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Research Article
Molecular Characterisation of Bacterial Species Isolated from Landfill Site

Mohd Arshad Siddiqqui

School of Environment and Sustainable Development, Central University of Gujarat, 382030 Gandhinagar, Gujarat

Abstract

Background and Objective: Globally solid waste production have increased enormously and the dumping of these wastes to landfills is commonly observed in every major city. Landfill contains various types of wastes and microbes growing in them are also diverse. Based on nature of waste and duration of dumping the microbial population varies. The present study was an attempt to isolate and characterise bacteria based on molecular techniques from samples collected from landfill site. **Materials and Methods:** Samples were collected from landfill site and analysed for physicochemical characteristics using standard procedures. The bacterial population was isolated and molecular characterisations were performed for identification. The physicochemical characteristics (pH, electrical conductivity, moisture content, water holding capacity, alkalinity, total hardness, calcium, magnesium, organic carbon, total nitrogen, sulphate, phosphate and chloride) were assessed. **Results:** The present analysis also revealed the presence of different bacterial species (*Halomonas* sp. (KY952739), *Bordetella petrii* (KY952740), *Luteimonas marina* (KY952741), *Bordetella petrii* (KY952742), *Bordetella petrii* (KY952743) and *Bacillus megaterium* (KY952744) in the samples collected from landfill site. **Conclusion:** The presence of bacterial species in dominance indicate the decomposition of landfill waste material. The study will further help to isolate species with greater degradation potential and it could be applied at large scale composting.

Key words: Municipal solid waste, dumping site, landfill, bio conversion, microbial activity

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Corresponding Author: Mohd Arshad Siddiqqui, School of Environment and Sustainable Development, Central University of Gujarat, 382030 Gandhinagar, Gujarat Tel: 9793823967

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Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Generally, municipal solid waste (MSW) is disposed off in low lying areas without taking any precautions or operational controls. Therefore, municipal solid waste is one of the major environmental problems of Indian megacities. It involves activities associated with generation, storage, collection, transfer and transport, processing and disposal of solid wastes. But, in most cities, the MSWM system comprises only 4 activities, i.e., waste generation, collection, transportation and disposal. The management of MSW requires proper infrastructure, maintenance and upgrade for all activities. This becomes increasingly expensive and complex due to the continuous and unplanned growth of urban centres. The difficulties in providing the desired level of public service in the urban centres are often attributed to the poor financial status of the managing municipal corporations[1].

The amount of waste generated around the world which stands at 12.7 billion tonnes in 2000 will be increased to approximately 19 billion tonnes in 2025 and to approximately 27 billion tonnes in 2050 as per the future prediction. There is a dramatic increase in the amount of waste generated, especially in Asia. Beside this the MSW generation amount in India, which was 0.46 kg per person per day in 1995 expected to grow to 0.7 kg per person per day by 2025 (Source: Secretariat of the Basal Convention) and the collection, transportation and disposal of MSW are unscientific and chaotic in India[2].

The organic waste found in MSW produce odors, sludge, pollution or unsightly mess during degradation. These problems can be reduced-by the bacteria if they can utilize it as nutrients. After consuming waste by the bacteria, they converted into safe by products and in due course of this conversion they actually produce several metabolites to break down the complex waste into simple compounds. Due to this there is an immense possibility to screen effective bacterial strains from waste dump sites with valuable applications. There have been a constant effort in isolating novel bacteria from diverse environment to cope up with the demand for new organisms with properties of production of unique enzymes/molecules for industrial application and waste degradation. Accordingly, the present research study was carried out with an objective to assess the physicochemical characters of the municipal solid waste and isolation and molecular characterization of bacteria from MSW dumping site at Pirana, Ahmedabad for waste degradation[3].

During the survey conducted for the present day, massive mounts of wastes which are more than 40 years old had been observed. The city has one major landfill site at Pirana with 84 acres of land which is receiving municipal solid waste for last 20 years. The total solid waste generated from the city is around 1,100-1,200 t/day. Nearly 95% of the solid waste is dumped at the Pirana landfill site, i.e. around 1,000 t/day goes to landfill area at Pirana and nearly 50 t/day consumed by the excel factory for composting. The pirana landfill site at Ahmedabad is not adopting any particular solid waste disposal method.

