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Research Article

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Bacteriological and physicochemical properties of sullage in the city of Ilhéus, Bahia, Brazil

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A B S T R A C T

The study evaluated the microbiological and physicochemical properties of sullage from sources like kitchens, showers, and laundry collected from various residential and commercial locations across four zones in Ilhéus City, Bahia State, Brazil. From October 2024 to February 2025, 100 sullage samples, 20 each from laundry, dishwashing, mopping, sink, and air conditioning (AC) outlets, were analyzed using standard bacteriological and biochemical techniques. Results showed a generally high bacterial load across all zones and sample types. Total bacterial counts ranged from $1.0\pm0.31\times10^3$ to $70.0\pm0.32\times10^3$ CFU/ml, while total coliform counts showed similar elevated ranges. Specifically, the Central Zone's laundry samples and the North Zone's mopping samples exhibited some of the highest bacterial counts. Gene sequencing identified five bacterial strains: *Enterobacter strain MF3714*, *Proteus strain FCC64*, *Achromobacter strain MZ-19*, *Bacillus strain RD_MAAMIA_19*, and *Shewanella strain ST305*. *Enterobacter* sp. was the most prevalent isolate across mopping (29.0%), dishwashing (27.0%), laundry (23.0%), and AC outlet (24.0%) samples. In sink samples, *Proteus* sp. was the most frequent (27.0%). While most physicochemical parameters and heavy metal contents were within WHO permissible limits, the levels of copper (Cu), iron (Fe), and cadmium (Cd) exceeded these standards. The high bacterial load observed in the study indicates serious contamination. Hence, proper treatment of sullage before re-use will help minimize the risk of pathogenic microbes that can cause diseases, negatively affecting plant growth, development, and overall productivity.

INTRODUCTION

Sullage is wastewater usually generated from the kitchen sink, shower, laundry or washing machine, and AC outlet (Samayamanthula *et al*., 2019). It is often referred to as Grey-water because when stored for even a short period, the water will often cloud and turn grey. It does not create bad smells as organic matter content is less or in negligible amount (Oteng-peprah and Nanne, 2018). Sullage contains microorganisms such as *Escherichia coli*, *Pseudomonas* sp. and *Staphylococcus aureus*. Also, soil contents such as sand, stones, and inorganic matter are associated with sullage (Kusumawardhana *et al*., 2021). Sullage usually contains some traces of human waste, and it is therefore not free of pathogens. The excreta come from washing the anal area in the bath and shower or from the laundry (Mohammed *et al*., 2017). The quality of sullage can deteriorate rapidly during storage because it is often warm and contains some nutrients and organic matter as well as pathogens (Mohammed *et al*., 2017). Stored sullage also leads to odour nuisances for the same reason. In households with conventional flush toilets, sullage makes up about 65% of the total wastewater produced by that household (Radha *et al*., 2019).

Much of the daily generated wastewater can be recognised as sullage. It can be used for different purpose, such as garden watering, ornamental uses in fountains and waterfalls, landscaping, lawn irrigation, car washing and toilet flushing. Sullage re-use utilizes on-site resource which could otherwise be wasted. As a result of re-use, fresh drinking

water are conserved which in turn enables the water to remain in natural ecosystem (Ungureanu *et al*., 2020).

Sullage re-use succeeds in saving money spent by water authorities, reduces sewage flows, and reduces the public demand on portable water supplies. By re-using sullage, the load on sullage disposal systems is reduced, and therefore, the life of the wastewater disposal system is prolonged and capital expenditure required for the upgrading and expansion system is delayed (Davis, 2003).

Demand on conventional water supplies and pressure on sewage treatment systems is reduced by the use of sullage. Re-using sullage also reduces the volume of sewage effluent entering watercourses, which can be ecologically beneficial (Ungureanu *et al*., 2020).

Ilhéus is a tourist City and one of the biggest exporters of cocoa beans in the world. Because the City focuses on agricultural production on a large scale, it became necessary to evaluate other water sources to enhance irrigational activities by assessing the bacteriological and physicochemical properties of various sullage water sources for use in the agricultural sector. The study also considered the significance of sullage recycling for domestic re-use for public health interest. The study was the first carried out in the region.

MATERIALS AND METHODS

Study Sites

The study was carried out in Ilhéus City. Ilhéus is a major City located in the southern coastal region of Bahia, Brazil. 211 km south of Salvador, the state's capital. The city was founded in 1534 as Vila de São Jorge dos Ilhéus and is known as one of the most important tourism centers of the northeast of Brazil. The city is located at coordinates 14°47′20″S 39°02′56″W.

