MICROBIAL POPULATION OF FOOD WASTE DUMP CONTAMINATED AREAS IN PARTS OF TARABA STATE

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Abstract: Untreated solid waste and sewage disposal is not only hazardous to human health but also to the environment. This study aim to determine the microbial populations linked with food waste dump in some part of Taraba State. A total of nine samples of food waste were collected from three dump sites located in three different local government areas which include Wukari, Ibi and Donga. After the isolation, the extracted and purified DNA of the isolates was used for a polymerase chain reaction. Gel electrophoresis was performed utilizing the UV lightbox system for viewing DNA bands. To precisely identify the isolates, DNA is denatured and converted into single-stranded and sequencer machine gives signals to the detector which transfers them to the computer and inspects the signals, converts into a nucleotide sequence and the blast was carried out. The highest of temperature on food waste dump site is 38^0C and lower temperature recorded is 34^0C respectively. The bacterial counts ranged from 10.4×10^5cfu/g to 0.5×10^5cfu/g. The fungal counts ranged from 6.4×10^5sfu/g to 0.1×10^5sfu/g. The microorganisms with their frequency of isolation during the investigation are; *Arthrobacter* spp. (3.16%), *Bacillus paramycoides* (28.14%), *Enterobacter larvae* (3.16%), *Escherichia coli* (3.16%), *Klebsiella* spp. (6.25%), *Micrococcus luteus* (9.38%), *Micrococcus roseus* (9.38%), *Proteus mirabilis* (9.38%), *Pseudomonas aeruginosa* (9.38%), *Staphylococcus aureus* (3.12%), *Staphylococcus epidermidis* (3.12%), *Streptomyces* spp. (3.12%), *Trichococcus paludicola* (3.12%), *Vagococcus fluvialis* (6.25%), *Aspergillus aculeatus* (4.76%), *Aspergillus flavus* (4.76%), *Aspergillus fumigatus* (23.81%), *Aspergillus niger* (23.81%), *Cladosporium* spp. (4.76%), *Penicillium citrinum* (4.76%), *Penicillium notatum* (28.58%) and *Penicillium* spp. (4.76%). The presence of these microorganisms poses potential health threat to the households within the area. It is therefore recommended that dumpsites be located at a minimum 1km distance away from residential areas.

Key Word: Bacteria, Donga, Food waste dump, Fungi, Ibi, Microorganism, waste and Wukari,

Introduction

The smallest and most basic form of life is referred to as a microorganism. Many microorganisms can be found in the soil, water, air, dead and live species, and plants. Microorganisms frequently cause disease (Ebe *et al.*, 2015). In all the microbial communities linked with the content of a food dump are diverse (Palaniveloo, *et al.*, 2020). Objects that are unwanted or useless are referred to as waste (also known as rubbish, trash, refuse, or junk) (Williams and Hakam, 2016). Domestic waste is waste produced by domestic sources and is collected before being recycled, burned, or dumped in landfills for municipal solid waste. Household waste is primarily composed of organic materials like waste food, waste fruit, cooked food, and other edible products, with a small amount of inorganic materials like newspaper and textiles (Ebe *et al*., 2015). Waste can be produced by a variety of human activities, including the extraction of raw materials, the processing of those materials into intermediate and final products, consumption of finished commodities, and others. At the time of generation, recycled or used leftovers are not included. Garbage pollution is a serious problem as the population rises and the amount of solid waste created (Williams and Hakam, 2016).

From the above, it appears almost every local government area (LGA) in Taraba State lack a sanitary landfill. In reality, waste items, including food waste, are placed in selected "open" dump sites in Wukari, Ibi, and Donga and are left to accumulate until they are removed or burnt. The dumping of untreated municipal solid waste poses risks to both the environment and human health (Williams and Hakam, 2016).

Unused foods that has been wasted or recycled are referred to as food waste. It's also referred to as the parts of food that aren't meant for human consumption. Households, dining venues, markets, shops and stores, and distribution channels can collect food waste such as fruit and vegetable scraps, eggshells, and tea leaves and use them as composting agents. Contrarily, foods like meat, seafood, and fatty foods should not be composted since they may contain pathogenic microorganisms that must be killed by composting at a very high temperature. Depending on the conditions of your pillage, it might not achieve the necessary temperature to destroy oily components and hazardous microbes. Moreover, the odour emanating from raw materials create may draw disease vectors (Jain *et al.*, 2018; Palaniveloo, *et al.*, 2020).

