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Kamundia Patrick
Department of Animal Health and Production, Maasai Mara University, P.O. Box 861-20500, Narok, Kenya

Mbuthia Paul
Department of Veterinary Pathology, Microbiology, and Parasitology, Faculty of Veterinary Medicine, University of Nairobi, P.O. Box 29053-00625, Nairobi, Kenya

Njagi Lucy
Department of Veterinary Pathology, Microbiology, and Parasitology, Faculty of Veterinary Medicine, University of Nairobi, P.O. Box 29053-00625, Nairobi, Kenya

Bebora Lilly
Department of Veterinary Pathology, Microbiology, and Parasitology, Faculty of Veterinary Medicine, University of Nairobi, P.O. Box 29053-00625, Nairobi, Kenya

Nyaga Phillip
Department of Veterinary Pathology, Microbiology, and Parasitology, Faculty of Veterinary Medicine, University of Nairobi, P.O. Box 29053-00625, Nairobi, Kenya

Corresponding Author:
Kamundia Patrick
Department of Animal Health and Production, Maasai Mara University, P.O. Box 861-20500, Narok, Kenya

Quality of Winam gulf water: Bacterial pathogens and their antimicrobial resistance patterns in Winam gulf, Lake Victoria, Kenya

Kamundia Patrick, Mbuthia Paul, Njagi Lucy, Bebora Lilly and Nyaga Phillip

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Abstract
This study assessed microbiological water quality and antimicrobial resistance (AMR) in Lake Victoria's Winam Gulf, Kenya. Water samples (n=86) from 14 sites (estuaries, fish landing areas, and an effluent stream) yielded 196 bacterial isolates, predominantly *Staphylococcus aureus* (19.4%) and *Escherichia coli* (11.2%), including pathogens like *E. coli* O157, *Vibrio parahaemolyticus*, and *V. cholerae*. AMR testing of 62 isolates against nine antibiotics revealed widespread resistance, with *Pseudomonas* spp. showing the highest multiple antibiotic resistance (MAR) index (0.667) and resistance to nine classes. Multidrug resistance (≥50% of antibiotics) was observed in *S. aureus*, *Enterobacter* spp., and *Pseudomonas* spp. Hierarchical clustering grouped isolates into four clusters, suggesting shared resistance mechanisms. The presence of resistant pathogens underscores urgent public health risks, necessitating enhanced antimicrobial stewardship, water quality management, and sanitation improvements to safeguard Lake Victoria's ecological and public health integrity.

Keywords: Water quality, Lake Victoria, Bacterial pathogens, antimicrobial resistance

1. Introduction
Water quality is a fundamental determinant of public health. With water being a critical natural resource in the sustenance of life where communities rely heavily on freshwater resources for drinking, agriculture, and fishing, it is crucial to protect its quality. However, with a rapidly increasing global population, the demand is amplifying the risks of microbial contamination which poses a serious health risk [1, 2]. This growing pressure on water resources has been linked to increased incidents of waterborne diseases and contamination events in both developed and developing nations [2]. Importance of access to clean and safe water for all is highlighted by the United Nations Sustainable Development Goal (SDG) targets 6, however 63% of the Kenya population has been documented not to have a reliable source of water [3].
The Lake Victoria basin supports the economic and environmental needs of approximately 42 million people [4]. Therefore, the Winam Gulf of Lake Victoria in Kenya experiences intensive human activities, primarily centered around fishing, agriculture, and urban development [5]. These anthropogenic activities have led to increased environmental pressures through industrial discharge, agricultural runoff, and inadequate sewage treatment, significantly impacting the gulf's water quality [6].
Lake Victoria's extensive catchment area encompasses diverse land-use patterns, including agricultural zones, industrial sectors, and urban settlements. This positioning makes the lake a crucial environmental receptor for various inputs [7]. The lake continuously receives agricultural runoff, domestic effluents, industrial waste, and both treated and untreated sewage, affecting its ecological balance [8]. These anthropogenic pressures have resulted in the introduction of pathogenic microorganisms and pollutants, including antimicrobial-resistant (AMR) bacteria, into the aquatic ecosystem, creating substantial risks for both human health and environmental integrity [9]. Thus, systematic monitoring of water quality through microbiological assessment and antimicrobial resistance surveillance is fundamental for identifying and managing waterborne health risks.

