ABSTRACT

AIMS: To evaluate the pollution index of municipal solid waste dumpsite site located at Obosi metropolis of Anambra state, Nigeria.

STUDY DESIGN: Study of the dumpsite bioload level using sabouraud dextrose agar and nutrient agar, heavy metal determination using atomic absorption spectrophotometry and assessment of the ecological impact of the dump using two selected agricultural plants maize (Zea mays) and beans (Vicia faba).

PLACE AND STUDY DURATION: Department of Applied Microbiology and Brewing Nnamdi Azikiwe University, PMB 5025, Awka, Anambra state, Nigeria between February, 2014 to September, 2015.

METHODOLOGY: Sample collection from two locations in Obosi, Nigeria, the dumpsite and sample collected 1.10 km away from the dumpsite was used as control, determination of the physicochemical characteristics of the two soils, microbial enumeration, chemical analysis and growing of plants (phytotoxicity assay).

RESULTS: Results showed that relatively alkaline pH was observed in the dumpsite soil (DSS) while slight acidity was reported in the control soil (CSS). The list of heavy metals and minerals quantified in this work via atomic absorption spectrophotometry (AAS) included mercury, lead, arsenic, cadmium, zinc, chromium, aluminum, iron, manganese, magnesium, calcium, sodium and potassium. The heavy metal concentration of dumpsite was higher than that of control. The microorganisms isolated from the present study included; Bacillus subtilis, Aspergillus candidus, and Aspergillus flavus. In the phytotoxicity assessment, the maize grain and beans exhibited good germination conditions in CSS with an extremely poor germination performance in DSS due to heavy metal toxicity as well as alteration of other physicochemical status such as pH, texture and particle size configurations.

In general, seed germination performance was higher in the maize (Zea mays) than beans (Vicia faba) with germination indices of 89.7 % and 51.2 % respectively. 2:1 DSS and CSS soil modification gave the best germination. Statistical analysis showed that there was a significant difference in the percentage seed germination at p<0.05.

CONCLUSION = Results of the present study showed that the study therefore, showed that Obosi dumpsite is polluted with heavy metals particularly mercury, chromium, lead and cadmium which reported very high in concentrations and if proper environment action is not carried out would affect the surrounding agricultural soil thus jeopardizing the health of humans in the area.

Keywords: Heavy metal, Soil, Pollution, municipal dumpsites, phytotoxicity

1. INTRODUCTION

Indiscriminate disposal of domestic, industrial and municipal waste can potentially contribute to elevated levels of various heavy metals; iron (Fe), lead (Pb), zinc (Zn) chromium (Cr) and cadmium (Cd) in the soil ecosystem [1, 2, 3]. These metals are known to accumulate in soil and have long
persistance time through interaction with soil component and consequently enter food chain through
plants or animals. Similarly, continuous disposal of these wastes and particularly in unlined surfaces
can enhance their mobility at environmentally hazardous levels [3, 4]. The concentrations of heavy
metals in soil and around dumps are influenced by type of wastes; topography, runoff and level of
scavenging and are eventually introduced to the ecosystem through infiltration or disposal of
leachates.
The presence of a poorly managed waste disposal scheme is often manifested through the use of
conventional landfills and dumpsites owing to their accessibility, inexpensiveness, and convenience of
methane gas recovery [5] although other options like composting and recycling are also available and
are often practised. The gradual increasing population and the proliferation of basic industrial
processes particularly in major cities of the world in which Obosi metropolis is a typical example has
led to emergency of civilization that have greater impact on the environment. The industrial revolution
gave birth to environmental pollution and the large volume of industrial chemical discharges has
added to the growing load of untreated domestic waste. The disposal of domestic, commercial and
industrial garbage in the world is a problem that continues to grow with human civilization and no
method so far is completely safe. Experience has shown that all forms of waste disposal have
negative consequences on the environment, public health, and local economies. The aims of the
present study therefore, were to ascertain the heavy metal concentration of Obosi dumpsite, bioload
level status and determine the relative mobility of some potential heavy into some agricultural crops in
the surrounding dumpsite environment.

