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Landfill Waste Effluents Increase the Population and Diversity of Soil Microorganisms: The Case of Olusosun Landfill, Lagos, Nigeria

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Authors' contributions

This work was carried out in collaboration between all authors. Authors EEN, ENA and ODT designed the study. Author EEN wrote the protocol, managed the analyses of the study, performed the statistical analysis and wrote the first draft of the manuscript. Authors EEN and ENA managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Aims: This study investigated the impact of landfill waste effluents on the population and diversity of soil microorganisms, and a comparative study between landfill soil and effluent-free field soil.
Study Design: A comparative, investigative survey.
Place and Duration of Study: Biotechnology Laboratory, Federal Institute of Industrial Research, Oshodi, Lagos, between August 2015 and February 2016.
Methodology: Soil samples were collected from the surface layers (1-20 cm) of alfisol at the landfill and a field located about 1000 meters from the landfill site. Isolation and characterization of bacteria, actinomycetes and fungi, physical and chemical analysis of the soil samples were performed. One-way analysis of variance (ANOVA) was used for statistical analysis, with level of significance at 0.05.

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Results: Mean microbial counts (CFU g^{-1} dry soil) in landfill soil (Lfs) and field soil (Fs) respectively were: Total bacterial counts 87 $\times 10^5$ and 72 $\times 10^5$, coliforms 51$\times 10^5$ and 38 $\times 10^5$, actinomycetes 44 $\times 10^5$ and 22 $\times 10^5$, and fungi 21$\times 10^5$ and 15 $\times 10^5$, Lfs counts exceeding Fs counts significantly ($P < 0.05$). The isolates included *Proteobacteria* (Lfs =16 spp.; Fs=7 spp.), *Firmicutes* (Lfs =20 spp.; Fs=10 spp.), *Actinobacteria* (Lfs =10 spp.; Fs=5 spp.), and Fungi (Lfs =15 spp.; Fs=13 spp.), Lfs yielding significantly higher diversity than Fs ($P < 0.05$). Lfs and Fs respectively contained: moisture (56.8 and 50.9%); pH (6.19 and 6.80); nitrogen (0.99 and 0.42%); phosphorus (553.4 and 371.8 mg/kg); Organic carbon (2.65 and 3.52%); cation exchange capacity (48.14 and 38.8 Cmmol/kg); sand (48.8 and 31.2%); clay (28.8 and 26.0%); silt (22.4 and 57.2%), highlighting differences in chemical and physical properties which support a greater diversity and population of microbes in Lfs more than Fs.
Conclusion: Effluents from landfills enhance the physical and chemical properties of soil, resulting in larger CFU, and greater diversity of all microorganisms. The greater diversity of microbes can be exploited for industry, medicine, agriculture, bioremediation, bio-control and research. The results reveal the importance of citing landfills far from farms, water bodies and residential areas to avoid health hazards in humans, livestock, and adverse effects on plants.

Keywords: Landfill; municipal waste; effluent; microorganisms; population; diversity.

1. INTRODUCTION

Municipal landfills receive thousands of tons of rubbish daily, comprising mainly of domestic, industrial, commercial, agricultural and hospital waste. Most wastes arriving at the landfills are untreated, and may contain organic and inorganic substances, as well as microorganisms which may be beneficial or otherwise hazardous to life and the environment. Studies conducted on the microbial diversity in landfills reveal that landfill soil offer a conducive environment for the growth of diverse kinds of microorganisms. Song et al. [1] used PCR-based 454 pyrosequencing to investigate the bacterial communities of landfill leachate samples from five different landfills in China. Bacterial isolated included Gammaproteobacteria, *Firmicutes*, and bacteroids, *Fusobacteria* and Tenericutes. Predominant among these bacteria were *Pseudomonas* species, cellulolytic bacteria, sulphate-reducing bacteria, sulphate-oxidizing bacteria and xenobiotic organic compound-degrading bacteria.

