



Bacteria Associated with Soils and Roots of Cucurbits (*Lagenaria guineensis* and *Luffa aegyptica*) in Open Waste Dump Sites

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Abstract

Cucurbits have been associated with the degradation of solid waste at refuse dump site. This research is dedicated to exploring the potential of rhizobacteria of cucurbits in the phytoremediation of components of solid wastes. A total of 84 soil and root samples were collected over a biweekly period from April to July, from six different stations of three different waste dump sites. The samples were examined for viable heterotrophic bacteria which were characterized and identified using standard microbiological techniques. The mean total viable heterotrophic bacteria population at the waste dump soil in Borokiri, Rugaraga and Eagle Island ranged from 2.00×10^3 to 2.80×10^5 CFU/g; from 1.70×10^4 to 3.10×10^5 ; and from 1.00×10^4 to 2.10×10^5 CFU/g respectively. The order of decreasing bacterial counts in the dump soils followed the order of Rugaraga > Eagle Island > Borokiri. The mean total viable heterotrophic bacteria population in the cucurbit roots in Borokiri, Rugaraga and Eagle Island ranged from 4.50×10^2 to 2.60×10^3 CFU/g; from 2.50×10^1 to 2.00×10^3 CFU/g; and from 2.00×10^2 to 7.80×10^2 CFU/g respectively. The order of decreasing bacterial counts in the roots of cucurbits across the waste dump sites followed the order of Borokiri > Rugaraga > Eagle Island. Various bacterial species were isolated during the study, including *Acinetobacter sp.*, *Arthrobacter sp.*, *Bacillus sp.*, *E. coli*, *Micrococcus roseus*, *Proteus sp.*, *Pseudomonas sp.*, *Serratia mercerscens*, *Staphylococcus sp.*, and *Streptococcus sp.* *Arthrobacter*, *Bacillus*, *Micrococcus*, *Serratia mercerscens* and *Staphylococcus* were isolated from both soils and roots at all sampling stations. Statistical analysis using ANOVA (F-test) indicated that the means of total bacterial counts (CFU/g soil) within the sampling sites were not significantly different at the 95% confidence level. However, the total bacterial counts (CFU/g of root) of the cucurbit plants demonstrated significant variations at the same confidence level.

Keywords: Waste Dump Soil; Cucurbit; Roots; *Pseudomonas*; *Acinetobacter*; *Arthrobacter*; Phytoremediation

Introduction

With urban industrialization, social development and population increases, solid waste production are growing rapidly, making garbage pollution a serious problem [1]. A waste is said to be hazardous if it is infectious, meaning containing viable microorganisms or their toxins which are known or suspected to cause disease in animals or humans [2]. Waste disposal poses threat to both, animals and the soil. Poisonous plants, insect, animal and indigenous pathogens are biological hazards that might be encountered at the waste site [2].

It is crucial to implement proper waste management strategies to mitigate these risks and protect the environment and public health.

Municipal solid waste generation in Port Harcourt, Nigeria (approximate $96,000 \text{ tons yr}^{-1}$) in an order of magnitude higher than industrial solid waste generation. Port Harcourt lacks a sanitary landfill [3].

The soil has been considered convenient repositories for solid and liquid waste. Every year, about 300 metric tons of pollutants, industrial wastes, and garbage are deposited into the natural environment. There is a common misconception that naturally occurring microbes will eventually biodegrade (breakdown) these waste materials over time [4].

Despite the production of waste is global issue, its management vary significantly. In Rivers State and Nigeria as a whole, the mismanagement of waste has had detrimental effects on motorable roads, drainage systems and immediate surroundings besides the proximity of dumpsites and untreated waste site to agricultural lands and drinking water sources thus resulting to socio-economic and health hazards impacting the ecology of the environment adversely [3].

Improper disposal of untreated municipal solid waste is not only harmful to human's health but also constitute a threat to ecological environment [5]. The future benefits of intervening are commensurably high. The city of Port Harcourt lack sanitary land-fill but there are several dumpsites in existence in Port Harcourt and its environs. These dump sites are usually surrounded by luxuriantly growing vegetation soil type and other environmental factors control the plant species or population at these dump sites. At the immediate vicinity of the dumpsite, luxuriantly growing or free growing weeds including some cucurbitaceae plants are abundant.

One plant group with most species widely used for bio-remediation is the cucurbitaceae family. The cucurbitaceae are a group of plants popularly known as "the gourd family" which consist of nearly 100 genera and 750 species [6], occurring mainly in warm climates, and consisting principally of herbaceous plants with juicy stems, often climbing by tendrils that arise near the bases of the leaf stalks [7]. This family of plants includes the cucumber (*Cucumis sativa*), sweet melon (*Cucumis melo*), water melon (*Citrullus lanatus*) and pumpkins and squashes (including marros and *Zucchini courgettes*), all of which are species of cucurbita. Gherkins (a small cucumber, preserved in vinegar), gourds and calabashes also belong to this family, as does loofah (*Luffa cylindrical*), and there are wild and cultivated types [6].

The waste dump soil ecosystem serves as an insightful model for studying the association and interactions between plants and microorganisms and the impact of waste and contaminants in the soil. Microorganisms are an essential part of the nutrient cycling and energy flow process of the ecosystem. Their indisputable roles in their degradative and mineralization capabilities in maintaining the carbon balance of the environment have a certain assimilatory capacity for the waste and their biodegradation potential determines the magnitude of this capacity. Therefore, man should not exceed this capacity. The generation and production of contaminants above the acceptable limit result in deleterious impact such as inhibiting nitrification that impacts plant communities and triggers a cascade effect leading to reduced photosynthesis across the ecosystem [8].

