



Impact of Dumpsites on Soil and Water Sources from Selected Locations in Akure, Ondo State, Nigeria

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Abstract: Dumpsites are created for waste disposal and management, unfortunately they have been revealed as habitat of numerous pathogenic microorganisms, heavy metals, and other hazardous materials that easily leachate into surrounding soils and water bodies. In this study we investigated microbial quality and presence of heavy metals in water and soil samples from 10 selected locations in Akure Ondo State, Nigeria. The samples were taken in triplicates, and analyzed using standard microbiological methods. Twelve heavy metals were analyzed using the flame atomic absorption spectrophotometry. The results showed the presence of *Enterobacter aerogenes*, *Citrobacter freundii*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Klebsiella pneumoniae*, *Proteus vulgaris* and *Bacillus subtilis* in the water samples. The highest bacterial load of 1.6×10^3 cfu/ml was recorded in water sample 2. The qualities of most of the water samples were below the WHO drinking water standard, and 3.74 mg/l lead value was observed in water sample 4. The soil samples were also heavily populated with bacteria and fungi. Heavy metals such as cobalt, lead, aluminum, argon and magnesium were detected at varying concentrations in all the soil samples. The highest lead value of 1.54 mg/ml was shown in soil sample 4. Hence, we recommend periodic testing, provision of affordable treatment, and monitoring of residential water-sources and soil by government regulatory bodies. This will invariably prevent the incidence of communicable diseases, and genetic mutations caused by heavy metals.

1. Introduction

Waste dumping as well as waste management is a major problem confronting developing countries (Graffariraad *et al.*, 2024). Indiscriminate dumping of refuse especially solid waste is still a norm in cities, towns, and villages in developing countries due to poor monitoring system (Kandeler *et al.*, 2019). According to Waste Atlas 2020 report, six of the biggest dumpsites in the world are located in Africa of which three are found in Lagos, Port Harcourt, and Ibadan in Nigeria, South West Africa (Kandeler *et al.*, 2019).

This is caused by the upsurge in generation of municipal solid waste (MSW) as a result of increase in urbanization of human population (Njoke *et al.*, 2022). MSW is a fast-growing pollutant than greenhouse gases and about 6.1 million metric tons MSW is generated per day by the urban

residents (Fadili *et al.*, 2022, Ojiego *et al.*, 2022). Recycling, landfilling, and composting are some of the methods used for handling the menace of MSW, however landfilling is the most adopted waste disposal option (Essien *et al.*, 2019, Fadili *et al.*, 2022). Landfill site also known as a tip, dump, rubbish dump, garbage dump or dumping ground is a site for the disposal of waste materials (Ojiego *et al.*, 2022).

The increase in urbanization has resulted in the increase in construction of residential and commercial centres most especially in area with proximity to dumpsites (Njoke *et al.*, 2022). Unfortunately, this closeness negatively impact the quality of water and soil due to pathogenic microbes harbored by the dumpsite (Akharayi and Omoya, 2004). On the other hand, heavy metal containing materials such as tyres, batteries, and metallic objects are also dumped along with the MSW on landfills (Briffa *et al.*, 2020, Rime *et al.*, 2016). Lead and cadmium which are major components of electronics, and batteries are also released into dumpsites. These heavy metals are extremely poisonous to human(s), animals, plants, and microbes as they induce their effects on the cells by damaging cell membranes, altering the peculiarity of enzymes, and destroy the structure of the DNA (Lehmann *et al.*, 2018, Elanga *et al.*, 2022). Other heavy metals such as chromium, iron, and mercury are also common on dump sites, and are also easily leached into underground drinking water source such as well and boreholes (Karimian *et al.*, 2021; El Hammari *et al.*, 2022).

Notably, these heavy metals have also been revealed to cause terminal diseases and mutation of human genomes (Elanga *et al.*, 2022, Kandeler *et al.*, 2019).

Although several studies have shown leachates from dumpsites as the principal channel of entry for heavy metals into water bodies and soil, environmental scientists have continued to study the quality of dumpsite impacted environs in order to monitor and proffer solutions (Agbeshie *et al.*, 2020, Mavakal *et al.*, 2022). Presently, there is no report on the presence and amount of heavy metals in the soil as well as water sources in Akure, Ondo State, Nigeria. The microflora of these locations, as well as the dominant bacteria and fungi species in these locations are unknown. Therefore, this research focus on determining the microbial load in soil, and drinking water samples from ten (10) selected locations in Akure, Ondo State, Nigeria. Similarly, the amount and types of heavy metals present in the soil and water samples in the locations were investigated.

2. Materials and Methods

2.1 Study area

Ten (10) residential locations in Akure, Ondo State, Nigeria were selected for the study. The locations are; Federal University of Technology Akure (FUTA) North gate area (A), Ipinsha area (B), Orita-Obele Estate area (C), Road block area (D), FUTA South gate area (E), Shagari village area (F), Oke-Aro area (G), Ijoka area (H), Oba-Ile Airport area (I) and Ado-road area (J).

2.2 Collection of samples

Soil samples from the locations were taken and kept in a labeled sterile polythene bags. Likewise, well-water samples, and borehole-water samples were collected as the water sample. The water samples were aseptically collected into labeled sterile bottles. The soil and water samples were then taken to laboratory for analysis. The samples were collected in triplicates (Ditterich *et al.*, 2016).