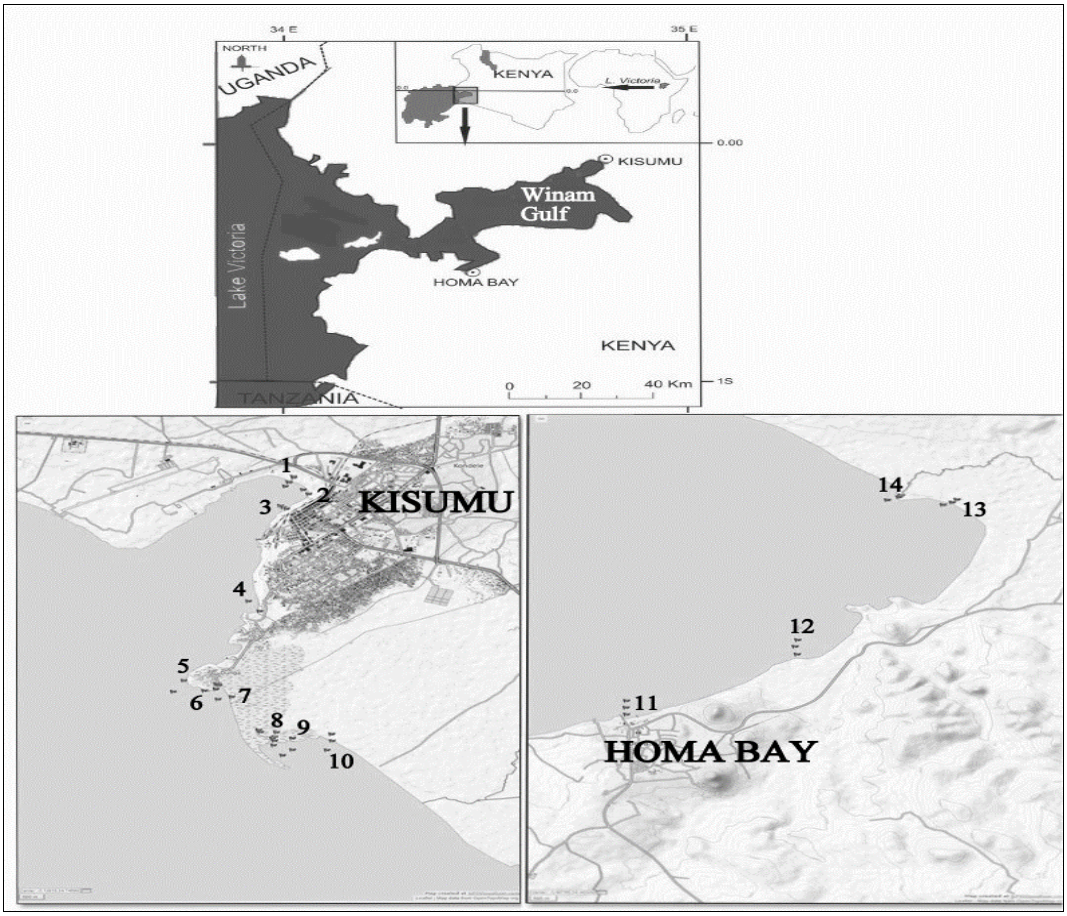
Escherichia coli and other fecal indicator bacteria serve as crucial markers for assessing fecal contamination and potential pathogen presence in aquatic environments [10]. Emergence of antimicrobial resistance in water systems has introduced additional complexities to water quality management protocols. Research has demonstrated that the release of antibiotics from various sources, including healthcare facilities, agricultural operations, and domestic waste streams, significantly contributes to the selection and proliferation of antimicrobial-resistant (AMR) bacteria in aquatic ecosystems [11]. These environments subsequently function as reservoirs for resistance genes, facilitating their transfer to human pathogens. This situation is particularly concerning in developing nations such as Kenya, where limited access to adequate water and sanitation infrastructure amplifies the impact of waterborne diseases [12].

Ecological services provided by water bodies face increasing pressure from both urban and rural activities. Fishing operations, livestock production, and agricultural practices contribute substantially to water pollution through farm runoff and domestic wastewater discharge [6,7]. River systems that drain catchment areas serve as primary conduits for microbial contaminants entering lake ecosystems. Additional sources of microbial pollution include inadequately treated human and animal waste [13]. The dynamic nature of these challenges, particularly regarding emerging issues such as antimicrobial resistance, necessitates continuous monitoring and adaptive management strategies. This research addresses a critical knowledge gap by conducting a comprehensive microbiological assessment of the Winam Gulf's water quality, taxonomic diversity, and antimicrobial resistance (AMR) patterns in isolated bacterial strains. The study's integrated approach to analyzing both river estuaries and landing sites aligns with recommendations for holistic water quality monitoring frameworks [14]. By examining microbial contamination patterns and AMR dynamics in this vital water system, this research aims to generate actionable insights for water quality management and antimicrobial resistance mitigation strategies. Furthermore, other tools such as the phenotypic hierarchical cluster analysis have been widely utilized to delineate relationships among bacterial isolates in antimicrobial resistance (AMR) studies, serving as a powerful approach to uncover phenotypic similarities that underpin resistance mechanisms [15].

2. Material and methods

2.1 Study area

The study was conducted in the Winam Gulf region of Lake Victoria, Kenya, encompassing two urban centers: Kisumu (0°6'0" S, 34°45'0" E) and Homa Bay (0°31'43" S, 34°27'19" E). In Kisumu County, eight river systems were selected for sampling: Rivers Kisat, Auji, Luanda, Nyamasaria, Oriatiko, Tako, and Wigwa, along with an effluent stream named Railway. Additionally, two major landing sites in Kisumu - Dunga Beach and Tilapia Beach - were included to assess the impact of fishing activities and urban development on water quality. The Homa Bay sampling sites comprised three river estuaries - Nyakwanya, Arujo, and Awach - and the Homa Bay landing site. A comprehensive spatial representation is shown in Figure 1.