The soil is the ultimate receptor of and incubation chamber for the decomposition and recycling of nutrients from organic materials back to plants, as well as detoxification of organic pollutants. Soil micro-organisms play important role in almost every chemical transformation taking place in the soil. In particular, they can improve the fertility status of the soil and contribute to plant growth. "Biofertilizers" which are microorganisms that play these roles are receiving increased attention for use as microbial inoculants in agriculture [9].

Similarly, other soil microorganisms have been found to produce compounds (such as vitamins and plants hormones) that can improve plant health and contribute to higher crop yield [9]. These microorganisms called "phytostimulators" are currently studied for possible use as microbial inoculants to improve crop yield. It is known that *Azospirillum* induces the proliferation of plant root hairs which can result in improved nutrient uptake [10].

The root of plants are involved in the uptake of mineral nutrients and water for plant growth, but they also releases a wide range of organic compounds in the surrounding soil. Many microorganisms are present at higher numbers on the surface of plant roots. The rhizosphere is a key soil habitat where numerous interactions taking place between plant root and soil microorganisms which determine growth conditions for both the plant and the microorganisms in the rhizosphere [9].

The process of degradation of waste in waste dump involves not only biological process, but also interrelated physical and chemical processes. Most organic materials can be degraded by micro-organisms in the waste dump. Microorganisms have been shown to degrade methane, synthetic compounds, such as 2,4-dichloro- phenoxyacetic acid (2, 4-D) [11] and some microbial degradation of isomers of polychlorinated biophenyls (PCB) among others [12].

Also members of the genera *Bacillus*, and *Pseudomonas*, *Enterobacter*, *Chromobacter*, *Escherichia*, *Corynebacterium*, *Staphylococcus*, *Microccus* and *Arthrobacter* have been found to be implicated in the degradation of surfactants in liquid detergents [13].

Microbes are sensitive to abrupt changes in their environment. Whenever the physical or chemical environment is suddenly changed, there is a transition time during which the microbial population gets reacquainted with the new conditions [14]. Microbial communities within contaminated ecosystems often tend to be dominated by those organisms capable of utilizing and or surviving toxic contaminants [15]. Plant associated microorganisms have been extensively examined for their roles in natural and induced suppressiveness of soil-borne diseases, and also for plant growth promotion [16]. They reside in the rhizosphere, phyllosphere and inside tissue of healthy plants. They include the rhizobacteria i.e. (root colonizing bacteria) that reside and colonize in the rhizosphere and endophytic bacteria isolated from within healthy plant tissues [16]. They tend to maintain a microniche within the roots of those plants. Rhizobacteria are a subset of total rhizosphere bacteria which have the capacity, upon re-introduction to seeds or vegetative plant parts to colonize the developing root system in the presence of competing soil microflora. Root colonization is typically examined by quantifying bacterial populations on root surfaces.

Rhizobacteria and endophytes are part of the natural microflora of healthy plants, they may be considered to be important contributors to plant health and general soil suppressiveness [16]. Specifically, they play the role of decomposing waste materials so that "liberated nutrients" (Like nitrogen, phosphorus and potassium) can readily be taken up-by the hair roots of a plant.

Recently, a number of alternatives have been developed using plants, fungi, and bacterial to clean up wastes [17]. These plants have been studied for their ability to remove metals from soils

thereby treating waste – soil containing metal contamination [18]. Phytoremediation (remediation, or clean-up, using plants) can include a variety of strategies for absorbing, extracting, or neutralizing toxic compounds. Certain types of mustards and sunflowers can extract lead, arsenic, zinc, and other metals (phytoextraction). Poplar trees can absorb and breakdown toxic organic chemicals (phytodegradation). Reeds and other water-loving plants can filter water tainted with sewage, metals, or other contaminants [17]. Natural bacteria in groundwater, when provided with plenty of oxygen, can neutralize contaminants in aquifers, minimizing or even eliminating the need to extract and treat water deep in the ground. Radioactive strontium and cesium have been extracted from soil near the Chernobyl nuclear power plant using common sunflowers [17].

The cucurbitaceae family is a plant group with the most species widely used for bio-remediation as they grow commonly at waste dump sites. Many of the biophysical details are poorly understood, but in general, plant roots are designed to efficiently extract nutrients, water, and minerals from soil and ground water. The mechanisms involved may aid extraction of metallic and organic contaminants [17].

Improper disposal of untreated municipal solid waste is not only harmful to human's health but also constitute a threat to ecological environment [1]. The future benefits of intervening are commensurably high [1]. The city of Port Harcourt does not have sanitary landfill but there are several dumpsites in existence in Port Harcourt and its environs. These dump sites are usually surrounded by luxuriantly growing vegetation soil type and other environmental factors control the plant species or population at these dump sites. At the immediate vicinity of the dumpsite, free growing weeds including some cucurbitaceae plants are abundant.

In Nigeria, little information is available on the types of bacteria associated with soils and roots of Cucurbits in open waste dump sites [3]. Therefore, there is a need for the cultivation, enumeration, isolation and identification of bacterial isolates associated with the soils and roots of Cucurbits (*Luffa aegyptica* and *Lagenaria guineensis*) found on waste dump found in open waste dump sites. The aim of this study is to evaluate the population and diversity of bacteria associated with the soils and roots of Cucurbits found in waste dump sites in Port Harcourt metropolis. The findings will assist in the selection and harnessing of bacteria with potentials for the degradation of solid wastes.