In a study that highlighted how contaminated effluents from landfills can impact on the surrounding communities, Ikpeme et al. [2] carried out a microbiological analysis of utisols polluted by dumpsite effluents in Cross River State, Southern Nigeria. The isolates included *Proteus* spp, *Pseudomonas* spp, *Bacillus* spp, *Escherichia coli*, *Campylobacter* spp, *Klebsiella* spp, *Shigella* spp, *Salmonella* spp, *Aeromonas* spp and *Vibrio cholerae*. Nearby water sources were analyzed and similarities in the properties of isolates from both dumpsite effluent-polluted soil and water sources indicated a possible infiltration of pathogens from dumpsite effluents to water sources in the community.

In the environment, microorganisms are extremely important in recycling of nutrients, balance of trophic chains, vital physiological activities in plants and animals, as well as conservation of natural habitats. Microbes are important in industrial and food production, in probiotics, and in synthesis of antimicrobial substances and vitamins essential to living beings. The diversity of microorganisms is critical to the functioning of the ecosystem, because there is the need to maintain ecological processes such as decomposition of organic matter, nutrient cycling, soil aggregation and controlling pathogens within the ecosystem [3].

Landfills constitute habitats for the growth of unusual microbes because of the diversity of waste materials they contain. In Nigeria, indiscriminate dumping of rubbish at unauthorized sites create similar habitats all over the landscape, thus amplifying the impact of microbial communities on the ecosystem. The study of microbial biodiversity in landfills, as well as its role and function in relation to environmental, industrial and health issues is at stake, since microbial diversity is directly related to ecosystem stability [4].

The few studies of microbial life on landfill soils did not compare the microbial diversity of landfills with other kinds of soil. The authors embarked on a microbiological, physical and chemical analysis of landfill soil in comparison with field soil in order

to highlight the changes in soil quality, microbial diversity and population when soil is polluted with landfill effluents.

There is good reason to undertake a study on microbial biodiversity since microorganisms are sensitive indicators of environmental quality [5]. The findings of the study revealed changes in population that could result in serious threats to human, plant and animal health. The study also unveiled rare microbial strains with potentially beneficial traits. Hopefully, information from this study will stimulate the implementation of policies for better control of the landfill system in order to prevent ecosystem destabilization.

2. MATERIALS AND METHODS

2.1 Study Area and Duration

The Study area was Olusosun landfill, Latitude 6.441158 and Longitude 3.417977 (6o 30' 0" N and 4o 48' 0" E) in Ojota area of Lagos Mainland. Olusosun landfill, is the largest in Africa and one of the largest in the world. The site receives up to 10,000 tons of rubbish each day [6]. The proximity of this massive dumpsite to homes and commercial areas, necessitates a study of the biodiversity of microbial life at the landfill, in order to elucidate the associated benefits and hazards. The study was conducted inbetween August 2015 and February 2016.

2.2 Soil Sample Collection

Soil sub-samples (10) were randomly collected from the surface layers (1-20 cm) of alfisol at the landfill and pooled to form composite sample. Soil samples were also collected from a field located about 1000 meters away from the landfill. The samples were stored in sterile cellophane bags and taken to the Biotechnology Laboratory, Federal Institute of Industrial Research, Oshodi, Lagos, for microbiological, chemical and physical analysis within 8 h. The samples were homogenized and spread in sterile trays to be cleaned of extraneous materials (pieces of plants, animals, etc) before analyses.

2.3 Microbial Counts

Ten g of each soil sample were added to 95 mL of 0.1% (w/v) solution of sodium pyrophosphate. After homogenization for 30 min, this solution was decimally diluted (10^{-1} to 10^{-7}). Aliquots of the resulting solutions were plated on appropriate culture media. Culture media included Tryptone soy agar for total microbial count, MacConkey agar for coliform counts, Casein-Starch agar for actinomycetes counts, and Czapek Dox agar for fungi counts [7]. After incubation at 30℃, for up to 10 days, the colonies in each plate were counted. Counts were calculated as y=log(x+1), where x was the number of CFU g^{-1} dry soil.

