



ASSESSMENT OF MICROBIOLOGICAL AND PHYSICOCHEMICAL QUALITIES OF OUTDOOR PUBLIC SWIMMING POOLS IN NNEWI NORTH LGA, ANAMBRA STATE

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Abstract: Swimming pools can act as reservoirs of pathogenic microorganisms when poorly maintained. This study assessed the microbiological and physicochemical quality of seven outdoor public swimming pools in Nnewi North, Anambra State, Nigeria, before use and after use by bathers on weekends, Saturdays and Sundays. Water samples were aseptically collected between September and November 2024 and analyzed using standard methods. Heterotrophic bacterial counts increased from 6.35×10^4 CFU/ml before use to 6.51×10^4 cfu/ml after use, while fungal counts ranged from $0-2.13 \times 10^5$ cfu/mL before and $0-3.0 \times 10^5$ cfu/mL after use. The mean $\pm$ SD total heterotrophic bacterial counts (THBC) before use (49.5714 ± 21.8210) and after use (50.8571 ± 22.4305), and the mean total heterotrophic fungal counts (THFC) before use (13.0476 ± 11.7195) and after use (14.8571 ± 13.5288) were considered statistically significant at $p = 0.05$. Bacterial isolates rose from 242 before use to 378 after use, with increased occurrence of *Escherichia coli* (11.9%), *Enterobacter intermedium* (11.1%), *Citrobacter freundii* (10.6%), and *Klebsiella pneumoniae* (10.1%). Fungal isolates also increased from 40 before use to 70 after use, predominantly *Penicillium* (28.6%), *Curvularia* (24.3%), and *Aspergillus* (21.4) species. Most Probable Number (MPN) index/100 ml for total coliforms ($<3-93$ MPN/100 ml) and fecal coliforms ($<3-12$ MPN/100 ml) exceeded WHO/EPA limits after use. Mean $\pm$ SD physicochemical parameters before and after use by bathers indicated deteriorating water quality of the swimming pools, with reduced pH ($5.56 \pm 1.23-5.32 \pm 1.11$), residual chlorine ($0.59 \pm 0.82-0.52 \pm 0.739$ mg/L), salinity ($438.64 \pm 178.92-231.42 \pm 104.71$), and calcium hardness ($199.670 \pm 181.80-78.51 \pm 73.31$ mg/L) alongside increased temperature ($26.18 \pm 0.69-28.31 \pm 0.64^\circ\text{C}$), turbidity ($9.91 \pm 0.458-14.83 \pm 2.47$ NTU), nitrate ($0.31 \pm 0.20-1.12 \pm 0.99$ $\mu\text{g/L}$), alkalinity ($92.83 \pm 60.75-160.00 \pm 81.86$ mg/L), and ammonia ($0.66 \pm 0.03-0.77 \pm 0.74$ mg/L) after use by bathers. The mean physicochemical parameters before and after use by bathers were considered statistically significant at $p = 0.05$. Bacterial isolates showed high susceptibility to fluoroquinolones but resistance to β -lactam antibiotics, while fungi exhibited notable antifungal resistance, particularly against fluconazole and griseofulvin. Most pools in this study failed to meet recommended standards, posing public health risks and highlighting the need for improved monitoring and maintenance.

Keywords: swimming pools; water quality; microbial contamination; antimicrobial resistance; public health.

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Introduction

Swimming pools are structures filled with water designed for swimming or recreational activities. They can be of various sizes, shapes, and types; including private, public, supervised, or unsupervised pools (WHO, 2006). Despite their recreational and health benefits, swimming pools may harbor pathogenic microorganisms, including bacteria, fungi, viruses, and parasites, often introduced by swimmers or from environmental sources (CDC, 2006; Sohrabi *et al.*, 2016). These microorganisms have been linked to infectious diseases, with gastrointestinal illnesses being the most commonly reported outcomes due to faecal contamination from swimmers (WHO, 2006; Rabi *et al.*, 2008). Other associated infections include cryptosporidiosis, otitis externa (swimmer's ear), skin, eye, and respiratory infections (CDC, 2006; Sohrabi *et al.*, 2016).

Proper pool maintenance using pumps, filters, and disinfectants helps reduce microbial transmission and maintain water clarity. However, studies in Nigeria and Ghana have shown high microbial contamination in public pools, with isolates such as *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus*, and other opportunistic pathogens exceeding acceptable limits (Osei-Adjei *et al.*, 2014; Amala and Aleru, 2016). Research indicates that over 36 infectious diseases can be transmitted directly through contaminated recreational waters (Akhionbare, 2009). Infected swimmers can contaminate pool water and surfaces, potentially causing infections in others, while some bacteria form biofilms that persist in the pool environment, increasing health risks (WHO, 2001; Nichols, 2006).

Pathogens of concern in pools include gastrointestinal bacteria such as *Salmonella*, *Shigella*, *Campylobacter*, and *E. coli*; parasitic protozoans such as *Cryptosporidium parvum* and *Giardia duodenalis*; free-living amoebae like *Acanthamoeba* and *Naegleria fowleri*; viruses such as small round structured viruses, rotaviruses, and hepatitis A; and fungi like *Trichophyton* species (Walsh *et al.*, 1996; Hunter, 1997; WHO, 2001; Kujundzic *et al.*, 2012). Chemical contaminants from swimmers, including sweat, urine, cosmetics, and lotions, react with disinfectants to form by-products such as chloramines, trichloramine, cyanogen chloride, and nitrosamines, which pose additional health hazards (WHO, 2016; Arnold and Henry, 2016; Engelhaupt, 2017).

In West Africa, most available studies indicate poor compliance with international water-quality standards (Van Heerden *et al.*, 2005; Abd ElSalam, 2010; Sule and Oyeyiola, 2012; Agbagwa and Young-Harry, 2012). Indicator organisms, such as *E. coli*, are commonly used to monitor faecal contamination due to the difficulty of detecting all pathogens directly (Al-Khatib *et al.*, 2003; Agbagwa *et al.*, 2012). Contaminated swimming pools therefore represent a potential public health hazard, emphasizing the need for regular monitoring, proper maintenance, and regulatory enforcement. The aim of this study was to assess the microbiological and physicochemical qualities of swimming pools in Nnewi North LGA, Nigeria.