MATERIALS AND METHODS

Sampling site: Ahmedabad, the industrial capital of Gujarat which lies on 23°01 N latitude and 72°61 E longitudes on the bank of River Sabarmati, located in the Southeast of the great Thar Desert and Northeast of the Arabian Sea, with an elevation of 49 m above mean sea level. The climate of Ahmadabad is hot and humid with typical characteristics of a semi-arid region with annual rainfall of 650-700 mm, mainly occurs during the South-West monsoon (June-August). Ahmedabad is underlain by thick alluvial deposits of Quaternary age. Lithologs of the city indicate that alluvium comprises of alternating beds of sand, silt, clay and gravel. There are several sand layers down to the depth of approximately 50 m. These are interspersed with lenses of silt and clay but are essentially in direct hydraulic communication with one another and may be treated as a single unconfined aquifer. In general, a 20-25 thick silt/clay layer separates the deeper (depth>100 m) aquifer from the upper unconfined group of aquifers. The deeper aquifers have large areal extent and presently supply most of the water consumed in the city. An initial survey was conducted to take the general information about the Pirana municipal solid waste dumping site, Ahmedabad during October, 2015, with the support of technical staff of landfill site.

Sample collection: Surface and subsurface municipal solid waste with soil samples were collected from 5 different sites of Pirana landfill. All of the collected samples were immediately filled in air tight zip lock bags and labelled. Samples were transported to the laboratory for physicochemical and microbial characterization. For microbial characterization, samples were preserved at a low temperature (4°C) in the laboratory to avoid any deviation and contamination of them.

Physicochemical characterization: Various physico-chemical parameters (pH, Electrical conductivity, moisture content, water holding capacity, alkalinity, total hardness, calcium,

magnesium, organic carbon, total nitrogen, sulphate, phosphate and chloride) and biological parameters were analyzed for waste characterizations.

Isolation and enumeration of bacteria: Isolation and enumeration of bacteria were performed by serial dilution plate technique using nutrient agar media.

Molecular characterization of isolated bacteria: The isolated bacteria were identified by standard morphological and biochemical tests. The bacterial samples were subjected to DNA analysis by manual method and observed by agarose gel electrophoresis. The 16s rRNA were obtained by PCR and sequenced by BLAST using NCBI BLAST tools and they were assigned accession numbers accordingly by GSBTM, Gandhinagar Gujarat.

RESULTS

The 5 samples collected from the landfill were assessed for physicochemical characters (Table 1). The pH of the samples on average showed a near neutral value of 7.09. Electrical conductivity of the sample was 8.20 µS and moisture content was recorded to be 14.79%, with water holding capacity of 43.98%. The alkalinity and total hardness were observed to be 2805.70 and 1354.66 mg L^{-1}. Minerals like calcium and magnesium were recorded as 347.5 and 136.39 mg L^{-1}. The organic carbon and total nitrogen were 2.12 and 0.68%, respectively. Sulphate and phosphate content of the sample were 89.01 and o.88 mg L^{-1} whereas chloride was 1412.99 mg L^{-1}.

Morphological characters of bacteria isolated from different sites: Municipal solid waste collected from the site was subjected to bacterial isolation and various morphological characters like shape, size, margin, pigmentation, optical character, surface, consistency were observed.

Molecular characterisation: Determination of microbial presence and diversity using molecular techniques have made possible the discovery of previously unknown microbes. In the present study the isolated bacteria were subjected to DNA analysis and sequencing (Table 2) Based on the molecular analysis, the bacterial species identified were, *Halomonas* sp., *Bordetella petrii*, *Luteimonas marina*, *Bordetella petrii*, *Bordetella petrii* and *Bacillus megaterium*.

DISCUSSION

In this study municipal solid waste was collected from Pirana municipal solid waste dumping site, Ahmedabad. The physicochemical characterisation followed by isolation and molecular characterisation of bacterial strains was performed. The results showed the presence of *Halomonas* sp., *Bordetella petrii*, *Luteimonas marina*, *Bordetella petrii*, *Bordetella petrii* and *Bacillus megaterium*, *bacterial* species at the site. The presence of microbes indicates the degradation of the waste materials. Similar studies have been conducted by other authors and have documented the isolation and molecular characterization of composting bacteria from municipal solid waste disposal sites in two Kenyan cities, Nairobi and Kisumu and found that the bulk of the isolates were of the genus *Bacillus* (68%). Others species of *Paenibacillus*, *Planococcus*, *Pseudomonas* and a mixture of other bacteria (*Stenotrophomonas maltophilia*, *Caryophanon* sp., *Ochrobactrum intermedium*, *Brevibacterium frigoritolerans* and *Blackwater bioreactor bacterium*) were also observed[4]. Saha and Santra[3] have also