Materials and Methods

Description of the study area

The study area for this research consisted of three specific locations: the first site is the Eagle Island, an island located South-West of Port Harcourt City. It is bounded on the East by Nkpolu-Oroworukwo (at the University Science and Technology) and surrounded by Elechi creek. It features mangrove vegetation and serves as both an industrial and residential area. The sampling site was an abandoned or active dump located in the Eagle Island, where a variety of waste materials were found, including paper products, cardboard materials, plastics, broken bottles, leaves, food wastes, feces, leather and rubber. It is a waste dump site used by Port Harcourt city council and Environmental Sanitation Authority for solid waste disposal. Most of the wastes disposed were mainly domestic and household wastes. The waste dump spanning an area of 4,355sq.m. Sampling stations were established on the waste dump site and were represented as stations A and B.

The second site is the Rugaraga, municipal waste dump site in a street located North-West of Port Harcourt City. It is a non-noisy street found after the transformer before reaching the Psychiatric hospital junction in Rumigbo. The sampling site was a borrow pit area used as a dump located immediately after the mechanic village found in the Rugaraga Street. It is a waste dump site used by the community in that area for solid waste disposal. The Rugaraga waste dump contained wooden products, batteries, textiles, bones glass, ferrous metal, ceramic and hazardous waste as reported for Port Harcourt waste dump site by Obire., *et al.* 2002. Most of the waste disposed are mainly domestic, household wastes, and of course industrial waste from the mechanic village. The waste dump covered an area of 4,000sq.m approximately. Sampling stations were established on the waste dump site and were represented as stations C and D. The Rugaraga Street is both an industrial and Residential area too. The sampling site has mangrove swamp vegetation with palm trees and plantain trees in the area, where there is a creek.

The third site is a vegetable garden located in Okarki Street in Borokiri layout, Port Harcourt. This area is located south of Port Harcourt city after Harold Wilson Drive. It is purely a Residential area and the garden has green vegetation more of garden vegetables. The Borokiri garden site contained the following waste, food waste and leaves or decomposing plant materials. Residents utilized the vegetable garden as a dumping ground for their kitchen waste. The dump area is small compared to the other two aforementioned sites. Sampling stations were established on the vegetable garden site and were represented as station E and F.

Collection and treatment of soil samples

Waste dump soil samples were collected from the two established stations on each dump site using standard method. At each sampling station, the surface debris was removed and subsurface soil was dug to a depth of about 5cm from one-foot square area. These soil samples were then scooped into sterile duplicate sampling black polythene bags and labeled accordingly. Twelve soil samples, two from each study site, were aseptically collected on each sampling visit. Samples were collected seven times at bi-weekly intervals. The soil samples were appropriately labeled and placed in a cool box containing ice packs and immediately transported to the laboratory and treated within 24 hours after collection. A total of 84 waste dump site soil samples were collected during the sampling period from April to July. The soil samples were air dried to obtain fine soil particles [19]. One gram (1g) of each air-dried fine soil sample was mixed in a test-tube containing 9ml of sterile distilled water using a sterile spatula, after which it was vigorously agitated. This solution constitutes the original 10^{-1} dilution of propagules.

Collection and treatment or processing of the cucurbit roots

Cucurbit root sample collection was also carried out biweekly during the study period. At each sampling station, the root of the desired cucurbit plant was dug out with the aid of a sterile hand trowel and inserted into sterile duplicate sampling black polythene bags and approximately labeled. Six (6) root samples, two from each sampling station were collected on each visit. The root samples were transported to the laboratory and processed within twenty four (24) hours after collection.

The root samples were processed by carrying out a thorough washing of parts of the root required, to remove all soil and most of the loose, decayed plant tissue, in which most of the saprophytes are present [20]. Several small sections (5-10mm square) from the margin of the tissue area were then cut and placed in one of the surface sterilant solutions (Clorox solution) making sure that the surface is wet. These were left for about 15 to 30 second and the sections were removed aseptically one by one for at least 5 to 10 second intervals, such that each of them has been surface sterilize for different times. The sections were dried on clean, sterile paper towels for different times [20].

Cultivation and enumeration of bacteria in soil and root samples

Each sample (1g) of previously air dried fine soil was thoroughly shaken in 9ml normal saline. An aliquot (1.0ml) of this mixture was then serially diluted in one-tenth stepwise increments to create a 10^{-3} dilution.

From the dilution of 10^{-3} of each soil sample, 0.1ml aliquot was aseptically transferred onto freshly prepared nutrient agar plates and spread with a sterile bent glass rod [3]. The dilution of 10^{-3} and 10^{-2} were used in bacteria plating as a preliminary study showed that the dilution of 10^{-1} gave a confluent growth. The inoculated plates were inverted and incubated at 37°C for 24- 48 hours after which the plates were examined for growth. The discrete colonies which developed were counted and the average counts for duplicate cultures were recorded as total viable aerobic heterotrophic bacteria in the soil sample.

After subjecting sections of the root samples to surface sterilization, the sections are ground aseptically in a sterile mortar but quite thoroughly in a small (1ml) volume of sterile water, and then part of this homogenate is diluted serially ten items the volume of the initial water. Each ground root sample solution was thoroughly shaken to get a homogenate. An aliquot (1.0ml) was transferred into the next test tube and diluted serially in one-tenth stepwise to 10^{-3} diluted just as was done or the soil sample [3]. From the 10^{-3} dilution of each root sample, 0.1ml aliquot was transferred aseptically onto freshly prepared nutrient agar plates and spread with a sterile bent glass rod [3]. The dilution of 10^{-3} and 10^{-2} were used in plating for bacteria because the dilution of 10^{-1} led to confluent growth. The inoculated plates were inverted and incubated at 37°C for 24-48 hours after which the plates were examined for growth. The discrete colonies which developed were counted and the average count for duplicate cultures was recorded as total viable aerobic heterotrophic bacteria in the root sample.