Sample Collection

The sources of sullage examined were: Mopping, Dishwashing, Laundry, Sink, and A.C. Outlet. A total of 100 samples, 20 each of the various sullage sources, were collected early in the morning when cleaning in most households was at its peak at different time intervals between October 2024 to February 2025. Residential areas, including both educated and uneducated households as well as a restaurant, were randomly selected for the study across the four zones of Ilhéus City. These zones comprise the North Zone (Iguape, Barra, Tabby, Savoia); South Zone (Pontal, Our Lady of Victoria, Olivenca, Hermanisa); West Zone (Salobrinho, Victoria Bank, Teitonio Viella, Waterfall Village); and Central Zone (Market Square and the vicinity of the Federal Police). At each sampling site, the sample bottles were opened under the sullage in a suitable container, filled up, and closed under water. Once collected, the samples were appropriately fixed in the field and transported in an ice-cooled cool box to the research laboratory at the Environmental Monitoring Laboratory and Microbial Biotechnology Laboratory of the State University of Santa Cruz. Bacteriological examination of the samples commenced within six hours after sampling. In cases where immediate laboratory analysis was not possible, the samples were held at 4°C until the time of analysis.

Preparation of serial dilution of water samples

This was carried out by procedure reported by Cheesebrough (2005). One mil (1 ml) of water sample was added to 9 ml of sterile distilled water, and the test tube was labeled $10^{-1,}$ then shaken to obtain a complete mixture. 1mil of the mixture was then transferred into the next tube containing 9mil distilled water, $10^{-2,}$ and this was repeated up to 10^{-6}.

Isolation and purification of bacterial isolates

The serially diluted samples, zero-point one mil (0.1ml), were transferred into sterile petri dishes and sterilized nutrient agar, Eosin methylene blue agar (EMB) were poured into the Petri dishes under aseptic conditions, and it was then allowed to solidify. The plates were incubated at 37^0C for 24 hours. After incubation, the number of discrete colonies was counted in terms of colony-forming units. Isolated single colonies were picked, purified on nutrient agar plates, sub-cultured, and stocked in brain heart broth slants with 1% NaCl for further studies.

Isolation of coliforms

The membrane filtration technique was carried out to isolate the microorganisms present in the water samples. The funnel of the membrane filtration unit has a capacity of 50ml and the funnel was mounted on a receptacle fixed to the vacuum pump, which allows the water to flow over the porous sterile membrane filter (0.45 µm). Aseptically, the membrane filters were placed on MacConkey agar plates using sterile forceps after passage of 100ml of the water sample. The media was prepared and autoclaved at 121 ^{O}C for 15 minutes at 15Ib before being inoculated with membrane filters (Cheesebrough, 2005).

Identification of Bacterial Isolates

This was carried out by the methods reported by Cheesebrough (2005). The various morphological and biochemical tests were Gram staining reaction, motility test, catalase test, citrate utilization test, oxidase test, urease test, indole test, and triple sugar iron test.

DNA Extraction

DNA extraction was carried out following the method described by Inceoglu *et al.* (2010). Single colonies grown on a solid medium were transferred to 1.5 ml of liquid medium, and the cultures were incubated on a shaker for 48 hours at 28°C. After incubation, the cultures were centrifuged at 4,600 g for 5 minutes. The resulting pellets were re-suspended in 520 µl of TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0). Next, 15 µl of 20% SDS and 3 µl of Proteinase K (20 mg/ml) were added to the suspension, which was then incubated for 1hr at 37°C. Afterward, 100 µl of 5 M NaCl and 80µl of a 10% CTAB solution in 0.7 M NaCl were added and the mixture was vortexed. The suspension was incubated at 65°C for 10 minutes and then placed on ice for 15 minutes. An equal volume of chloroform: isoamyl alcohol (24:1) was added, followed by a 5-minute incubation on ice and centrifugation at 7,200 g for 20 minutes. The aqueous phase was carefully transferred to a new tube, and isopropanol was added in a 1:0.6 ratio to

precipitate the DNA, which was then stored at –20°C for 16 hours. The DNA was collected by centrifugation at 13000 g for 10 minutes, washed with 500 µl of 70% ethanol, air-dried at room temperature for approximately three hours, and finally dissolved in 50 µl of TE buffer.

Polymerase Chain Reaction

The PCR sequencing preparation cocktail included 10 µl of 5x Go Taq colorless reaction buffer, 3 µl of 25 mM MgCl2, 1 µl of a 10 mM dNTPs mix, and 1 µl of each primer (27F: 5'-AGA GTT TGA TCM TGG CTC AG-3' and 1525R: 5'-AAGGAGGTGATCCAGCC-3'). Additionally, it contained 0.3 units of Taq DNA polymerase (Promega, USA) and was made up of a total volume of 42 µl with sterile distilled water, along with 8 µl of DNA template.

