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BACTERIAL COMMUNITY OF SELECTED WASTE DUMPS IN LUGBE, ABUJA AND THEIR HEALTH SIGNIFICANCE

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ABSTRACT

Introduction: The health hazard associated with indiscriminate dumping of solid waste in any area influences the mortality and morbidity profile of its community as it affects all age group.

Aim: To determine the bacterial community of selected waste dumps in Lugbe, Abuja and their health significance.

Methods: Using standard microbiological methods a total of 720 samples were analyzed; comprising of 360 dump and 360 soil samples of ten different refuse dumps in Lugbe, Abuja. There pH and temperatures were also recorded and compared.

Results: The mean temperature (^{0}C) of the soil samples was 31.3^{0}C and 30.1^{0}C for the dump samples. The mean pH value of the soil and dump samples were 6.61 and 6.72 respectively. The mean total viable microbial count of the soil samples ranged from 3.49 x 10^7 CFU/g/ml to 8.22 x 10^7 CFU/g/ml for wet season and 2.69 x 10^7 CFU/g/ml to 5.71 x 10^7CFU/g/ml for the dry season. The mean total viable microbial count of the dump samples ranged from 4.29 x 10^7 CFU/g/ml to 8.19 x 10^7 CFU/g/ml for wet season and 3.32 x 10^7 CFU/g/ml to 5.98 x 10^7 CFU/g/ml for the dry season. Statistical analysis using analysis of variance (ANOVA) at 5% significance level revealed a significant difference between the total microbial count wet and dry season for both the soil and dump samples. Eight different bacteria were isolated namely: *Staphylococcus aureus, S. saprophyticus, Streptococcus pyogens, Bacillus cereus, Escherichia coli, Proteus vulgaris, Klebsiella pneumonia, Pseudomonas aeruginosa, Aspergillus niger, A. fumigatus, A. flavus, Rhodoturula, Candida, Mucor mucedo, Scedosporium apiospermum,* Zygomyeces and *Penicillum sp.*

Conclusion: Large bacteria community known for their significant public health implications at different percentages were isolated from the environment studied. These bacteria could contribute to the health deteroration of people living within its environ and could contribute to disease outbreak if not well managed.

Keywords: Bacteria, Refuse Dumps, Soil Samples, Public Health

INTRODUCTION

Indiscriminate dumping of refuse is a major problem in Nigeria especially in rural areas, and this pose a potential hazard as they are associated with many microorganisms. According to United Nation Environmental Programme [1], the magnitude of waste generation is increasing with population expansion and economic development.

Archives of Pharmaceutical Sciences and Biotechnology Journal

Volume 2 Issue 1 January, 2022 Page 52 - 58 ISSN: 2971_611X

APSB-05

APSBJournal

Inadequate solid waste disposal is the second most pressing problem facing city residents in developing countries after unemployment, according to United Nations Development Programme (UNDP) survey report of one hundred and fifty-one different cities from around the world [2]. Nigeria is a developing country with persistent solid waste management problem, an average Nigerian generates about 0.49 kg of solid waste per day [2]. These waste dumps are rapidly populated by microorganisms such as bacteria and fungi using their components as their sources of nutrition for growth and multiplication, many of these microorganisms have been found to be harmful to man and the environment [3]. Many pathogenic microorganisms may as well be present in the faecal matter, soil and the decaying refuse. Children playing and people living around these dump sites could be affected by these pathogens.

The magnitude of indiscriminate refuse dumps is worsening by the day in Lugbe, Abuja due to inadequate sanitary landfill. No evidence of work on health significance of bacteria associated with refuse dumps in Lugbe community of Abuja. The objectives of this study are to examine the dump and soil samples of different refuse dump sites and assay them for the presence of bacteria and asses the public health implications.