Isolation, characterization and identification of bacteria in the waste dump soil

Pure cultures of bacteria were obtained by aseptically streaking representative colonies of different morphological types onto nutrient agar plates, followed by incubation at 28°C for 24 hours. Discrete bacteria colonies which developed were sub-cultured on nutrient agar slopes and incubated at 20°C for 24 hours.

These pure stock cultures were then subjected to various standard characterization tests. The following standard characterization tests were performed. Gram staining, catalase test, coagulase test, sugar fermentation test, Methyl Red test, Voges – Proskauer test, indole test, and citrate utilization test. The pure cultures were identified on the physiological characterization in accordance with methods described by Cruickshank, *et al.* [21] and with reference to Holt [22].

Results

The results of Total heterotrophic Bacterial Count of soil and root samples of cucurbits in waste dump sites is presented in Table 1. The values presented are the means of three replicates. The values of total bacterial count per gram of soil ranged from 2.00×10^3 to 2.80×10^5 CFU/g with a mean value of 8.82×10^4 CFU/g in Borokiri Garden site, 1.70×10^4 to 3.10×10^5 CFU/g with a mean value of 1.19×10^5 CFU/g in Rugaraga waste dump site and from 1.00×10^4 to 2.10×10^5 with a mean value of 7.83×10^4 CFU/g in Eagle Island waste dump site.

Table 1: Mean values of total viable heterotrophic bacteria soil and root samples of cucurbits in waste dump site.

Sampling Period	Total Heterotrophic Bacteria Count (CFU/g)					
	Waste dump soil sample			Cucurbit root sample		
Days	Borokiri	Rugaraga	Eagle Island	Borokiri (<i>Lagenaria guineensis</i>)	Rugaraga (<i>Luffa aegyptica</i>)	Eagle Island (<i>Luffa aegyptica</i>)
1	4.50×10^4	4.20×10^4	1.00×10^4	4.50×10^2	3.80×10^2	2.00×10^2
14	8.0×10^3	1.70×10^5	2.10×10^5	6.50×10^2	2.40×10^2	2.30×10^2
28	1.20×10^5	3.70×10^4	7.10×10^4	5.50×10^2	4.80×10^2	4.00×10^2
42	5.20×10^4	4.60×10^4	4.30×10^4	1.00×10^3	1.20×10^3	7.80×10^2
56	2.00×10^3	3.10×10^5	1.20×10^5	1.80×10^3	2.50×10^1	2.30×10^2
70	2.80×10^5	2.10×10^5	8.10×10^4	2.60×10^3	2.80×10^2	2.80×10^2
84	5.10×10^4	1.70×10^4	1.30×10^4	2.30×10^3	2.00×10^3	2.30×10^2
Mean	8.82×10^4	1.19×10^5	7.83×10^4	1.33×10^3	6.57×10^2	3.35×10^2

The values of total bacterial count per gram of root ranged from 4.50×10^2 to 2.60×10^3 with a mean value of 1.33×10^3 CFU/g in *Lagenaria guineensis* plant root from Borokiri garden site, 2.50×10^1 to 2.00×10^3 CFU/g with a mean value of 6.57×10^2 CFU/g in *Luffa aegyptica* plant root from Rugaraga waste dump site, and 2.00×10^2 to 7.80×10^2 CFU/g with a mean value of 3.35×10^2 CFU/g in *Luffa aegyptica* plant root from Eagle Island waste dump site.

The results of the analysis of variance (ANOVA) of the data obtained showed that the critical or tabulated F- values for the mean bacterial counts CFU/g of the soil sample population at the three different sites 3.55 and 6.01 was found to be higher than the calculated F value 0.306 at both 0.05 and 0.01 probability level, which is not statistically significant. The calculated F-values of 5.008 for mean bacterial counts CFU/g of root samples at the three different sites was greater than the critical F-value 3.55 at 0.05 probability level only and therefore is statistically significant.

The Occurrence of bacteria in soil and cucurbit root samples in Borokiri, Rugaraga and Eagle Island waste dump sites are presented in Figure 1, Figure 2, and Figure 3 respectively.

In the Borokiri waste dump soil, *Micrococcus roseus*, had the highest occurrence of 22.22% while *Acinetobacter* sp, *E. coli*, and *Streptococcus* sp., each recorded the least value of 2.77%. In the Borokiri waste dump site cucurbit roots, *Staphylococcus* sp had the highest occurrence of 29.62% while *Acinetobacter* sp, *E. coli*, and *Serratia mercescens*, each recorded the least value of 3.7%.

However, *Proteus* sp, and *Pseudomonas* sp., were not isolated from the roots (Figure 1). Means that *Micrococcus roseus* had the highest occurrence in soil samples, while *Staphylococcus* sp. was highest in cucurbit roots.

In the Rugaraga waste dump soil, *Bacillus* and *Staphylococcus* species, each recorded the highest occurrence of 25% while *Proteus* sp, and *Streptococcus* sp., each recorded the least value of 3.12%. However, *Pseudomonas* sp., was not isolated from the soil samples. In the Rugaraga waste dump site cucurbit roots; *Bacillus* sp had the highest occurrence of 23.53% while *E. coli*, and *Pseudomonas* sp, each recorded the least value of 2.94%. However, *Streptococcus* sp. was not isolated from the roots (Figure 2). Means that *Bacillus* and *Staphylococcus* species were prevalent in soil samples, while *Bacillus* sp. dominated in cucurbit roots.