PCR was performed using a Gene Amp 9700 PCR System Thermal Cycler (Applied Biosystems Inc., USA) with the following profile: an initial denaturation step at 94°C for 5 minutes, followed by 30 cycles consisting of denaturation at 94°C for 30 seconds, annealing at 50°C for 60 seconds, and extension at 72°C for 1 minute and 30 seconds. The program concluded with a final termination step at 72°C for 10 minutes, followed by chilling at 4°C.

To confirm the amplification of the approximately 1.5 Mb gene fragment, the integrity of the PCR product was checked on a 1.5% agarose gel. The agarose gel was prepared using 1X TAE buffer. This procedure was previously done by (Inceoglu *et al*., 2010; Odeyemi *et al*., 2018).

Purification of Amplified Product

After confirming the gel integrity, the amplified fragments were purified using ethanol to remove the PCR reagents. In a new sterile Eppendorf tube (1.5 ml), 7.6 µl of 3M sodium acetate and 240 µl of 95% ethanol were added to approximately 40 µl of the PCR amplified product. The mixture was thoroughly vortexed and then stored at -20°C for at least 30 minutes.

Following this, the samples were centrifuged at 13000g and 4°C for 10 min. The supernatant was carefully removed by inverting the tube over a trash container. The pellet was then washed by adding 150 µl of 70% ethanol, mixed, and centrifuged again for 15 min at 7500 g and 4°C. The supernatant was removed once more, and the tube was inverted on a paper towel to allow it to dry in the fume hood at room temperature for 10-15 minutes. Finally, the pellet was resuspended in 20 µl of sterile distilled water and stored at -20°C before sequencing. The purified fragment was checked on a 1.5% agarose gel, which was run at a voltage of 110V for about 1 hour, as previously described, to confirm the presence of the purified product. The concentration was quantified using a NanoDrop model 2000 from Thermo Scientific. This was performed following the report of Inceoglu *et al*. (2010) and Odeyemi *et al*. (2018).

Sequencing

The amplified fragments were sequenced using an Applied Biosystems 3130xl Genetic Analyzer, following the manufacturer's manual. The sequencing kit utilized was the BigDye Terminator v 3.1 cycle sequencing kit. For all genetic analyses, Bio-Edit software and MEGA 6 were employed. Initially, samples were identified through sequencing and by performing a BLAST search of the 16S ribosomal RNA. This procedure was performed as reported by (Inceoglu *et al*., 2010; Odeyemi *et al*., 2018).

Physicochemical Analysis of Water Samples

The temperature of the water samples was recorded at the collection sites using a simple thermometer calibrated in degrees Celsius (°C), as described by Inceoglu *et al*. (2010). Electrical conductivity was measured with a CDM 83 conductivity meter (Radio Meter A/S, Copenhagen, Denmark). Turbidity and pH were assessed on-site using the Water Proof Scan 3+ Double Junction and HI 98311-HI 98312 (Hanna) meters from Wagtech International, UK. The samples were stored under deep freezing conditions at a temperature of –°C until analysis. Other physicochemical characteristics measured included hardness, which was determined by titrimetric methods; total dissolved solids and total suspended solids, assessed by gravimetric methods; acidity and alkalinity, evaluated through titrimetric tests; and both nitrate and sulfate, determined colorimetrically using Spectronic-20 (Gallenkamp, UK) as described by AOC (2005). Calcium and magnesium levels were analyzed using the EDTA titration method.

Data analysis

The data were presented using numerical counts and percentages. Descriptive statistics were employed for data analysis, and the results were shown as percentages.