2. MATERIAL AND METHODS

2.1 Sample collection

1 kg of the soil (Dumpsite) was collected at a depth of 10 cm as measured with a metre rule after an
excavator was used to remove the heaps of the solid waste before collecting the soil sample on the
substratum. Equal quantity of soil sample was also collected from location away from the dumpsite
(1.10 km) while ensuring the same depth and collection procedures and this however, served as
experimental control. Both soil samples were collected into separate sampling bottles which were
previously sterilized with cotton wool soaked in 70% alcohol [6] and taken to the laboratory for
analyses. Two plastic bowls were separately used to collect to the brims each of the soil samples for
phytotoxicity assay.

2.2 Microbial Enumeration

The bioload levels (total microbial count) present in the two different experimental groups were
determined. The spread plate methods on nutrient and sabouraud dextrose agar (Oxoid LTD, UK)
were used for bacterial and fungal isolates. The dumpsite soil and control soil suspensions prepared
and serially diluted to $10^{-3}$ via serial dilution with 1g of each of the soils using distilled water as
diluents. 0.1ml aliquots of the $10^{-3}$ dilutions were spread on triplicates of sterile agar plates. Dissolved
nutrient and Sabouraud dextrose agar were amended with chloramphenicol and nystatin to exclude
bacteria and fungi respectively. Plates were incubated for 18 – 24 hours for bacteria and 18 – 72
hours for fungi. Colonies were counted and expressed in colony forming unit per gram (CFU/g).

2.3 Characterization of microbial isolates

The identification of bacteria was based on morphological and biochemical characterization such as
Gram staining, motility, sugar and alcohol fermentation tests, citrate, catalase, indole, methyl red,
Voges Prauskauer, starch hydrolysis, and oxidase [7]. The identification of fungi was based on colony
appearance, wet mount preparation, use of lactophenol blue and comparison with different fungal
Atlases [8,9,10]. The isolates were further identified to species level at CABI Microbial Identification
Services (United Kingdom, Bakem Lane, Egham Surrey TW20 9TY, UK ) where partial 16S rDNA
sequencing analysis was used for bacterial isolates and internally transcribed spacer (ITS), rDNA
sequencing analyses used on fungal isolates. Briefly, total of four (4) microbial isolates were submitted to CABI for microbial identification. A
unique CABI reference number (IMI number) was assigned to each of the samples. Bacterial
samples (both Bacillus species IMI504618, and IMI 504619 were processed using partial 16S rDNA
sequencing analysis. Fungi samples IMI 504614 and IMI 504615 were processed using ITS rDNA
sequencing analysis. All procedures were validated and processing undertaken in accordance with CABI's in-house methods as documented in TPs 61-68 and TP70 for bacteria and TPs 72-80 for fungi. Procedures involved the following steps: All original samples were subjected to a purity check. Molecular assays were carried out on each sample using nucleic acid as a template. A proprietary formulation [microLYSIS®-PLUS (MLP), Microzone, UK] was subjected to the rapid heating and cooling of a thermal cycler, to lyse cells and release deoxyribonucleic acid (DNA). Following DNA extraction, Polymerase Chain Reaction (PCR) was employed to amplify copies of the partial 16S fragment of rDNA in vitro for bacteria and the ITS fragment of rDNA in vitro for fungi. The quality of the PCR product was assessed by undertaking gel electrophoresis. PCR purification step was carried out to remove unutilised dNTPs, primers, polymerase and other PCR mixture compounds and obtain a highly purified DNA template for sequencing. This procedure also allowed concentration of low yield amplicons. Sequencing reactions were undertaken using BigDye® Terminator v3.1 kit from Applied Biosystems (Life Technologies, UK) which utilises fluorescent labelling of the chain terminator ddNTPs, to permit sequencing. Removal of excess unincorporated dye terminators was carried out to ensure a problem-free electrophoresis of fluorescently labelled sequencing reaction products on the capillary array AB 3130 Genetic Analyzer (DS1) DyeEx™ 2.0 (Qiagen, UK). Modules containing prehydrated gel-filtration resin were optimized for clean-up of sequencing reactions containing BigDye® terminators. Dye removal was followed by suspension of the purified products in highly deionised formamide Hi-Di™ (Life Technologies, UK) to prevent rapid sample evaporation and secondary structure formation. Samples were loaded onto the AB 3130 Genetic Analyzer and sequencing undertaken to determine the order of the nucleotide bases, adenine, guanine, cytosine, and thymine in the DNA oligonucleotide. Following sequencing, identifications were undertaken by comparing the sequence obtained with those available in European Molecular Biology Laboratory (EMBL) via the European Bioinformatics Institute (EBI).