MATERIALS AND METHODS

Description of Study Area

Study area was Lugbe, Abuja Municipal Area Council (AMAC) of the Federal Capital Territory Abuja. It is located on 8^0 57'20" North of the equator and latitude 7^0 24' 53" East of the Greenwich meridian. It is largely residential and densely populated. Samples of soil and dump were collected from ten common dump sites located and labelled as follows

1. Kapwa refuse dump A
2. Tudun wada refuse dump B
3. Sector F refuse dump C
4. Solid rock school refuse dump D
5. LEA primary school refuse dump E
6. Woodwox refuse dump F
7. FHA junction refuse dump G
8. Lugbe zone 1 refuse dump H
9. Lugbe village refuse dump I
10. VIO refuse dump J

Collection and Processing of Samples

Dump samples were obtained in a sterile bottle from three different points at each of the ten sites and labeled. All soil samples were taken from depth of 0-30cm after clearing the surface debris and scooping with the aid of spatula in a sterile bottle within the perimeter of each refuse collection point[4]. Two visits were made each month and six samples (three dump and soil samples) were collected at each visit from each site. The temperature of each sample was determined immediately after collection using a thermometer (Omron MC 246 E), after which the sample were conveyed to the department of microbiology of National Institute for Pharmaceutical Research and Development (NIPRD) for analysis. One gram (1g) of each sample was mixed in a sterile tube containing 9ml of sterile distilled water and the pH was determined with a pH meter (Model HI 2550 Hanna instrument ltd).

Cultivation and Enumeration of Bacteria

The dump sample was pounded and one gram (1g) of the sample was thoroughly shaken in a test-tube containing 10ml of sterile distilled water (stock) and serially diluted in a one-tenth stepwise to 10^{-6} dilution. One gram (1g) of each soil sample was thoroughly shaken in a test-tube containing 10ml of sterile distilled water as stock. 1ml was transferred into the next test-tube and diluted serially in a one-tenth stepwise

Archives of Pharmaceutical Sciences and Biotechnology Journal

Volume 2 Issue 1 January, 2022 Page 52 - 58 ISSN: 2971_611X

APSB-05

APSBJournal

to 10^{-6} dilution. From each of the dilution 1ml was transferred into a universal bottle containing nutrient agar using sterile micropippate (1000ul) and then poured into plate. The plates were labeled and incubated at 37^0C for 18 t0 24 hrs. The discrete colonies which developed were counted and the average count was recorded as total viable aerobic heterotrophic bacteria in the sample. Mixed growth of different bacterial isolate was observed.

Isolation and Identification of Bacteria

Pure cultures of the bacteria were obtained by aseptically streaking representative colonies of different morphological types which appeared on the cultured plates onto freshly prepared nutrient agar plates which were incubated at 37^0C for 24hrs. These served as pure stock cultures for cultural and morphological identification. The following standard characterization tests were performed in duplicates: Gram staining, catalase test, coagulase test, sugar fermentation test, methyl red test, Voges-proskauer test, indole test, citrate test, starch hydrolysis test and urease test.

Statistical Analysis

Statistical analysis was conducted using analysis of variance (ANOVA). In all the analysis, $P < 0.05$ was set for significance.

RESULTS

A total of 720 samples were analyzed, comprising of 360 soil and 360 dump samples. Table 1 shows the mean temperature and pH values of the soil and dump samples of the ten dump sites. The mean temperature (^{0}C) of the soil samples from the ten sites was 31.3^0C and that of the dump was 30.1^0C. The degree of acidity (pH), reported in this investigation for all the sampling sites ranged from pH 5.10 to 7.60 and mean pH values of the soil samples from the ten dumps was 6.61 and 6.72 for the dump samples.

Table 1: Mean Temperature (^{0}C) and pH Values of the Soil and Dump Samples

Dump sites	Temperature (^{0}C)		pH	
	Soil	Dump	Soil	Dump
A	27	28	7.15	6.92
B	30	31	6.71	6.80
C	31	34	6.49	6.65
D	30	30	6.35	6.50
E	32	35	5.10	6.60
F	29	29	7.30	6.84
G	29	31	7.04	6.91
H	32	34	6.50	6.67
I	31	30	7.60	6.95
J	30	31	5.87	6.40
Total	301	313	66.11	67.24
Mean	30.1	31.3	6.61	6.72

Archives of Pharmaceutical Sciences and Biotechnology Journal

Volume 2 Issue 1 January, 2022 Page 52 - 58 ISSN: 2971_611X
APSB-05

APSBJournal

Mean Total Viable Bacterial Count of the Soil and Dump Samples

Table 2 shows the mean total viable bacterial counts of the soil and dump samples. The mean value of total bacterial count per gram of the samples ranged from 7.5 x 10^7 to 16.1 x 10^7cfu wet season while that of dry season ranges from 5.8 x 10^7 to 11.3 x 10^7 (Table 2). Refuse dump C had highest mean total bacterial count of 16.1 x 10^7 cfu/g/ml and 11.3 x 10^7 cfu/g/ml for wet and dry season respectively. Refuse dump A had the lowest bacterial count of 7.5 x 10^7cfu/g/ml and 6.8 x10^7cfu/g/ml for wet and dry season respectively.