Materials and Methods

Study area and sampling universe

The study was carried out in Nnewi North Local Government Area of Anambra State, Nigeria. Nnewi North LGA is situated in the

southeastern part of Nigeria at latitude 6.010519° N and longitude 6.910345° E coordinates. The area comprises the villages of Otolu, Uruagu, Umudim, and Nnewi-ichi, under the traditional ruler Igwe Kenneth Orizu III. Nnewi has an estimated population of 221,500. In the study area, outdoor public swimming pools from seven preselected hotels located in the different villages were the sampling universe. The swimming pools were all rectangular in design, made of concrete and covered with glazed tiles. The pools were also of different sizes, with depths of 1.83 meters respectively, while the average number of swimmers per day ranged between 3 and 25. The pools were filled with water sources from the hotels' borehole facilities, and chlorination was applied for pool water treatment.

Water Sample Collection

Water samples were collected aseptically from seven outdoor swimming pools in Nnewi North LGA using 250 mL sterile glass bottles. The water samples were collected before use and after use by bathers on Saturdays and Sundays between September and November 2024. In this study, 2 samples, 1 before and 1 after use by bathers, were collected from each swimming pool. Water samples were collected from the subsurface of the swimming pools at a depth of approximately 30 cm below the water surface using sterile 250 ml glass bottles. The water samples from the seven swimming pools were labelled A to G, and transported in ice box to Perfect Glory Research Laboratory and Environmental Services Nnewi for analysis.

Determination of total coliforms and faecal coliforms

Total and faecal coliforms were determined using the Most Probable Number (MPN) 3–3–3 method as described by Akeju and Awojobi (2015). Results were expressed using the standard APHA MPN index table. The procedure involved presumptive, confirmed, and completed tests. In the presumptive test, 10 mL of water sample was inoculated into double-strength lactose broth, while 1 mL and 0.1 mL were inoculated into single-strength lactose broth and incubated at 37°C for 24 h, with acid and gas production indicating positive results. Positive tubes were subjected to confirmation test using Brilliant Green Bile Lactose (BGBL) broth and Eosin Methylene Blue (EMB) agar, for total coliform and faecal coliform growth respectively. Gas production in (BGBL) broth and characteristic colonies in (EMB) agar indicated coliform and faecal coliform presence. The completed test involved subculturing on nutrient agar, Gram staining, and biochemical tests like Indole test, Methyl Red test, Voges–Proskauer test, Citrate utilization test (IMVC) to identify the faecal coliforms.

Isolation of bacterial and fungal organisms

Total viable heterotrophic plate counts were determined using pour plate method and spread plate method as described by American Public Health Association (APHA, 2017). One milliliter (1 mL) of the swimming pool water samples were serially diluted with sterile peptone water in ten folds. Total heterotrophic bacteria count was determined using Nutrient agar while total heterotrophic fungal count was estimated using Potato Dextrose Agar (PDA). Using the pour plate method, 1 mL of each water sample was collected using a sterile pipette from 10³ dilution factor, and dropped into sterilized petri plates in triplicate, then a sterilize Nutrient media agar in molten form was poured over the water samples. The mixture of the medium and water sample was rocked on a flat surface to

ensure even mixing. The inoculation was done in triplicate. Afterwards, the plates were incubated in inverted manner at 37°C for 48 h. After incubation, the total viable heterotrophic bacteria count was counted using a colony counter. Using the spread plate method, 0.1 mL of each water samples was collected using a sterile pipette from 10³ dilution factor, and dropped onto the surface of sterile potato dextrose agar plates. The inoculum was evenly spread over the agar surface using a sterile glass spreader. The inoculation was done in triplicate. The inoculated plates were incubated at 28°C for 72–120 h. Afterwards, the visible fungal colonies were counted using a colony counter. The bacterial and fungal colony counts were recorded as colony-forming units per millilitre (CFU/ml).

Characterization and identification of the bacterial and fungal isolates

The characterization and identification of the isolates were identified using standard microbiological methods as described by Holt *et al.* (1994); Cheesbrough (2006), and Willey *et al.* (2008). The bacterial isolates were identified based on morphological characteristics such as shape, size, elevation, surface, colour, structure and biochemical tests such as Gram staining reaction, spore formation, catalase production, coagulase production, motility, indole and urease production, citrate utilization, sugar fermentation, oxidase production, starch hydrolysis, nitrate reduction, hydrogen sulfide production, methyl red and Voges Proskauer. The fungal isolates were identified based on morphological characteristics such as colony texture, colony color, growth rate, colony topography, pigmentation and microscopic examination such as hyphael structure, type and shape of spores, arrangement of spores, specialized structures using Lactophenol cotton blue staining.

Physicochemical Analysis of the water samples

From water samples collected separately as a duplicate of the one used for culture, physicochemical parameters: temperature, pH, turbidity, residual chlorine, calcium hardness, alkalinity, salinity, nitrate, and ammonia were determined using calibrated instruments and standard analytical methods in accordance with APHA (2012). Temperature and pH were measured *in situ* using a mercury thermometer and a calibrated handheld pH meter, respectively. Turbidity was determined using a turbidometer, while residual chlorine was analyzed by iodometric titration. Nitrate and ammonia concentrations were measured spectrophotometrically using brucine and phenate methods, respectively. Calcium hardness, alkalinity, and salinity were determined using standard titrimetric methods.

Antimicrobial sensitivity test of the bacterial and fungal isolates

Antimicrobial susceptibility of bacterial and fungal isolates was determined using the disc diffusion method as described by CLSI (2005) guidelines. Standardized bacterial suspensions equivalent to 0.5 McFarland turbidity standard were prepared in sterile normal saline and inoculated onto Mueller–Hinton agar plates using sterile swab sticks. The antibiotic discs tested were: ciprofloxacin (10 µg), ofloxacin (10 µg), gentamicin (10 µg), ceftazidime (30 µg), pefloxacin (10 µg), ceporex (10 µg), amoxicillin (20 µg), rifampicin (20 µg), ceftriaxone (30 µg), levofloxacin (5 µg), erythromycin (30 µg), streptomycin (30 µg), cefuroxime (30 µg), augmentin (30 µg), and azithromycin (10 µg). The inoculated plates were incubated at 37°C for 24 h, after which zones of inhibition were measured and interpreted as susceptible, intermediate, or resistant according to CLSI N100-S15 (2005) and HiMedia breakpoints criteria. Standardized fungal suspensions equivalent to 0.5 McFarland turbidity standard were prepared in sterile normal saline and inoculated onto Mueller–Hinton agar plates using sterile swab sticks. The antifungal agents tested were: fluconazole (25 µg), griseofulvin (25 µg), itraconazole (10 µg), miconazole (10 µg), nystatin (100 units), and ketoconazole (15 µg). The inoculated plates were incubated at 37°C for 24 h, after which zones of inhibition were measured using calibrated meter rule and interpreted as susceptible, intermediate, or resistant according to HiMedia breakpoints.