2.3 Preparation of media

The media was prepared based on manufactures' specifications (Cheesbrough 2014).

2.4 Sample analysis

The pour plate technique was used for plating out the appropriate dilution of the water and soil sample (10^{-2} and 10^{-4}) (Cheesbrough 2014). Purification, and identification of the isolates was done according to the method of Prescott *et al.*, 2018.

2.5 Biochemical and sugar fermentation test

The biochemical and sugar fermentation tests were done aseptically on the isolates following the methods described by Baker *et al.*, 2016, and Prescott *et al.*, 2018.

2.6 Bacteria colony count

The visible colonies in the nutrient agar plate were counted with a colony counter and recorded based on the dilution factor:

$$\text{Number of organisms} = \frac{\text{Number of colonies}}{0.1} * \frac{\text{Dilution factor}}{1}$$

2.7 Heavy metal determination

The flame atomic absorption spectrophotometry (55AA Atomic Absorption Spectrometer, 2016 Tokyo model) was used to determine the presence of heavy metals in the water and soil samples (Ojiegbo *et al.*, 2022, Emenike *et al.*, 2018). Heavy metals analyzed includes; cobalt, silver, aluminum, arsenic, mercury, manganese, zinc, copper, chromium, iron, lead, and cadmium.

2.8 Statistical analysis

The data were analyzed using the one-way analysis of variance. The mean values were correlated with the Duncan test and statistical package for social sciences (SPSS) by IBM version 16 was used.

3. Results

3.1 Microbial isolation from the water samples

The result of the bacteria load in the water samples from the ten locations are presented in **Table 1**. Seven (7) bacteria (*Enterobacter aerogenes*, *Citrobacter freundii*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Klebsiella pneumoniae*, *Proteus vulgaris*, and *Bacillus subtilis*) were isolated from the water samples. All the bacteria are *Enterobacteriaceae* (with enteric coliforms) with exception of *Bacillus*. The highest bacterial load of 1.6×10^3 cfu/ml was obtained in well-water sample B. Very low bacteria load was seen in borehole-water sample C from Obele Estate, and borehole-water sample J from Ado road. *Proteus vulgaris* was only isolated in borehole-water sample C, while *Klebsiella* and *Bacillus* were isolated in borehole-water sample J.

3.2 Fecal coliform test of the water samples

The fecal coliform test of the water samples at 44.5 °C is presented in **Table 2**. The result shows that only borehole-water samples C and J are fecal negative while the other water samples are fecal positive.

Table 1. Mean bacterial load and types of bacteria in water samples

| S/N | Sample Identity | Description | Bacterial Load (cfu/ml) | Bacterial Type |
|-----|-----------------|-------------|-------------------------|--|
| 1 | A | Well | 1.5×10^2 | <i>Enterobacter aerogenes</i> , <i>Citrobacter freundii</i> and <i>Pseudomonas aeruginosa</i> |
| 2 | B1 | Borehole | 1.2×10^2 | <i>Proteus vulgaris</i> , <i>Enterobacter aerogenes</i> . |
| 3 | B2 | Well | 1.6×10^3 | <i>Escherichia coli</i> , <i>Pseudomonas aeruginosa</i> , <i>Enterobacter aerogenes</i> , <i>Bacillus subtilis</i> and <i>Citrobacter freundii</i> |
| 4 | C1 | Borehole | 2.0×10^1 | <i>Proteus vulgaris</i> |
| 5 | C2 | Well | 2.3×10^2 | <i>Enterobacter aerogenes</i> , <i>Proteus vulgaris</i> , <i>Klebsiella pneumoniae</i> and <i>Bacillus subtilis</i> |
| 6 | D | Well | 3.0×10^2 | <i>Escherichia coli</i> , <i>Enterobacter aerogenes</i> and <i>Citrobacter freundii</i> |
| 7 | E | Well | 2.3×10^2 | <i>Enterobacter aerogenes</i> , <i>Klebsiella pneumoniae</i> , <i>Proteus vulgaris</i> and <i>Bacillus subtilis</i> |
| 8 | F | Well | 3.0×10^2 | <i>Enterobacter aerogenes</i> , <i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> |
| 9 | G | Well | 1.0×10^2 | <i>Escherichia coli</i> , <i>Enterobacter aerogenes</i> , |
| 10 | H | Well | 1.0×10^3 | <i>Escherichia coli</i> , <i>Enterobacter aerogenes</i> |
| 11 | I | Well | 1.0×10^3 | <i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> and <i>Bacillus subtilis</i> |
| 12 | J1 | Borehole | 3.0×10^1 | <i>Klebsiella pneumoniae</i> and <i>Bacillus subtilis</i> |
| 13 | J2 | Well | 1.9×10^2 | <i>Klebsiella pneumoniae</i> , <i>Citrobacter freundii</i> and <i>Bacillus subtilis</i> |