In the Eagle Island waste dump soil, *Staphylococcus* sp had the highest occurrence of 29.63% while *Arthrobacter* sp, *Micrococcus roseus*, and *Streptococcus* sp., each recorded the least value of 3.7%. However, *Acinetobacter* and *Pseudomonas* species were not isolated from the soil samples. In the Eagle Island waste dump site cucurbit roots; *Micrococcus roseus* and *Staphylococcus* sp each recorded the highest occurrence of 22.85% while *Bacillus* and *Pseudomonas* sp each recorded the least value of 2.85%. However, *E. coli* and *Proteus* sp were not isolated from the roots (Figure 3). Means that *Staphylococcus* sp. was prominent in soil samples, and *Micrococcus roseus* and *Staphylococcus* sp. were prevalent in cucurbit roots.

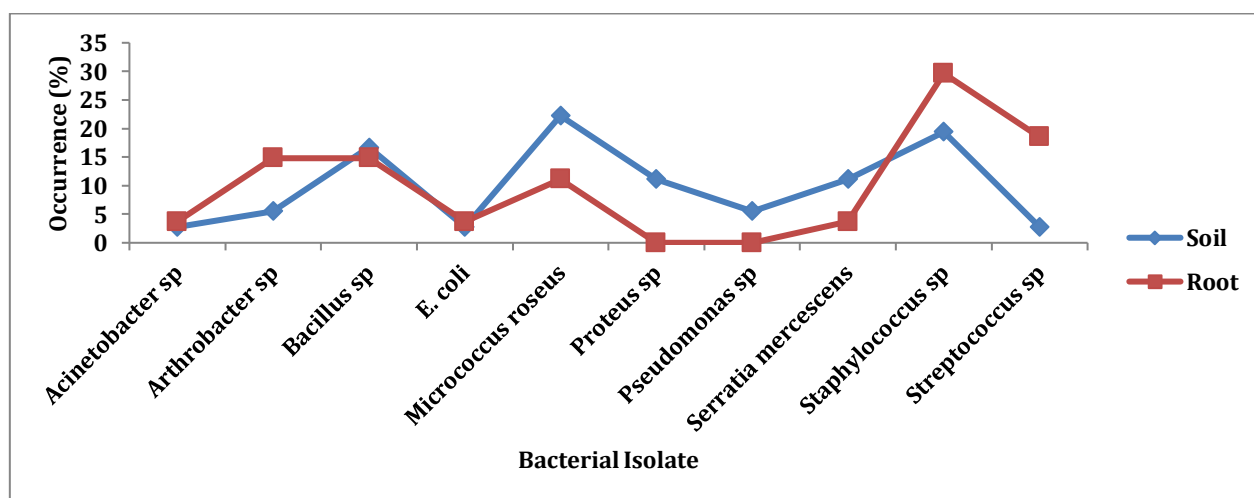


Fig. 1: Occurrence of bacteria in soil and cucurbit root samples in Borokiri waste dump site

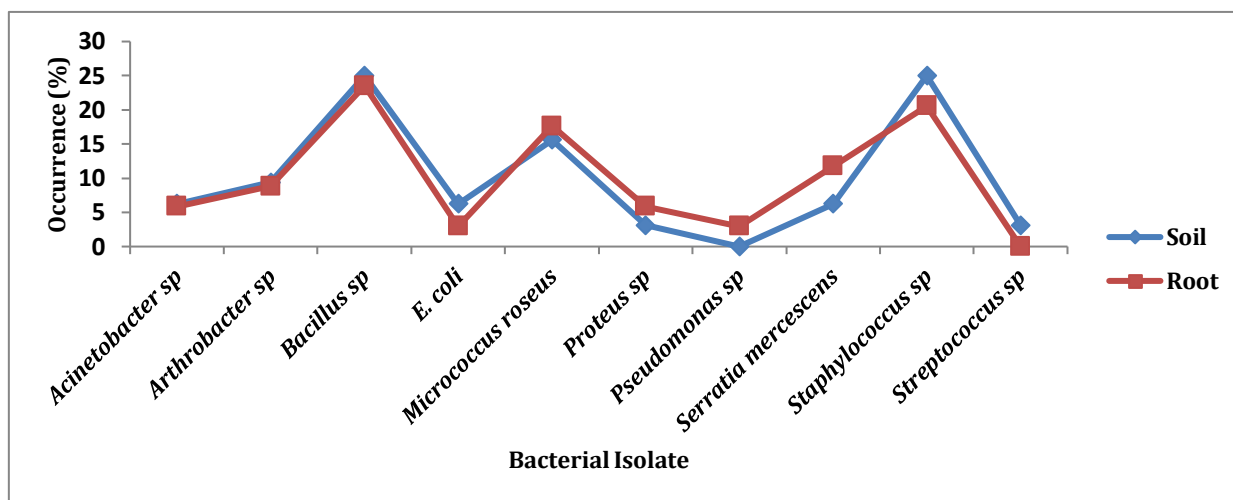


Fig. 2: Occurrence of bacteria in soil and cucurbit root samples in Rugaraga waste dump site

