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Bacteria Associated with Domestic Solid Waste Dump in Egbu, Owerri North Local Government Area in Imo State, Nigeria.

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ABSTRACT

The prevalence of bacteria in solid waste dump from domestic waste in Owerri was studied. Six samples were collected from Egbu community in Owerri North and examined bacteriologically using Nutrient agar and macconkey agar and were serially diluted, cultured, identified and characterized. Five genera of bacteria were isolated. They were *Staphylococcus aureus, Klebsiella sp, Escherichia coli, lactobacillus sp* and *Corynebacterium sp* and from the findings,*Klebsiella* exhibited the highest number of bacterial activity (66.6%) while *Corynebacterium* and *Iactobacillus* exhibited the lowest number of bacterial activity (16.67%). Futhermore, location D had the highest total heterotropic bacterial count of 5.75x 10^8 and the least was location E with 6.25x10^7. The presence of *Escherichia coli, Staphylococcus aureus, Cornebacteria* and *Klebsiella* in the waste dump site is an indication that the contamination is of human and plant orign or their activities.

Keywords: Nutrient agar ,macconkey agar , *Staphylococcus aurous, Klebsiellasp, Escherichia coli, Lactobacillus sp* and *Corynebacterium sp*.

1.0 INTRODUCTION

Bacteria can be described as the simplest and smallest form of plant life. Bacteria exist in large numbers in air, water, and soil and also in a dead and living creatures and plants, and often cause diseases.

Domestic waste is waste generated by house hold sources that is collected and either recycles, incinerated or disposed in municipal solid waste landfills. Domestic waste is mainly organic matter such as vegetables waste food etc and few inorganic wastes such as newspaper, clothing, etc. A solid waste generation is a function of land use and its composition is inversely proportional to the potential solid damage and bacterial contamination of the environment and public health (Lobber, 1996, Omuta, 1999 and Shakibaie *et al.,* 2009). Thus a healthy environment is dependence upon the maintenance of proper wastes disposal practices. The increased population density in modern Nigeria is generating a massive amount of domestic wastes, to the extent that failure of local authorities to cope adequately with waste collection has resulted in indiscriminate dumping of waste, (Olaore, 1983).

In natural environments, such as soil or the surfaces of plants, the majority of bacteria are bound to surfaces in biofilms (Branda *et al.,* 2005).

Bacteria growth follows three phases when a population of bacteria first enter a high nutrient environment that allows growth, the cells need to adapt to their new environment. The first phase of growth is the log phase, a period of slow growth when the cells adapting the high nutrient environment and preparing for fast growth. The log phase has high biosynthesis rates, as proteins necessary for rapid growth are produced (Prats *et al.,* 2006).

This work is aimed at identification and prevalence of bacteria in this location.

2.0 METHODOLOGY

2.1 TEST SAMPLE

The samples used for this study were domestic solid wastes collected from different household waste dumps in Egbu, Owerri North L.G.A., Imo State of Nigeria on the 21^{ST} September, 2013.

2.2 COLLECTION OF SAMPLES

A total of six (A-F) domestic solid wastes were collected using sterile cellophane bag disinfected with absolute alcohol. These samples were collected differently and were transported to the microbiology laboratory at Federal University of Technology Owerri for examination and analysis.

2.3 PROCEDURE

40g of waste in 150ml distilled water contained in sterile conical flask (250ml) stoppard with cotton wool and wrapped in foil and left for an hour. Mixture, was filtered using fine silky cloth which was sterilized with autoclave, and were serially diluted and cultured on Nutrient agar and Macconkey media using pour plate technique (Nwanebu *et al.*, 2007).

All the plates inoculated were incubated at 37^0c in reduced carbon dioxide tension, for 24hours and examined for bacterial growth. All the isolate after 24hours incubation were characterized and identified using standard methods as in Nwanebu *et al.*, (2007).

3.0 RESULTS AND DISCUSSION

3.1 MICROORGANISMS ASSOCIATED WITH DOMESTIC SOLID WASTE DUMPS

The study showed that five genera of bacteria, three gram positive and two gram negative organisms (bacterial) were associated with the domestic solid waste dumps collected in Egbu, Owerri North L.G.A. among the organisms isolated the most prevalent bacteria associated with the solid waste was *Klebsiella sp*. From the seven samples analyzed, *Klebsiella sp* was found present in four different samples (A-D), followed by *Staphylococcus aureus* and *Esherichia coli* (A, B, and F), (C, D AND F) respectively while the least bacteria was found were *Corynebacterium* and *Lactobacillus sp* (D and E) respectively.