Table 2. Fecal coliform test at 44.5 °C for the water samples

| Sample No | Sample Identity | Production of Acid | Production of Gas | Remarks |
|-----------|-----------------|--------------------|-------------------|----------|
| 1 | A | Yes | Yes | Positive |
| 2 | B1 | Yes | No | Positive |
| 3 | B2 | Yes | Yes | Positive |
| 4 | C1 | No | No | Negative |
| 5 | C2 | Yes | Yes | Positive |
| 6 | D | Yes | Yes | Positive |
| 7 | E | Yes | Yes | Positive |
| 8 | F | Yes | Yes | Positive |
| 9 | G | Yes | Yes | Positive |
| 10 | H | Yes | Yes | Positive |
| 11 | I | Yes | Yes | Positive |
| 12 | J1 | No | No | Negative |
| 13 | J2 | Yes | Yes | Positive |

3.3 WHO compliance test of the water samples

Table 3 shows the compliance level of the water samples to the WHO drinking water standard. Unfortunately, almost all the well-water samples analyzed showed bacterial load higher than the WHO drinking water standard. Likewise, the borehole-water sample B from Ipinsha did not comply with the WHO standard, as bacterial load of 1.2×10^2 cfu/ml was recorded.

Table 3. Compliance of water samples with WHO standard of drinkable water

| Sample No | Sample Identity | Bacterial Load (cfu/ml) | Bacterial Counts | Compliance with WHO Standard |
|-----------|-----------------|-------------------------|------------------|------------------------------|
| 1 | A | 1.5×10^2 | 150 | No |
| 2 | B1 | 1.2×10^2 | 120 | No |
| 3 | B2 | 1.6×10^3 | 1600 | No |
| 4 | C1 | 2.0×10^1 | 2 | Yes |
| 5 | C2 | 2.3×10^2 | 230 | No |
| 6 | D | 3.0×10^2 | 300 | No |
| 7 | E | 2.3×10^2 | 230 | No |
| 8 | F | 3.0×10^2 | 300 | No |
| 9 | G | 1.0×10^2 | 100 | No |
| 10 | H | 1.0×10^3 | 1000 | No |
| 11 | I | 1.0×10^3 | 1000 | No |
| 12 | J1 | 3.0×10^1 | 3 | Yes |
| 13 | J2 | 1.9×10^2 | 190 | No |

3.4 Microbial isolation from the soil samples

Table 4 shows the result of the bacteria load and type in the soil samples. Twenty bacteria were isolated from the soil samples. Among the bacteria isolated are *Bacillus subtilis*, *Sphingomonas sp*, *Rhizobium sp*, *Clostridium sp*, *Enterobacter aerogenes*, *Proteus vulgaris*, *Salmonella typhi*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Methanococcus sp*, *Streptococcus faecalis*, *Lactobacillus sp*, *Staphylococcus aureus*, *Staphylococcus saprophiticus*, *Klebsiella pneumoniae*, *Escherichia coli*, *Arthrobacter sp*, *Streptomyces sp*, *Campylobacter jejuni*, and *Shigella dysenteriae*. However, soil sample A from FUTA North gate area showed the highest bacteria load of 6.9×10^6 cfu/g, while soil samples I from Oba-Ile Airport area, and soil sample J from Ado-road area had the lowest bacterial load of 1.0×10^6 cfu/g. The fungi load and type from the soil samples is equally represented in the **Table 4**. Thirteen (13) fungal isolates were obtained. The fungi isolated are *Pithomyces sp*, *Penicillium notatum*, *Rhizopus oligosporus*, *Penicillium oxalicum*, *Fusarium oxysporium*, *Aspergillus niger*, *Rhizopus stolonifer*, *Geotrichum candidum*, *Penicillium fulfur*, *Aspergillus flavus*, *Neurospora crassa*, *Penicillium italicum* and *Mucor mucedo*. The highest fungal load of 6.0×10^6 sfu/g was found in soil sample F from Shagari village area, and soil sample J from Ado-road area.

Table 4. Results of bacteria and fungi load and types isolated from soil samples

| S/N | Sample | Bacterial Load (cfu/g) | Fungal Load (Sfu/g) | Bacterial Type | Fungal Type |
|-----|--------|------------------------|---------------------|--|---|
| 1 | A | 6.9×10^6 | 1.2×10^6 | <i>Bacillus subtilis</i> , <i>Sphingomonas sp</i> , <i>Rhizobium sp</i> , <i>Clostridium sp</i> , <i>Enterobacter aerogenes</i> | <i>Aspergillus niger</i> , <i>Rhizopus stolonifer</i> , <i>Mucor mucedo</i> , <i>Penicillium fulfur</i> |
| 2 | B | 2.2×10^6 | 3.0×10^6 | <i>Proteus vulgaris</i> , <i>Rhizobium sp</i> , <i>Clostridium sp</i> , <i>Salmonella typhi</i> , <i>Pseudomonas aeruginosa</i> , <i>Streptomyces sp</i> | <i>Fusarium oxysporium</i> , <i>Aspergillus niger</i> , <i>Rhizopus stolonifera</i> |
| 3 | C | 1.9×10^6 | 4.0×10^6 | <i>Proteus vulgaris</i> , <i>Rhizobium sp</i> , <i>Clostridium sp</i> , <i>Salmonella typhi</i> , <i>Shigella cdysenteriae</i> , <i>Lactobacillus sp</i> | <i>Penicillium oxalicum</i> , <i>Fusarium oxysporium</i> , <i>Aspergillus niger</i> , |