Legend: 1 = River Kisat, 2 = Tilapia beach, 3 = Railways Point, 4 = River Tako, 5 = River Nyamasaria, 6 = River Wigwa,7 = Dunga beach, 8 = River Otiatiko, 9 = River Luanda, 10 = River Auji, 11 = Homa Bay, 12 = River Arujo, 13 = R. Awach, 14 = River Nyakwanya

Fig 1: Map of Lake Victoria basin, Kenya showing the drainage area and the sampling sites [16]

2.2 Sampling strategy
Eighty-six water samples were collected from Kisumu (KSM) and Homa Bay (HB) counties in Kenya to evaluate microbial contamination risks. Sampling sites were strategically selected to encompass diverse hydrological environments and anthropogenic influences: 62 samples from ten river estuaries and one effluent stream, prioritized for their ecological sensitivity and proximity to human activity, and 24 samples from three high-traffic fish landing sites to assess contamination risks in areas critical to local livelihoods and food security. Sampling was conducted in 5 campaigns: Kisumu County (KSM1, n = 12; KSM2, n = 20, KSM3, n = 30) and Homa Bay County (HB1, n = 12, HB2, n = 12). This stratified design balanced spatial representation (riverine and fishing zones), ensuring robust analysis of contamination trends across ecologically and socioeconomically significant environments.

2.3 Sample Collection Methodology
Water was collected in Kisumu (KSM) three times and Homa Bay (HB), times. At each study site, water samples were collected along a 300-meter transect. For river estuaries, sampling points along the transect were established at 100 meters upstream, at the shoreline (0 meters), and 100 meters offshore. At fish landing sites, sampling sites along the transect were at the shoreline (0 meters), 100 meters offshore, and 200 meters offshore. A Garmin eTrex GPS device was utilized to measure distances between collection points with precision.

Water samples were obtained using sterile 250 ml glass bottles. The collection procedure involved submerging the bottles approximately 15 centimeters below the water surface, with strict adherence to protocols preventing sample contamination. Following collection, all samples were maintained at 4 °C through ice storage in cool boxes during transportation to the laboratory for subsequent bacterial analysis.

2.4 Isolation and identification of bacteria
Plates were incubated aerobically at 37 °C for 24 hours. For bacterial culture and identification, blood agar (colony morphology), MacConkey agar (for selection and differentiation of members of family Enterobacteriaceae), Selenite broth (used as an enrichment medium for *Salmonella* bacteria), Sorbitol MacConkey (used as a selective and differential medium for *Escherichia coli* O157), and Thiosulfate-Citrate-Bile Salts-Sucrose (TCBS) Agar (used for the selective isolation of *Vibrio cholerae* and *Vibrio parahaemolyticus*) were utilized. The media used in the study were manufactured by Oxoid, Basingstoke, United Kingdom. Bacterial identification was carried out through observation of colony morphology on blood agar, Gram staining to determine the bacteria's staining characteristics and cell shape, and biochemical tests for further characterization of the bacteria. Latex agglutination test was used for detection of *Escherichia coli* serotype O157 (Prolex™ Blue E. coli O157 Latex Test Reagent Kit, Prolab Diagnostics).

2.5 Antibiotic susceptibility Testing
Antimicrobial susceptibility testing was conducted using the standardized disc diffusion method as described by [16]. Sixty-two bacterial isolates comprising 9 different species were analyzed for their resistance to 9 antibiotics. The bacterial species included *Escherichia coli* (n=10), *Vibrio cholerae* (n=4), *Staphylococcus aureus* (n=8), *Aeromonas hydrophila* (n=10), *Enterobacter* spp. (n=4), *Proteus mirabilis* (n=7), *Pseudomonas* spp. (n=5), *Klebsiella* spp. (n=4), and *Salmonella* spp. (n=10). The antibiotics tested were Ampicillin (AMP), Chloramphenicol (CHL), Cefuroxime (CXM), Ciprofloxacin (CIP), Erythromycin (ERY), Ceftriaxone (CTR), Cloxacillin (CLX), Trimethoprim-Sulfamethoxazole (STX), and Nalidixic Acid (NAL). The antimicrobial discs were procured from Sigma-Aldrich (St. Louis, MO, USA). Zone diameters were measured using calipers and the resistance was quantified by calculating resistance percentages. Multiple drug resistance (MDR) was defined as resistance to more than two classes of antibiotics among all antibiotics tested as described by [17]. The Multiple Antibiotic Resistance (MAR) index for each isolate was calculated using the formula MAR = a/b, where a = number of antibiotics to which the isolate shows resistance, and b = total number of antibiotics tested [18]. Hierarchical clustering analysis was applied to nine bacterial antibiotic resistance profiles using Euclidean distance and four linkage methods (single, complete, average, and Ward's) [19]. The optimal four-cluster solution was determined using the elbow method and validated by silhouette analysis [20]. This methodological approach quantified dissimilarities in resistance patterns and identified robust, biologically meaningful groupings, ensuring standardized and comparable results across studies in antimicrobial resistance research, yielding a consistent framework for comparative data analysis [21].

2.6 Statistical Analysis
Antibiotic susceptibility patterns were quantified by calculating the resistance ratio, defined as the proportion of bacterial isolates exhibiting resistance relative to the total number of isolates tested for each antibiotic [18]. MDR (Multi-Drug Resistance) Formula: MDR Status = {MDR, if resistant to $\geq$ 3 antibiotic classes, non-MDR, if resistant to < 3 antibiotic class}[19]. Statistical analyses were conducted using Python 3.13. Hierarchical clustering employed Ward's method with Euclidean distances (hclust package). Optimal cluster number was determined through Elbow method (factoextra package), Silhouette analysis (cluster package) and Gap statistic (cluster package).

