Original Research Article

Impact of Solid Waste Disposal on the Bacteriological Quality of Soil around Hostels of a Tertiary Institution in Port Harcourt, Nigeria

ABSTRACT

The production of waste has increased to such an extent that it generates hurdles in the daily lives of today as well as the future generations. This study was aimed at assessing Impact of Solid Waste Disposal on the Bacteriological Quality of Soil around Hostels of a Tertiary Institution in Port Harcourt, Nigeria. Soil samples from two different layers (0 - 30cm and 30 - 60cm) from waste contaminated sites and control sites (100 meters away from the dumpsites) were collected and analysed using standard bacteriological procedures. Statistical analysis was carried out using a one-way Analysis of Variance (ANOVA). The result of the Total Heterotrophic Bacterial Count (THBC) showed the highest value of 11.05±5.16 x 10^7cfu/g was obtained from the contaminated topsoil sample while the least value of 3.6±0.14 x 10^7cfu/g was obtained from the control subsoil. Similar pattern was recorded for the other bacterial groups. The results for the Total Coliform Count (TCC) indicated that the individual samples' values varied between 1.0 x 10^5cfu/g (for Control Subsoil 2) and 5.8 x 10^5cfu/g (for Contaminated Topsoil 1), while for the Fecal Coliform Count (FCC) showed that the individual samples' values varied between 1.2 x 10^4cfu/g (for Control Subsoil 2) and 14.9 x 10^4cfu/g (for Contaminated Topsoil 2). A total of 50 isolates were obtained and characterized belonging to six genera, and their prevalence showed *Bacillus* and *Staphylococcus* species were the most occurring with a frequency of 100%, followed by *Shigella* spp. (50%), *Salmonella* spp. (33.3%), *Pseudomonas* and *Klebsiella* (167%) species. The study therefore, showed notable bacteriological implications, thereby necessitating the need for proper design plan for constructing and allocating waste disposal sites and placing them away from sensitive areas like halls of residence.

Keywords: Bacteriology, hostels, solid waste, soil, tertiary institution

1.0 Introduction

For ages, waste management have been a source of concern for public health. Any item that is considered unusable by humans is considered waste. Wastes from daily activities, including the mix of residential, industrial and commercial activity in a specific location, make up or surround the human environment. Eventually, these pollutants are disposed of at a landfill following collection and sweeping. Landfills are the most often used location for the disposing of solid waste worldwide. Open dumping accounts for the bulk of landfill

disposal in Nigeria. Piling these waste in an uncontrolled disposal site without taking into account how they can eventually leach appears to be the easiest and least expensive way of handling waste [1].

The dumpsites, particularly those that are poorly managed contain varying numbers of pathogenic and opportunistic bacteria, due to the presence of various domestic, industrial and clinic waste. *Bacillus* spp. is known for its predominance in soil [2] and is found in dumpsites alongside *Escherichia coli*, *Salmonella* spp., *Shigella* spp., *Clostridium perfringens*, and *Vibrio cholerea* (known to be found in dumpsites close to water bodies, can be carried by leachates into nearby water sources) are common pathogenic bacteria found in dumpsites [3]. Opportunistic bacteria like *Pseudomonas aeruginosa, Klebsiella pneumonia, Staphylococcus aureus* and *Enterococcus* spp. can be seen in dumpsite environment and can be transmitted to humans and animals through direct contact with contaminated environment, ingestion of contaminated food and water and through airborne particles or aerosols [4]. The presence of these bacteria in the environment can degrade the soil quality and lead to the spread of infectious diseases, posing risk to the human health and environment [5]; [6].

In Nigeria, the majority of waste materials are discharged into the environment without receiving much treatment. This is still one of the fundamental concerns that needs to be addressed in the planning, and administration of the waste disposal facilities.

Waste workers and waste pickers are particularly susceptible to many chronic ailments and infectious disorders that might arise from direct handling of solid trash. Hospital waste disposal calls for extra caution because it poses serious health risks. Bandages, syringe needles, cotton, plaster, and other contagious waste products are generated by hospitals and other health facilities, and they are often disposed of alongside ordinary non-infectious waste [7]. Employee that deal with waste containing chemicals and metals run the risk of being exposed to harmful substances [8]. Due to the fact that discarded needles can spread serious health risks like Hepatitis B and C, the removal of medical waste requires extra caution. People who dig through waste in search of recyclable materials,

such as waste-pickers, run the risk of cutting themselves or coming into close contact with these infectious materials.