2.4 Isolation and Identification of Microorganisms

Three grams of soil were diluted in 100 ml of saline solution (0.85% NaCl) and shaken in an orbital shaker at 200 rpm for 30 min. The mixtures were allowed to settle and three different dilutions (1:10, 1:100, 1:1000) were prepared using sterile saline solutions in a total volume of 10 ml.

2.4.1 Isolation and identification of bacteria

An aliquot of 0.1 ml of each dilution was taken and spread evenly over the surface of Nutrient agar and MacConkey agar. Plates were incubated overnight at 30℃. Identification of bacteria was done using standard microbiological and biochemical methods [8-10]. Gram staining, motility tests, starch, gelatin and casein hydrolysis were performed for genus identification. Biochemical tests for catalase, oxidase, indole production, urease, Methyl Red and Voges Proskauer tests, Nitrate (NO_3) reduction, and utilization of different carbon sources such as such as citrate, starch, glucose, sucrose, xylose, lactose, mannitol, maltose, raffinose, arabinose, sorbitol, fructose, and salicin were used to establish possible species identity. The biochemical tests were performed by the conventional phenotypic method.

2.4.2 Isolation and identification of *Actinomyces* and *Streptomyces*

2.4.2.1 Isolation of Actinomyces and Streptomyces

An aliquot of 0.1 ml of each dilution was taken and spread evenly over the surface of Casein-Starch agar and *Streptomyces* agar (HiMedia, Mumbai, India). Rifampin 2.5 µl /ml and amphotericin B 75 µl /ml were added to the media to inhibit bacterial and fungal contamination. Plates were incubated at 30℃, and monitored after 48, 72, and 96 h. Representative colonies were selected and streaked on new plates of selective medium [11,12].

2.4.2.2 Genus identification and morphological characteristics of Actinomyces and Streptomyces

Visual observation of both morphological and microscopic characteristics were performed, using light microscopy, and Gram-stain properties [11]. The isolates were classified and differentiated using the aerial mass color, color of substrate mycelium, production of melanoid pigment, and spore chain morphology, according to Bergey's Manual of Systematic Bacteriology [13].

2.4.2.3 Biochemical screening of Actinomyces and Streptomyces

Physiological criteria such as the ability to hydrolyse starch, gelatin and casein were used for genus confirmation. The utilization of different carbon sources, utilization of urea, Nitrate (NO_3) reduction and production of melanin were studied for possible species classification.

2.4.3 Isolation and identification of fungi

An aliquot of 0.1 ml of each dilution was taken and spread evenly over the surface of Sabouraud's Dextrose agar. Chloramphenicol 0.1 g/L and Rose Bengal 0.05 g/L were added to the media to inhibit bacterial growth and overgrowth of rapidly growing moulds. Plates were incubated at 30℃, and monitored after 48, 72, and 96 h. Representative colonies were selected and sub-cultured on new plates of selective medium. Fungi were identified according to colonial morphology and color on agar, as well as microscopic morphologic features such as hyphae and conidiophores [14].

2.5 Determination of Physical and Chemical Properties of Soil Samples

Physical and chemical properties of the soil samples were determined according to established standards. This analysis included moisture (%), pH (H_2O), Nitrogen (%), P ($mgdm^{-3}$), organic matter (gdm^{-3}), Effective Cation exchange capacity (CEC) and Exchangeable Cations in Cmmol/kg (Ca, Mg, K, Na, Al, H^+), Sand (%), Clay (%), and Silt (%) [15,16,17].

2.6 Statistical Analysis

One-way Analysis of variance (ANOVA) was used for statistical analysis, and Duncan Multiple Range Test was used to separate the means. The level of significance was set at 0.05.