2.7 Ethical Considerations
This study was conducted under approval from the Biosafety, Animal Use and Ethics Committee (BAUEC) of the Faculty of Veterinary Medicine, University of Nairobi (approval number: FVM BAUEC/2015/220).

3. Results
3.1 Bacterial isolates distribution

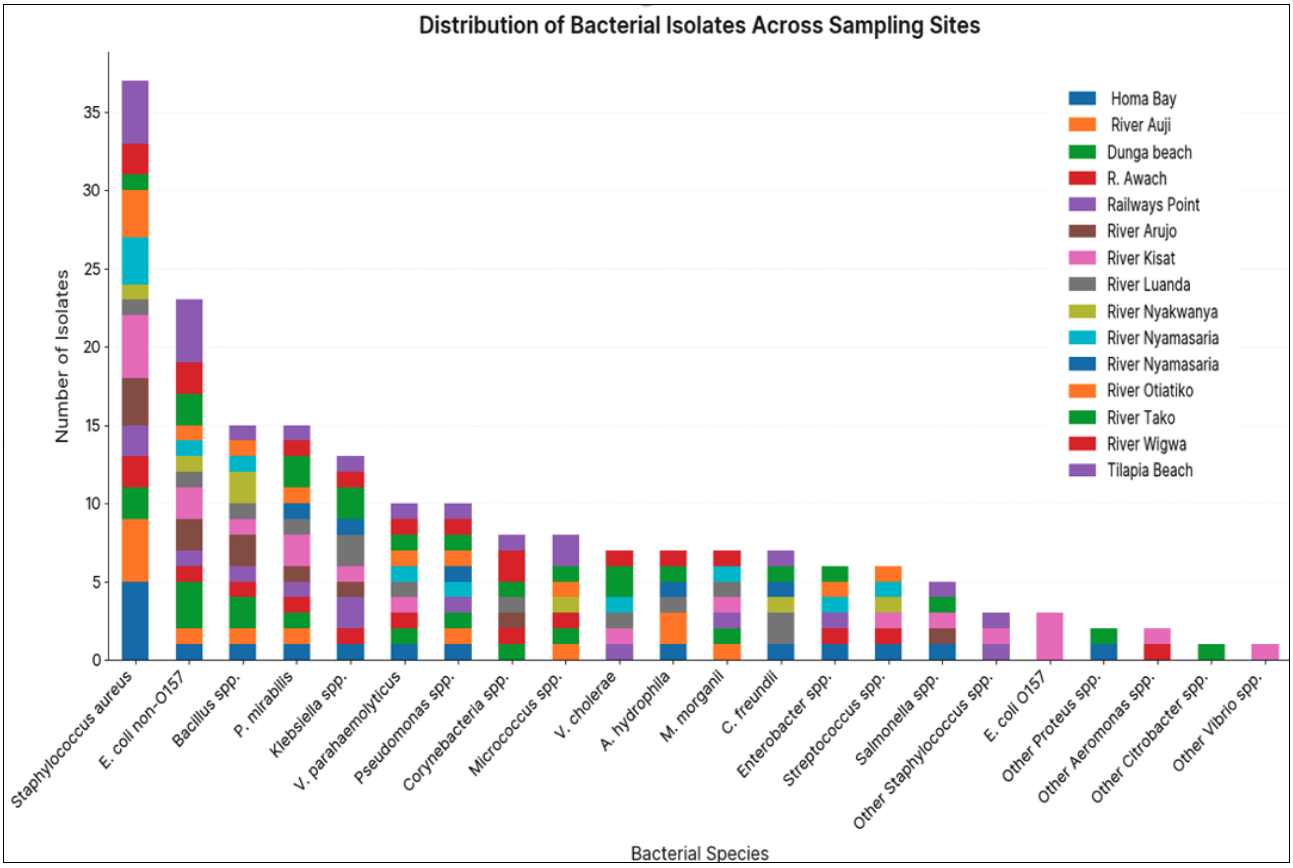


Fig 2: Distribution of bacterial isolates across the sampling sites

The analysis revealed widespread distribution of several bacterial species across sampling locations (Figure 2). *Staphylococcus aureus*, *E. coli* non-O157, *Bacillus* spp., and *Pseudomonas* spp. demonstrated presence across multiple sites, indicating their adaptability to various aquatic environments. River Kisat and Tilapia Beach sampling sites consistently showed elevated bacterial counts, particularly for *S. aureus* and *E. coli* non-O157. These locations exhibited distinct bacterial community profiles, suggesting site-specific environmental conditions favorable for bacterial persistence. *S. aureus* and *Bacillus* spp demonstrated moderate to high abundance across most sampling locations. *E. coli* O157 and *Proteus* spp showed sporadic distribution with localized occurrence. Lastly, *Klebsiella* spp. and *Pseudomonas* spp exhibited variable abundance patterns across sampling sites.