Table 1: Physicochemical characterization of solid waste (landfill site conditions)

Parameters	Site 1	Site 2	Site 3	Site 4	Site 5	Average	Standard deviation
pH	6.50	7.20	7.80	6.40	7.80	7.09	0.70
EC (µS)	7.95	8.05	8.67	7.58	8.76	8.20	0.44
Moisture content (%)	14.87	15.09	13.99	14.98	15.03	14.79	0.40
Water holding capacity (%)	45.80	41.93	42.58	45.84	43.76	43.98	1.61
Alkalinity (mg L^{-1})	9764.54	1057.47	1045.97	1125.21	1035.32	2805.70	3479.56
Total hardness (mg L^{-1})	1476.43	1237.67	1327.76	1438.45	1292.99	1354.66	89.51
Calcium (mg L^{-1})	372.35	304.00	360.37	312.65	388.21	347.51	33.30
Magnesium (mg L^{-1})	135.00	146.21	121.67	138.11	140.98	136.39	8.23
Organic carbon (%)	1.99	2.57	2.18	1.89	2.01	2.12	0.23
Total nitrogen (%)	0.87	0.92	0.34	0.56	0.74	0.68	0.21
Sulphate (mg L^{-1})	84.65	91.20	87.34	88.98	92.90	89.01	2.88
Phosphate (mg L^{-1})	0.99	0.85	0.78	0.88	0.93	0.88	0.07
Chloride (mg L^{-1})	1437.10	1399.01	1477.76	1323.76	1427.36	1412.99	51.26