| | | | | | |
|----|---|-------------------|-------------------|---|---|
| 4 | D | 3.1×10^6 | 3.0×10^6 | <i>Bacillus subtilis</i> , <i>Sphingomonas sp</i> , <i>Rhizobium sp</i> , <i>Pseudomonas</i> <i>aeruginosa</i> , <i>Streptococcus faecalis</i> , <i>Lactobacillus sp</i> | <i>Pithomyces sp</i> , <i>Penicillium</i> <i>notatum</i> , <i>Rhizopus</i> <i>oligosporus</i> , <i>Penicillium</i> <i>fulfur</i> |
| 5 | E | 2.5×10^6 | 1.1×10^6 | <i>Staphylococcus aureus</i> , <i>Staphylococcus</i> <i>saprothiticus</i> , <i>Escherichia coli</i> , <i>Proteus</i> <i>vulgaris</i> , <i>Enterobacter aerogenes</i> | <i>Mucor mucedo</i> , <i>Fusarium</i> <i>oxysporium</i> , <i>Aspergillus</i> <i>niger</i> , <i>Penicillium fulfur</i> . |
| 6 | F | 3.0×10^6 | 6.0×10^6 | <i>Enterobacter aerogenes</i> , <i>Escherichia</i> <i>coli</i> , <i>Klebsiella pneumoniae</i> , <i>Shigella</i> <i>dysenteriae</i> , <i>Campylobacter jejuni</i> , <i>Lactobacillus sp</i> | <i>Rhizopus stolonifer</i> , <i>Fusarium oxysporium</i> , <i>Aspergillus niger</i> , |
| 7 | G | 1.4×10^6 | 5.0×10^6 | <i>Enterobacter aerogenes</i> , <i>Staphylococcus aureus</i> , <i>Staphylococcus</i> <i>saprothiticus</i> , <i>Escherichia coli</i> , <i>Bacillus subtilis</i> | <i>Geotrichum candidum</i> , <i>Fusarium oxysporium</i> , <i>Aspergillus niger</i> |
| 8 | H | 1.9×10^6 | 4.0×10^6 | <i>Staphylococcus aureus</i> , <i>Arthrobacter</i> <i>sp</i> , <i>Staphylococcus saprothiticus</i> , <i>Escherichia coli</i> , <i>Salmonella typhi</i> , <i>Lactobacillus sp</i> | <i>Mucor mucedo</i> , <i>Aspergillus flavus</i> , <i>Geotrichum candidum</i> , <i>Fusarium oxysporium</i> |
| 9 | I | 1.0×10^6 | 5.0×10^6 | <i>Enterobacter aerogenes</i> , <i>Pseudomonas</i> <i>aeruginosa</i> , <i>Pseudomonas putida</i> , <i>Methanococcus sp</i> , <i>Bacillus subtilis</i> , <i>Streptococcus faecalis</i> | <i>Fusarium sp</i> , <i>Neurospora</i> <i>crassa</i> , <i>Geotrichum</i> <i>candidum</i> , <i>Fusarium</i> <i>oxysporium</i> , |
| 10 | J | 1.0×10^6 | 6.0×10^6 | <i>Escherichia coli</i> , <i>Pseudomonas</i> <i>aeruginosa</i> , <i>Pseudomonas putida</i> , <i>Methanococcus sp</i> , <i>Campylobacter</i> <i>jejuni</i> , <i>Bacillus subtilis</i> | <i>Mucor mucedo</i> , <i>Penicillium italicum</i> , <i>Geotrichum candidum</i> , <i>Fusarium oxysporium</i> , |

3.5 Morphology and biochemical test

The result of different morphological and biochemical tests used to identify the bacterial isolates in the water and soil samples are seen in **Table 5**, while the result of the complete morphological and microscopic characteristics of the fungal isolates in the samples are presented in **Table 6**.

Table 5. Morphological characteristics and sugar fermentation of bacteria in the water and soil samples

| S/N | Morphological characteristics | Morphological characteristics | | | | | | Probable isolates |
|-----|--|-------------------------------|----------|-----------|---------|--------|----------|----------------------------|
| | | Gram reaction | Catalase | Coagulase | Citrate | Indole | Motility | |
| 1 | Circular, milky white | - | + | + | + | + | - | <i>Proteus vulgaris</i> |
| 2 | Circular, , milky white | - | + | - | + | - | - | <i>Rhizobium</i> |
| 3 | Circular, milky white | - | + | + | + | - | - | <i>Sphingomonas sp</i> |
| 4 | Irregular, white opaque | + | - | + | + | - | - | <i>Streptococcus mitis</i> |
| 5 | Irregular, white, flat, small, opaque, rough, lobate, butyrous | + | + | + | - | - | - | <i>Bacillus subtilis</i> |
| 6 | Circular, light yellow | + | + | + | - | - | - | <i>Arthrobacter sp</i> |
| 7 | Circular, creamy, butyrous | + | + | + | ++ | ++ | - | <i>Streptomyces sp</i> |
| 8 | Irregular, milky white | - | + | + | + | - | - | <i>Azotobacter aceti</i> |