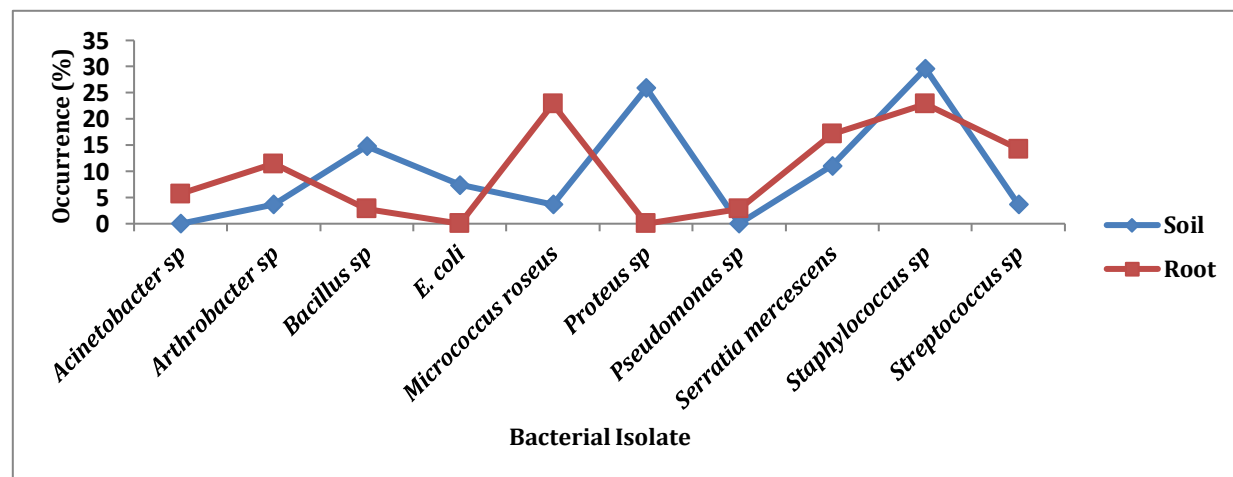


Fig. 3: Occurrence of bacteria in soil and cucurbit root samples in Eagle Island waste dump site

Discussion

The present investigation focuses on the population and diversity of bacteria associated with waste dump soils and in the roots of cucurbits growing in the waste dump sites.

Some members of the cucurbitaceae family are being envisaged for bioremediation [23]. The cucurbit plant growth is important in soil fertility, equally important are their plant death, decomposition, and recycling. These plants are constantly releasing leaves, branches, and other plant parts which enter the soil. These re- leased soluble materials create a residue sphere, an area between decaying plant material and the soil [24]. This has been described as a hot bed of microbial activity, which drives a wide range of microbiological processes. In anaerobic “hot sports” soluble plant materials support identification and possible genetic exchange processes [24].

The mean total viable heterotrophic bacteria population in the waste dump soil in Borokiri, Rugaraga and Eagle Island ranged from 2.00×10^3 to 2.80×10^5 CFU/g; from 1.70×10^4 to 3.10×10^5 ; and from 1.00×10^4 to 2.10×10^5 CFU/g respectively. The order of decreasing bacterial counts in the dump soils was Rugaraga > Eagle Island > Borokiri. The mean total viable heterotrophic bacteria population in the cucurbit roots in Borokiri, Rugaraga and Eagle Island ranged from 4.50×10^2 to 2.60×10^3 CFU/g; from 2.50×10^1 to 2.00×10^3 CFU/g; and from 2.00×10^2 to 7.80×10^2 CFU/g respectively. The order of decreasing bacterial counts in the roots of cur- cubits in the waste dump sites was Borokiri (*Lagenaria guineensis*) > Rugaraga (*Luffa aegyptica*) > Eagle Island (*Luffa aegyptica*). These results showed that, the total values of the total bacteria count of the soil and root samples were generally moderate according to the specific standard (Cruishank., et al. 1975).

The ANOVA results indicated that the means of total bacterial counts (CFU/g soil) within the sampling sites were not significantly different at the 95% confidence level. The ANOVA result depicted that the means of total bacterial counts (CFU/g of root) of the cucurbit plants within the sampling sites were significantly different at 95% confidence level.

Growth pattern of bacteria in waste dump soils of the three study locations decreased in the sequence of Rugaraga dump site > Eagle Island dump site > Borokiri garden site. The soil matrix of the Rugaraga dump site may have provided a substratum for attachment of more bacteria cells than the two other sites [25]. The lower bacterial count as observed in the two other locations may be due to the nature of the microenvironment and niche, level of waste and soil nutrients which may have attenuated microbial proliferation as rightly reported by Liu, *et al.* [26].

The present investigation has also shown that the nature of the microenvironment and niche, addition of waste and soil nutrients can affect microbial proliferation as reported by Liu, *et al.* [26]. The Borokiri garden site has the lowest number of microorganisms compared to the other study locations. This might be owing to the fact that in the Borokiri garden site, the nature of the micro-environment, the type of waste and soil nutrients added was not on the favourable side compared to the other experimental plots.

This is in agreement with the findings of Rodríguez-Espinosa, *et al.* [24] who reported that the specific physical location of a microorganism is its microenvironment. In this physical microenvironment, the flux of required oxidants, reductants, and the nutrients to the actual location of the microorganisms can be limited thus affecting the microbial proliferation as seen in the case observed in the Borokiri garden site. While the physical structured environment also can limit the predatory activities of protozoa. Rodríguez-Espinosa, *et al.* [24], also stated that if the microenvironment has pores with diameters of 3 to 6µm, microorganisms in the pores will be protected from predation, while allowing diffusion of nutrients and waste products, thus, increasing the microbial population in that niche. This is seen mostly in the case of the other study locations with higher microbial population.

Growth pattern of bacteria in the three sampled root plants decreased in the sequence of The order of decreasing bacterial counts in the roots of cucurbits in the waste dump sites was Borokiri (*Lagenaria guineensis*) > Rugaraga (*Luffa aegyptica*) > Eagle Island(*Luffa aegyptica*).

The higher bacterial growth in the root of *Lagenaria guineensis* plant Borokiri may be due to the fact that different plant species have different soil pH and nutrient requirements thus incidentally selecting for a higher microbial proliferation [27]. The lower bacterial growth recorded in the root of *Luffa aegyptica* plant of Eagle Island is an indication that probably the flux of required nutrients to the actual location of the microorganism surrounding the root may have been limited.