A total of 196 bacterial isolates in 15 genera were characterized across sampling sites. Analysis of bacterial prevalence (Table 1) revealed *Staphylococcus aureus* (19.4%) and *Escherichia coli* (11.2%), *Bacillus* (7.7%) and *Proteus mirabilis* (7.7%) as the predominant species. Additional bacterial species isolated across multiple sites included *Klebsiella spp*. (6.6%), *Pseudomonas spp.* (5.1%), and *Vibrio parahaemolyticus* (5.1%). Pathogens such as *Vibrio cholerae* and *E. coli* O157 were exclusively detected in the Kisumu (Figure 2), while Homa Bay, despite its lower overall diversity, exhibited higher proportions of certain species, such as *Bacillus* spp. at 12.5% in HB2. Additionally, site-specific patterns emerged: river estuaries were characterized by greater bacterial diversity, while landing sites harbored more human-associated pathogens like *S. aureus* and *E. coli*.

An examination of the pathogen-specific trends, *S. aureus* was consistently present across all sites (ranging from 9.1% to 25%), with its highest occurrence in Homa Bay (25%). The non-O157 strains of *E. coli* showed a marked increase from 4.5% in KSM1 to 16.9% in KSM3, while the O157 strain appeared sporadically, exclusively in Kisumu.

3.2 Antibiotic Resistance Profile

The analysis revealed distinct antimicrobial resistance profiles across bacterial species against nine antibiotics, as visualized in the heatmap (Figure 3), with resistance percentages represented by a color gradient. Overall resistance patterns showed highest resistance to cloxacillin (72.6%) and ampicillin (70.9%), while ciprofloxacin demonstrated the lowest resistance (17.7%). *Escherichia coli* demonstrated high resistance to ampicillin (80%) and erythromycin (80%). *Pseudomonas spp*. showed 100% resistance to erythromycin, ceftriaxone, and cloxacillin. Ampicillin resistance was noted in *Aeromonas hydrophila* (90%) and *Staphylococcus aureus* (87.5%). *Enterobacter* spp. exhibited complete resistance to erythromycin and nalidixic acid. Conversely, *Vibrio cholerae*, *Aeromonas hydrophila*, and *Salmonella* spp. demonstrated comparative susceptibility to cefuroxime and ciprofloxacin.

Table 1: Distribution of Bacterial Isolates from Winam Gulf Water Samples by Sampling Period

Genus	Species	KSM1 (n=12)	KSM2 (n=20)	KSM3 (n=30)	HB1 (n=12)	HB2 (n=12)	Total (n=86)
Staphylococcus	*S. aureus*	4 (9.1%)	7 (21.2%)	15 (21.1%)	8 (25.0%)	4 (25.0%)	38 (19.4%)
	Staphylococcus spp.	1 (2.3%)	0 (0.0%)	2 (2.8%)	0 (0.0%)	0 (0.0%)	3 (1.5%)
Escherichia	*E. coli* non-O157	2 (4.5%)	4 (12.1%)	12 (16.9%)	4 (12.5%)	1 (6.3%)	22 (11.2%)
	E. coli O157	1 (2.3%)	0 (0.0%)	2 (2.8%)	0 (0.0%)	0 (0.0%)	3 (1.5%)
Proteus	*P. mirabilis*	5 (11.4%)	2 (6.1%)	5 (7.0%)	2 (6.3%)	1 (6.3%)	15 (7.7%)
	Other *Proteus* spp.	0 (0.0%)	0 (0.0%)	1 (1.4%)	1 (3.1%)	0 (0.0%)	2 (1.0%)
Bacillus	*Bacillus* spp.	3 (6.8%)	4 (12.1%)	2 (2.8%)	4 (12.5%)	2 (12.5%)	15 (7.7%)
Klebsiella	*Klebsiella* spp.	2 (4.5%)	5 (15.2%)	3 (4.2%)	3 (9.4%)	0 (0.0%)	13 (6.6%)
Vibrio	*V. parahaemolyticus*	1 (2.3%)	2 (6.1%)	5 (7.0%)	1 (3.1%)	1 (6.3%)	10 (5.1%)
	V. cholerae	2 (4.5%)	3 (9.1%)	2 (2.8%)	0 (0.0%)	0 (0.0%)	7 (3.6%)
	Other *Vibrio* spp.	0 (0.0%)	0 (0.0%)	1 (1.4%)	0 (0.0%)	0 (0.0%)	1 (0.5%)
Pseudomonas	*Pseudomonas* spp.	3 (6.8%)	1 (3.0%)	5 (7.0%)	1 (3.1%)	0 (0.0%)	10 (5.1%)
Corynebacteria	*Corynebacteria* spp.	4 (9.1%)	0 (0.0%)	2 (2.8%)	1 (3.1%)	1 (6.3%)	8 (4.1%)
Micrococcus	*Micrococcus* spp.	4 (9.1%)	0 (0.0%)	2 (2.8%)	1 (3.1%)	1 (6.3%)	8 (4.1%)
Aeromonas	*A. hydrophila*	1 (2.3%)	1 (3.0%)	4 (5.6%)	0 (0.0%)	1 (6.3%)	7 (3.6%)
	Other *Aeromonas* spp.	0 (0.0%)	0 (0.0%)	1 (1.4%)	0 (0.0%)	1 (6.3%)	2 (1.0%)
Citrobacter	*C. freundii*	3 (6.8%)	0 (0.0%)	2 (2.8%)	1 (3.1%)	1 (6.3%)	7 (3.6%)
	Other *Citrobacter* spp.	1 (2.3%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.5%)
Morganella	*M. morganii*	2 (4.5%)	4 (12.1%)	1 (1.4%)	0 (0.0%)	0 (0.0%)	7 (3.6%)
Enterobacter	*Enterobacter* spp.	2 (4.5%)	1 (3.0%)	1 (1.4%)	2 (6.3%)	0 (0.0%)	6 (3.1%)
Streptococcus	*Streptococcus* spp.	1 (2.3%)	0 (0.0%)	2 (2.8%)	1 (3.1%)	2 (12.5%)	6 (3.1%)
Salmonella	*Salmonella* spp.	2 (4.5%)	0 (0.0%)	1 (1.4%)	2 (6.3%)	0 (0.0%)	5 (2.6%)
Total		44	33	71	32	16	196