There are many species of microorganisms that have been reported in some of the recent scientific reports according to the respective food dump composition and composting stages (Palaniveloo, *et al.*, 2020). Therefore, there is need for the assessment of microbial population and molecular analysis of food waste dumps contaminated areas in parts of Taraba State.

In various way when solid waste, such as food waste, is not adequately handled, pathogenic bacteria and hazardous substances can be released into the environment. The aim of this study is to determine the microbial populations linked with food waste dump in some part of Taraba State.

Materials and Methods

Description of study area

This study was carried out in three Local Government areas in southern Taraba State. Taraba State is located in the north east part of Nigeria and has an undulating topography with a few isolated mountainous features. The picturesque and well-known Mambilla Plateau is one typical example. Southern State has low woodland in the south and grassland in the north and it is mostly located in the savannah zone. At 1,800 meters (6,000 feet) above sea level, the Mambilla Plateau has a mild temperature all year long. The Taraba River inspired the state's name. The Jukun, Chamba, Kuteb, Ichen, Fulani, and Hausa are the main ethnic groups in the state's southern region. Southern Taraba comprises of five local government areas (Wukari, Ibi, Donga, Takum and Ussa). According to the 2006 Nigerian population census, Taraba state has a total population of 2,294,800 people and a total area of 54,473 km2 (21,032 sq mi).

Sample sites

Food wastes was collected from trash dumps and drainages in various sites in Wukari, Ibi, and Donga local government areas of Taraba State, Nigeria (Ebe *et al.,* 2015). Food waste samples was mixed with soil that were collected from three dump sites located in three different local government areas which include Wukari, Ibi and Donga LGAs in Taraba State, Nigeria.

Sample collection

With a hand shovel, the subsurface soil was dug up to a depth of roughly 15 cm after the surface material was cleared away. At each refuse collection point's perimeter, samples of food waste were collected by scooping them from 0 to 15 cm deep into plastic bags (Iwegbu *et al*., 2005). In sterile cellophane or polythene bags, twenty to thirty grams (20g-30g) of soil (food waste) from trash sites were gathered (Ochei and Kolhatkar, 2007). With the use of a thermometer, a well label, and quick transportation to the lab, the temperature of each sample was ascertained (Williams and Hakam, 2016; Imarenezor *et al*., 2019).

Physicochemical analyses

The Association of Official Analytical Chemists (AOAC) method was used to determine the physicochemical characteristics of the samples. The pH and temperature were measured using a pH meter and a mercury thermometer respectively (Williams and Hakam, 2016).

Preparation of culture media

For the isolation of bacteria and fungi, Media Nutrient agar and potato dextrose agar or sabouraud dextrose agar were employed, respectively. Every medium was created in accordance with the manufacturer's instructions (Ogodo *el al*., 2022)

Determination of microbial load

By transferring 1ml of the sample into 9ml of distilled water, the samples were serially diluted using the pour plate method (Obidah *at al*., 2018). Each sample of food waste underwent ten-fold serial dilution. To determine the total bacterial count, total coliform count, and total fungal count, respectively, 0.1ml from the 10^{-5} dilution factor was transferred to three different media, Nutrient Agar, MacConkey Agar, and Sabroud Dextrose Agar, using the spread plate technique as described by Agwaranze *et al*. (2017). The plates were incubated for 28 hours at 37°C. cfu/g were calculated from the number of discrete colonies (Agwaranze *et al*., 2017; 2018).

Microbial analyses

To create pure cultures, the discrete colonies were sub-cultured on new nutrient agar medium and incubated at 37°C for 24 hours (Agwaranze *et al*., 2018). When the incubation time was over, isolation for pure culture was carried out (Williams and Hakam, 2016). As described by Agwaranze *et al.* (2018) the acquired pure cultures were evaluated using microscopy, biochemical, and sugar fermentation tests.

To obtain fungi isolates, acidified potato dextrose agar plates with streptomycin (1 mg/100 ml) or any other antibiotic were utilized. Following the isolation of pure isolates, the plates were incubated at 30-37^{0}C for 48 hours for yeasts and 96 hours for mould (Williams and Hakam, 2016).