| | | | | | | | | |
|----|--|---|---|---|----|----|---|-------------------------------------|
| 9 | Circular, creamish yellow | + | + | + | + | - | - | <i>Lactobacillus casei</i> |
| 10 | Circular and white | + | + | + | + | - | + | <i>Bacillus cerceus</i> |
| 11 | Irregular, brownish | - | + | + | + | - | + | <i>Pseudomonas aeruginosa</i> |
| 12 | Circular, cream, flat | - | + | + | + | - | + | <i>Pseudomonas putida</i> |
| 13 | Circular, milky white | + | - | + | + | - | - | <i>Staphylococcus aureus</i> |
| 14 | Irregular, white opaque | + | + | + | - | - | - | <i>Clostridium sp</i> |
| 15 | Irregular, white, flat, small, opaque, rough, lobate, butyrous | + | + | + | - | - | - | <i>Methanococcus sp</i> |
| 16 | Circular, light yellow | + | + | + | ++ | ++ | - | <i>Staphylococcus saprophyticus</i> |
| 17 | Circular, creamy, butyrous | - | + | + | + | - | - | <i>Escherichia coli</i> |
| 18 | Irregular, milky white | + | + | + | + | - | - | <i>Streptococcus thermophiles</i> |
| 19 | Circular, creamish yellow | + | + | + | + | - | + | <i>Nitrosomonas sp</i> |
| 20 | Circular and white | - | + | + | + | - | + | <i>Klebsiella pneumonia</i> |
| 21 | Irregular, brownish | - | + | + | + | - | + | <i>Enterobacter aerogenes</i> |
| 22 | Circular, cream, flat | - | + | + | + | - | - | <i>Salmonella typhi</i> |

Table 6. Microscopic characteristics of identified fungi isolates

| Isolates | Cultural Characteristics | Arrangement of Spores | Probable Microorganisms |
|----------|---|--|--------------------------------|
| 1 | White base with black conidiophores | Conidia heads radiate, conidiophores stripes smooth wall. Conidia are 1-celled and vesicles globose | <i>Aspergillus niger</i> |
| 2 | White base with yellowish green color in appearance | Conidia heads radiate and typically vesicles globose, surface contain many flask shaped phialides and chains of conidia. Hyphae septate, no collumella | <i>Aspergillus flavus</i> |
| 3 | White cotton like mycelia turning dirty with development of black spores. | Non-septate hyphae and coenocytic thin sporangiophores. Sporangium have well developed collumella which is umbrella-like in form. Spores are of various shapes but generally oval. | <i>Rhizopus stolonifer</i> |
| 4 | Fluffy white in appearance which grows rapidly | Mycelium extensive, with some tinge of yellow, conidiophores variable, slender and simple. | <i>Fusarium oxysporium</i> |
| 5 | Yellow base with black conidiophores | Conidia heads radiate, conidiophores stripe smooth wall. Conidia are 1-celled and vesicles globose | <i>Mucor mucedo</i> |
| 6 | Blue base with brown conidiophores which makes it brown in color | An upright conidiophore that terminate in a clavate swelling, bearing phialides at the apex. Conidia are 1-celled and vesicles globose. Hyphae septate, non-collumella. | <i>Penicillium chrysogenum</i> |

| | | | |
|----|--|--|-----------------------------|
| 7 | White to cream colored smooth, glabrous, yeast like. | Sphere to sub-spherical budding blastoconidia $2.7 \times 3-8\mu\text{m}$ in size | <i>Canidada albican</i> |
| 8 | Colonies are white cream, smooth, large globose to ellipsoidal budding yeast-like cells or blastoconidia | Presence of large central vacuole formation of a septum (cross wall) $3.0 \times 10.0 \times 4.5 - 21\mu\text{m}$ | <i>Geotrichum candidum</i> |
| 9 | Yellow-green base with yellowish green color in appearance | Conidia heads radiate and typically vesicles globose, surface contain many flask shaped phialides and chains of conidia. Hyphae septate, no collumella | <i>Rhizopus oligosporus</i> |
| 10 | Blue base with black conidiophores | Conidia heads radiate, conidiophores stripe smooth wall. Conidia are 1-celled and vesicles globose | <i>Penicillium notatum</i> |
| 11 | Bluish-white base with brown conidiophores which makes it brown in color | An upright conidiophore that terminate in a clarate swelling, bearing phialides at the apex. Conidia are 1-celled and vesicles globose. Hyphae septate, non-collumella. | <i>Penicillium oxalicum</i> |
| 12 | White cotton like mycelia turning dirty brown with development of black spores. | Non-septate hyphae and coenocytic thin sporangiophores. Sporangium have well developed collumella which is umbrella-like in form. Spores are of various shapes but generally oval. | <i>Penicillium fulfur</i> |
| 13 | Yellowish base with yellowish green color in appearance | Conidia heads radiate and typically vesicles globose, surface contain many flask shaped phialides and chains of conidia. Hyphae septate, no collumella | <i>Neurospora crassa</i> |

3.6 Heavy metals analysis of the soil and water samples

The analysis of heavy metals in the water samples are shown in **Table 7**. Twelve heavy metals (lead, cadmium, zinc, chromium, copper, manganese, iron, silver, cobalt, aluminum, arsenic, magnesium) were analyzed. The result obtained showed very high 3.74 mg/L lead value in water sample 4 (Road block area) while low 0.0717 mg/ml lead value was recorded in water sample 6 (Shagari village area). Cadmium was detected in all the water samples with the highest in water sample 2 (Ipinsha area). Ditto for zinc, with the highest value of 0.3577 mg/ml detected in water sample 7 (Oke-Aro area). Chromium was not detected in most of the water sample except water sample 6 (Shagari village area) with 1.1152 mg/ml chromium value.