3. RESULTS AND DISCUSSION

3.1 Microbial Counts

Microbial counts for aerobic mesophiles were obtained in duplicate plates, and recorded as CFU g^{-1} dry soil on different media. Average counts obtained from landfill soil and field soil, respectively were:total bacterial count on Tryptone soy agar: 87×10^5 CFU g^{-1} dry soil and 72×10^5 CFU g^{-1} dry soil; Coliform counts on MacConkey agar: 51×10^5 CFU g^{-1} dry soil and 38×10^5 CFU g^{-1} dry soil; Actinomycetes counts on Casein-Starch agar: 44×10^5 CFU g^{-1} dry soil and 22×10^5 CFU g^{-1} dry soil; Fungi count on Czapek Dox agar: 21×10^5 CFU g^{-1} dry soil and 15×10^5 CFU g^{-1} dry soil in landfill soil and field soil respectively (Table 1).

3.2 Genera and Species of Microorganisms Isolated from Landfill Soil and Field Soil

3.2.1 *Proteobacteria* from landfill soil and field soil

Eleven (11) genera and 16 species of *Proteobacteria* (Gram-negative bacteria) were isolated from landfill soil. These included *Alcaligenes* (2 species), *Acinetobacter* (1 species), *Citrobacter* (1 species), *Enterobacter* (3 species) *Escherichia coli* (1 species), *Klebsiella* (1 species), *Proteus* (1 species), and *Serratia* (1 species). Also isolated were *Flavobacteria* (2 species) and *Pseudomonas* (2 species).Six (6) genera and 7 species of Gram-negative bacteria were isolated from field soil. These included *Alcaligenes* (1 species), *Acinetobacter* (2 species) *Enterobacter* (1 species), *Klebsiella* (1 species) *and Serratia* (1 species). Also isolated was *Flavobacterium* (1 species) (Table 2).

3.2.2 *Firmicutes* from landfill soil and field soil

Five (5) genera and 20 species of *Firmicutes* (Gram-positive bacteria) were isolated from landfill soil, including members of the genera *Bacillus* (11 species) *Clostridium* (1 species), *Corynebacterium* (3 species), *Micrococcus* (3 species) and *Staphylococcus* (1 species).

Three (3) genera and 10 species of Gram-positive bacteria were isolated from field soil, including members of the genera *Bacillus* (6 species), *Corynebacterium* (2 species), and *Micrococcus* (2 species) (Table 3).

3.2.3 *Actinobacteria* from landfill soil and field soil

One (1) genera and 10 species of *Actinobacteria* (Gram-positive branching bacteria) were isolated from landfill soil. All were members of the genus *Actinomyces*.

Two (2) genera and 5 species of *Actinobacteria* were isolated from field soil, including members of the genera *Actinomyces* (2 species) and *Streptomyces* (3 species) (Table 4).

3.2.4 Fungi from landfill soil and field soil

Eleven (11) genera and 15 species of fungi were isolated from landfill soil. These included members of the genera *Absidia* (1 species), *Aspergillus* (5 species), *Cladosporium* (1 species), *Fusarium* (1 species), *Monilia* (1 species), *Mucor* (1 species), *Nigrospora* (1 species), *Penicillium* (1 species), *Rhizopus* (1 species), *Sepedonium* (1 species), and *Talaromyces* (1 species).

Ten (10) genera and 13 species of fungi were isolated from field soil. These included members of the genera *Absidia* (1 species), *Alternaria* (1 species), *Aspergillus* (3 species), *Fusarium* (1 species), *Gliomastix* (1 species), *Humicola* (1 species), *Moniliella* (1 species), *Mucor* (1 species), *Penicillium* (2 species), *Rhizopus* (1 species) (Table 5).