Also, bacterial contaminants leaching through soil column pose a serious health challenge to humans relying on underground water sources, as these leachates may aid the transport of pathogenic, including antibiotics resistant strains [9];[10] of microorganisms into aquifers and eventual ground water pollution. It is therefore important to evaluate the bacterial dynamics associated with different soil column.

This study is therefore aimed at assessing Impact of Solid Waste Disposal on the Bacteriological Quality of Soil around Hostels of a Tertiary Institution in Port Harcourt, Nigeria.

2.0 MATERIALS AND METHOD

2.1 Description of Study Area

The study was carried out around two hostels (NDDC hostel and Hostel H) university studied, within latitude N 4^{o}47’46.53708” and longitude E 6^{o}58’58.29636 for Hostel H, and latitude N 4^{o}47’39.17652” and longitude E 6^{o}58’51.14964” for NDDC hostel while the control was taken hundred meters (100m) away within latitude N 4^{o}47’38.8896” and longitude E 6^{o}58’50.39976”.

2.2 Method of Sample Collection

Soil samples were collected into sterile zip lock bags using a sterile soil auger at a depth of 0-30cm and 30-60cm. The samples were labelled properly and transported aseptically to the laboratory for bacteriological procedures.

2.3 Description of the Sample Points

The soil samples were collected from different points as indicated below

CT1-Contaminated Topsoil 1	-	Hostel H (0-30cm depth)
CT2-Contaminated Topsoil 2	-	NDDC Hostel (0-30cm depth)
CS1-Contaminated Subsoil 1	-	Hostel H (30-60cm depth)
CS2-Contaminated Subsoil 2	-	NDDC Hostel (30-60cm depth)
CNT1-Control Topsoil 1	-	Hostel H (0-30cm depth)
CNT2-Control Topsoil 2	-	NDDC Hostel (0-30cm depth)
CNS1-Control Subsoil 1	-	Hostel H (30-60cm depth)
CNS2-Control Subsoil 2	-	NDDC Hostel (30-60cm depth)

2.4 Enumeration of bacteria in the water samples

A 10-fold serial dilution of the water samples was carried out aseptically and transferred into test tubes up to 10^{-5} with sterile pipette and agitated properly to allow even distribution. After serial dilution of the samples, an aliquot (0.1ml) was inoculated in duplicates on Nutrient Agar, Mannitol Salt Agar (MSA), MacConkey Agar (MCA) and Eosin Methylene Blue (EMB), Salmonella-Shigella agar (SSA), using the spread plate method. The inoculated plates were incubated at 37°C for 24hours after which the colonies were counted and recorded.

2.5 Storage of Pure Cultures and Characterization of the Bacterial Isolates

Pure isolates was stored as frozen 10% (v/v) glycerol suspension at -4°C. Pure bacterial isolates were identified in accordance with the method described by [11] and [12]. Pure cultures from respective samples was identified based on their cultural and biochemical features. This included the colonial color of the isolates, the shape of the isolates, the elevation of the isolates, the edge of the isolates, and the consistency.

2.6 Statistical Methods

A One-way Analysis of Variance (ANOVA) was used to check for significant difference between each of the different samples. The mean separation was analyzed using Tukey High significant difference (SD).

The percentage prevalence was calculated using the formula;

$$P = (Fi/\sum Sn) \times 100$$

Where;

P= Prevalence of the isolate (%)

Fi= Frequency of respective isolate

∑Sn= Summation of samples.

3.0 RESULTS

3.1 Bacterial population in the different soil samples studied

The results obtained for the bacterial population in the various soil samples as shown in Table 1, indicated the value for Total Heterotrophic Bacterial Count (THBC) varied between 3.5 x 10^7cfu/g (for Control Subsoil 2) and 14.7 x 10^7cfu/g (for Contaminated Topsoil 1), while Table 2 showed that the mean value of THBC for Contaminated Topsoil had a greater value of 11.05±5.16 x 10^7cfu/g than that of Control Topsoil which had a value of 4.55±0.07 x 10^7cfu/g.

The data obtained from Table 2 showed that the Contaminated Subsoil had higher THBC (6.1±0.57 x 10^7cfu/g) than the Control Subsoil (3.6±0.14 x 10^7cfu/g). Similarly, the THBC value for Contaminated Topsoil had was greater (11.05±5.16 x 10^7cfu/g) than the Contaminated Subsoil (6.1±0.57cfu/g), as shown in Table 2. Also, the study obtained higher THBC from the Control Topsoil (4.55±0.07 x 10^7cfu/g) than the Control Subsoil (3.6±0.14 x 10^7cfu/g). There was however, no significant statistical difference ($p > 0.05$) recorded for the mean THBC value between the various soil types and layers compared except for the contaminated subsoil and control subsoil, as well as control topsoil and control subsoil that recorded significant differences in the their values ($p < 0.05$).