Data analysis

Data obtained from the physicochemical parameters, total heterotrophic bacterial counts, total fungal counts, and antimicrobial susceptibility patterns of the bacterial and fungal isolates from the swimming pool water samples before and after use by bathers were subjected to one-way ANOVA using Statistical Package for Service Solutions (SPSS) version 21 for windows evaluation. A p-value = 0.05 was considered statistically significant, indicating whether the swimming pools composition before and after use by bathers is safe for public swimming. Results were presented in texts, Tables, and Figures.

Results

Total heterotrophic bacterial counts ranged from 0–6.33 × 10⁴ cfu/mL before use and 0–6.50 × 10⁴ cfu/mL after use, while fungal counts ranged from 0–2.13 × 10⁵ cfu/mL and 0–3.0 × 10⁵ cfu/mL, respectively (Table 1). The mean total heterotrophic bacterial counts (THBC) before use (49.5714±21.8210) and after use (50.8571±22.4305), and the mean total heterotrophic fungal counts (THFC) before use (13.0476±11.7195) and after use (14.8571±13.5288) obtained from the swimming pools were subjected to one-way ANOVA using the Statistical Package for Service Solution (SPSS) version 21. Before and after use were considered statistically significant at p = 0.05.

Table 1: Total heterotrophic microbial count of the swimming pools before use by bathers

Swimming pools	Bacterial count (CFU/ml)		Fungal count (CFU/ml)	
	BEFORE USE	AFTER USE	BEFORE USE	AFTER USE
A	0	0	0	0
B	5.00×10^4	5.17×10^4	0	0
C	6.30×10^4	6.43×10^4	2.2×10^5	2.23×10^5
D	6.23×10^4	6.27×10^4	2.4×10^5	2.53×10^5
E	5.93×10^4	6.17×10^4	2.4×10^5	3.0×10^5
F	6.33×10^4	6.50×10^4	2.13×10^5	2.67×10^5
G	4.90×10^4	5.07×10^4	0	0

Key: CFU/mL = Coliform forming unit per milliliter; 0 = No colony detected and CFU/mL calculated.

The MPN three-tube results for total coliforms ranged from 0–28 MPN/100 mL before use and 0–93 MPN/100 mL after use (Table 2). Pools C–F recorded the highest counts, with positive tubes varying across the three volumes, reflecting coliform distribution within each pool, while Faecal coliforms also varied across tube volumes, ranging 0–9 MPN/100 mL before use and 0–23 MPN/100 mL after use (Table 2). Pools D, E, and F showed the highest faecal coliform counts, with positive reactions primarily in

the 10 mL and 1 mL tubes. The total coliform and faecal coliform counts before and after bather use were determined using the 3-tube MPN method and reported as MPN index/100 mL. Results were obtained from standard APHA MPN index tables. Values of <3 MPN/100 mL were interpreted as not detected, while values ≥ 3 MPN/100 mL were recorded as positive, indicating the presence of coliforms.

Table 2: Most probable number of total coliforms and faecal coliforms counts in the swimming pools before and after use by bathers

Swimming pools	Total coliforms (MPN index/100 ml)		Faecal coliforms (MPN index/100 mL)	
	before use	after use	before use	after use
A	<3	<3	<3	<3
B	<3	<3	<3	<3
C	4	15	3	4
D	4	11	4	7
E	9	43	4	23
F	28	93	9	11
G	<3	<3	<3	<3

Key: <3 = Not detected; MPN = Most probable number; mL = Millilitre;

The bacterial isolates were characterized based on their colony morphology on nutrient agar and biochemical reactions. Colony features such as shape, size, elevation, surface appearance, colour, and structure, together with biochemical characteristics, facilitated the identification of ten isolates such as *Providencia stuartii*,

Enterobacter intermedius, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus vulgaris*, *Staphylococcus aureus*, *Escherichia coli*, *Bacillus macerans*, *Citrobacter freundii*, and *Salmonella Typhimurium* (Tables 3 and 4).

Table 3: Colonial description of the bacterial strains

Isolate	Colour	Shape	Margin	Elevation	Optic	Surface	Size (mm)
<i>Providencia stuarti</i>	Greyish - white	Round	Convex	Raised	Opaque	Smooth/Moist	3.80
<i>Enterobacter intermedius</i>	Yellow	Round	Entire	Flat	Translucent	Smooth	1.70
<i>Klebsiella pneumonia</i>	Greyish - white	Round	Convex	Raised	Translucent	Mucoid	2.40
<i>Pseudomonas aeruginosa</i>	Grey/Metallic sheen	Round	Convex	Flat	Translucent	Smooth	1.20
<i>Proteus vulgaris</i>	Colourless	Round	Entire	Flat	Transparent	Smooth/Shiny	3.40
<i>Staphylococcus aureus</i>	Golden-yellow	Round	Entire	Raised	Opaque	Smooth/Shiny	2.60
<i>Escherichia coli</i>	Greyish - white	Round	Entire	Raised	Translucent/Opaque	Smooth/Moist	3.10
<i>Bacillus macerans</i>	Greyish - white	Round	Lobate	Flat	Opaque	Dull/Dry	4.10
<i>Citrobacter freundii</i>	Grey	Round	Entire	Flat	Translucent/Opaque	Smooth/Shiny	2.80
<i>Salmonella typhimurium</i>	Greyish - white	Round	Entire	Raised	Translucent	Smooth/Moist	2.20

Table 4: Morphological and biochemical characteristics of the bacterial isolates from the swimming pools

Isolate/ Parameter	1	2	3	4	5	6	7	8	9	10
Gram reaction	-	-	-	-	-	+	-	+	-	-
Shape	rod	rod	rod	rod	rod	coccus	rod	rod	rod	rod
Spore reaction	-	-	-	-	-	-	-	+	-	-
Hydrogen sulphide	-	-	-	+	+	+	-	-	+	+
Coagulase	-	-	-	-	-	+	-	-	-	-
Motility	-	+	-	+	+	-	+	-	-	+
Glucose	-	-	-	+	-	+	+	+	+	+
Sucrose	-	-	-	+	-	+	+	+	+	+
Lactose	-	+	+	-	-	-	+	-	+	-
Inositol	-	-	-	+	+	-	-	+	-	+
Arabinose	-	-	-	+	+	-	-	+	+	+
Mannitol	-	-	-	+	-	+	-	+	-	-
Xylose	-	-	-	+	+	-	-	+	-	-
Rhamnose	-	+	-	+	-	+	-	+	-	+
Sorbitol	+	-	-	+	+	-	-	+	-	-
Citrate	+	+	+	+	+	-	-	-	+	+
Indole	+	-	-	+	+	-	+	+	-	-