RESULTS

Table 1 represents the total bacterial count of sullage samples. The total bacterial counts of sullage samples collected from the North Zone ranged from 1.0 ± 0.11 to 52.0 ± 0.22 × 10^3 CFU/ml for A.C. Outlet and mopping, respectively. In the Central Zone, bacterial counts varied from 1.0 ± 0.16 to 70.0 ± 0.32 × 10^3 CFU/ml for A.C. Outlet and laundry, respectively. For the West Zone, total bacterial counts ranged from 1.0 ± 0.31 to 14.0 ± 0.13 × 10^3 CFU/ml for A.C. Outlet and mopping. In the South Zone, the total bacterial count spanned from 1.0 ± 0.24 to 16.0 ± 0.19 × 10^3 CFU/ml for A.C. Outlet and dishwashing. The total coliform count of sullage samples is presented in Table 2. The total coliform counts of sullage samples in the North Zone ranged from 1.0 ± 0.44 to 28.0 ± 0.40 × 10^3 CFU/ml for A.C. Outlet and mopping, respectively. In the Central Zone, counts ranged from 1.0 ± 0.11 to 52.0 ± 0.22 × 10^3 CFU/ml for A.C. Outlet and mopping. The West Zone reported total coliform counts from 1.0 ± 0.16 to 20.0 ± 0.40 × 10^3 CFU/ml for A.C. Outlet and laundry, while the South Zone showed counts from 1.0 ± 0.16 to 36.0 ± 0.40 × 10^3 CFU/ml for A.C. Outlet and dishwashing. The total fungal counts for the various zones are presented in Table 3. Total fungal counts in the North Zone ranged from 1.0 ± 0.5 to 34.0 ± 0.17 × 10^3 CFU/ml for A.C. Outlet and laundry. In the Central Zone, counts varied from 2.0 ± 0.15 to 48.0 ± 0.12 × 10^3 CFU/ml for A.C. Outlet and dishwashing. The West Zone reported total fungal counts ranging from 1.0 ± 0.41 to 28.0 ± 0.42 × 10^3 CFU/ml for A.C. Outlet and laundry, while the South Zone showed a range of 3.0 ± 0.25 to 44.0 ± 0.28 × 10^3

CFU/ml for A.C. Outlet and mopping. Gene sequencing identified five bacterial strains, including *Enterobacter* sp. MF3714, *Proteus mirabilis* strain FCC64, *Achromobacter* strain MZ-19, *Bacillus* strain RD_MAAMIA_19, and *Shewanella* strain ST305 as represented in Figures 1 to 5. Table 5 presents the frequency of bacterial isolates identified from sullage samples. *Enterobacter* sp. was the most prevalent bacterium found in mopping samples, comprising 29.0% of the isolates, while *Shewanella* sp. was the least common, at 12.0%. In dishwashing samples, *Enterobacter* sp. again emerged as the predominant isolate at 27.0%, with *Shewanella* sp. being the least dominant at 14.0%. In laundry samples, *Enterobacter* sp. represented 23.0% of the isolates, while *Shewanella* sp. was the least prevalent at 15.0%. For sink samples, *Proteus mirabilis* was the most frequently isolated bacterium, accounting for 27.0%, whereas *Bacillus* sp. was the least dominant at 10.0%. Lastly, in A.C. outlet samples, *Enterobacter* sp. made up 24.0% of the isolates, with *Shewanella* sp. again being the least common, comprising 17.0%. The physicochemical and heavy metal compositions of the sullage samples are presented at Table 6 and Table 7 respectively. Although the temperature of the sullage samples were higher than the allowable limit. The alkaline pH and all other physicochemical parameters were within the permissible limit of the World Health Organisation (2011) and Federal ministry of Environment. Heavy metals content observed also fell within the permissible limit except (Cu), (Fe) and (CD) which were significantly higher

Table 1: Total bacterial count (CFU/ml) of the sullage samples obtained from various zones ($\times 10^3$)

Samples	North	Central	West	South
Mopping	52.0± 0.22	23.0± 0.32	14.0± 0.13	7.5± 0.19
Dish washing	16.4± 0.55	18 ± 0.12	5.0 ± 0.12	16.0± 0.12
Laundry	20.0± 0.36	70.0 ± 0.10	6.0 ± 0.55	5.3± 0.55
Sink	1.4 ± 0.22	3.6 ± 0.21	4.0 ± 0.21	3.2± 0.21
A.C outlet	1.0 ± 0.11	1.0 ± 0.16	1.0 ± 0.31	1.0± 0.24

Table 2: Total coliform count (CFU/ml) of the sullage samples obtained from various zones ($\times 10^3$)

Samples	North	Central	West	South
Mopping	25.0± 0.27	52.0± 0.22	12.0± 0.27	16.0 ± 0.27
Dish washing	16.0± 0.35	18± 0.15	9.0± 0.35	36.0 ± 0.35
Laundry	28.0± 0.40	31± 0.42	20.0± 0.40	12.0 ± 0.40
Sink	11.0± 0.19	24.0± 0.27	12.0± 0.19	13.0± 0.19
A.C outlet	1.0± 0.44	1.0± 0.11	1.0± 0.16	1.0 ± 0.32

Table 3: Total fungal count (CFU/ml) of the sullage samples from various zones ($\times 10^3$)