The present investigation shows that seasonal influence can affect microbial proliferation. Generally, the mean total bacterial count was higher in the wet season than the dry season for both the soil and dump samples (Table 2). Statistical analysis, using analysis of variance (ANOVA) at 5% significance level revealed a significant difference between the total bacterial count wet and dry season ($P<0.05$). This is in agreement with Achudume and Olawale[5] which recorded higher bacterial count in the wet season.

Table 2: Mean Total Viable Bacterial Counts of the Soil and Dump samples.

Dumps	Wet season (CFU/g/ml)			Dry season (CFU/g/ml)		
	Soil sample	Dump sample	TBCW	Soil sample	Dump sample	TBCD
A	3.2 x 10^7	4.3 x 10^7	7.5 x 10^7	3.0 x 10^7	3.8 x 10^7	6.8 x 10^7
B	6.2 x 10^7	7.2 x 10^7	13.4 x 10^7	4.3 x 10^7	4.5 x 10^7	8.8 x 10^7
C	8.1 x 10^7	8.0 x 10^7	16.1 x 10^7	5.6 x 10^7	5.7 x 10^7	11.3 x 10^7
D	7.1 x 10^7	6.8 x 10^7	13.9 x 10^7	5.2 x 10^7	4.9x 10^7	10.1 x 10^7
E	4.5 x 10^7	5.5 x 10^7	10.0 x 10^7	3.1 x 10^7	4.5 x 10^7	7.6 x 10^7
F	5.3 x 10^7	7.0 x 10^7	12.3 x 10^7	3.8 x 10^7	3.8 x 10^7	7.6 x 10^7
G	4.0 x 10^7	4.1 x 10^7	8.1 x 10^7	2.6 x 10^7	3.2 x 10^7	5.8 x 10^7
H	7.1 x 10^7	5.5 x 10^7	12.6 x 10^7	4.7 x 10^7	4.0 x 10^7	8.7 x 10^7
I	5.0 x 10^7	5.7x 10^7	10.7 x 10^7	3.7 x 10^7	4.4 x 10^7	8.1 x 10^7
J	6.2 x 10^7	6.2 x 10^7	12.4 x 10^7	3.4 x 10^7	4.8 x 10^7	8.2 x 10^7

Keys: TBCW: Total bacterial count wet season, TBCD: Total bacterial count dry season
F=58.33071416, F crit=2.38607, df=5, p< 0.05

Bacterial Isolates and their Dump Distribution

A total of eight bacteria were isolated from the dump sites. The bacteria isolated includes, *Staphylococcus saprophyticus, Staphylococcus aureus, Streptococcus pyogenes, Bacillus cereus, Escherichia coli, Proteus vulgaris, Klebsiella pneumonia* and *Pseudomonas aeruginosa.*

Table 3 shows the soil bacterial isolates and their dump distribution. Only three bacteria; *Staphylococcus aureus, Bacillus cereus* and *Escherichia coli* were isolated from the soil samples of all the ten dumps. Table 4 shows the dump bacterial isolates and their dump distribution. Only *Staphylococcus aureus* and *Escherichia coli* were isolated from the dump sample of all the ten refuse dumps.

Archives of Pharmaceutical Sciences and Biotechnology Journal

Volume 2 Issue 1 January, 2022 Page 52 - 58 ISSN: 2971_611X

APSB-05

APSBJournal

Table 3: Bacterial Isolates Observed in Various Dump Soil Samples

Microorganisms	A	B	C	D	E	F	G	H	I	J	No of Dumps
Staphylococcus saprophyticus	+	+	+	+	-	+	+	-	+	+	8
Staphylococcus aureus	+	+	+	+	+	+	+	+	+	+	10
Streptococcus pyogenes	-	+	+	+	-	-	-	+	-	-	4
Bacillus cereus	+	+	+	+	+	+	+	+	+	+	10
Escherichia coli	+	+	+	+	+	+	+	+	+	+	10
Proteus vulgaris	+	-	+	-	+	-	+	-	-	-	4
Klebsiella pnemoniae	-	-	+	+	-	-	-	+	-	-	3
Pseudomonas aeruginosa	-	-	+	-	+	-	-	-	-	+	3