Catalase	+	+	+	+	+	+	+	+	+	+
Methyl red	+	+	+	+	+	+	+	+	+	+
Voges Proskauer	-	+	-	+	+	-	-	-	-	+
Oxidase	-	-	-	+	-	-	-	-	-	-
Urease	-	-	+	+	+	+	-	+	-	-
Starch	+	+	+	+	+	+	+	+	+	+
Nitrate reduction	-	+	+	+	+	+	+	+	+	+
Identity	<i>Providencia stuartii</i>	<i>Enterobacter intermedius</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Proteus vulgaris</i>	<i>Staphylococcus aureus</i>	<i>Escheria coli</i>	<i>Bacillus macerans</i>	<i>Citrobacter freundii</i>	<i>Salmonella typhimurium</i>

Five fungal isolates: *Penicillium* sp, *Rhizopus* sp, *Aspergillus* sp, *Curvularia* sp and *Syncephalastrum* sp. were identified using both macroscopic and microscopic characteristics. Colony texture, colour, growth rate, topography, and pigmentation, as well as hyphal characteristics, spore morphology,

spore arrangement, and specialized structures, were used to identify the fungal isolates recovered from the swimming pools (Table 5).

Table 5: Macroscopic and microscopic features of the fungal isolates from the swimming pools.

	Macroscopic characteristics	Microscopic characteristics	Identity
1	White colony at first but developing blue to green color	Small, round spores borne in “brush-like” formations	<i>Penicillium</i> sp.
2	Gray to brown to black colony filling a Petri dish in 2 to 3 days	It has foot-like structures (rhizoids) at base of spore bearing hyphae. Spores sporangium clear, coenocytic hyphae	<i>Rhizopus</i> sp.
3	Flat, compact colonies, white at first then becoming black, green, bluish or yellow	Small one-celled spores irradiating out from swollen base	<i>Aspergillus</i> sp.
4	Dark brown to black colony on both sides ragged in appearance	Large, bent spores with 3 to 5 cells. Similar to <i>Helminthosporium</i> spp. Brown, septate hyphae	<i>Curvularia</i> sp.
5	Gray to brown to black fluffy colony that may fill a Petri dish in a few days.	Broad, clear, nonseptate hyphae, spores in many slender sac-like structures (sporangia) adhere to a swelling on the terminal end of hypha.	<i>Syncephalastrum</i> sp.

Table 6 showed the distribution of bacterial isolates from swimming pools before and after use by bathers. Swimming pools C, D, E and F showed positive occurrences for most bacterial isolates

before and after use, while swimming pool A remained negative to all isolates. Variations in the occurrence of some bacterial isolates were observed in swimming pools B and G.

Table 6: Distribution of the bacterial isolates from the swimming pools before and after use by bathers

Isolate Swimming pools	<i>Providencia stuartii</i>		<i>Enterobacter intermedius</i>		<i>Klebsiella pneumoniae</i>		<i>Pseudomonas aeruginosa.</i>		<i>Proteus vulgaris</i>		<i>Staphylococcus aureus</i>		<i>Escherichia coli</i>		<i>Bacillus macerans</i>		<i>Citrobacter freundii</i>		<i>Salmonella typhimurium</i>	
	Before	After	Before	After	Before	After	Before	After	Before	After	Before	After	Before	After	Before	After	Before	After	Before	After
A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
B	+	-	-	-	-	+	+	+	+	-	+	+	-	-	+	+	-	-	+	-
C	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
D	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
E	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
F	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
G	-	+	-	-	-	-	+	+	-	+	-	+	-	-	+	+	-	-	-	-

Key: + = positive and - = negative

Table 7 showed the distribution of fungal isolates from swimming pools before and after use by bathers. Swimming pools D and E showed positive occurrences for all fungal isolates, while

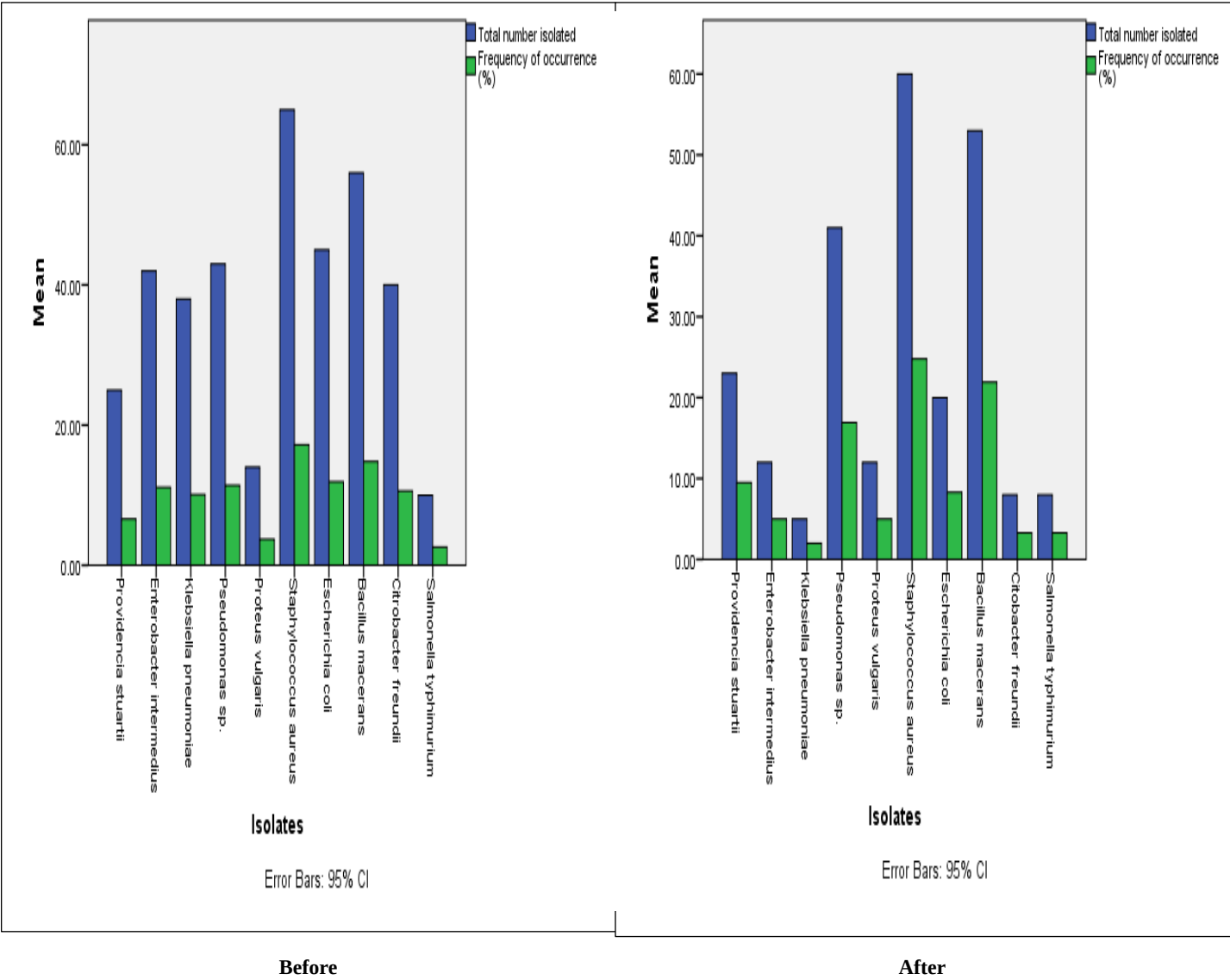
swimming pools A, B and G remained negative to all fungal isolates. Partial occurrence of fungal isolates was observed in swimming pools C and F after use by bathers.