Samples	North	Central	West	South
Mopping	25.0± 0.32	31.0± 0.28	17.0± 0.28	44.0± 0.28
Dish washing	20.0± 0.12	48.0± 0.12	23.0± 0.12	19.0 ± 0.12
Laundry	34.0± 0.17	26.0± 0.42	28.0± 0.42	21.0 ± 0.42
Sink	1.0± 0.23	09.0± 0.38	04.0± 0.38	10.0 ± 0.38
A.C outlet	1.0± 0.25	2.0± 0.15	1.0± 0.41	3.0 ± 0.25

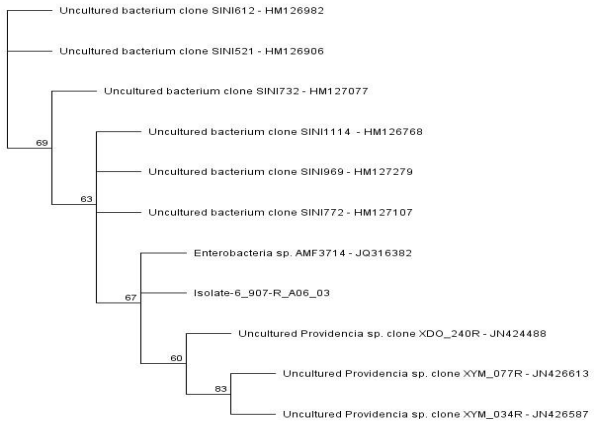

Fig. 1: Phylogenetic analysis of water sample based on the nucleotide sequence of part of the 16S rRNA nucleotide sequence of bacteria. The phylogenetic tree was constructed by the Neighbor-Joining method program in the Geneious package (version 9.0.5). The numbers at the forks show the number of occurrences of the repetitive groups to the right out of 100 bootstrap samples. Isolate 1 has a similar sequence to *Enterobacteria* sp. AMF3714

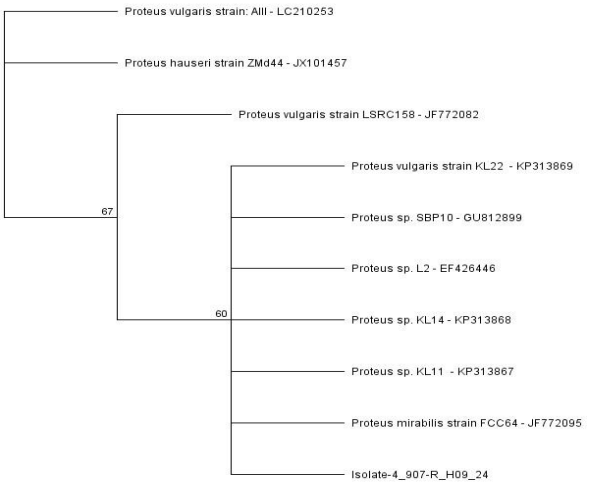

Fig. 2: Phylogenetic analysis of water sample based on the nucleotide sequence of part of the 16S rRNA nucleotide sequence of bacteria. The phylogenetic tree was constructed by the Neighbor-Joining method program in the Geneious package (version 9.0.5). The numbers at the forks show the numbers of occurrences of the repetitive groups to the right out of 100 bootstrap samples. Isolate 2 has similar sequence with *Proteus* strain FCC64

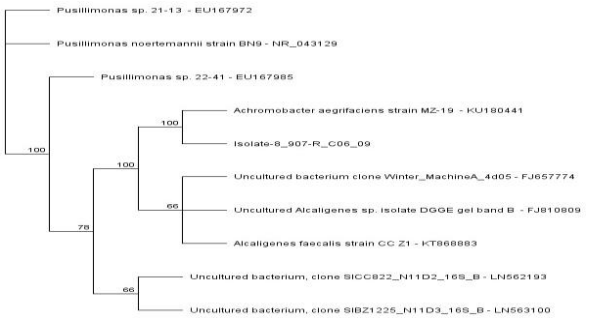

Fig. 3: Phylogenetic analysis of water sample based on the nucleotide sequence of part of the 16S rRNA nucleotide sequence of bacteria. The phylogenetic tree was constructed by the Neighbor-Joining method program in the Geneious package (version 9.0.5). The numbers at the forks show the

number of occurrences of the repetitive groups to the right out of 100 bootstrap samples. Isolate 3 has a similar sequence to *Achromobacter* strain MZ-19