Table 1. Average microbial counts of aerobic mesophiles in landfill soil and field soil (CFU g^{-1} dry soil)

Soil sample	Total viable bacterial count on Tryptone soy agar	Coliform count on MacConkey agar	Actinomycetes count on starch casein agar	Fungi count on czapek dox agar
Landfill soil	84 $\times10^5$	49 $\times10^5$	46 $\times10^5$	22 $\times10^5$
	89 $\times10^5$	52 $\times10^5$	42 $\times10^5$	20 $\times10^5$
	Av. 87$\times10^5$	Av. 51$\times$ 10^5	Av. 44 $\times10^5$	Av. 21$\times10^5$
Field soil	73 $\times10^5$	36 $\times10^5$	20 $\times10^5$	16 $\times10^5$
	70 $\times10^5$	39 $\times10^5$	24 $\times10^5$	14 $\times10^5$
	Av. 72 $\times10^5$	Av. 38 $\times10^5$	Av. 22 $\times10^5$	Av. 15 $\times10^5$

Table 2. *Proteobacteria* isolated from landfill soil and field soil

Landfill soil bacteria isolate	Number of isolates	Field soil bacteria isolate	Number of isolates
Alcaligenes eutrophus	1	*Alcaligenes latus*	1
A. faecalis	1	-	-
Acinetobacter anitratus	1	*Acinetobacter mallei*	1
-	-	*A. iwoffi*	1
Citrobacter diversus	1	-	-
Enterobacter aerogenes	1	*Enterobacter intermedius*	1
E. agglomerans	1	-	-
E. cloacae	1	-	-
Escherichia coli	1	-	-
Flavobacterium gleum	1	*Flavobacterium aquantile*	1
F. rigense	1	-	-
Klebsiella pneumoniae	1	*Klebsiella terrigena*	1
Proteus vulgaris	1	-	-
Pseudomonas aeruginosa	1	-	-
P. putida	1	-	-
Serratia liquifasciens	1	*Serratia rubidaea*	1
Number of genera	11		6
Number of species	16		7
Total Number of isolates	16		7

Table 3. *Firmicutes* isolated from landfill soil and field soil

Landfill soil bacteria isolate	Number of isolates	Field soil bacteria isolate	Number of isolates
Bacillus brevis	1	*Bacillus brevis*	1
B. cereus	2	*B. fastidiosus*	1
B. circulans	1	*B. licheniformis*	1
B. coagulans	1	*B. polymyxa*	1
B. laterosporus	1	*B. sphaericus*	1
B. licheniformis	1	*B. subtilis*	1
B. mycoides	1	-	-
B. pastearii	1	-	-
B. (Paenibacillus) plymyxa	1	-	-
B. subtilis	1	-	-
B. thuringensis	1	-	-
Clostridium tertium	1	-	-
Corynebacterium kutscheria	1	*Corynebacterium pilosum*	1
C. pilosum	1	*C. fascians*	1
C. striatum	1	-	-
Micrococcus roseus	1	*Micrococcus kristinae*	1
M. luteus	1	*M. candidus*	1
M. varians	1	-	-
Staphylococcus aureus	1	-	-
Number of genera	5		3
Number of species	20		10
Total Number of isolates	21		10

Table 4. *Actinobacteria* isolated from dump soil and field soil

Landfill Soil Bacteria Isolate	Number of isolates	Field Soil Bacteria Isolate	Number of isolates
Actinomyces bovis	1	*Actinomyces pyogenes*	1
A. eriksonii	1	*A. viscosus*	1
A. humiferus	1	-	-
A. israelii	1	-	-
A. meyeri	1	-	-
A. naellundii	1	-	-
A. odontolyticus	1	-	-
A. pyogenes	1	-	-
A. suis	1	-	-
A. viscosus	1	-	-
-	-	*Streptomyces phaeofaciens*	1
-	-	*S. nigrescens*	1
-	-	*S. cretosus*	1
Number of genera	1		2
Number of species	10		5
Total number of isolates	10		5

3.3 Physical and Chemical Properties of Soil Samples

From the results, the mean moisture content of the landfill soil sample was 56.75%, while the mean moisture content of the field soil sample was 50.90%. The mean nitrogen (N) content of landfill soil was 0.985%, while mean nitrogen content of field soil was 0.42%. The mean available phosphorus (P) found in landfill soil sample was 553.395 mg/kg, while mean available phosphorus found in field soil sample was 371.81 mg/kg. Cation exchange capacity (CEC) was found to be 48.14 and 38.74 Cmmol/kg for landfill soil and field soil respectively. Percentage sand, clay and silt were 48.82, 28.8 and 22.4% respectively for landfill soil, and 31.2, 26.0 and 57.2 respectively for field

soil. The pH of landfill soil and field soil were 6.19 and 6.80 respectively (Table 5).