Identification and characterization of bacteria and fungi isolates

The bacterial isolates were identified and characterized using common biochemical tests based on their morphology (Akinnibosun and Ayejuyoni, 2015). The pure cultures of the bacterial isolates were subjected to various morphological and biochemical characterization tests, including colonial, Gram stain, motility indole production, urease activity, citrate utilization, glucose, sucrose, and lactose utilization tests (Williams and Hakam, 2016). These tests included color, shape, elevation, consistency, margin, catalase test, MRVP (Methyl Red-Voges Proskauer test) (Akinnibosun and Ayejuyoni, 2015). Results were compared with accepted references from Bergey's Manual of Determinative Bacteriology in order to identify bacteria isolates (Williams and Hakam, 2016).

Based on their physical traits, such as the color of the aerial hyphae, the substrate mycelium, the organization of the hyphae, and the arrangement of the conidials, the fungal species were recognized and described. Fungi colonies were examined under a microscope and the reproductive and vegetative structures were looked into. During microscopy, spores, sporangia, hyphae, and septa were examined (Awujo *et al*., 2022) while also investigation was performed utilizing taxonomic references and industry standards (Akinnibosun and Ayejuyoni, 2015).

DNA isolation and purification

Microbial isolates were subjected to DNA isolation and purification employing the polymerase chain reaction and gel electrophoresis using PCR and gel electrophoresis machine (DNAlab, 2022).

Statistical Analysis

To ascertain whether there were significant differences in the counts obtained, the results were subjected to statistical analysis (Williams and Hakam, 2016) of variance (ANOVA) (Akinnibosun and Ayejuyoni, 2015) using the student t-test at 95% confidence levels and the SPSS (LATEST VERSION) statistical package or program (Williams and Hakam, 2016).

Results and Discussion

Despite the fact that many of the bacteria and fungi species isolated in this study were not directly pathogenic or suggestive of the presence of other disease-carrying organisms, the presence of heterotrophic bacteria at a given distributed sampling site may indicate a decline in the microbiological quality of that environment.

From three different dump sites, nine samples of food waste dump were collected, examined, and tested for the presence of microorganisms. The physiochemical properties of food waste dump samples in parts of Taraba state include different sample locations and guideline values are provided in (Tables 1). Higher pH values 8.12 was recorded from the food waste dump sample as shown in the waste site were alkaline, Tables 1 and 2, and these were typical of the samples from age wastes dump (Mekonnen *et al*., 2020). Waste dump sample from both locations had lower pH readings 7.52. Other studies conducted in the solid waste dump sites of Nigeria, South Sudan, Sri Lanka, and Ethiopia substantiate this finding which shows slightly basic pH in the waste dump (Dharmarathne and Gunatilake 2013; Karija *et al*., 2013; Hailemariam and Ajeme, 2014; Mekonnen *et al*., 2020).

The pH of the contaminated soil samples influences the microflora's quantitative and qualitative abundance. Thus, it could be concluded that the polluted soils' pH (Table 1) had an impact on the distribution of the microorganisms. This is supported by the article of Nazina *et al.* (2002) and Akinnibosun *et al.* (2015), that the number and activity of microflora in soil strata are controlled by factors such as the availability of water, nutrients, pH, metal ion concentrations, and hydrogen dynamic communication with the ground surface. The finding collaborate with that of Zhen et al. (2019) on article "Significant impacts of both total amount and availability of heavy metals on the functions and assembly of soil microbial communities in different land use patterns".

The highest physicochemical temperature parameters of food waste dump is 38^0C. Lower temperature was recorded as 34^0C. By comparing the obtained values of the physicochemical parameters with the standard limit, the impact of the food waste on the physic-chemical parameter of soil from the sample sites was identified. This very study support Akinnibosun *et al.* (2015) finding.

Table 1: The Physicochemical analysis obtained for food waste dump samples

Sample Location	Samples Point	Temperature (^{0}C)	pH
Wukari	0M (Edge)	36.0	8.09
	5M	37.5	7.95
	10M	38.0	7.71
Ibi	0M (Edge)	36.5	7.52
	5M	37.2	7.83
	10M	38.0	8.12
Donga	0M (Edge)	34.0	7.86
	5M	35.0	7.88
	10M	34.0	7.84
	WHO Standard	NS	6.5 – 8.5

Key: M = Meter, WHO = World Health Organization, NS = Not Specified

The physicochemical properties of food waste dump samples in the areas, sample locations and guideline values are provided in (Tables 1). The table shows that the food waste dump site, the temperature and pH values obtained are within the range of WHO standard limit.