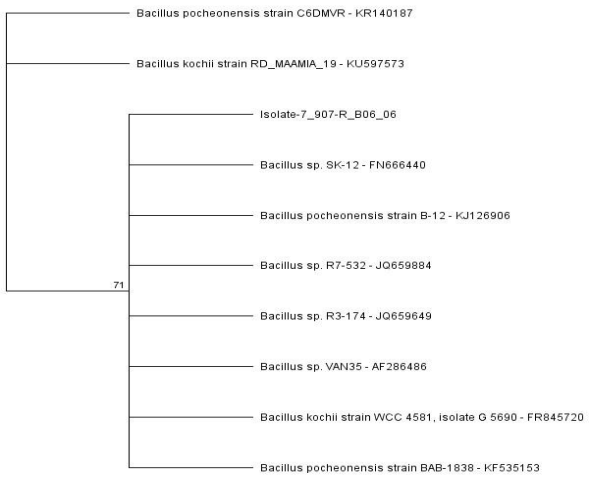

Fig. 4: Phylogenetic analysis of water sample based on the nucleotide sequence of part of the 16S rRNA nucleotide sequence of bacteria. The phylogenetic tree was constructed by the Neighbor-Joining method program in the Geneious package (version 9.0.5). The numbers at the forks show the number of occurrences of the repetitive groups to the right out of 100 bootstrap samples. Isolate 4 has a similar sequence to *Bacillus* strain RD_MAAMIA_19

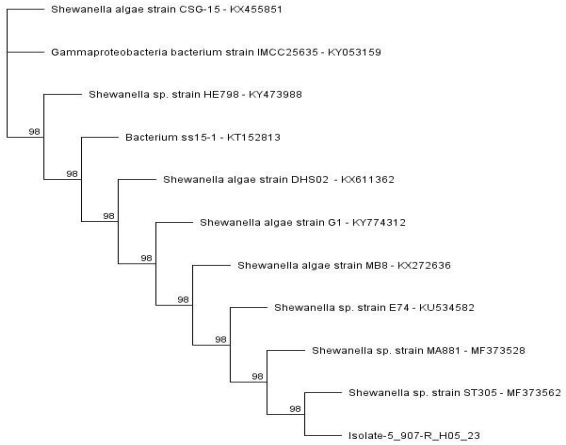

Fig. 5: Phylogenetic analysis of water sample based on the nucleotide sequence of part of the 16S rRNA nucleotide sequence of bacteria. The phylogenetic tree was constructed by the Neighbor-Joining method program in the Geneious package (version 9.0.5). The numbers at the forks show the numbers of occurrences of the repetitive groups to the right out of 100 bootstrap samples. Isolate 5 has similar sequence with *Shewanella* strain ST305

Table 5: Frequency (%) of occurrence of bacterial isolates in sullage samples

Samples	*Enterobacter* sp.	*Proteus mirabilis*	*Achromobacter* sp.	*Bacillus* sp.	*Shewanella* sp.
Mopping	29.0	25.0	20.0	14.0	12.0
Dishwashing	27.0	23.0	19.0	17.0	14.0
Laundry	23.0	21.0	21.0	20.0	15.0
Sink	25.0	27.0	22.0	10.0	16.0
A.C Outlet	24.0	20.0	21.0	18.0	17.0

Table 6: Physicochemical compositions of sullage from collection points

Location/source	Temperature	Turbidity	Ph	TDS	Total hardness	Electrical conductivity
Mopping	32.7 ± 0.55	15.1±0.09	9.0 ±0.13	33.5± 0.33	42.8 ± 0.23	11.5 ± 0.41
Dish washing	32. ± 0.13	20.3±0.04	8.3 ±0.36	33.9±0.11	34.3±0.11	11.0±0.28
Laundry	32.3±0.20	23.0±0.22	8.2±0.28	24.7±0.22	37.4±0.35	14.7±0.23
Sink	27.8±0.16	30.4±0.43	9.0±0.17	30.5±0.20	33.4±0.37	15.0±0.12
A.C Outlet	32.2±0.34	25.8±0.42	7.1±0.13	29.2±0.8	34.2±0.25	13.6±0.23
Mopping	32.4±0.52	32.6±0.75	9.0±0.40	35.0±0.16	23.8±0.44	15.1±0.50
Dish washing	31.4±0.22	33.0±0.25	8.1±0.32	31.0±0.12	35.5±0.18	11.1±0.38
Laundry	32.4±0.11	35.1±0.36	9.2±0.43	37.0±0.25	33.3±0.21	16.1±0.42
Sink	32.2±0.25	32.8±0.51	8.9±0.17	34.0±0.48	28.7±0.19	13.1±0.37
A.C Outlet	24.3±0.32	38.3±0.55	7.0±0.10	31.0±0.18	31.4±0.30	14.1±0.22
P – value	**0.8345**	**0.0882**	**0.1024**	**0.1026**	**0.0345**	**0.0000**
WHO Limit	**25 – 27**	**0.1 – 4.0**	**6.5 – 9.0**	**500**	**120 – 180**	**1000**