Table 2: 16s r-RNA sequencing of different bacteria

Bacteria	16s r-RNA sequencing
Halomonas sp. (KY952739)	TTCACCCCAGTCATGAACCACACCGTGGTGATCGCCCTCCCGAAGGTTAGGCTAACCACTTCTGGTGCAGTCCACTCCCATGGTGTGACG GGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGACATTCTGATTCACGATTACTAGCGATTCCGACTTCACGGAGTCGAGTTGCAG ACTCCGATCCGGACTGAGATCAGCTTTCTGGGATTGGCTCACTCTCGCAAGTTCGCAACCCTTTGTACTGACCATTGTAGCACGTGTGTAG CCCTACCCGTAAGGGCCATGATGACTTGACGTCGTCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCCCTAGAGTTCCCGACCGAATCG CTGGCAAATAGGGACAAGGGTTGCGCTCGTTACGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTC TCTGCGTTCCCGAAGGCACCCCTTCGTCTCCGAAGGGTTCGCAGGATGTCAAGGGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACC ACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTATCGCGTTTA ACTGCGCCACAAAGTCCGCGAAGGACCCAACGGCTAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTACCC ACGCTTTCGCACCTCAGCGTCAGTGTCAGTCCAGAAGGCCGCCTTCGCCACTGGTATTCCTCCCGATCTCTACGCATTTCACCGCTACACC GGGAATTCTACCTTCCTCTCCTGCACTCTAGCCTGACAGTTCCGGATGCCGTTCCCAGGTTGAGCCCGGGGCTTTCACAACCGGCTTATCA AGCCGCCTACGCGCGCTTTACGCCCAGTAATTCCGATTAACGCTCGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTG CTTCTTCTGTGGGTGATGTCCCTCCTCCCGGGTATTAACCGGAAGGCTTTCTTCCCCACTGAAAGTGCTTTACAACCCGAGGGCCTTCTTCA CACACGCGGCATGGCTGGATCAGGCTTGCGCCCATTGTCCAATATTCCCCACTGCTGCCTCCCGTAGGAGTTCGGGCCGTGTCTCAGTCC CGATGTGGCTGATCATCCTCTCAGACCAGCTACGGATCGTCGCCTTGGTGAGCCATTACCTCACCAACCAGCTAATCCGACATAGGCTCAT CCGATAGCGCAAGGCCCGAAGGTCCCCTGCTTTCTCCCGTAGGACGTATGCGGTATTAGCCTGGGTTTCCCCAGGTTATCCCCCACTACC GGGCAGATTCCTATGCATTACTCACCCGTCCGCCGCTCGCCACCAGGGAGCAAGCTCCCCGTGCTGCCGCTCGACTTGCATGTGTTAGGC CTGCCCGCCCAGCGTTCAATCTGAGCCA
Bordetella petrii (KY952740)	CGACTTCACCCCAGTCATGAATCCTACCGTGGTAATCGCCCCCCTTGCGGTTAGGCTAACTACTTCTGGTAAAACCCACTCCCATGGTGTG ACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCGACATGCTGATCCGCGATTACTAGCGATTCCGACTTCACGCAGTCGAGTTG CAGACTGCGATCCGGACTACGATCGGGTTTCTGGGATTGGCTCCCCCTTGCGGGTTGGCAGCCCTCTGTCCCGACCATTGTATGACGTGTG AAGCCCTACCCATAAGGGCCATGAGGACTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCATTAGAGTGCCCTTTCGTA GCAACTAATGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGCCATGCAGCACCTGTGTTCC GGTTCTCTTGCGAGCACTGCCAAATCTCTTCGGCATTCCAGACATGTCAAGGGTAGGTAAGGTTTTTCGCGTTGCATCGAATTAATCCACA TCATCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTTAATCTTGCGACCGTACTCCCCAGGCGGTCAACTTCACGCGTTAGCTGC GCTACCAAGGACCGAAGTCCCCAACAGCTAGTTGACATCGTTTAGGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTT CGTGCATGAGCGTCAGTGTTATCCCAGGAGGCTGCCTTCGCCATCGGTGTTCCTCCGCATATCTACGCATTTCACTGCTACACGCGGAATT CCACCTCCCTCTGACACACTCTAGCCCGGTAGTTAAAAATGCAGTTCCAAGGTTAAGCCCTGGGATTTCACATCTTTCTTTCCGAACCGCCT GCGCACGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGTGCTTATTCTG CAGGTACCGTCAGTTGCTCCAGATATTAGCCAGAGCCGTTTCTTTCCTGCCAAAAGTGCTTTACAACCCGAAGGCCTTCATCGCACACGCG GGATGGCTGGATCAGGGTTGCCCCCATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGG CTGGTCGTCCTCTCAAACCAGCTACGGATCGTTGCCTTGGTAGGCCTTTACCCCACCAACTAGCTAATCCGATATCGGCCGCTCCCAATAG TGCGAGGCCCCGAAGGTCCCCCGCTTTCCCCCCGTAGGGCGTATGCGGTATTAGCCACGCTTTTCGCGTAGTTTATCCCCCGCTACTGGGC ACCGTTCCGATACATTTACTCACCCGTTCGCCACTCGCCGCCAGACCGAAATCCGCGCTGCCGTTCGACTTGCATGTGTAAAGCATCCCGC TAGCGTTCA