The table 2 shows that the food waste dump site mean pH values obtained is 7.86±0.18, which when equaled to the limit value agreed by WHO is between 6.5 to 8.5 which demonstrates that the pH is virtually basic and the values were within the acceptable range (Akinnibosun *et al*., 2015). The results are consistent with the report of Mekonnen *et al.* (2020). Also in table 2, however, reveals that the mean temperature values recorded at the food waste dump is 36.24±1.50, which is below the WHO-recommended ranges. The discovery complements that of Akinnibosun *et al.* (2015) on article "Microbial and physico-chemical assessment of soil and water around waste dump sites in Lagos".

Table 2: Comparison of values of physicochemical properties obtained with standard limit.

Samples	Parameters	N	Mean	WHO limit
Food waste dump	pH	9	7.86±0.18	6.5 – 8.5
	Temperature	9	36.24±1.50	NS

Key: N = Number samples, WHO = World Health Organization, NS = Not Specified

The wastes may have played a significant role in the highest values of bacteria and fungi. With 10.4×10^5 cfu/mg, Ibi 10M sample point has the highest food waste dump bacterial count, while Wukari 10M sample point has the lowest, at 0.5×10^5 cfu/mg. The Donga 30M sample point had the highest fungal load of food waste dump with 6.4×10^5sfu/mg while Ibi 5M sample point had the lowest fungal load with $0.1x10^5$sfu/mg (Table 3).

Table 3: Enumeration of bacteria and fungi of food waste dump

Organism	Location	Samples Point	Microbial count	cfu/g
	Wukari	0M (Edge)	45	4.5×10^5
		5M	10	1.0×10^5
		10M	05	0.5×10^5
Bacteria	Ibi	0M (Edge)	52	5.2×10^5
		5M	42	4.2×10^5
		10M	104	10.4×10^5
	Donga	0M (Edge)	37	3.7×10^5
		5M	40	4.0×10^5
		10M	64	6.4×10^5
Organism	**Location**	**Samples Point**	**Microbial count**	**sfu/g**
	Wukari	0M (Edge)	13	1.3×10^5
		5M	28	2.8×10^5
		10M	05	0.5×10^5
Fungi	Ibi	0M (Edge)	04	0.4×10^5
		5M	01	0.1×10^5
		10M	02	0.2×10^5
	Donga	0M (Edge)	37	3.7×10^5
		5M	40	4.0×10^5
		10M	64	6.4×10^5

Key: M = Meter, cfu/g = colony forming unit/gram and sfu/g = spore forming unit/gram,

Tables 4 shows the percentage frequency of occurrence for the bacteria and fungus isolated from the food waste dump samples. In this study, the bacteria isolated were *Arthrobacter* spp. (3.16%), *Bacillus paramycoides* (28.14%), *Enterobacter larvae* (3.16%), *Escherichia coli* (3.16%), *Klebsiella* spp. (6.25%), *Micrococcus luteus* (9.38%), *Micrococcus roseus* (9.38%), *Proteus mirabilis* (9.38%), *Pseudomonas aeruginosa* (9.38%), *Staphylococcus aureus* (3.12%), *Staphylococcus epidermidis* (3.12%), *Streptomyces* spp. (3.12%), *Trichococcus paludicola* (3.12%) and *Vagococcus fluvialis* (6.25%). However, several of the samples showed no development on some of the various media used. As a result, gram-positive organisms, particularly those belonging to the Staphylococcus, Micrococcus, and Bacillus families, were isolated in greater numbers than gram-negative ones. Higher concentrations of gram positive bacteria (*Bacillus paramycoides*) and gram negative bacteria (*Pseudomonas aeruginosa* and *Proteus mirabilis*) were present in the study samples. According to the study's analysis of strain concentration, the Bacillus had the highest concentration followed by the Micrococcus of two strains. It is evident from Table 4 that *Bacillus paramycoides* had the largest percentage frequency of occurrence (28.14%), while *Arthrobacter* species, *Enterobacter larvae*, *Escherichia coli*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptomyces* species, and *Trichococcus paludicola* had the lowest (3.12%). The results support the findings of previous research by Ebe *et al.* (2015) and Ogbonna and Igbenijie, (2006). This is consistent with a study by Sintayehi (2011) that found certain potentially harmful bacteria in waste effluents, including *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Klebsiella* species, and *Escherichia coli*. This is in contrast to Omini *et al.* (2015) findings, which demonstrated that more gram negative organisms (particularly those belonging to the enteriobacteriaceae) than gram positive organisms were isolated. *Escherichia coli*, a gram-negative organism, and *Staphylococcus aureus*, a gram-positive organism, were identified in greater amounts from the waste samples, which in this study showed that there were more gram positive than gram negative organisms.