Similar pattern was recorded for the other bacterial groups. Data obtained for the Staphylococcus Count (SC) indicated that the individual samples had values that varied between 1.1 x 10^4cfu/g (for Control Subsoil 1) and 12.7 x 10^4cfu/g (for Contaminated Topsoil 1) as shown in Table 1. From Table 2 it was however recorded that the mean value of SC for Contaminated Topsoil had a greater value of 8.25±6.29 x 10^4cfu/g than that of Control Topsoil which had a value of 1.15±0.21 x 10^4cfu/g. There was no significant statistical difference recorded for the mean Staphylococcal counts for the various soil layers and types studied ($p > 0.05$).

The results for the Total Coliform Count (TCC) as also reported in Table 1 indicated that the individual samples' values varied between 1.0 x 10^5cfu/g (for Control Subsoil 2) and 5.8 x 10^5cfu/g (for Contaminated Topsoil 1), while Table 2 reported that the mean value of TCC for Contaminated Topsoil had a greater value of 5.65±0.21 x 10^5cfu/g than that of Control Topsoil which had a value of 1.85±0.07 x 10^5cfu/g. The data obtained from Table 2 also showed that the value 1.9±0.57 x 10^5cfu/g (for Contaminated Subsoil) was higher than Control Subsoil which had 1.2±0.28 x 10^5cfu/g.

Data obtained for the Fecal Coliform Count (FCC) shown in Table 1, showed that the individual samples' values varied between 1.2 x 10^4cfu/g (for Control Subsoil 2) and 14.9 x 10^4cfu/g (for Contaminated Topsoil 2), while Table 2 indicated the mean value of FCC for Contaminated Topsoil had a greater value of 14.55±0.49 x 10^4cfu/g than that of Control Topsoil which had a value of 7.8±0.14 x 10^4cfu/g. The results obtained from Table 2 further showed that the value 8.65±0.64 x 10^4cfu/g (for Contaminated Subsoil) was higher than Control Subsoil which had 1.3±0.14 x 10^4cfu/g. There was however no significant statistical difference recorded for the mean FCC values recorded.

The results for the Salmonella-Shigella Count (SSC) as shown in Table 1, indicated that the individual samples' values varied between 2.5 x 10^3cfu/g (for Control Subsoil 2) and 8.7 x 10^3cfu/g (for Contaminated Topsoil 2), while Table 2 showed the mean value of SSC for Contaminated Topsoil had a greater value of 8.65±0.07 x 10^3cfu/g than that of Control Topsoil which had a value of 3.45±0.07 x 10^3cfu/g. There was a significant statistical difference recorded for the mean value of SSC between the topsoil of the contaminated and control samples.

Table 1 Bacterial population in the various study points

Samples	**THBC x10^7 cfu/g**	**SC x 10^4 cfu/g**	**TCC x 10^5 cfu/g**	**SSC x10^3 cfu/g**	**FCC x10^4 cfu/g**
CT1	14.7	12.7	5.8	8.6	14.2
CT2	7.4	3.8	5.5	8.7	14.9
CS1	6.5	3.9	2.3	7.4	8.2

CS2	5.7	2.3	1.5	5.7	9.1
CNT1	4.5	1.3	1.9	3.5	7.7
CNT2	4.6	1.0	1.8	3.4	7.9
CNS1	3.7	1.1	1.4	3.0	1.4
CNS2	3.5	1.5	1.0	2.5	1.2

KEY

CT1-Contaminated Topsoil 1 - Hostel H (0-30cm depth)
CT2-Contaminated Topsoil 2 - NDDC Hostel (0-30cm depth)
CS1-Contaminated Subsoil 1 - Hostel H (30-60cm depth)
CS2-Contaminated Subsoil 2 - NDDC Hostel (30-60cm depth)
CNT1-Control Topsoil 1 - Hostel H (0-30cm depth)
CNT2-Control Topsoil 2 - NDDC Hostel (0-30cm depth)
CNS1-Control Subsoil 1 - Hostel H (30-60cm depth)
CNS2-Control Subsoil 2 - NDDC Hostel (30-60cm depth)

Table 2: Mean Bacterial Counts obtained from the Soil Samples

Samples	THBC $x10^7$ cfu/g	SC $x\ 10^4$ cfu/g	TCC $x\ 10^5$ cfu/g	SSC $x10^3$ cfu/g	FCC $x10^4$ cfu/g
CT	11.05±5.16	8.25±6.29	5.65±0.21	8.65±0.07	14.55±0.49
CNT	4.55±0.07	1.15±0.21	1.85±0.07	3.45±0.07	7.8±0.14
P-value	0.2169	0.2518	0.0017	0.0002	0.0029