Table 7: Distribution of the fungal isolates from the swimming pools before and after use by bathers

Isolate Pools	<i>Penicillium</i> sp.		<i>Rhizopus</i> sp.		<i>Aspergillus</i> sp.		<i>Curvularia</i> sp.		<i>Syncephalastrum</i> sp.	
	Before	After	Before	After	Before	After	Before	After	Before	After
A	-	-	-	-	-	-	-	-	-	-
B	-	-	-	-	-	-	-	-	-	-
C	+	+	+	-	+	+	+	+	+	-
D	+	+	+	+	+	+	+	+	+	+
E	+	+	+	+	+	+	+	+	+	+
F	+	+	+	-	+	-	+	+	+	-
G	-	-	-	-	-	-	-	-	-	-

Key: + = positive and - = negative

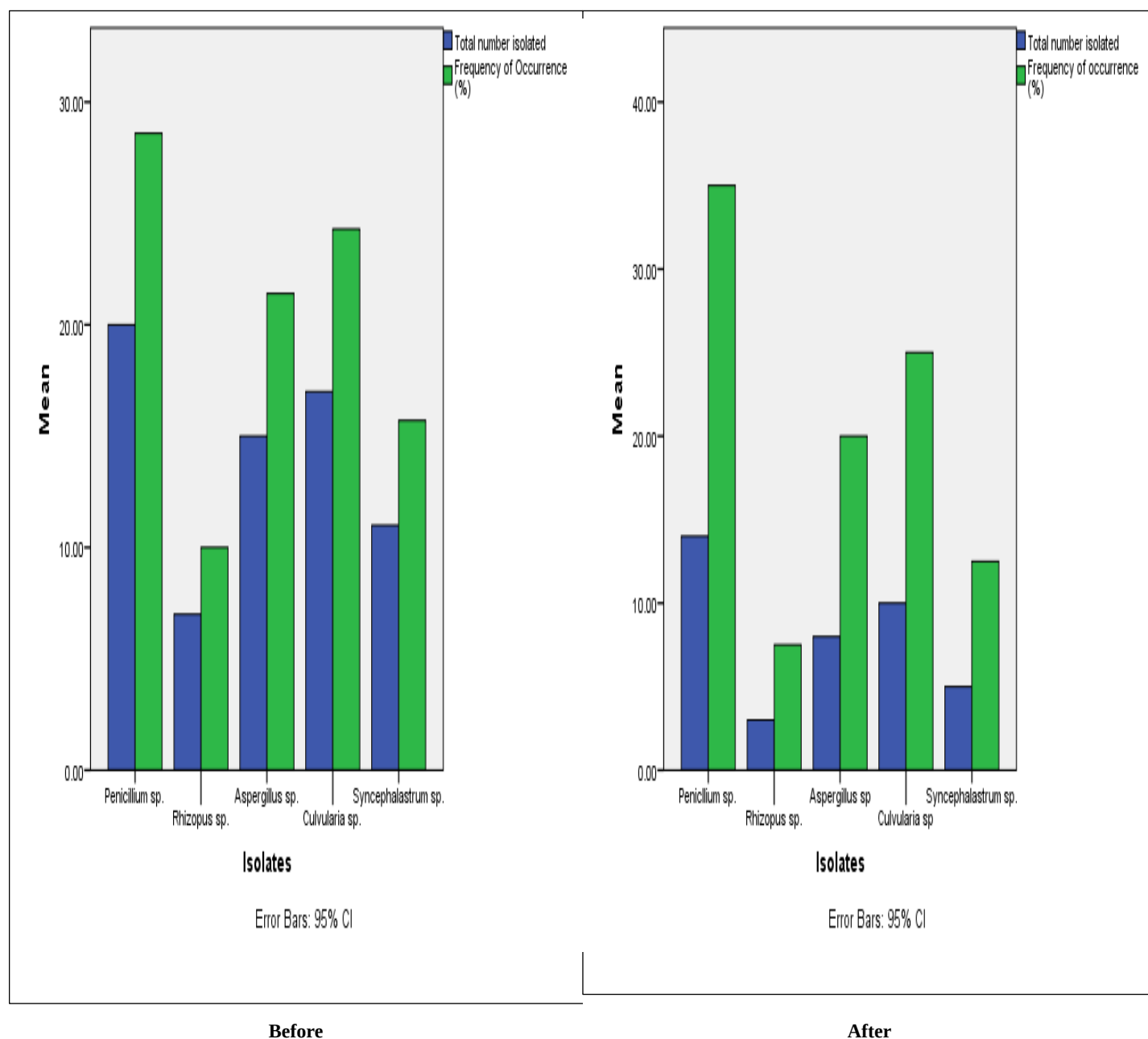
Figures 1 and 2 showed the occurrence of bacterial isolates from swimming pools before and after use by bathers. A total of 242 isolates were identified from the swimming pools before use by bathers. *Staphylococcus aureus* had the highest occurrence 60 (24.8%), followed by *Bacillus macerans* 53 (21.9%) and *Pseudomonas aeruginosa* 41 (16.9%) while *Klebsiella pneumoniae* had the lowest occurrence 5 (2.0%) (Figure1). A total of 378 isolates were identified from the swimming pools after use by bathers. *Staphylococcus aureus* had the highest frequency 65 (17.2%), followed by *Bacillus macerans* 56 (14.8%) and *Escherichia coli* 45 (11.9%) and *Pseudomonas aeruginosa* 43 (11.4) while *Salmonella typhimurium* had the lowest frequency 10 (2.6%) (Figure 2).