Likewise, the result of heavy metals analysis in the soil samples are represented in **Table 8**. The highest level of lead value of 1.54 mg/ml was recorded in soil sample 4 (Road block area) had, while it was not detected in soil samples 1, 5, and 8. High cadmium and zinc values were recorded in all the soil samples while chromium was not detected in most of the soil samples. Very high copper, manganese and iron were also detected in all the soil samples. Cobalt, aluminum, argon and magnesium were all seen in all the soil samples with varying values for all the samples, and silver was only detected in some of the soil sample.

Table 7. Types and amount of heavy metals present in the water samples

| Sample | Pb (mg/L) | Cd (mg/L) | Zn (mg/L) | Cr (mg/L) | Cu (mg/L) | Mn (mg/L) | Fe (mg/L) | Ag (mg/L) | Co (mg/L) | Al (mg/L) | Ar (mg/L) | Mg (mg/L) |
|--------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| WS1 | ND | 0.091 | 0.1238 | ND | 0.014 | 0.080 | 2.201 | 0.0051 | 0.2904 | 0.091 | 0.1238 | 2.5675 |
| WS2 | ND | 0.230 | 0.0978 | ND | 0.035 | 0.024 | 0.233 | 0.0134 | 0.3577 | 0.230 | 0.0978 | 1.6123 |
| WS2 b | ND | 0.084 | 0.0110 | ND | 0.006 | 0.005 | 0.196 | 0.0049 | 0.0075 | 0.0019 | 0.0046 | 0.644 |
| WS3 | ND | 0.061 | 0.0833 | ND | 0.144 | 0.000 | 0.571 | 0.0479 | 0.2513 | 0.061 | 0.0833 | 1.3087 |
| WS3b | ND | 0.090 | 0.0260 | ND | 0.008 | 0.006 | 0.220 | 0.0050 | 0.0055 | 0.0023 | 0.0090 | 0.560 |
| WS4 | 3.74 | 0.097 | 0.0522 | ND | 0.074 | 0.225 | 0.450 | 0.0365 | 0.2374 | 0.097 | 0.0522 | 1.2824 |
| WS5 | ND | 0.0237 | 0.2933 | ND | ND | ND | 2.5675 | 0.0140 | 0.2144 | 0.0237 | 0.2933 | 3.3282 |
| WS6 | 0.0717 | 0.0051 | 0.2904 | 1.1152 | ND | ND | 1.6123 | 0.097 | 0.0522 | 0.0051 | 0.2904 | 2.3113 |
| WS7 | ND | 0.0134 | 0.3577 | ND | ND | 0.0807 | 1.3087 | 0.0237 | 0.2933 | 0.0134 | 0.3577 | 2.201 |
| WS8 | ND | 0.0479 | 0.2513 | ND | ND | 0.0255 | 1.2824 | 0.0051 | 0.2904 | 0.0479 | 0.2513 | 0.233 |
| WS9 | ND | 0.0365 | 0.2374 | ND | 0.0013 | 0.0952 | 3.3282 | 0.0134 | 0.3577 | 0.0365 | 0.2374 | 0.571 |
| WS10 | ND | 0.0140 | 0.2144 | ND | ND | 0.1512 | 2.3113 | 0.0479 | 0.2513 | 0.0140 | 0.2144 | 0.450 |
| WS10 b | ND | 0.0092 | 0.0193 | ND | 0.002 | 0.052 | 0.326 | 0.0092 | 0.0180 | 0.0091 | 0.0122 | 0.133 |

Key: WS=Water sample; Pb=Lead; Cd=Cadmium; Zn=Zinc; Cr=Chromium; Cu=Copper; Mn=Manganese; Fe=Iron; Ag=Silver; Co=Cobalt, Al=Aluminum; Ar= Arsenic; Mg=Magnesium, ND=Not detected