A wide variety of bacteria and fungi were isolated and identified from the soil samples in the present study. Total counts, coliform, Actinomyces, and fungi counts from landfill soil were all significantly higher than in field soil (Table 1). The groups of microbes found respectively in landfill soil (Lfs) and field soil (Fs) were: *Proteobacteria* (Lfs =16 spp.; Fs=7 spp.), *Firmicutes* (Lfs =20 spp.; Fs=10 spp.), *Actinobacteria* (Lfs =10 spp.; Fs=5 spp.), and Fungi (Lfs =15 spp.; Fs=13 spp.) showing significant differences were ($P < 0.05$). (Tables 2-5). All the isolates are associated with the environment such as soil, water, plants, and sewage. Genera and species diversity for dump soil were higher in dump soil than in field soil, for all the groups isolated. This may imply that landfill effluent-contaminated soil supports a greater population and diversity of microbes, than uncontaminated field soil. These findings are in consonance with reports of similar studies conducted in China and Cross River State of Nigeria [1,2].

Bacillus (11 species) and Actinomyces (10) were the most abundant species found in the landfill soil in the present study. Similarly, Krishnamurthi and Chakrabarti [18] reporting from a study in a landfill in India, isolated *Firmicutes* (86.6%), *Actinobacteria* (9.6%), and *Proteobacteria* (3.7%), with *Bacillus* species yielding at least 17 species as the most abundant inhabitants of the landfill. They suggested that irrespective of the composition of municipal solid waste and climate, the members of bacterial and archaeal communities in landfills of many countries remains broadly similar.

Table 5. Fungi isolated from dump soil and field soil

Landfill Soil Fungi Isolate	Number of isolates	Field Soil Fungi Isolate	Number of isolates
Absidia spinosa	2	*Absidia spinosa*	1
-	-	*Alternaria tenius*	1
Aspergillus amstelodami	1	*Aspergillus niger*	1
A. chevalieri	1	*A. flavus*	1
A. flavus	1	*A. fumigates*	1
A. melleus	1	-	-
A. niger	1	-	-
Cladosporium sphaerospermum	1	-	-
Fusarium oxysporum	2	*Fusarium culmorum*	1
Monilia sitophila	1	-	-
-	-	*Gliomastix murorum*	1
-	-	*Humicola grisea*	1
-	-	*Moniliella accetoabutans*	1
Mucor plumbeus	1	*Mucor plumbeus*	1
Nigrospora oryzae	1	-	-
Penicillium digitatum	1	*Penicillium islandicum*	1
-	-	*P. verruculosum*	1
Rhizopus arrhizus	2	*Rhizopus stolonifer*	1
Sepedonium sp	1	-	-
Talaromyces thermophilus	1	-	-
Number of genera	11		10
Number of species	15		13
Total number of isolates	18		13

Table 6. Mean values for physical and chemical properties of soil samples

Sample	Moisture (%)	N (%)	P (mg/kg)	Organic carbon (%)	Cation exchange (Cmmol/kg)	Sand (%)	Clay (%)	Silt (%)	pH
Landfill soil	56.8	0.985	553.4	2.65	48.14	48.82	28.8	22.4	6.19
Field soil	50.9	0.42	371.8	3.52	38.74	31.2	26.0	57.2	6.80

