	_	+	+	K	A	+	Proteus mirabilis
Site 28	+	+	_	_	_	A	A	_	Klebsiella pneumoniae
	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 29	+	–	_	+	–	A	A	+	Citrobacter freundii
Site 30	+	–	_	+	–	A	A	+	Citrobacter freundii

Legend

Citrate, Urease, SIM; I Indole, M (motility), SIM H_2S, TSI (Butt/Slant/H_2S): + = positive; and – = negative; TSI A = acid (yellow), K = alkaline (red).

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Table 2 shows that the isolated organisms had five E. coli isolates, two P. mirabilis isolates, three K. pneumonia isolates, and 21 C. freundii isolates.

Table 3: Summary Table of Bacterial Isolates Identified

Bacterial Species	Number of Isolates	Primary Source Media
Citrobacter freundii	21	MacConkey Agar
Escherichia coli	5	MacConkey Agar
Klebsiella pneumoniae	3	MacConkey Agar
Proteus mirabilis	2	MacConkey Agar
Staphylococcus aureus	5	Mannitol Salt Agar
Enterococcus faecalis	18	Bile Esculin Agar

Figure 1: Showing the different isolated organisms.

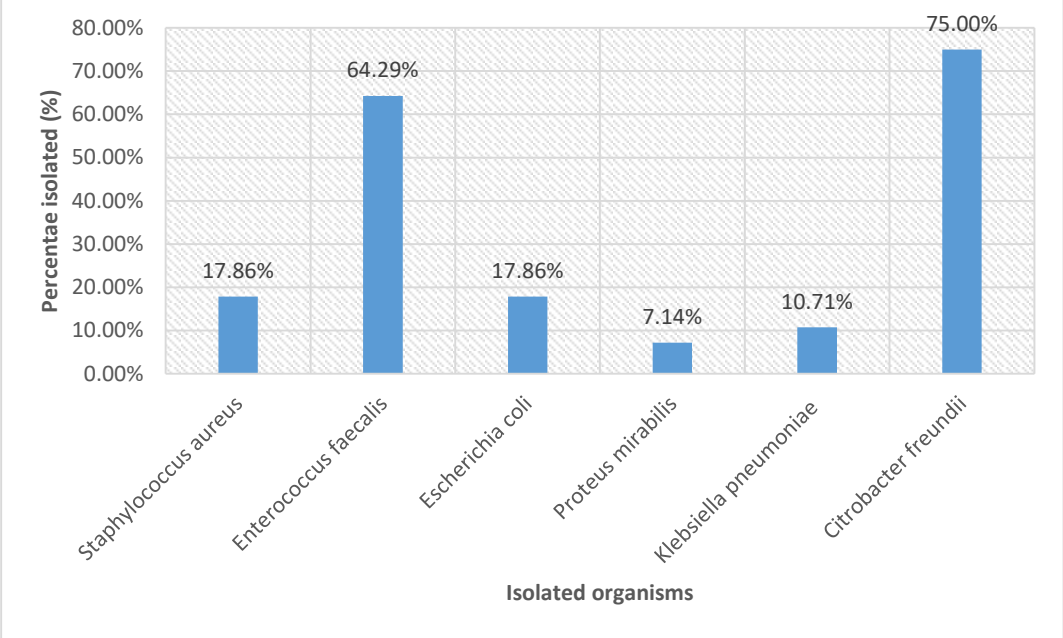

Figure 3 shows that Citrobacter freundii was the most frequently isolated and identified bacterium; it accounted for 75.00% of all positive isolates. The overall detection of C. freundii indicates significant fecal contamination in the tested water sources, which implies there may have been poor sanitation and contaminated areas in the vicinity of the water source. C. freundii is poorly associated with clean water. Enterococcus faecalis was the second most frequently isolated bacterium, which accounted for 64.29% of the total isolates, indicative of a more widespread fecal contamination of human origin due to its strong association with the human gastrointestinal tract.

Staphylococcus aureus and Escherichia coli were both present in equal proportions at 17.86%, with E. coli being a sensitive indicator organism for fecal pollution in the water sources and contributing to the health concerns associated with the potential microbial hazards. While S. aureus is associated with human skin, it may also indicate contamination has occurred either at the time of water collection or handling.

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Proteus mirabilis and Klebsiella pneumoniae were the least frequently isolated bacteria, with P. mirabilis accounting for 7.14%, and K. pneumoniae accounting for 10.71% of the total isolates. Both percent prevalence is low, but both organisms are opportunistic pathogens; therefore, their presence further indicates that some sanitary failings had occurred in the handling, storage, or source of the water.

Discussion

Isolation and identification of pathogenic bacteria present in wastewater effluents at Mukuuba Landing Site, Wakiso District, Uganda.

The research established a high isolation frequency for Citrobacter freundii (75%), followed by Enterococcus faecalis (64.3%), while E. coli and S. aureus were isolated in lesser proportions (17.9% each), Klebsiella pneumoniae (10.7%), and Proteus mirabilis (7.1%). The presence of C. freundii was consistent with studies from wastewater tracking in Uganda and East Africa in which Citrobacter species are frequently isolated, which typically have high resistance to ampicillin due to an inducible AmpC β-lactamases ('Citrobacter', 2025). C. freundii can cause opportunistic infections, form biofilms, and can persist in contaminated water and sewage, and these factors may have contributed to its abundance in samples from Mukuuba Landing Site.