Table 8. Types and amount of heavy metals present in the soil samples

| Element (conc) | Pb (mg/L) | Cd (mg/L) | Zn (mg/L) | Cr (mg/L) | Cu (mg/L) | Mn (mg/L) | Fe (mg/L) | Ag (mg/L) | Co (mg/L) | Al (mg/L) | Ar (mg/L) | Mg (mg/L) |
|----------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| S1 | ND | 0.494 | 21.1846 | 0.804 | 8.072 | 3.764 | 204.561 | 1.31 | 0.326 | 5.9111 | 9.853 | 4.697 |
| S2 | 1.31 | 0.326 | 5.9111 | 0.355 | 9.853 | 4.697 | 92.848 | 0.0875 | 0.0363 | 13.7278 | 0.5987 | 0.3356 |
| S3 | 0.0875 | 0.0363 | 13.7278 | ND | 0.5987 | 0.3356 | 170.386 | ND | 0.0111 | 6.4572 | 0.2828 | 1.8935 |
| S4 | 1.54 | 0.0111 | 6.4572 | ND | 0.2828 | 1.8935 | 173.904 | 0.0412 | 0.0379 | 14.4564 | 1.1702 | 3.5150 |
| S5 | 0.0412 | 0.0379 | 14.4564 | ND | 1.1702 | 3.5150 | 250.036 | ND | 0.0292 | 7.1913 | 0.0746 | 2.2534 |
| S6 | ND | 0.0292 | 7.1913 | ND | 0.0746 | 2.2534 | 155.378 | 1.0544 | 0.0614 | 15.4005 | 1.6966 | 5.0491 |
| S7 | 1.0544 | 0.0614 | 15.4005 | ND | 1.6966 | 5.0491 | 187.825 | ND | 0.0163 | 6.7915 | 0.3640 | 2.2367 |
| S8 | ND | 0.0163 | 6.7915 | ND | 0.3640 | 2.2367 | 159.422 | 0.4834 | 0.0768 | 15.6518 | 1.6790 | 2.4825 |
| S9 | 0.4834 | 0.0768 | 15.6518 | ND | 1.6790 | 2.4825 | 190.288 | 0.0412 | 0.0379 | 14.4564 | 2.0197 | 0.6038 |
| S10 | 0.1483 | 0.0496 | 15.3782 | ND | 2.0197 | 0.6038 | 187.988 | ND | 0.0292 | 7.1913 | 1.54 | 0.494 |

Key: S=Soil sample; Pb=Lead; Cd=Cadmium; Zn=Zinc; Cr=Chromium; Cu=Copper; Mn=Manganese; Fe=Iron; Ag=Silver; Co=Cobalt, Al=Aluminum; Ar= Arsenic; Mg=Magnesium. ND=Not detected

4. Discussion

4.1 Microbial isolation from the water samples

The result of the bacterial load in the water samples shows the well-water samples are all polluted by enteric bacteria (*Escherichia*, *Pseudomonas*, *Klebsiella* and *Citrobacter*). The presence of the pathogenic *Escherichia*, *Pseudomonas*, *Klebsiella*, and *Citrobacter* in the well-water samples shows the water samples has been polluted by the dumpsite in the environments. Babalola *et al.* (2017), Pino-Herrera *et al.* (2017) showed that there is a direct link between a dumpsite and the bacteria inherent in the surface and underground water found within the environment. Also, Gana *et al.* (2018) revealed that the type of microorganisms isolated from the ground water as well as the surface water about 500 m distance from dumpsites are about 95% similar with the microorganisms isolated from the dumpsites. Also, these bacteria may have entered the water sources through seepages from nearby septic tanks, deliberate and indiscriminate deposition of animal waste and human faeces into the water sources, aside from the wash off from the dumpsites (Nguendo-Tongsi *et al.*, 2011). Previous study have shown these bacteria as human pathogens associated with varieties of infectious diseases such as gastroenteritis, urinary tract infections, and have revealed them as causative agents of many water borne diseases (Nwido *et al.*, 2018, Bada *et al.*, 2018).

4.2 WHO compliance test of the water samples

Table 1 shows the well-water samples did not meet the WHO standard, and thus are not suitable for domestic use such as drinking, bathing, and cooking. This is an indication of the closeness of the well-water samples to a dumpsite, and the users of these water sources may be prone now or in the future to communicable diseases infection such as cholera, dysentery, diarrhoea, food poisoning etc. Notably, two of the three borehole water samples analyzed (borehole-water samples C and J) met the WHO drinking water standard despite their proximity to dumpsites. The borehole-water samples C (Obele Estate) and J (Ado road) had very low bacteria load, showed no presence of coliform, and complied with WHO standard of drinkable water making them the only water samples suitable for domestic use (WHO 2013, 207, and 2019). This result shows borehole-water as the best and safest water drilling technique. According to Prescott *et al.* (2018), Brooks *et al.* (2018) borehole is the safest public source of drinking water microbiologically after spring water.

4.3 Microbial isolation of the soil samples

The presence of *Sphingomonas specie*, and *Rhizobium specie* indicates nitrogenous wastes such as groundnut peels, sorghum wastes, and soya beans wastes in the soil etc. *Enterobacteriaceae* was also isolated from the soil showing house-hold waste pollution. Likewise, *Methanococcus specie* was isolated from some of the soil samples showing the presence of faeces in some of the dumpsites which was probably washed into the soil. According to Babalola *et al.* (2017), *Methanococcus* are anaerobes that love hot septic tank as well as soak-away.

On the other hand, saprophytic fungi were isolated from the soil. These fungi include *Aspergillus niger*, *Rhizopus stolonifer*, *Mucor mucedo*, *Penicillium fulfur*. These fungi are water loving however, they easily adapt to soil with low water activities. According to Nester *et al.* (2018), these fungi are more involved in putrefaction and has the ability to digest their substrate through the production of extracellular enzymes that aid their activities.