From the results obtained, there is variability in pattern of sequence for the bacteria in this study. Environmental factors and climate conditions may have contributed to the variation.

The bacterial isolated from the sites include, *Acinetobacter* sp., *Arthrobacter* sp., *Bacillus* sp., *E. coli*, *Micrococcus roseus*, *Proteus* sp., *Pseudomonas* sp., *Serratia mercescens*, *Staphylococcus* sp., *Streptococcus* sp., *Bacillus* sp., *Micrococcus* sp., and *Staphylococcus* sp., were isolated from all the sites. The other bacterial isolates occurred in one or two sites of the different genera of bacteria isolated from the waste dump soils. All the bacterial isolates reported in this study have been reported to be associated with waste and waste biodegradation. Faecal coliforms and *Streptococci* have been reported to be associated with waste [28]. *Arthrobacter*, *Bacillus* and *Pseudomonas* species were reported by Obire, *et al.* [3] to be associated with waste. *Bacillus*, *E. coli*, *Klebsiella*, and *Pseudomonas* were also reported by Karungamye, *et al.* [29]. Janda and Abbott [30] reported *Enterobacter*, *E. coli* and *Serratia* among others.

Dangi, *et al.* [28] reported *Bacillus*, *E. coli*, *Proteus*, *Pseudomonas*, *Micrococcus*, *Serratia*, *Staphylococcus*, and *Streptococcus* among others. *Pseudomonas* has been widely reported to be associated with waste [25,31], some of these organisms are pathogenic while others can be opportunistic [32]. *Bacillus*, *Serratia* and *Pseudomonas* are protolytic in nature i.e. they breakdown proteins and carbohydrate in soil. Their being most abundant could be attributed to the fact that they are the most prevalent in the soil environment as a result of the abundance of proteins and carbohydrate wastes and other nutrients in the waste dump soils [3].

Most of the bacteria isolated in this study are potential pathogens. The presence of these potential pathogens reported in this investigation is attributed to the disposal of human faecal discharges and other waste emanating from human exudates at the waste dump sites [3]. The implicating presence of these pathogenic organisms in open dump sites within the Port Harcourt metropolis might involve huge expenditure on public health and reduction in the productivity of the populace.

All the bacterial genera reported in this study with the exception of *Arthrobacter* have been reported by Kaur., *et al.* [33] and Chesborough (2000) as potential pathogens. That is, they are capable of causing diseases. Kumar., *et al.* [34] reported that truly pathogenic forms may survive in waste. The presence of these potential pathogens reported in the present investigation may be attributed to the disposal of raw human faecal discharges and other human waste at the waste dump site.

Conclusion

Africa's agricultural viability and food security depend heavily on its soil quality. To understand the potential for feeding the world on a sustainable basis, we need to know how soil forms, how it is lost, and what we can do to protect and rebuild good agricultural soil. The cucurbitaceae plants, well associated with the waste dump site are important in the agricultural sector, equally important are their death, decomposition and recycling. That is to say that they can be used as fertilizers. Other economic importance of the species includes degradation in the environment, sales, medicine, and food.

The health hazard associated with the indiscriminate dumping of waste around residential areas and other ecologically sensitive areas such as rivers and streams and arable land cannot therefore be under-estimated. Nigeria should therefore direct her efforts towards not only treatment of waste before disposal but also cultivate the habit of incorporating these plants that can withstand toxic condition of these waste dump sites in the treatment (phytoremediation) of waste as to minimize the health hazards associated with dumping of waste.

The present investigation has revealed the presence of various bacteria known to be associated with waste and the cucurbit plant root. It has also revealed that the presence of cucurbits is beneficial to the soil fertility. This is owing to the fact microorganisms in the rhizosphere of the cucurbits can enhance the uptake of nutrients and other elements or metals from the soil or waste dump site. Thus, the activities of these bacteria in conjunction with these plants if properly harnessed can be used in future treatment plants in Nigeria in accelerating the bioconversion of waste compost into organic fertilizer for use in gardening, agriculture and horticulture. In addition, in the Borokiri waste dump soil, *Micrococcus roseus* stood out with the highest occurrence, while *Acinetobacter* sp, *E. coli*, and *Streptococcus* sp had the least values. *Staphylococcus* sp dominated in the Borokiri waste dump site. In the Rugaraga waste dump soil, *Bacillus* and *Staphylococcus* species both exhibited high occurrences.

Bacillus sp had the highest occurrence in the Rugaraga waste dump site cucurbit roots. *Staphylococcus* sp led in the Eagle Island waste dump soil, while *Micrococcus roseus* and *Staphylococcus* sp were prevalent in Eagle Island waste dump site cucurbit roots.