Figures 1 and 2: Occurrence of the bacterial isolates from the swimming pools before and after use by bathers.

Figures 3 and 4 showed the occurrence of fungal isolates from swimming pools before and after use by bathers. A total of 40 fungal isolates were identified before use by bathers, with *Penicillium* sp. showing the highest occurrence 14 (35.0%), followed by *Culvularia* sp. 10 (25.0%) and *Aspergillus* sp 8 (20.0%) while *Rhizopus* sp. had the lowest occurrence 3 (7.5%)

(Figure 3). A total of 70 fungal isolates were identified from the swimming pools after use by bathers with *Penicillium* sp. showing the highest occurrence 20 (28.6%), followed by *Culvularia* sp. 17 (24.3%) and *Aspergillus* sp. 15 (21.4%) while *Rhizopus* sp. had the lowest occurrence 7 (10.0%) (Figure 2).



Figures 3 and 4: Occurrence of the fungal isolates of the swimming pools before and after use by bathers

Physicochemical parameters of the swimming pools before use ranged as follows: temperature 25.40–27.20 °C, pH 3.64–7.23, residual chlorine 0.00–2.30 mg/L, total alkalinity 0–150 mg/L, salinity 227.50–796.00 ppt, calcium hardness 0–425 mg/L, turbidity 4.77–14.77 NTU, nitrate 0.13–0.74 µg/L, and ammonia 0.67–0.74 ppm (Table 8) and the mean physicochemical parameters: temperature 26.1800±0.6892°C, pH 5.5629±1.2342, residual chlorine 0.5886±0.8249 mg/L, total alkalinity

92.8329±60.7487 mg/L, salinity 438.6400±178.9208 ppt, calcium hardness 199.6986±181.8023 mg/L, turbidity 9.9071±4.5824 NTU, nitrate 0.3086±0.2040 µg/L, and ammonia 0.6600±0.0265 ppm obtained from the swimming pools before and after bather use were subjected to one-way ANOVA using the Statistical Package for Service Solution (SPSS) version 21. Before use were considered statistically significant at $p = 0.05$

Table 8: Physicochemical properties of the swimming pools before use by bathers

Swimming pools	Temperature (°C)	pH	Residual chlorine level (mg/L)	Total (mg/L)	Alkalinity	Salinity (ppt)	Calcium (mg/L)	hardness	Turbidity (NTU)	Nitrate (µg/L)	Ammonia (ppm)
A	26.70±0.01	7.23±0.16	2.30±0.20	150.00±0.01		796.00±0.01	303.00±0.01		10.35±0.03	0.22±0.04	0.67±0.03
B	25.70±0.02	6.65±0.02	1.24±0.05	150.00±0.02		454.90±0.02	90.00±0.03		14.77±0.04	0.22±0.05	0.68±0.06
C	25.60±0.12	3.64±0.27	0.00	0.00		341.20±0.01	0.00±0.00		14.64±0.03	0.32±0.03	0.74±0.05
D	26.35±0.20	5.43±0.02	0.00	150.00±0.01		454.90±0.02	0.00±0.00		11.50±0.04	0.46±0.02	0.68±0.01
E	27.20±0.15	5.10±0.05	0.00	50.00±0.03		341.20±0.03	170.00±0.01		4.77±0.02	0.13±0.01	0.70±0.02
F	25.40±0.03	5.17±0.01	0.00	50.00±0.04		227.50±0.02	425.00±0.03		10.73±0.02	0.74±0.03	0.73±0.05
G	26.90±0.06	6.27±0.02	0.89±0.10	100.00±0.01		454.90±0.01	410.00±0.03		2.81±0.03	0.26±0.02	0.67±0.03

Key: °C = Degree centigrade; mg/L = Milligram per litre; ± = values represent standard error of mean of triplicate values; 0.00 = Not detected; ppt = Part Per Thousand, µg/L = Microgram per litre; mg/L = Milligram per litre; ppm = Part Per Million.

After use ranged as follow: temperature 27.50–28.90 °C, pH 3.28–6.50, residual chlorine 0.00–1.95 mg/L, total alkalinity 0–250 mg/L, salinity 227.50–341.30 ppt, calcium hardness 0–210 mg/L, turbidity 13.04–18.62 NTU, nitrate 0.15–2.77 µg/L, and ammonia 0.71–0.93 ppm (Table 9) and the mean physicochemical parameters: temperature 28.3129±0.6415 °C, pH 5.3186±1.101, residual chlorine 0.5171±0.7393 mg/L, total alkalinity 160.0043±81.8627 mg/L, salinity 231.4200±104.7148 ppt, calcium hardness 78.5114±73.3146 mg/L, turbidity 14.8271±2.4729 NTU, nitrate 1.1171±0.9865 µg/L, and ammonia 0.7729±0.7387 ppm obtained from the swimming pools after bather use were subjected to one-way ANOVA using the Statistical Package for Service Solution (SPSS) version 21. Before and after use were considered statistically significant at p = 0.05

Table 9: Physicochemical properties of the swimming pools after use by bathers

Swimming pools	Temperature (°C)	pH	Residual chlorine level (mg/L)	Total (mg/L)	Alkalinity	Salinity (ppt)	Calcium (mg/L)	hardness	Turbidity (NTU)	Nitrate (µg/L)	Ammonia (ppm)
A	28.90±0.03	6.47±0.03	1.95±0.04	250.00±0.02		341.20±0.02	90.00±0.02		13.04±0.03	0.30±0.06	0.75±0.01
B	27.90±0.10	6.50±0.01	0.98±0.04	200.00±0.01		227.50±0.04	50.00±0.04		18.62±0.06	2.77±0.04	0.75±0.03
C	27.50±0.04	3.28±0.02	0.00	0.00		341.30±0.02	0.00±0.00		16.14±0.05	0.76±0.01	0.78±0.01
D	28.60±0.23	5.36±0.03	0.00	200.00±0.02		227.50±0.03	0.00±0.00		15.54±0.02	0.47±0.04	0.79±0.01
E	29.50±0.13	4.82±0.03	0.00	200.00±0.02		227.50±0.01	120.00±0.04		10.73±0.06	0.15±0.01	0.93±0.02
F	28.20±0.05	4.96±0.02	0.00	150.00±0.03		227.50±0.03	210.00±0.05		14.97±0.03	1.53±0.05	0.85±0.04
G	28.00±0.02	5.88±0.02	0.80±0.05	120.00±0.03		227.50±0.02	80.00±0.02		14.97±0.03	2.04±0.02	0.71±0.02

Key: °C = Degree centigrade; mg/L = Milligram per litre; ± = values represent standard error of mean of triplicate values; 0.00 = Not detected; ppt = Part Per Thousand, µg/L = Microgram per litre; mg/L = Milligram per litre; ppm = Part Per Million.