Key: += Present, - =Absent, A-J= Refuse dump sites

Table 4: Bacterial Isolates Observed in Various Dump Samples

Microorganisms	A	B	C	D	E	F	G	H	I	J	Dumps site	%
Staphylococcus saprophyticus	+	-	+	-	+	+	-	+	+	-	7	13.1
Staphylococcus aureus	+	+	+	+	+	+	+	+	+	+	10	18.9
Streptococcus pyogenes	-	+	+	+	-	-	-	-	-	-	3	5.7
Bacillus cereus	+	+	+	+	-	+	+	-	+	+	8	15.1
Escherichia coli	+	+	+	+	+	+	+	+	+	+	10	18.9
Proteus vulgaris	-	-	+	-	-	-	-	+	-	-	2	3.8
Klebsiella pnemoniae	+	+	+	+	-	-	-	+	-	-	5	9.4
Pseudomonas aeruginosa	+	+	+	-	+	+	+	+	+	-	8	15.1
Total											**53**	**100**

Keys: A-J = dump sites, += Present, - = absent

DISCUSSION

The bacterial isolates are in agreement with a reports [3] in which *Staphylococcus sp, Bacillus sp, Escherichia coli, Proteus sp, Klebsiella sp* and *Pseudomonas sp* were isolated. Another researcher [4] also isolated *Staphylococcus sp, Streptococcus sp, Bacillus sp, Escherichia coli, Proteus sp, Klebsiella sp, and Pseudomonas sp.* All the bacterial isolates reported in this study have been associated with waste and waste biodegradation [3]. The presence of *K. pneumonia* and *E. coli* is an indication of faecal contamination at the dump site [6].

Most of the microorganisms recovered in this study are soil-inhabiting microorganisms which form symbiotic associations in the soil [3]. Some non symbiotic nitrogen fixing bacteria like *Klebsiella* and *Bacillus* which are facultative anaerobes where isolated in this research [7]. It has been reported that truly pathogenic form may survive in waste [8]. In line with this all the bacteria isolated in this study have been reported as potential pathogens (they are capable of causing disease) [9, 10].

Archives of Pharmaceutical Sciences and Biotechnology Journal

Volume 2 Issue 1 January, 2022 Page 52 - 58 ISSN: 2971_611X
APSB-05

APSBJournal

Staphylococcus aureus is the most dangerous of all *Staphylococcus* bacteria [11]. It is a normal commensal of the nose but it may become pathogenic and cause pneumonia in a child with measles or influenza, bronchopneumonia, conjunctivitis, skin infections, food poisoning, and some urinary tract infection associated with instrumentation [11, 12]. *S. saprophyticus* is a normal vaginal flora but can cause urinary tract infections usually in young women that are sexually active [13].

Streptococcus pyogenes could cause systemic infections including sore throat, scarlet fever, soft tissue infections, toxic shock-like syndrome and some burn infections [14]. *Escherichia coli* is a normal inhabitant of the intestinal tract but if it enters the urinary tract it can cause urinary infection. It can also cause dysentery, infantile diarrhea, traveler's diarrhea, primary bacteremia, occasionally meningitis and some wound infections [12]. *E. coli* when ingested even in small amount can cause infection [15].

Proteus, Pseudomonas and *Klebsiella* are frequently involve in urinary tract infections, bacteremia, occasionally causes nosocomial infections of the lower respiratory tract, burn and wound infections [12]. *Bacillus cereus* is associated with food poisoning and some gastrointestinal illnesses [12].

The presence of these potential pathogens in the soil and refuse dump ultimately leads to their presence in the air as they are taken up by air currents into the atmosphere from where they are inhaled by the population. The health hazard associated with the indiscriminate dumping of wastes in these dump sites cannot therefore be under estimates.

CONCLUSION

The health hazard associated with indiscriminate dumping of solid waste within lugbe cannot be underestimated. The data suggest there is need to control dumping of waste as these waste dumps are sources of potential health hazards.

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Competing Interests: Authors have declared that no competing interest exist.

Authors' Contribution

FD designed the study, wrote the protocol and wrote the first batch of the manuscript. ZB managed the literature searches while HD performed the statistical analysis. All authors read and approved the final manuscript.

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Archives of Pharmaceutical Sciences and Biotechnology Journal

Volume 2 Issue 1 January, 2022 Page 52 - 58 ISSN: 2971_611X
APSB-05

APSBJournal

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