However, the identical observation from Omini *et al.* (2015) concurs with this discovery that comparable organisms were

isolated. This research supports Anitha and Jayraaj's (2012) findings that gram-positive isolates, including *Bacillus subtilis* and *Staphylococcus aureus*, were present in biomedical wastes gathered from a public and private hospital in Coimbatore, India. Similar to this research, Oyeleke and Istifanus' (2009) investigation found that Bacillus and Staphylococcus species were the pathogens most frequently isolated from wastes. However, *Pseudomonas aeruginosa* was the most often identified Gram negative bacteria from wastes, making up 25.00% of all isolates, according to research by Oviasogie *et al.* (2010). Similar bacterial isolates from waste have been reported by a number of researchers as well (Bolaji *et al*., 2011; Rastogi *et al*., 2011). In contrast to this presence finding, which indicates that *Bacillus paramycoides* is the most isolated organism, a study conducted in the city of Erbil by Aziz *et al.* (2014) indicated that *Escherichia coli* was primarily isolated from a wastewater. This study contradicts Anitha and Jayraaj's (2012) findings, which claimed that *Escherichia coli* were the main bacteria in hospital trash.

Bacillus species are native to the soil environment and are known to remain there, therefore their presence in the contaminated soil is expected (Atlas and Bartha, 2007; Akinnibosun *et al*., 2015). Similar observations were made by Ezeronye and Ubalua (2005), Bala (2006) and Rabah *et al.* (2010).

Table 4: Bacterial isolates with frequency and percentage frequency of occurrence

Isolated Bacteria	Frequency	Percentage Frequency (%)
Arthrobacter spp.	01	3.12
Bacillus paramycoides	09	28.14
Enterobacter larvae	01	3.12
Escherichia coli	01	3.12
Klebsiella spp.	02	6.25
Micrococcus luteus	03	9.38
Micrococcus roseu	03	9.38
Proteus mirabilis	03	9.38
Pseudomonas aeruginosa	03	9.38
Staphylococcus aureus	01	3.12
Staphylococcus epidermidis	01	3.12
Streptomyces spp.	01	3.12
Trichococcus paludicola	01	3.12
Vagococcus fluvialis	02	6.25
Total	**32**	**100**

The fungal isolates were *Aspergillus aculeatus* (4.76%), *Aspergillus flavus* (4.76%), *Aspergillus fumigatus* (23.81%), *Aspergillus niger* (23.81%), *Cladosporium* spp. (4.76%), *Penicillium citrinum* (4.76%), *Penicillium notatum* (28.58%), *Penicillium* spp. (4.76%), in table 5.

The research revealed that *Aspergillus aculeatus*, *Aspergillus flavus*, *Cladosporium* spp., *Penicillium citrinum* and *Penicillium* spp. were the lowest fungi isolates with (4.76%), while *Penicillium notatum* was recorded as having the highest in the fungi isolates with a percentage occurrence of 31.8% (table 5). The findings are consistent with a study of Akinnibosun *et al.* (2015) that presented the isolation of fungi from effluent-contaminated soil. The isolated fungi have been identified as typical food spoiling organisms (Akinnibosun *et al*., 2015) and as soil-dwelling microbes (Atlas and Bartha, 2007). The *Aspergillus* species can cause aspergillosis in humans, cattle, and poultry and are typically found where there is a lot of organic material (Akinnibosun *et al*., 2015). Asthma with breathing problems may arise from inhaling *Aspergillus* species according to Ronald (2003) and Akinnibosun *et al.* (2015). A significant Aspergilloma in the lungs might obstruct respiratory gas exchange and result in asphyxiation death. According to Ogbonna and Igbenijie (2006), the microbial contamination found in this study is a sign of potential pollution and may have an impact on the ecological balance of the soil. Waste contaminated soil should not be used for residential purposes or released untreated directly into the environment (Akinnibosun *et al*., 2015).