Bacterial Isolates were mostly sensitive to ofloxacin, ciprofloxacin and levofloxacin, intermediate to gentamicin, streptomycin, rifampicin, erythromycin, azithromycin, cefuroxime, ceftriaxone and ceftazidime and resistant to amoxicillin, augmentin, cefuroxime, ceftriaxone, ceftazidime (Table 10).

Table 10: Antibacterial sensitivity patterns (mm) of the bacterial isolates from the swimming pools before and after use by bathers

Antibiotic agents/breakpoint sources	<i>Providencia stuartii</i>	<i>Enterobacter intermedium</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Proteus vulgaris</i>	<i>Staphylococcus Aureus</i>	<i>Escherichia coli</i>	<i>Bacillus macerans</i>	<i>Citrobacter freundii</i>	<i>Salmonella typhimurium</i>
Ceporex 10 µg HiMedia S _≥ 18, I 15-17, R _≤ 14	29.00±0.10 (S)	0.00 (R)	14.00±0.02 (R)	0.00 (R)	0.00 (R)	16.00±0.03 (I)	12.00±0.05 (R)	0.00 (R)	24.00±0.10 (S)	0.00 (R)
Ofloxacin 10 µg HiMedia S _≥ 16, I 13-15, R _≤ 12	28.00±0.10 (S)	21.00±0.04 (S)	30.00±0.04 (S)	22.00±0.09 (S)	21.00±0.05 (S)	28.00±0.02 (S)	24.00±0.10 (S)	24.00±0.08 (S)	0.00 (R)	20.00±0.04 (S)
Augmentin 30 µg CLSI S _≥ 18, I 14-17, R _≤ 13	0.00 (R)	0.00 (R)	11.00±0.05 (R)	0.00 (R)	0.00 (R)	12.00±0.01 (R)	0.00 (R)	0.00 (R)	22.00±0.02 (S)	0.00 (R)
Peflacin 10 µg HiMedia S _≥ 21, I 16-20, R _≤ 15	30.00±0.05 (S)	21.00±0.05 (S)	26.00±0.10 (S)	12.00±0.05 (R)	29.00±0.10 (S)	29.00±0.01(S)	36.00±0.20 (S)	26.00±0.06 (S)	0.00 (R)	22.00±0.01 (S)
Ceftazidime 30 µg CLSI S _≥ 18, I 15-17, R _≤ 14	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)	12.00±0.04 (R)	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)
Gentamicin 10 µg CLSI S _≥ 15, I 13-14, R _≤ 12	20.00±0.10 (S)	14.00±0.04 (I)	18.00±0.10 (S)	0.00 (R)	0.00 (R)	18.00±0.04 (S)	16.00±0.20 (S)	16.00±0.07 (S)	16.00±0.03 (S)	14.00±0.04 (I)
Ciprofloxacin 10 µg HiMedia S _≥ 21, I 16-20, R _≤ 15	30.00±0.03 (S)	20.00±0.03 (I)	28.00±0.08 (S)	18.00±0.03 (I)	24.00±0.10 (S)	32.00±0.10 (S)	26.00±0.06 (S)	26.00±0.08 (S)	0.00 (R)	22.00±0.10 (S)
Ceftriaxone 30 µg CLSI S _≥ 21, I 14-20, R _≤ 13	13.00±0.06(R)	0.00 (R)	0.00 (R)	16.00±0.10 (I)	0.00 (R)	0.00 (R)	0.00 (R)	14.00±0.02 (I)	22.00±0.01 (S)	0.00 (R)
Streptomycin 30 µg HiMedia S _≥ 15, I 12-14, R _≤ 11	22.00±0.10 (S)	18.00±0.10 (S)	22.00±0.10 (S)	14.00±0.05 (I)	19.00±0.06 (S)	20.00±0.10 (S)	22.00±0.10 (S)	0.00 (R)	22.00±0.03 (S)	12.00±0.10 (I)
Cefuroxime 30 µg CLSI S _≥ 18, I 15-17, R _≤ 14	16.00±0.05 (I)	0.00 (R)	14.00±0.04 (R)	0.00 (R)	0.00 (R)	4.00±0.03 (R)	0.00 (R)	0.00 (R)	22.00±0.07 (S)	0.00 (R)
Rifampicin 20 µg HiMedia S _≥ 20, I 17-19, R _≤ 16	22.00±0.05 (S)	13.00±0.01 (R)	16.00±0.02 (R)	0.00 (R)	0.00 (R)	15.00±0.06 (R)	11.00±0.01 (R)	14.00±0.03 (R)	22.00±0.01 (S)	12.00±0.01 (R)

Azithromycin 10 µg HiMedia S _≥ 18, I 14-17, R _≤ 13	22.00±0.03 (S)	17.00±0.03 (I)	20.00±0.05 (S)	15.00±0.03 (I)	0.00 (R)	24.00±0.02 (S)	18.00±0.05 (S)	0.00 (R)	26.00±0.08 (S)	16.00±0.10 (I)
Amoxicillin 20 µg HiMedia S _≥ 17, I 14-16, R _≤ 13	22.00±0.01 (S)	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)	14.00±0.01 (I)	0.00 (R)	0.00 (R)	26.00±0.10 (S)	0.00 (R)
Erythromycin 30 µg HiMedia S _≥ 23, I 14-22, R _≤ 13	26.00±0.03 (S)	29.00±0.08 (S)	12.00±0.01 (R)	0.00 (R)	0.00 (R)	18.00±0.01(I)	0.00 (R)	20.00±0.02 (I)	28.00±0.10 (S)	16.00±0.02 (I)
Levofloxacin 5 µg CLSI S _≥ 17, I 14-16, R _≤ 13	29.00±0.02 (S)	28.00±0.07 (S)	31.00±0.07 (S)	18.00±0.05(S)	30.00±0.05 (S)	12.00±0.04 (R)	28.00±0.01 (S)	24.00±0.02 (S)	0.00 (R)	0.00 (R)

Key: 0.00 = No zone of inhibition; ± values represent standard error of mean of triplicate values

R = Resistant, I = Intermediate, S = Susceptible

All fungal isolates were resistant to tested antifungal agents, except *Penicillium* sp., which showed intermediate sensitivity to miconazole (Table 11).

Table 11: Antifungal sensitivity patterns (mm) of the fungal isolates from the swimming pools before and after use by bathers.