CS	6.1±0.57	3.1±1.13	1.9±0.57	6.55±1.2	8.65±0.64
CNS	3.6±0.14	1.3±0.28	1.2±0.28	2.75±0.35	1.3±0.14
P-value	0.0261	0.1607	0.2580	0.0503	0.0039
CT	11.05±5.16	8.25±6.29	5.65±0.21	8.65±0.07	14.55±0.49
CS	6.1±0.57	3.1±1.13	1.9±0.57	6.55±1.2	8.65±0.64
P-value	0.3100	0.3727	0.0127	0.1325	0.0092
CNT	4.55±0.07	1.15±0.21	1.85±0.07	3.45±0.07	7.8±0.14
CNS	3.6±0.14	1.3±0.28	1.2±0.28	2.75±0.35	1.3±0.14
P-value	0.0136	0.6094	0.0876	0.1110	0.0005

KEY

CT = Contaminated Topsoil (0-30cm depth)
CS = Contaminated Subsoil (30-60cm depth)
CNT = Control Topsoil (0-30cm depth)
CNS = Control Subsoil (30-60cm depth)

3.2 Types and Prevalence of Bacteria associated with the study sites

The study identified a diverse array of bacterial species with varying prevalence rates. Data presented in figure 1 indicated that *Bacillus* spp. and *Staphylococcus* spp. were the overall predominant bacterial species, having a prevalence of 100% each. While *Salmonella* had a prevalence of 50%, *Shigella* spp. was recovered from 33.3% of the soil samples, with *Klebsiella* spp. and *Pseudomonas* spp. recording the least prevalence, occurring in 16.7% of the soil samples. Data reported in Table 3 further showed that *Salmonella* spp. were the only enteric bacteria isolated from the control (topsoil) samples, while *Klebsiella* and *Shigella* species were the only enteric bacteria associated the contaminated subsoil samples. The study also showed that the waste inundated or contaminated topsoil (CT1) had more bacterial genera (5) compared to the other soil types and layers (Table 3).

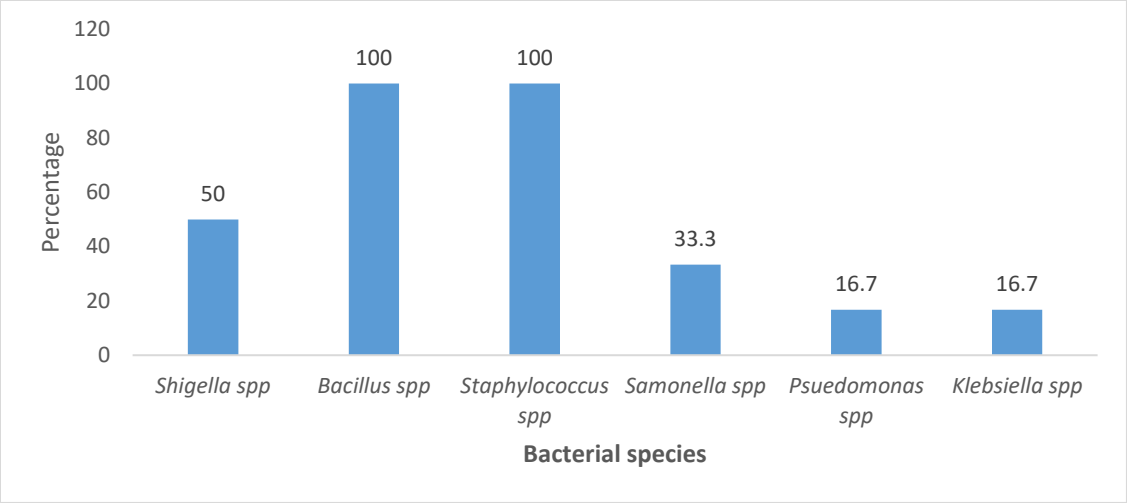

Figure 1: Prevalence of the Bacterial Species in the study.