Luteimonas marina (KY952741)	TTACCCTTTGTTACGACTTCACCCCAGTCATCGGCCACACCGTGGCAAGCGCCCTCCTTGCGGTTAGGCTACCTGCTTCTGGTGCAACAGA CTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCAGCAATGCTGATCTGCGATTACTAGCGATTCCGACTTC ACGGAGTCGAGTTGCAGACTCCGATCCGGACTGAGAGAAGGTTTCTGGGATTGGCTTGCCCTCGCGGGTTCGCAGCCCTCTGTCCTTCCC ATTGTAGTACGTGTGTAGCCCTGGCCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCGGTCTCCTTA GAGTTCCCACCATTACGTGCTGGCAACTAAGGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGA CAGCCATGCAGCACCTGTCTCACGGTTCCCGAAGGCACCAATCCATCTCTGGAAAGTTCCGTGGATGTCAAGGCCAGGTAAGGTTCTGCG CGTTGCATCGAATTAAACCACATACTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGGC GGCGAACTTAACGCGTTAGCTTCGATACTGAGTTCCTAGTTGAACCCAACATCCAGTTCGCATCGTTTAGGGCGTGGACTACCAGGGTATC TAATCCTGTTTGCTCCCCACGCTTTCGTGCCTCAGTGTCAGTACTGGTCCAGGTGGCCGCCTTCGCCACGGGTGTTCCTCCTGATCTCTACG CATTTCACTGCTACACCAGGAATTCCGCCACCCTCTACCGTACTCTAGCCCGCCAGTATCCAATGCAATTCCCAGGTTGAGCCCAGGGCTT TCACATCAGACTTAACGAACCACCTACGCACGCTTTACGCCCAGTAATTCCGAGTAACGCTTGCACCCTTCGTATTACCGCGGCTGCTGGC ACGAAGTTAGCCGGTGCTTATTCTTTGGGTACCGTCATTCTCTCCGGGTATTAGCCGGAAAGTTTTCTTTCCCAACAAAAGGGCTTTACAAC CCGAAGGCCTTCTTCACCCACGCGGCATGGCTGGATCAGGCTTTCGCCCATTGTCCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGG ACCGTGTCTCAGTTCCAGTGTGGCTGATCATCCTCTCAGACCAGCTACGGATCGTCGCCTTGGTGGGCCATTACCCCGCCAACTAGCTAAT CCGACGTCGGCTCATCTTTCTGCGTGAGGCCTTGCGGTCCCCCACTTTCACCCGTAGGTCGTATGCGGTATTAGCGTAAGTTTCCCTACGTT ATCCCCCACAAAAAGGCAGATTCCGACGTATTCCTCACCCGTCCGCCACTCGCCACCCGGGGAGCAAGCTCCCCTGTGCTGCCGTTCGAC TTGCATGTGTTAGGCCTGCCGCCAGCGTTCACTCTGA
Bordetella petrii (KY952742)	CGACTTCACCCCAGTCATGAATCCTACCGTGGTAATCGCCCCCCTTGCGGTTAGGCTAACTACTTCTGGTAAAACCCACTCCCATGGTGTGA CGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCGACATGCTGATCCGCGATTACTAGCGATTCCGACTTCACGCAGTCGAGTTGC AGACTGCGATCCGGACTACGATCGGGTTTCTGGGATTGGCTCCCCCTTGCGGGTTGGCAGCCCTCTGTCCCGACCATTGTATGACGTGTG AAGCCCTACCCATAAGGGCCATGAGGACTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCATTAGAGTGCCCTTTCGTA GCAACTAATGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGCCATGCAGCACCTGTGTTCC GGTTCTCTTGCGAGCACTGCCAAATCTCTTCGGCATTCCAGACATGTCAAGGGTAGGTAAGGTTTTTCGCGTTGCATCGAATTAATCCACA TCATCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTTAATCTTGCGACCGTACTCCCCAGGCGGTCAACTTCACGCGTTAGCTGC GCTACCAAGGACCGAAGTCCCCAACAGCTAGTTGACATCGTTTAGGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTT CGTGCATGAGCGTCAGTGTTATCCCAGGAGGCTGCCTTCGCCATCGGTGTTCCTCCGCATATCTACGCATTTCACTGCTACACGCGGAATT