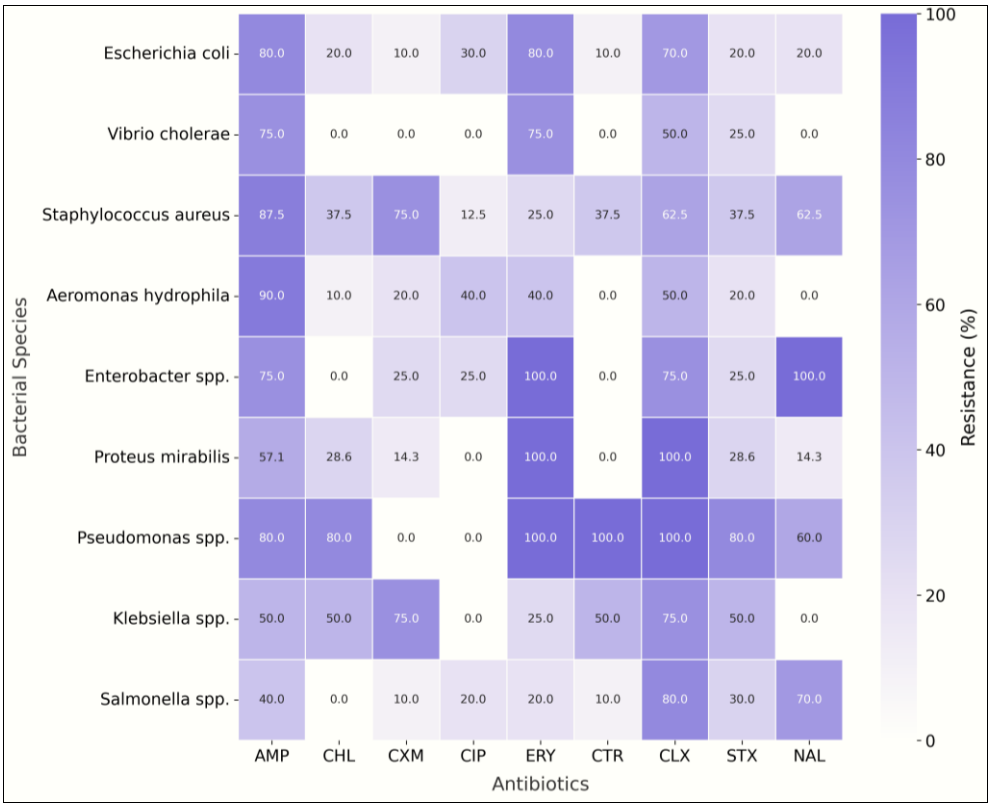


Fig 3: Heatmap showing antibiotic resistance patterns (%). Purple indicates higher resistance; light purple indicates lower resistance.

Multi-Drug Resistance (MDR) is defined as resistance to three or more classes of antibiotics, was observed in 51 out of 62 isolates (82.3%). Notably, the isolates from *Staphylococcus aureus, Enterobacter* spp., and *Pseudomonas* spp. exhibited MDR characteristics (Table 2). The overall MAR index across all isolates was 0.392, suggesting a concerning level of antibiotic resistance in the aquatic bacterial population studied. *Pseudomonas* spp. records the highest MAR index (0.667), whereas *Vibrio cholerae* exhibits the lowest MAR index (0.250) with resistance to just two antibiotics.

Table 2: Multiple antibiotic resistance indices and multiple drug resistance patterns of bacterial isolates

Bacterial Species	Antibiotics with Resistance (≥50%)	Number of Resistant Classes	MAR Index
Pseudomonas spp.	AMP, CHL, ERY, CTR, CLX, STX, NAL	6***	0.667
Staphylococcus aureus	AMP, CXM, CLX, NAL	3***	0.486
Enterobacter spp.	AMP, ERY, CLX, NAL	3***	0.472
Klebsiella spp.	CXM, CLX	2	0.417
Proteus mirabilis	ERY, CLX	2	0.381
Escherichia coli	AMP, ERY, CLX	2	0.378
Salmonella spp.	CLX, NAL	2	0.311
Aeromonas hydrophila	AMP	1	0.300
Vibrio cholerae	AMP, ERY	2	0.250