The higher moisture content in landfill soil could be one of the factors that encouraged microbial growth, leading to a higher population of all the groups of microbes found in the study, as against field soil. Both nitrogen and phosphorus contents in landfill soil were found to be higher than in field soil. This implies that the dumpsite contained organic waste which mineralized to add nitrogen and phosphorus to the soil. Contrarily, the field soil contained much less nitrogen and phosphorus than the landfill soil (Table 5). The presence of decomposing organic matter in the landfill, adding more N and P to the soil, would encourage the growth of all genera of microbes, and this resulted in the larger microbial counts in landfill soil. The Cation Exchange Capacity, (CEC) is a measurement of the soil's capacity to hold cation nutrients. CEC is useful in comparing the potential for different soils to hold and supply nutrients for plant growth. [19]. CEC of 48.14 and 38.74 Cmmol/kg for landfill soil and field soil respectively implies that the dump soil had a higher potential to hold and supply nutrients for plant growth, and by implication, microbial growth.

The mean pH value of the landfill soil sample was found to be 6.19, while the mean pH value of the field soil sample was 6.80. This shows that the two soils have a low acidity, with the landfill soil more acidic than field soil. According to most nutrients needed by plants are readily available when the pH of the soil ranges from 6.0 to 7.5. In addition, other authors reported a wider range of soil pH (5.5 – 8) which favor plant growth and most soil processes, including nutrient availability and microbial activity. This implies that both the landfill soil and field soil pH values fall into the range most suitable for both microbial and plant growth. Furthermore, the higher acidity found in landfill soil can be attributed to organic matter mineralization [20,21].

The present investigation yielded important bacterial isolates from landfill waste effluent-contaminated soil, not found in the control field soil. Notable among these is *Pseudomonas putida*, which has a very diverse metabolism, including the ability to degrade organic solvents such as toluene [22]. It is used as a soil inoculant to remedy naphthalene-contaminated soils, with the advantage of being non-pathogenic [23]. In addition, *P. putida* is able to convert styrene oil into the biodegradable plastic PHA [24]. This may be of use in the effective recycling of polystyrene foam, otherwise thought to be non-biodegradable. *P. putida* has also demonstrated potential biocontrol properties, as an effective antagonist of damping off diseases such as *Pythium* [25] and *Fusarium* [26].

Some of the Gram negative bacteria isolated from landfill soil are implicated in heavy metal remediation of soil. Oxidation of AsO^{-}_{2} to AsO^{3-}_{4} by strains of *Alcaligenes faecalis*, and reduction of CrO^{2-}_{4} to Cr $(OH)_3$ by *Enterobacter cloacae* have been reported [27]. Another important Gram negative bacterium isolated from landfill soil is the non-sporing *Alcaligenes eutrophus* (re-classified as *Ralstonia eutropha*), which is naturally facultatively chemolithoautothropic, and thrives in environments containing millimolar concentrations of some toxic heavy metals such as zinc, cadmium, cobalt, lead, mercury, nickel and chromium. This property is exploited by scientists by specially engineering the bacterium to sequester heavy metals from polluted soils [28].

An important fungi isolated from landfill soil is the ubiquitous saprobe *Cladosporium sphaerospermum* [29] which has the ability to produce melanin [30]. In addition, the fungi can survive and thrive in areas of high radioactivity and can reduce levels of radiation [31]. Industrial off-gas emissions, namely aromatic hydrocarbons, ketones and some aromatic acids can be degraded by the organism [32]. *C. sphaerospermum* can possibly become a substitute for chemical fertilizers due to its ability to produce gibberellins [33].

4. CONCLUSION

The findings of the present study, in corroboration with similar reports elsewhere indicate that soil contaminated by landfill waste effluents support a high population and great diversity of microbes. Most of the microorganisms that inhabit landfill soils have tremendous importance in medicine, industrial production, bio-control, biodegradation, bioremediation and agriculture. On the negative side is the presence of potential pathogens such as *Pseudomonas aeruginosa*, *Escherichia coli*, *Klebsiella pneumonia*e and *Staphylococcus aureus* with the inherent danger of contaminating nearby water bodies and farm crops. This calls for improved urban planning by the relevant authorities, and citing of landfills far from farms, water bodies and residential areas to avoid health hazards in humans, livestock, and adverse effects on plants.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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