Table 2: Continued

Bacteria	16s r-RNA sequencing
	CCACCTCCCTCTGACACACTCTAGCCCGGTAGTTAAAAATGCAGTTCCAAGGTTAAGCCCTGGGATTTCACATCTTTCTTTCCGAACCGCCT
	GCGCACGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGTGCTTATTCTG
	CAGGTACCGTCAGTTGCTCCAGATATTAGCCAGAGCCGTTTCTTTCCTGCCAAAAGTGCTTTACAACCCGAAGGCCTTCATCGCACACGCG
	GGATGGCTGGATCAGGGTTGCCCCCATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGG
	CTGGTCGTCCTCTCAAACCAGCTACGGATCGTTGCCTTGGTAGGCCTTTACCCCACCAACTAGCTAATCCGATATCGGCCGCTCCCAATAG
	TGCGAGGCCCCGAAGGTCCCCCGCTTTCCCCCCGTAGGGCGTATGCGGTATTAGCCACGCTTTTCGCGTAGTTTATCCCCCGCTACTGGGC
	ACCGTTCCGATACATTTACTCACCCGTTCGCCACTCGCCGCCAGACCGAAATCCGCGCTGCCGTTCGACTTGCATGTGTAAAGCATCCCGC
	TAGCGTTCA
Bordetella petrii (KY952743)	CGACTTCACCCCAGTCATGAATCCTACCGTGGTAATCGCCCCCCTTGCGGTTAGGCTAACTACTTCTGGTAAAACCCACTCCCATGGTGTG
	ACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCGACATGCTGATCCGCGATTACTAGCGATTCCGACTTCACGCAGTCGAGTTG
	CAGACTGCGATCCGGACTACGATCGGGTTTCTGGGATTGGCTCCCCCTTGCGGGTTGGCAGCCCTCTGTCCCGACCATTGTATGACGTGTG
	AAGCCCTACCCATAAGGGCCATGAGGACTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCATTAGAGTGCCCTTTCGTA
	GCAACTAATGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGCCATGCAGCACCTGTGTTCC
	GGTTCTCTTGCGAGCACTGCCAAATCTCTTCGGCATTCCAGACATGTCAAGGGTAGGTAAGGTTTTTCGCGTTGCATCGAATTAATCCACA
	TCATCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTTAATCTTGCGACCGTACTCCCCAGGCGGTCAACTTCACGCGTTAGCTGC
	GCTACCAAGGACCGAAGTCCCCAACAGCTAGTTGACATCGTTTAGGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTT
	CGTGCATGAGCGTCAGTGTTATCCCAGGAGGCTGCCTTCGCCATCGGTGTTCCTCCGCATATCTACGCATTTCACTGCTACACGCGGAATT
	CCACCTCCCTCTGACACACTCTAGCCCGGTAGTTAAAAATGCAGTTCCAAGGTTAAGCCCTGGGATTTCACATCTTTCTTTCCGAACCGCCT
	GCGCACGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGTGCTTATTCTG
	CAGGTACCGTCAGTTGCTCCAGATATTAGCCAGAGCCGTTTCTTTCCTGCCAAAAGTGCTTTACAACCCGAAGGCCTTCATCGCACACGCG
	GGATGGCTGGATCAGGGTTGCCCCCATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGG
	CTGGTCGTCCTCTCAAACCAGCTACGGATCGTTGCCTTGGTAGGCCTTTACCCCACCAACTAGCTAATCCGATATCGGCCGCTCCCAATAG
	TGCGAGGCCCCGAAGGTCCCCCGCTTTCCCCCCGTAGGGCGTATGCGGTATTAGCCACGCTTTTCGCGTAGTTTATCCCCCGCTACTGGGC
	ACCGTTCCGATACATTTACTCACCCGTTCGCCACTCGCCGCCAGACCGAAATCCGCGCTGCCGTTCGACTTGCATGTGTAAAGCATCCCGC
	TAGCGTTCA
Bacillus megaterium (KY952744)	GACTTCACCCCAATCATCTGTCCCACCTTAGGCGGCTAGCTCCTTACGGTTACTCCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGA
	CGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGC
	AGCCTACAATCCGAACTGAGAATGGTTTTATGGGATTGGCTTGACCTCGCGGTCTTGCAGCCCTTTGTACCATCCATTGTAGCACGTGTGT
	AGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTAAAT
	GCTGGCAACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGT
	CACTCTGTCCCCCGAAGGGGAACGCTCTATCTCTAGAGTTGTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAA
	CCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGGCGGAGTGCTTAATGCGTT
	AGCTGCAGCACTAAAGGGCGGAAACCCTCTAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCC
	CACGCTTTCGCGCCTCAGCGTCAGTTACAGACCAAAAAGCCGCCTTCGCCACTGGTGTTCCTCCACATCTCTACGCATTTCACCGCTACAC
	GTGGAATTCCGCTTTTCTCTTCTGCACTCAAGTTCCCCAGTTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAGA
	AACCGCCTGCGCGCGCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGTGG
	CTTTCTGGTTAGGTACCGTCAAGGTACAAGCAGTTACTCTTGTACTTGTTCTTCCCTAACAACAGAGTTTTACGACCCGAAAGCCTTCATCA
	CTCACGCGGCGTTGCTCCGTCAGACTTTCGTCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCC
	AGTGTGGCCGATCACCCTCTCAGGTCGGCTATGCATCGTTGCCTTGGTGAGCCGTTACCTCACCAACTAGCTAATGCACCGCGGGCCCAT
	CTGTAAGTGATAGCCGAAACCATCTTTCAATCATCTCCCATGAAGGAGAAGATCCTATCCGGTATTAGCTTCGGTTTCCCGAAGTTATCCC
	AGTCTTACAGGCAGGTTGCCCACGTGTTACTCACCCGTCCGCCGCTAACGTCATAGAAGCAAGCTTCTAATCAGTTCGCTCGACTTGCATG
	TATTAGGCACGCCGCCAGCGTTCATCCT