Legend: *** - Antibiotic showing multiple drug resistance patterns

Hierarchical cluster analysis revealed four distinct clusters of bacterial isolates based on their antibiotic resistance patterns. Cluster 1, comprising *Escherichia coli*, *Vibrio cholerae*, *Aeromonas hydrophila*, and *Proteus mirabilis*, exhibited pronounced resistance to Ampicillin (75.5%), Erythromycin (73.8%), and Cloxacillin (67.5%), while showing minimal resistance to Ceftriaxone (2.5%), with an average MAR index of 0.750. Cluster 2, consisting of *Enterobacter* spp. and *Salmonella* spp., demonstrated the highest resistance to Nalidixic Acid (85.0%) and Cloxacillin (77.5%), while maintaining complete susceptibility to Chloramphenicol, yielding an average MAR index of 0.833. Cluster 3, containing *Staphylococcus aureus* and *Klebsiella* spp., showed marked resistance to Cefuroxime (75.0%), Ampicillin, and Cloxacillin (both 68.8%), but minimal resistance to Ciprofloxacin (6.2%), with the highest average MAR index of 0.889. Cluster 4, consisting solely of *Pseudomonas* spp., displayed complete resistance (100%) to Erythromycin, Ceftriaxone, and Cloxacillin, high resistance (80%) to Ampicillin, Chloramphenicol, and Trimethoprim-Sulfamethoxazole, while maintaining complete susceptibility to Cefuroxime and Ciprofloxacin, with a MAR index of 0.778. Notably, all clusters exhibited elevated MDR prevalence, indicating widespread multiple drug resistance across all identified bacterial groups.

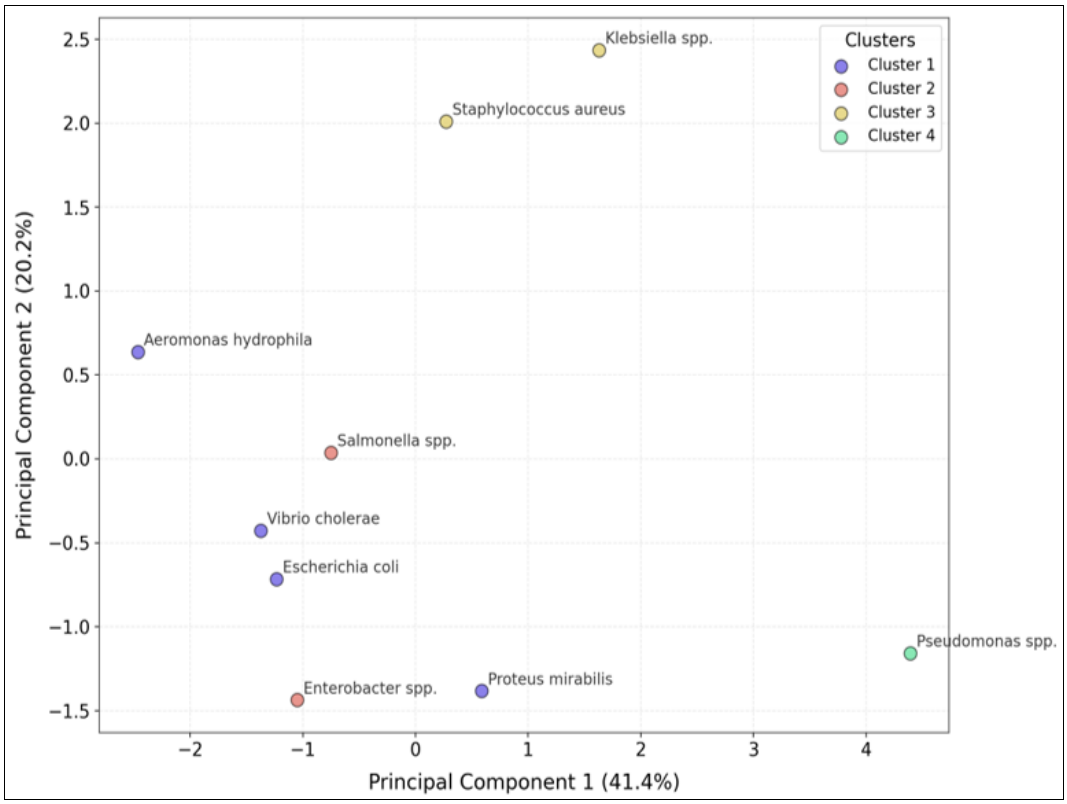


Fig 4: Bacteria species clustered by antibiotic resistance profiles

4. Discussion

The present study is the first to indicate the predominance of *Staphylococcus aureus* (19.4%) and *Escherichia coli* (11.2%) in Lake Victoria waters, and this aligns with Izbicki *et al.* [22] that suggested substantial anthropogenic influence on these aquatic environments. Furthermore, the isolation of *E. coli* O157 (1.5%), albeit in lower frequencies, raises significant public health concerns due to its association with severe gastrointestinal illness [23]. The presence of *Escherichia coli O157* in aquatic environments represents a significant public health concern due to its severe pathogenicity and low infectious dose [24]. *E. coli O157*, particularly serotype O157:H7, is recognized as a dangerous waterborne pathogen [25] due to its ability to cause severe gastrointestinal and renal infection, and potentially fatal complications [26]. Its persistence in various water sources [27] and potential for widespread transmission make it a critical target for public health surveillance and control measures.