Bibliography

1. Abubakar IR., *et al.* "Environmental Sustainability Impacts of Solid Waste Management Practices in the Global South". *International Journal of Environmental Research and Public Health* 19 (2022): 12717.
2. Uzal FA., *et al.* "Clostridium perfringens Toxins Involved in Mammalian Veterinary Diseases". *Open Toxicology Journal* 2 (2010): 24-42.
3. Obire O., *et al.* "Microbial community of a waste dump site". *Journal of Applied Sciences and Environmental Management* 6.1 (2002): 78-84.
4. Maglione G., *et al.* "Microbes' role in environmental pollution and remediation: a bioeconomy focus approach". *AIMS Microbiology* 10.3 (2024): 723-755.
5. Vinti G., *et al.* "Municipal Solid Waste Management and Adverse Health Outcomes: A Systematic Review". *International Journal of Environmental Research and Public Health* 18.8 (2021): 4331.
6. Schaefer H and Renner S S. "Phylogenetic relationships in the order Cucurbitales and a new classification of the gourd family (Cucurbitaceae)". *Taxonomy* 60.1 (2011): 122-138.
7. Watson L and Dallwitz M J. "Cucurbitaceae Juss". In: The families of flowering plants. The Hutchinson Encyclopedia. Helicon Publishing Ltd.
8. Zayed O., *et al.* "Nitrogen Journey in Plants: From Uptake to Metabolism, Stress Response, and Microbe Interaction". *Biomolecules* 13.10 (2024): 1443.
9. Dzvene AR and Chiduza C. "Application of Biofertilizers for Enhancing Beneficial Microbiomes in Push-Pull Cropping Systems: A Review". *Bacteria* 3 (2024): 271-286.
10. Thepbandit W and Athinuwat D. "Rhizosphere Microorganisms Supply Availability of Soil Nutrients and Induce Plant Defense". *Microorganisms* 12 (2024): 558.
11. Mierzejewska E., *et al.* "Removal and Ecotoxicity of 2,4-D and MCPA in Microbial Cultures Enriched with Structurally-Similar Plant Secondary Metabolites". *Water* 11 (2019): 1451.

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12. Borja JQ., *et al.* "Biodegradation of polychlorinated biphenyls using biofilm grown with biphenyl as carbon source in fluidized bed reactor". *Chemosphere* 64.4 (2023): 555-559.
13. Mbpom RE and Okpokwasili GC. "Primary Degradation of surfactants in liquid Detergents". *Nigerian Journal of Microbiology* 19.1-2 (1988): 387-391.
14. Ibáñez A., *et al.* "Microorganisms and Climate Change: A Not So Invisible Effect". *Microbiology Research* 14 (2023): 918-947.
15. Abo-Alkasem ML, *et al.* "Microbial bioremediation as a tool for the removal of heavy metals". *Bulletin of the National Research Centre* 47 (2023): 31.
16. Todorović I, *et al.* "Microbial diversity in soils suppressive to Fusarium diseases". *Frontiers in Plant Science* 14 (2023).
17. Cunningham W., *et al.* "Principles of Environmental Science" (10th Edn). McGrawHill.
18. Priya AK, *et al.* "Clean-Up of Heavy Metals from Contaminated Soil by Phytoremediation: A Multidisciplinary and Eco-Friendly Approach". *Toxics* 11.5 (2023): 422.
19. US-EPA. United States Environmental Protection Agency. "Microbiological Methods for Monitoring the Environment, Water and Waste" (1978): 14-86.
20. Ogbulie JN and Ojiako OA. "Biological and Agricultural Techniques" (2000): 50-66.
21. Cruickshank R., *et al.* "Medical Microbiology, 2" 12th Edition. Churchill Livingstone, New York (1975).
22. Holt JG. "The Shorter's Bergey's Manual of Determinative Bacteriology". 8th Edition. William and Wilkins Co., Baltimore, USA (1977).
23. Yiblet Y. "Overview of Cucurbitaceae Families". In: H. Wang (ed.) *Biological and Abiotic Stress in Cucurbitaceae Crops* (2023).
24. Rodríguez-Espinosa T., *et al.* "Soluble Elements Released from Organic Wastes to Increase Available Nutrients for Soil and Crops". *Applied Science* 13 (2023): 1151.
25. Obire O and Dollah S A. "Bacterial community and antibiotic resistance of bacteria of a municipal solid waste dumpsite soil, leachate and surrounding borehole Water". *Current Studies in Comparative Education, Science and Technology* 4.1 (2017): 95-111.
26. Liu Z., *et al.* "Differential response of the soil nutrients, soil bacterial community structure and metabolic functions to different risk areas in Lead-Zinc tailings". *Frontiers in Microbiology* 14 (2023): 1131770.
27. Xia Y., *et al.* "Effects of soil pH on the growth, soil nutrient composition, and rhizosphere microbiome of *Ageratina adenophora*". *Peer Journal* 12 (2024): e17231.
28. Dangi PL, *et al.* "BOD, Total and Faecal coliforms bacteria status of Lake Pichhola, Udaipur, Rajasthan". *International Journal of Fisheries and Aquatic Studies* 5.3 (2017): 176-180.
29. Karungamye P., *et al.* "Antibiotic Resistance Patterns of *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* Isolated from Hospital Wastewater". *Applied Microbiology* 3 (2023): 867-882.
30. Janda JM and Abbott SL. "The Changing Face of the Family Enterobacteriaceae (Order: "Enterobacterales"): New Members, Taxonomic Issues, Geographic Expansion, and New Diseases and Disease Syndromes". *Clinical Microbiology Review* 34.2 (2021): e00174-20.
31. Simon-Oke IA., *et al.* "Microorganisms in Soil and Groundwater of Epe and Laje Solid Waste Dumpsites in Ondo Town, Nigeria". *Journal of Applied Sciences and Environmental Management* 27.2 (2023): 317-322.
32. Cheesbrough, M. (2000). "District Laboratory Practice in Tropical Countries, Part. 2". Cambridge University Press, U.K: 55- 80.
33. Kaur, A., van der Peet, P.L., Mui, J.W., Herisse, M., Pidot, S. and Williams, S.J. (2022). "Genome sequences of *Arthrobacter* spp. that use a modified sulfoglycolytic Embden-Meyerhof-Parnas pathway". *Arch Microbiol*, 204(3): 193.
34. Kumar, V. Saikumar, G., Jana, C. K., Kumar, P., Babu, S. and Kumar, V. (2023). "Biomedical waste management for risk pathogens". *The Pharma Innovation Journal*, 12(5): 735-740.