Table 3: Occurrence of the Isolates at the study locations

Isolates	CT1	CS1	CT2	CS2	CT	CS
Bacillus spp.	+	+	+	+	+	+
Staphylococcus spp.	+	+	+	+	+	+
Salmonella spp.	+	-	-	-	+	-
Pseudomonas spp.	+	-	-	-	-	-
Klebsiella spp.	-	+	-	-	-	-
Shigella spp.	+	+	+	-	-	-
Total	**5**	**4**	**3**	**2**	**3**	**2**

KEY
CT = Contaminated Topsoil (0-30cm depth)
CS = Contaminated Subsoil (30-60cm depth)
CNT = Control Topsoil (0-30cm depth)
CNS = Control Subsoil (30-60cm depth)

4.0 Discussion

Waste generation and management has for years remained a growing environmental and public health issues. Disposal of untreated solid waste alters the bacteriological quality of the receiving soil [6], as bacterial degradation of the waste materials result in the proliferation of soil dwelling bacterial population due to nutrient enrichment in the soil.

The number of the distinct bacterial species found in the soil samples were investigated and it was revealed that the Total Heterotrophic Bacterial Count had the highest obtained from the solid waste inundated topsoil (0-30cm depth), while the control subsoil sample on the other hand had the least count. The population of the other bacterial groups (TCC, TSC, TFCC and TSSC) investigated followed a trend similar to that of the THBC.

Compared to the soils from the dumpsites, the control soil had a noticeably reduced bacterial burden. The study also showed that the bacterial population decreased with increase in soil depth, implying the subsoil samples had lower bacterial count for the different bacteria population characterized.

Several factors however influence soil bacterial population, including edaphic and anthropogenic factors. The higher bacterial population associated with the topsoil, compared to the subsoil samples is however attributable effect of abiotic factors such as aeration (oxygen), temperature, relative humidity, etc. the topsoil layer receives higher amount of oxygen, compared to the subsoil with reduced oxygen concentration. This could therefore account for the higher aerobic plate count observed with the topsoil samples compared to the subsoil sample.

The study recorded higher bacterial count in the waste contaminated sites than the control stations. This observation is however, attributable to the fact that the topsoil layer serves as the primary receptacle for the disposed waste, and thus greater part of the biodegradable activities takes places at the topsoil layer before leaching to the subsoil. This degradation in turn releases mineral components required by soil dwelling bacteria for growth. Therefore the higher bacterial number observed with the contaminated sites is most likely due to the continual deposition of different types of municipal waste at these

locations, which increases the availability of biodegradable organic and inorganic substrates.

These findings were also similar to previous reports [13, 14] that also had lesser counts from the control samples and higher counts from the soil receiving solid waste.

This present study observed that the majority of the microorganisms identified were soil-dwelling species that collaborates to develop symbiotic relationships in the soil [15]. This study recovered six bacterial species such as *Bacillus* spp., *Staphylococcus* spp., *Pseudomonas* spp., *Salmonella* spp., *Klebsiella* spp., and *Shigella* spp. from the different soil samples studied. Similar bacterial species were reported by Egbenyah *et al*., [16], who also identified *Pseudomonas* spp., *Staphylococcus* spp., *E. coli* and *Bacillus* spp., from dumpsite's soil samples. Also, a study conducted by Williams & Hakam [17] identified *Klebsiella* spp., *Pseudomonas* spp., *Bacillus* spp., *Staphylococcus* spp., *Proteus* spp., and *Streptococcus* spp. to be associated with dumpsites in Port Harcourt Metropolis, Nigeria.

The study further characterized *Bacillus and Staphylococcus* species as the predominant bacterial group in the soil samples. *Bacillus* species is known for its predominance in soil [2], and its ability to thrive in various environment including dumpsites with noted ecological importance, including waste biodegradation [18].

Although, a number of variables, including location, waste type, and environmental circumstances, might affect the dominating species found in dumpsites [19], the solid waste contaminated sites had more bacterial types than the control locations. This was also in line with the report of Selvarajan *et al*., [20], who isolated diverse bacterial in an informal dumpsite compared to the control.

While *Bacillus* spp. was noted for its ecological functions, including lignocellulose degradation, the other bacterial species isolated may pose some public health concerns [21, 22], causing an array of health syndromes when exposed to these organisms via inhalation of aerosolized soil particles, direct contact with contaminated soil or ingestion soil aggregates.

5.0 Conclusion

The study has revealed that the impact of the solid waste disposal varied with respect to soil depth. The study discovered a downward trend of bacterial groups as the soil depth increased. From the study, *Bacillus* and *staphylococcus* species were the predominant species while species of *Klebsiella* and *Pseudomonas* were the least prevalent. This therefore, implies that solid waste disposal led to the increase in the population of the soil bacterial community, including those with the potential to cause diseases in humans.

Waste disposal sites should therefore be situated away from delicate areas like students' halls of residence. Also, regular monitoring of the biological characteristics of the soil is required to establish the seasonal bacteriological impact associated with solid waste disposal at these locations. This will provide informed decision to be made towards reducing the risk connected with waste disposal.

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