The detection of various *Vibrio* species, including *V. parahaemolyticus* (5.1%) and *V. cholerae* (3.6%), suggests that these water bodies could serve as reservoirs for potentially pathogenic bacteria [28]. Studies by Wong *et al*. [29] have shown that *Vibrio* species can persist in aquatic environments due to their ability to adapt to varying environmental conditions. The presence of these organisms, particularly in KSM sites, may be attributed to favourable environmental conditions and possible anthropogenic activities in these areas [30]. Furthermore, the isolation of opportunistic pathogens such as *Aeromonas* species (4.6% combined) and *Pseudomonas* species further emphasizes the potential public health risks associated with these water bodies [31]. These organisms are known for their ability to persist in aquatic environments and their potential to cause infections in both immunocompetent and immunocompromised individuals [32].

The antimicrobial resistance (AMR) patterns among bacterial isolates from aquatic environments observed in this study are alarming and reflect the global challenge of AMR in aquatic environments. The high resistance rates observed for Cloxacillin (72.6%) and Ampicillin (70.9%) are particularly alarming, as these antibiotics are commonly used in both human and veterinary medicine. This finding aligns with previous studies that have reported increasing resistance to beta-lactam antibiotics in aquatic environments [33].

The significant resistance observed in *Pseudomonas spp.*, *Staphylococcus aureus*, and *Enterobacter spp.* raises concerns regarding potential multi-drug resistance mechanisms. In contrast, the lower resistance levels seen in *Vibrio cholerae* imply either less selective pressure or different niche adaptations. There were high resistance rates to commonly used antibiotics such as ampicillin, cloxacillin, and sulfamethoxazole among bacterial isolates such as *Aeromonas hydrophila* and *Staphylococcus aureus*. These findings align with previous investigations conducted in similar aquatic environments, particularly those documented by Elkenany *et al*. [34] in *Aeromonas hydrophila* and *Staphylococcus aureus* isolated from seafood in Egypt, who reported comparable resistance patterns in freshwater ecosystems. The observed resistance patterns suggest the presence of selective pressures in these environments, potentially driven by varying levels of antibiotic exposure from surrounding areas. The widespread resistance profiles documented may result from two key mechanisms: (1) environmental contamination with antibiotic compounds and resistance genes, leading to adaptive resistance development in aquatic bacteria, and (2) direct introduction of resistant bacteria through disposal into aquatic ecosystems [35]. These selective pressures appear to be driving the evolution of resistance traits as a survival strategy among bacterial populations in these environments. These findings call for stricter antibiotic stewardship, species-specific treatment, enhanced surveillance, and new antimicrobial development, along with routine susceptibility testing, careful empiric therapy choices, and local guideline development.

The overall MAR index of 0.393 across all isolates exceeds the threshold value of 0.2, which is considered indicative of high-risk environments where antibiotics are frequently used [36]. This suggests that the aquatic environments sampled in this study are likely impacted by anthropogenic activities, such as discharge of untreated sewage, agricultural runoff, or aquaculture practices that involve antibiotic use. P*seudomonas* spp. exhibited the highest MAR index (0.667), demonstrating resistance to seven antibiotics; this is in concurrence to studies that have shown a high MAR of 0.5-1.0 in *P. aeruginosa* [37] and multiple drug resistance pattern [38]. The resistance by *Pseudomonas* spp is particularly concerning as members of this genus are known opportunistic pathogens with intrinsic resistance to many antibiotics and disinfectants [39]. This was followed by *S. aureus* (0.486) with resistance to four classes, potentially indicating Methicillin-resistant Staphylococcus aureus (MRSA). *E. coli* (0.378) and *Enterobacter* spp. (0.472) showed moderate resistance to three classes. Gram-negative bacteria, especially *Pseudomonas* and *Enterobacter*, showed higher MAR indices. All species exceeded the 0.2 MAR index threshold, indicating significant antibiotic exposure and this further suggests a high-risk setting conducive to the dissemination of antimicrobial resistance [40]. Wanja *et al*. [18] documented high *Campylobacter* species MDR and resistance genes in Kajiado an upcountry location. Surface water from such areas can contaminate aquatic environment resulting to situations as in this study. The hierarchical clustering analysis revealed distinct bacterial resistance patterns, with all clusters showing 100% MDR prevalence and high MAR indices (0.750-0.889). Notable findings include shared resistance mechanisms within clusters and *Pseudomonas* spp. forming an isolated cluster with extensive resistance, emphasizing the need for targeted surveillance and treatment strategies in aquatic environments.

5. Conclusion

In conclusion, this study highlights the need for comprehensive water quality monitoring and management in the Winam Gulf of Lake Victoria to mitigate the risks of waterborne diseases and the spread and evolution of antimicrobial resistance to be implemented by the stakeholders such as the regional and national governments and the intergovernmental organizations that operate in the region. Detection of antimicrobial resistance in all bacterial species studied underscores the urgent need for intervention to preserve antibiotic effectiveness and reinforce the global antimicrobial resistance crisis, highlighting the necessity for coordinated action at all levels. The high levels of MDR and elevated MAR indices observed in this study call for urgent action to address antibiotic pollution in aquatic environments as part of a One Health approach to combating the global crisis of antimicrobial resistance. This study's findings underscore the importance of continuous monitoring, improved sanitation infrastructure, and sustainable environmental practices to safeguard public health and the ecological integrity of this vital water resource. Addressing these challenges will require collaborative efforts among policymakers, researchers, and local communities to ensure the sustainable use of Lake Victoria for future generations.

6. Competing Interests

The authors affirm that they do not possess any identifiable financial conflicts or personal affiliations that could have potentially influenced the outcomes presented in this research article.

7. Acknowledgements

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