4.4 Heavy metal analysis of the soil and water samples

The presence of varying concentration of silver, arsenic, mercury, manganese, zinc, copper, chromium, iron, lead, and cadmium in the water samples shows the proximity of the water to dumpsites. Most of these heavy metals have been reported to be capable of causing diseases, and their accumulations in the body has devastating effects on vital organs such as the liver, kidneys, heart, testis, brain and the pancreas (Emenike *et al.*, 2018). Mercury, lead and arsenic have also been implicated in causing lots of autoimmune diseases, cancers and mutation in man (Boateng *et al.*, 2019; Naveen *et al.*, 2017). In addition, Emenike *et al.* (2018) discovered high level of lead in a water sample, and suggested the use of biotransformation mechanism for the reduction of heavy metals from the water sample. Since this water serves drinking and cooking purposes to the dwellers of the community, there is an urgent need for sensitization on the dangers of using these source of water, and provision of alternative source of water to the community is imminent.

Similarly, the presence and high level of arsenic, mercury, manganese, zinc, copper, chromium, iron, lead, and cadmium was seen in the soil samples analyzed which is also a major concern. This is because most of these metals in the soil will either eventually seep into underground water, plant roots, or aquatic bodies (Girma, 2015). Unfortunately, consumption of products of any plant contaminated with these heavy metals will be detrimental to the human health (Babalola *et al.*, 2017). Also, the accumulation of these heavy metals in aquatic animals such as fish will ultimately affect man who is majorly the final consumer (Pino-Herrera *et al.*, 2017).

Conclusion

In this study the presence of pathogenic microorganisms and heavy metals in soil and water samples (wells and bore holes) from 10 selected locations in Akure, Ondo State, Southwest, Nigeria were investigated. The result showed that, more than 90% of the water samples analyzed did not meet up to the WHO drinking water standard. Well-water sample B2 had the highest pathogenic microorganisms with 1.6×10^3 cfu/ml bacteria load, and highest lead concentration of 3.74 mg/l was seen in well-water sample 4 (Road block area). Varying concentrations of cobalt, aluminum, argon and magnesium were detected in the soil and water samples. In conclusion, the results obtained in this research has shown that the soil and water samples except for the two borehole-water samples (C, and J) are polluted and unfortunately, majority of the people particularly those that depend on the wells as a source of drinking water are highly exposed unaware to both microbial pollutants and heavy metals even though the water is odorless and physically clean. Hence, periodic visit of government agencies, and officials to these areas for campaign on the dangers of polluted water and soil on human health, as well as testing and treatments of the soil and water sources are recommended. This will help mitigate the effects of heavy metals on the residents, and prevent the outbreak of communicable disease in Ondo state, and Nigeria.

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Compliance with Ethical Standards: This article does not contain any studies involving human or animal subjects.

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Appendix

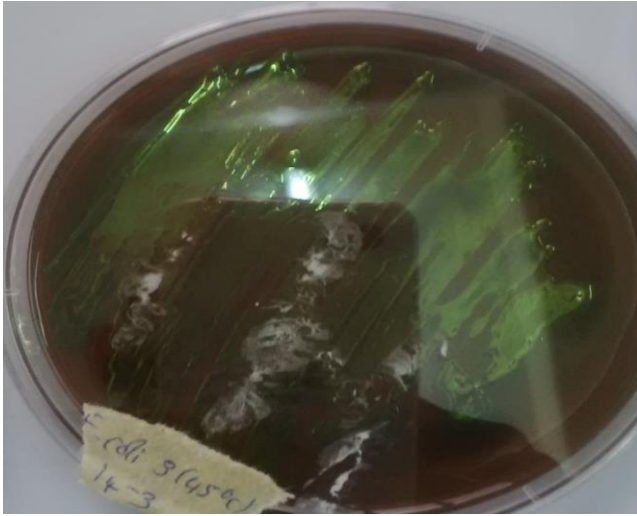


Plate 1. Purified *Escherichia coli* plate



Plate 2. Purified *Nitrosomonas* plate

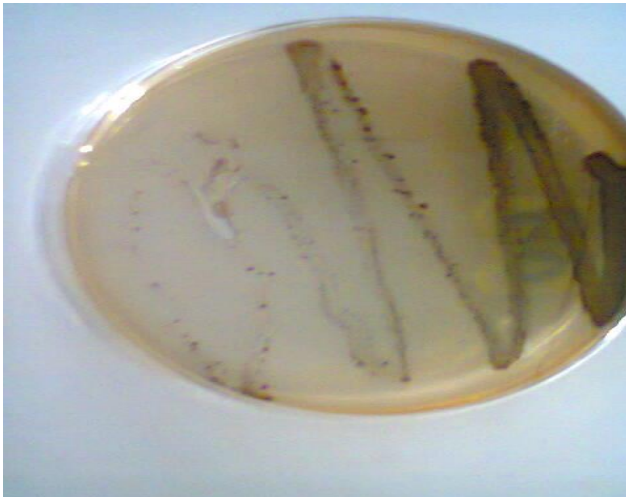


Plate 3. Purified *Pseudomonas* plate



Plate 4. Purified *Aspergillus niger*

(2026); <http://www.jmaterenvironsci.com>