reported the isolation and characterization of bacteria isolated from municipal solid waste for production of industrial enzymes and waste degradation and results shows that the scope of finding industrially important bacteria from municipal waste dump sites and these isolates could be vital source for the discovery of industrially useful enzymes/molecules and waste degradation.

The isolation and molecular identification of landfill bacteria capable of growing on di-(2-ethylhexyl) phthalate and deteriorating PVC materials[5]. Similarly[6] also reported the isolation of microorganisms associated with dump sites in Port Harcourt Metropolis, Nigeria and found the 4 strains LHM1, LHM2, LHM3 and LHM4, not previously reported as DEHP degraders, were identified via 16s rRNA gene sequence. Grampositive strains LHM1 and LHM2 had a greater than 97% similarity with *Chryseomicrobium imtechense* MW 10(T) and *Lysinibacillus fusiformis* NBRC 15717(T), respectively. Gramnegative strains LHM3 and LHM4 were related to *Acinetobacter calcoaceticus* DSM 30006(T) (90.7% similarity) and *Stenotrophomonas pavanii* ICB 89(T) (96.0% similarity), respectively.

Five bacterial strains were isolated and identified using biochemical tests and API 20E and 50 CH from landfill sites in Kumasi which degrade pre-treated plastic bags and found the five bacterial strains were isolated. The bacteria were used to degrade plastic bags previously treated with

concentrated hydrochloric acid[7]. Accordingly, Velsivasakthivel and Nandini[8] have also reported the airborne multiple drug resistant bacteria isolated from concentrated municipal solid waste dumping site of Bangalore, Karnataka, India and results showed that the MDR organisms like *Staphylococcus aureus* was recorded higher in number in the ambient air near the dump sites. Maximum populations of multi drug resistant bacteria were recorded near the dumping site. Bacterial organisms like *Staphylococcus aureus* and *Enterococcus* sp., were the most prevalent organisms recovered. The characterization of solid waste for microbial status will help to isolate the bacteria and developing a consortium which in turn can be used for bio degradation of organic waste at the landfill site.

In accordance with the present study, other researchers have also reported the isolation and molecular characterization of bacteria from E-waste contaminated site and results showed the presence of *Bacillus licheniformis*, *Bacillus subtilis* and *Bacillus badius*. 16s rRNA sequencing studies confirmed the identified strain as *Bacillus licheniformis* with an accession no. CP000002.3[9].

In a study by Aaisha and Barate[10] have also reported the pectinolytic bacteria from soil samples of Akola region, India and the results showed that the isolates were *Bacillus firmus* (P1), *Bacillus coagulans* (P13), *Bacillus endophyticus* (P57) and *Bacillus vietnamensis* (P58). Anitha and Jayraaj[11] have also documented the isolation and identification of bacteria from biomedical waste and the results showed the presence of different bacteria with their frequency of isolation from the biomedical waste were *Bacillus subtilis* (12%), *Staphylococcus aureus* (9%), *Klebsiella pneumonia* (6%) and *Escherichia coli* (15%).

CONCLUSION

This study has demonstrated that the physicochemical conditions existing at the Pirana MSW dumping site are sub-optimum for survival of different bacterial species which are very helpful in MSW management. Molecular characterization has revealed that municipal dump sites are inhabited by vast bacteria with the ability to efficiently compost the major MSW components (including cellulose, proteins and lipids). MSW dump sites are indeed a home to many safe biotechnologically usable bacteria. These can be mined for economic exploitation through job creation, improvement of agricultural yields as well as enhancement of environmental conditions for the urban and the peri-urban dwellers.

SIGNIFICANCE STATEMENT

Conversion of solid waste at the landfill site by microbial activity could be a positive approach to reduce pollution. This could be accomplished through identification of successive degrading microorganisms at the landfill sites and utilising them for bio conversion. The present study identified the species at landfill sites using molecular techniques.

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