Table 7: Concentration of metal ions (mg/l) in sullage sampled sites (M±SE)

Location/source	Cu	Fe	Cd	Zn	Ca	Cb	Na	K
Mopping	0.8±0.16	15.0±0.42	0.5±0.42	0.3±0.30	3.7±0.22	0.2±0.30	0.1±0.33	2.2±0.52
Dish washing	1.2±0.35	25.8±0.56	0.3±0.51	0.3±0.12	2.3±0.45	0.2±0.26	0.2±0.02	2.6±0.12
Laundry	1.6±0.37	16.1±0.17	0.3±0.31	0.8±0.37	2.2±37	0.2±0.44	0.9±0.09	3.2±0.06
Sink	0.3±0.01	15.9±0.45	0.8±0.14	0.2±0.17	3.1±0.28	0.1±0.10	0.3±0.20	2.4±0.24
A.C Outlet	0.6±0.27	24.8±0.41	1.0±0.56	0.3±0.13	2.9±0.33	0.2±0.12	0.2±0.18	3.5±0.39
Mopping	1.7±0.23	12.0±0.27	0.4±0.34	1.2±0.09	3.5±0.41	0.2±0.30	0.1±0.37	2.6±0.13
Dish washing	1.3±0.46	15.1±0.15	0.3±0.19	1.4±0.52	2.9±0.44	0.1±0.18	0.3±0.23	1.4±0.43
Laundry	1.8±0.33	14.9±0.18	0.5±0.22	1.6±0.22	3.8±0.11	0.1±0.12	0.4±0.47	1.3±0.26
Sink	1.4±0.32	24.0±0.40	0.3±0.44	1.0±0.02	3.3±0.21	0.2±0.38	0.3±0.17	2.4±0.33
A.C Outlet	1.0±0.21	22.0±0.24	0.1±0.25	1.1±0.07	2.0±0.26	0.1±0.11	0.2±0.39	2.3±0.28
P – value	**0.0521**	**0.0000**	**0.0145**	**0.2657**	**0.1402**	**0.2314**	**0.2976**	**0.5341**
WHO limit	**0.5 – 1.5**	**0.1 – 1.0**	**0.02-0.05**	**10 – 15**	**75 – 200**		**200**	

DISCUSSION

The total bacterial counts of sullage samples collected from the North Zone ranged from 1.0 ± 0.11 to 52.0 ± 0.22 × 10^3 CFU/ml for A.C. Outlet and mopping, respectively. In the Central Zone, bacterial counts varied from 1.0 ± 0.16 to 70.0 ± 0.32 × 10^3 CFU/ml for A.C. Outlet and laundry, respectively. For the West Zone, total bacterial counts ranged from 1.0 ± 0.31 to 14.0 ± 0.13 × 10^3 CFU/ml for A.C. Outlet and mopping. In the South Zone, the total bacterial count spanned from 1.0 ± 0.24 to 16.0 ± 0.19 × 10^3 CFU/ml for A.C. Outlet and dishwashing. The counts were higher than the recommended limit of 1.2 × 10^3 CFU/ml set by the World Health Organization (WHO, 2011). The reason for the high bacteria count might be because household cleaning and laundry generally increase the bacterial load of wastewater (Wolde and Bacha, 2016).

The total coliform counts of sullage samples in the North Zone ranged from 1.0 ± 0.44 to 28.0 ± 0.40 × 10^3 CFU/ml for A.C. Outlet and mopping, respectively. In the Central Zone, counts ranged from 1.0 ± 0.11 to 52.0 ± 0.22 × 10^3 CFU/ml for A.C. Outlet and mopping. The West Zone reported total coliform counts from 1.0 ± 0.16 to 20.0 ± 0.40 × 10^3 CFU/ml for A.C. Outlet and laundry, while the South Zone showed counts from 1.0 ± 0.16 to 36.0 ± 0.40 × 10^3 CFU/ml for A.C. Outlet and dishwashing. The counts exceeded the allowable limit set by the WHO (2011). The result was similar to that reported by Morka *et al*. (2021) on the physicochemical and bacteriological screening of household water supplies in selected communities in Edo State, Nigeria. The A.C outlet had low count because the sullage from A.C droplets is slightly contaminated, although not portable which could be due to sterilization of the storage medium. It was observed that most of the storage medium was usually used paint rubbers, which have been washed and kept outside the building to trap water droplets arising from the A.C disposals. On the other hand, Sinks and Dishwashing systems are usually contaminated due to inadequate washing practices Also, during cleaning, food residues may adhere to the sponge surface and damp sites such as sink areas can act as further microbial reservoirs that can contaminate the sponges during their use.