Five genera of bacteria were isolated from the waste analyses and *Klebsiella sp* was most common organism present.

TABLE 1: PERCENTAGE OF EACH BACTERIA ASSOCIATED WITH DOMESTIC WASTE

Samples	***Staphylococcus sp***	***Klebsiella sp***	***Corynebacterium sp***	***Escherichia sp***	***Lactobacillus sp***
A	1	1	-	-	-
B	1	1	-	-	-
C	-	1	-	1	-
D	-	1	1	1	-
E	-	-	-	-	1
F	1	-	-	1	-
TOTAL	3	4	1	3	1
%AGE	50.00	66.67	16.67	50.00	16.67

Klebsiellasp has the highest percentage occurrence, followed by *Staphylococcussp*and *Escherichia sp.* Then the least occurred in *Corynebacteriumsp* and *Lactobacillus sp*

Table 2: Total Heterotrophic Bacteria Count

Sample	**Count**	**Total**	**Count**	**Total**	**Mean**
A	130	$1.3X10^8$	92	$9.2X10^8$	$5.3X10^8$
B	150	$1.5X10^8$	97	$9.7X\ 10^8$	$5.6X\ 10^8$
C	93	$9.3X10^7$	80	$8.0X\ 10^8$	$8.7X10^7$
D	160	$1.6X10^8$	99	$9.9X\ 10^8$	$5.75X10^8$
E	35	$3.5X10^7$	90	$9.0X\ 10^7$	$6.25X10^7$
F	190	$1.9X10^8$	94	$9.4X\ 10^8$	$5.65X10^8$

Location F has the highest bacterial count, this is followed by D and the least is location E.

3.2 DISCUSSION

Although many of the bacteria species isolated in this study were not themselves pathogenic or directly indicative of the presence of other disease carrying organisms, the number of heterotrophic bacteria (HTB) at a particular distributed sampling site may indicate deterioration in the microbiological quality in that environment.

The finding agrees with the report of previous works done by (Norton and Lechuevallier, 2002, Colford *et al.*, 2002). The predominant genera were the *Klebsiella sp*, *Escherichia coli*, *Corynebacterium sp*, *Staphylococcus sp* and *Lactobacillus sp*. These are considered ubiquitous and opportunistic pathogens by forming spores and

becoming dehydrated. Dehydrated spores can then be packaged and sold as viable cultures. Waste becomes a limited liability in an ecological area, acquiring the spread of ticks, mosquitoes, rodents etc.
Although the bacteria are not hazardous to healthy individuals, it is possible that some of them in addition to *legionellae* and *Nonturbaculosis mycobacterium* are opportunistic pathogens and could be hazardous to those body defenses that are compromised. The populations at greatest potential risk of exposure are infants and toddlers, who may ingest soil through mouthing of hands, toys and other hap ten objects. It has been reported that infants and toddler ingest 10mg to 10g day $^{-1}$ of soil (Lewis *et al.,* 1994).

Other pathogens like the prevalence of *Staphylococcus aureus* and *Pseudomonas sp.* in dried materials during bedding, handling handkerchiefs , sweeping floor account for the entry of microorganisms in human population (Nandalal and Somasheka 2007) and represent a significant microbial disease health risk, epidemics may occur periodically as a result.

While the most common bacteria associated with the samples were *Klebsiella, Staphylococcus* and *Escherichia coli*, these little variations may be as a result of the difference in the waste dump sites.

4.0 CONCLUSION

The research suggest that there is need for control dumping of wastes into the commons by source recovery and or intermediate point sources where wastes could be held for treatment or combined for neutralization and treatment before being brought to common refuse areas.
Conclusively, the presence of *Escherichia coli, Staphylococcus sp Corynebacterium* and *Klebsiella sp* in the waste indicate possible contamination of the human and animal origin or activities, while *lactobacterium sp* might be as a result of the bacteria that are helping in the degrading of the waste.

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