Isolates	Nystatin 100 units HiMedia S _≥ 15, I 10-14, R _≤ 9	Fluconazole 25 µg HiMedia S _≥ 19, I 15-18, R _≤ 14	Griseofulvin 25 µg HiMedia S _≥ 20, I 10-19, R _≤ 9	Itraconazole 10 µg Himedia S _≥ 20, I 10-19 R _≤ 9	Miconazole 10 µg HiMedia S _≥ 20, I 12-19, R _≤ 11	Ketoconazole 15 µg HiMedia S _≥ 28, I 21-27, R _≤ 20
<i>Penicillium</i> sp.	6.00 (R)	0.00 (R)	0.00 (R)	6.00 (R)	12.00 (I)	6.00 (R)
<i>Rhizopus</i> sp.	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)
<i>Aspergillus</i> sp.	7.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)
<i>Curvularia</i> sp.	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)	0.00 (R)
<i>Syncephalastrum</i> sp.	0.00 (R)	0.00 (R)	0.00 (R)	6.00 (R)	5.00 (R)	0.00 (R)

Key: 0.00 = No zone of inhibition; ± values represent standard error of mean of triplicate values

R = Resistant, I = Intermediate, S = Susceptible

Discussion

Swimming pool water quality is critical due to the risk of waterborne illnesses (Dufour *et al.*, 2006; Fewtrell *et al.*, 2015). In this study, total heterotrophic bacterial counts (THBC) before bather use ranged from 0 CFU/mL (Pool A) to 6.33×10^4 CFU/mL (Pool F) (Table 1), increasing slightly after use, reflecting bather contamination and inadequate disinfection. Total heterotrophic fungal counts (THFC) similarly showed elevated levels, particularly in Pools D and E (Table 1), suggesting fungal proliferation due to organic matter accumulation and moist conditions (Akinyemi *et al.*, 2011; Papadopoulou *et al.*, 2008).

The total coliform counts and faecal coliform counts (Table 2) recorded in swimming pools C, D, E, and F before and after use indicate microbial contamination, with higher counts observed after use by bathers. Similar findings by Amala *et al.* (2016) associated increased coliform levels with inadequate disinfection, poor hygiene, and high bather load. The presence of coliforms above WHO (2006) and EPA (2003) recommended limits of 0 MPN/100 ml for total and faecal coliforms suggests poor sanitary conditions and potential public health risks.

The bacterial (ten) and fungal (five) isolates (Tables 3-5) were identified from the swimming pools. The predominance of bacteria such as *Providencia stuartii*, *Enterobacter intermedius*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus vulgaris*, *Escherichia coli*, *Citrobacter freundii*, *Salmonella typhimurium* agrees with the findings of Papadopoulou *et al.* (2008) and Akinyemi *et al.* (2011), who associated their occurrence with faecal contamination and their ability to survive in moist chlorinated environments. The presence of *Staphylococcus aureus* and *Bacillus* species is also consistent with the reports of Bello *et al.* (2012) and Willey *et al.* (2020), who linked them to human skin flora and spore-forming ability, respectively. Similarly, the fungal isolates such as *Penicillium* sp., *Rhizopus* sp., *Aspergillus* sp., *Curvularia* sp., and *Syncephalastrum* sp identified correspond with reports by WHO (2006), Nanbakhsh *et al.* (2004) and Rezaei *et al.* (2021), which attributed their occurrence in swimming pools to airborne spores, organic matter accumulation, high moisture levels, and inadequate sanitation.

The distribution of bacterial and fungal isolates (Tables 6 and 7) varied among the swimming pools before and after use by bathers. *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Escherichia coli*, and *Salmonella typhimurium* were among the commonly isolated bacteria, particularly in swimming pools C, D, E, and F, while fungal isolates included *Penicillium* sp., *Aspergillus* sp., *Curvularia* sp., *Fusarium* sp., and *Rhizopus* sp. Similar findings have been reported by Amala *et al.* (2016), Jankowski *et al.* (2017), Nanbakhsh *et al.* (2004) and Rezaei *et al.* (2021), who associated these microorganisms with poor sanitation, inadequate disinfection, high humidity, and high bather load. The persistence of these isolates before and after use suggests varying levels of contamination and differences in pool management practices.

The overall rise in microbial isolates from 242 before use to 378 after use by bathers for bacteria and 40 before use to 70 after use for fungi (Figures 1–4), indicates increased microbial contamination associated with bather activities and inadequate disinfection. *Staphylococcus aureus* and *Penicillium* sp. were the predominant bacterial and fungal isolates, respectively, before and

after use. Similar findings have been reported by Amala *et al.* (2016), Nanbakhsh *et al.* (2004) and Rezaei *et al.* (2021), who associated the presence of *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Aspergillus* sp., and *Penicillium* sp. with heavy bather load, environmental contamination, and poor pool hygiene. The detection of *Escherichia coli* and *Salmonella typhimurium* further suggests possible faecal contamination and potential public health risks.

Increases in temperature, turbidity, nitrate, ammonia, and alkalinity, alongside reduced pH and residual chlorine after use (Table 9), indicate bather-induced deterioration of pool water quality and compromised disinfection efficiency. These findings align with EPA (2003), and Omotayo *et al.* (2016), highlighting organic loading and poor maintenance as major contributing factors. The widespread resistance of bacterial isolates to amoxicillin, augmentin, cefuroxime, ceftriaxone, ceftazidime, and high antifungal resistance (Tables 10 and 11) further raise concerns about antimicrobial-resistant organisms in recreational waters. The high resistance observed is likely driven by sewage and agricultural runoff selecting for resistant strains (Chigor *et al.*, 2020; WHO, 2018; Fisher *et al.*, 2022).

Overall, statistical analysis showed significant p-values = (0.05) before and after use by bathers in the mean microbiological and physicochemical analysis carried out, indicating potential water quality issues. These findings underscore the need for regular monitoring, improved disinfection, and strict adherence to pool hygiene standards to mitigate the risk of waterborne infections.

Conclusion

Most swimming pools evaluated in this study failed to comply with recommended microbiological and physicochemical standards of the World Health Organization (WHO, 2006) and Environmental Protection Agency (EPA, 2003) for recreational water quality, particularly after bather use. Elevated microbial contamination, reduced residual chlorine, and imbalanced pH indicate ineffective disinfection and poor management practices, posing significant public health risks. The high level of antimicrobial resistance observed among bacterial and fungal isolates further highlights the potential of recreational waters as reservoirs of resistant pathogens. The significant p-values (0.05) before and after bather use indicate contamination of the swimming pools. Overall, these findings emphasize the risk of waterborne infections and the need for stricter monitoring and adherence to water-quality standards.

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