The fairly high abundance of E. faecalis at 64.3% is consistent with worldwide monitoring of enterococci in environmental waters. Enterococci are useful indicators of fecal contamination; they are hardy and can survive in harsh conditions of aquatic environments. In addition, enterococci usually have intrinsic resistance against several antibiotics, including vancomycin, quinolones, and β-lactam ('Enterococcus Faecalis', 2025; Katumba et al., 2024).

Interestingly, a recent surveillance programme looking at Uganda's water sector (2021-2023) noted that Enterococcus species constituted approximately 24.1% of all the priority pathogens that were retrieved, and this demonstrates the organisms' persistence in the culture and risk-factor conclusion (Katumba et al., 2024).

The detection of E. coli, K. pneumoniae, S. aureus, and P. mirabilis (albeit with a lower prevalence) reflects the microbial diversity and health implications. E. coli and K. pneumoniae are common enteric pathogens that are commonly found in Ugandan wastewater and surface waters and most commonly exhibit high resistance to antibiotics such as ampicillin and ciprofloxacin, which diminishes treatment options for infection (Katumba et al., 2024). S. aureus isolates presumably indicate skin/nasal direct contact of humans with water, while P. Mirabilis, despite lower prevalence, can lead to urinary and wound infections in immunocompromised individuals (Katumba et al., 2024). In sum, the diversity and abundance of these isolates indicate a very high degree of fecal and environmental contamination present at the landing site. The presence of these human and enteric pathogens in wastewater effluents indicates a large risk to waterborne illness potential in the health of communities that access the lake for domestic use (drinking, washing, and harvesting) and fishing/recreational activities.

Conclusion

Contamination of effluent water has the potential for serious public health risks, and there is a significant risk contribution from these bacteria in wastewater effluents, indicating a stronger requirement for action on wastewater effluents and monitoring of microbial content of waterways utilized by humans and animals.

Moreover, regarding the antibiotics investigated, the results showed a concerning trend of resistant bacteria, and many of the isolates showed very low susceptibility to the antibiotics ampicillin, tetracycline, and amoxicillin-clavulanic acid. Some variations did exhibit some susceptibility to the antibiotics gentamicin and ciprofloxacin. This resistance pattern is showing a significantly increased risk of antimicrobial resistance (AMR) globally, especially in water systems with the indiscriminate disposal of pharmaceuticals, untreated sewage, and agricultural runoffs. These study results suggest that effluent water has the potential to act as a reservoir or source of drug-resistant bacteria to humans and animals through water or direct contact.

Study limitations

Due to unavoidable circumstances, there was a possibility of a negative effect on the bacterial viability, thereby potentially affecting the culture results.

Natural fluctuations in wastewater effluent composition from the sample collection sites introduced inconsistencies in the findings of the study.

Recommendation

Ongoing monitoring and microbial testing of effluents and surface waters at places of landing, such as Mukuuba, should be enhanced by the Ministry of Health. The aim should be to monitor for pathogenic bacteria early, deterring

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any outbreaks. There should be an ideal surveillance function and become part of that Ministry's environmental health programming at a national level, so it becomes a trigger point to invoke the appropriate action from public health-conscious actors acting in authority in risk zones.

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List of Abbreviations

AMR – Antimicrobial Resistance
AST – Antimicrobial Susceptibility Testing
BEA- Bile Esculine Agar
BOD – Biological Oxygen Demand
CFU – Colony-Forming Unit
COD – Chemical Oxygen Demand
E. coli – Escherichia coli
e.g, for example
etc. – Et cetera
MAC – MacConkey Agar
MDR – Multidrug Resistance
MHA – Muller Hinton Agar
lab – Laboratory
MSA – Mannitol Salt Agar
NA – Nutrient Agar
NTDs – Neglected Tropical Diseases
QA & QC – Quality Assurance and Quality Control
S. aureus – Staphylococcus aureus
SDGs – Sustainable Development Goals
SIM – Sulphur Indole Motility
SOPs – Standard Operating Procedures
Spp – Species
TSI - Triple Sugar Iron Agar
UniK– University of Kisubi
SSA – Sub-Saharan Africa
WHO – World Health Organization
WWTP – Wastewater Treatment Plant
XLD – Xylose Lysine Deoxycholate Agar

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Conflict of interest

The author declares no conflict of interest.

Author contributions

SD served as the Principal Investigator and was responsible for the overall conception, design, and coordination of the study.

JK and **HM** supervised the research project, provided technical guidance, and oversaw the progress of the work.

LF, MD, WWH, AJB, SC, OBW, SV, MS, KJ, SF, NJ, and AM actively participated in data collection and made significant contributions to the review of the manuscript.

Data availability

Data is available upon request.

Informed consent

All the participants consented to this study

Author Biography

Seldon Duluga is a student of the Bachelor's Degree in Biomedical Laboratory Technology

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of the University of Kisubi.
James Kasozi is a lecturer at the University of Kisubi.
Habert Mabonga is a lecturer at the University of Kisubi.

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