Table 5: Fungal isolates with frequency and percentage frequency of occurrence

Isolated Fungi	Frequency	Percentage Frequency (%)
Aspergillus aculeatus	1	4.76
Aspergillus flavus	1	4.76
Aspergillus fumigatus	5	23.81
Aspergillus niger	5	23.81
Cladosporium spp.	1	4.76
Penicillium citrinum	1	4.76
Penicillium notatum	6	28.58
Penicillium spp.	1	4.76
Total	**21**	**100**

Table 6 showed the bacteria and fungi that were recovered from samples of three different food waste dumps. From the results obtained, Donga has the greatest number of organisms (8 species), followed by Wukari and Ibi, each with 6 species. Fungi species were highest at the Donga site (5 species), then at Ibi and Wukari (4 species each)

Table 6: Bacterial and Fungal isolates from the food waste dump samples

Organism	Locations		
	Wukari	Ibi	Donga
Bacteria	*B. paramycoides, P. aeruginosa, V fluvialis, S. aureus, M. roseus, M. luteus, Arthrobacter* spp.	*B. paramycoides, M. luteus, V. fluvialis, T. paludicola, P. aeruginosa, M. roseus, Klebsiella* spp.	*S. epidermidis, Streptomyces* spp. *M. roseus, M. luteus, E. coli, B. paramycoides, E. Larvae, P. mirabilis,*
Fungi	*A. niger, A. fumigatus, A. flavus, P. notatum, A. aculeatus*	*A. niger, A. fumigatus, P. notatum, P. citrinum*	*A. niger, A. fumigatus, P. notatum, Penicillium* spp. *Closdoporium* spp.

Table 7 showed the molecular analysis of bacterial and fungal isolates from the GenBank using 16S rRNA sequence. The table explained on the six organisms that undergo the molecular analysis which include *Bacillus paramycoides, Enterococcus larvae, Staphylococcus epidermidis, Trichococcus paludicola, Vagococcus fluvialis, Aspergillus aculeatus* which have undergone molecular identification with percentage ranged between 89.02% and 99.86%.

Table 4.7: Molecular Analysis of bacterial and fungal isolates from GenBank using 16S rRNA sequence.

Organisms	Query ID	Query	E-Value	% ID	Accession Number
Bacillus paramycoides,	12491	100%	0.0	99.86%	NZ MAO101000012.1
Enterococcus larvae	81061	93%	5e-171	92.55%	NZ JAEDXU010000020.1
Staphylococcus epidermidis	51071	100%	0.0	96.63%	NZ CP010820.1
Trichococcus paludicola	240601	86%	8e-145	89.02%	NZ QBLC01000005.1
Vagococcus fluvialis	63075	99%	0.0	99.72%	CP081461.1
Aspergillus aculeatus	57933	100%	0.0	99.60%	MN187297.1

Conclusion

This study demonstrated that food waste dumps had a significant impact on the microbiological quality of the environment. Despite exceeding the permissible limitations, the heterotrophic microbial counts from this research work. In the investigation, a number of microbial pathogens are found. The prevalence of these diseases has been directly linked to food waste dump sites, which can result in fatalities. As a result of the discovery, it has been established that residents of these areas are more susceptible to health risks because the air they breathe every day is of poor quality and contains a high concentration of microorganisms. It is observed that, in order to significantly minimize the risk of severe disease outbreaks and to lessen the occurrence of endemic soil-borne diseases, much more attention needs to be paid in controlling waste site pathogens in dumpsites than is currently done.

Recommendation

It's crucial to create a legislative framework and, more critically, to supply enough clearing vehicles with cover to safeguard the public health from pathogenic agents in food waste sites and along transit routes. The implementation of waste diversion and clean-up school recycling programs, the enactment of legislation banning open burning, and the provision of waste management education programs should all be priorities for governments at all levels. To lower environmental contamination and the occurrence of linked diseases, better waste and sewage inspection and stringent law enforcement are required. For the sake of protecting the environment and promoting public health, government agencies and other stakeholders should develop techniques for treating food waste. In addition, microbial pathogens at waste facilities should be given top priority for regulatory activities, research, funding, and control.

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