Gene sequencing identified five bacterial strains, including *Enterobacter* sp. MF3714, *Proteus* strain FCC64, *Achromobacter* strain MZ-19, *Bacillus* strain RD_MAAMIA_19, and *Shewanella* strain ST305. Among the isolated bacteria, *Enterobacter* sp. was the most prevalent bacterium found in mopping samples, comprising 29.0% of the isolates, while *Shewanella* sp. was the least common, at 12.0%. In dishwashing samples, *Enterobacter* sp. again emerged as the predominant isolate at 27.0%, with *Shewanella* sp. being the least dominant at 14.0%. In laundry samples, *Enterobacter* sp. represented 23.0% of the isolates, while *Shewanella* sp. was the least prevalent at 15.0%. For sink samples, *Proteus mirabilis* was the most frequently isolated bacterium, accounting for 27.0%, whereas *Bacillus* sp. was the least dominant at 10.0%. Lastly, in A.C. outlet samples, *Enterobacter* sp. made up 24.0% of the isolates, with *Shewanella* sp. again being the least common, comprising 17.0%. The isolates are common causes of diseases and infections like dysentery, typhoid, and cholera, and may likely affect plant productivity as well if not treated before reuse. These results are consistent with those reported by Peter *et al*. (2013) regarding *Lysinibacillus* contaminants sp. nov. isolated from surface water and by Bouali *et al.* (2016), who characterized some soil isolates of the *Bacillus cereus* group from Algeria. These organisms represent examples of the normal flora within soil and water, as noted by Oranusi and Braide (2012). Other identified bacterial strains included *Enterobacter* sp., *Achromobacter* sp., and additional *Shewanella* sp. findings align with those reported by Yardena *et al*. (1980) regarding *Achromobacter xylosoxidans* infections. These organisms also signify examples of normal flora found in soil and water, as discussed by Oranusi and Braide (2012).

The temperature of the various sullage samples was higher than the allowable standard of the WHO (2011). This could influence the microbial types in the sample waters. The level of turbidity was quite high and unsatisfactory below the acceptable standard by WHO (2011). The findings of turbidity may arise from dirt and a mixture of chemicals such as soaps and other organic matter during mopping, washing and laundry. This agrees with the finding of Zdeb *et al.* (2020) for rainwater quality from roofs possibility of its economic use.

The alkaline pH of the sampled waters fell within the acceptable standard (6.8-9.0) by WHO (2011). This might be a result of the level of dissolved minerals leached into the tanks. The report was similar to the report of Ogbeifun *et al.* (2019).

The values of total dissolved solids in the study also fell within the allowable limit by WHO (2011), which is an indication that the waters do not contain a heavy load of decaying organic matter. This also had a great impact on the growth rate of coliform bacteria being isolated. The report is in line with the findings of Iyasele and Idiata (2011) and Ogbeofun *et al*. (2019). The values of Total hardness also fell within the allowable limit or standards by WHO (2011). The values of electrical conductivity fell within the range of 11.0 to 0.28 to 15.1 to 0.50. The values fell within the allowable standard (1000 us/cm and 50 mg/1) recommended by WHO (2011). This influences the ionic compositions of the harvested waters (Ogbeofun *et al*., 2019).

Virtually all the heavy metals compositions examined including: Calcium (ca), zinc (zn), cobalt (cb), sodium (na) and potassium (k) fell within the allowable limits by WHO (2011) except copper (Cu), iron (Fe) and cadmium (CD) which were significantly higher. The water is thus free of harmful and toxic chemicals that might cause serious health challenges to the users. This finding agrees with Odiana and Edosomwan (2019), who also recorded low values of certain trace metals in research conducted in Edo State, Nigeria.

CONCLUSION

This study shows that the values obtained from bacteriological counts of the various water samples were higher than the maximum stipulated microbial load by the World Health Organization and the National Water Agency (ANA). Physicochemical compositions showed that sullage obtained from the sampled locations was chemically safe, as the parameters studied were within the acceptable limit except copper (Cu), iron (Fe), and cadmium (CD), which were significantly higher. It is recommended that proper treatment be implemented to ensure that sullage is completely clean and safe for reuse. This will help minimize the risk of pathogenic microbes that can cause diseases,

negatively affecting plant growth, development, and overall productivity. Additionally, rather than allowing sullage to go to waste, individuals should explore the potential benefits of recycling sullage. This approach can help save costs and resources, especially during times of drought.

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