2.4 Heavy metal quantification

Heavy metal analysis of the two soils was by atomic absorption spectrophotometry and values expressed in part per million (ppm)

2.5 Phytotoxicity Assay

Evaluation of agricultural performance of the two soils using seed germination as monitoring tool to measure phytotoxic level of the dumpsite soil relative to the control. The method of seed germination and growth with little modification in temperature and time was employed [11] using two different agricultural crops; cereal grain of Zea mays species and beans seed Vicia faba species (Fabaceae). 10g each of the two different experimental soils were placed in petri-dishes. Ten seeds each of Zea mays and Vicia faba respectively were distributed in the different dishes equally spaced. The plates were incubated for 4-5 days at room temperature. The soils containing the planted seeds were periodically moistened to check diffusional limitations of substrate supply and adverse physiological effect associated with cell dehydration as water penetrates the soil matrix and also to facilitate the swelling of the endosperm as well as the cotyledons and quicken germination. After this time, the number of germinated crops was counted and the elongations of the roots were measured from the transition point among the hypocotile to its extremity, root elongations and shoot lengths were also measured. The germination index (%IG) and percentage seed germination were calculated as thus:

% IG = (% SG) X (% GR)  

(1)

% SG = (% EG) x 100  

(% CG)  1  

(2)

% GR = GERm x 100  

GERCm  1  

(3)

Where % SG = Seed germination % GR = Growth of the roots, % EG = Germination in dumpsite soil %CG = Germination in control soil, GERm = Elongation of roots in dumpsite soil, GERCm = Elongation of roots in control soil.
2.6 Statistical analysis

Each set of data in the experiments conducted was collected in three replicates and the analytical result was the mean of three data sets. The standard deviations (error bars) and statistical differences (5% level of significance) were analyzed by using GraphPad Prism 6® software (full version) (GraphPad Software, CA, USA).

3. RESULTS AND DISCUSSION

3.1 Soils physicochemical and microbiological status

The physicochemical characteristics of the dumpsite soil (DSS) and the control soil (CSS) are shown in Table 1. The pH conditions of dumpsite soil and the control soil are 8.113 and 6.800 respectively.

Table 1. Physicochemical properties of the soil

<table>
<thead>
<tr>
<th>Parameters</th>
<th>DSS</th>
<th>CSS</th>
</tr>
</thead>
<tbody>
<tr>
<td>pH</td>
<td>8.113</td>
<td>6.800</td>
</tr>
<tr>
<td>Temperature (°C)</td>
<td>66.71</td>
<td>40.23</td>
</tr>
<tr>
<td>Nitrate (mg/l)</td>
<td>2.337</td>
<td>3.374</td>
</tr>
<tr>
<td>Density (g/ml)</td>
<td>1.532</td>
<td>1.356</td>
</tr>
<tr>
<td>Organic Carbon (%)</td>
<td>0.299</td>
<td>0.458</td>
</tr>
<tr>
<td>Electrical conductivity EC (µs/cm)</td>
<td>12.320</td>
<td>11.800</td>
</tr>
<tr>
<td>Silt (%)</td>
<td>9.002</td>
<td>20.318</td>
</tr>
<tr>
<td>Sand (%)</td>
<td>72.616</td>
<td>79.566</td>
</tr>
<tr>
<td>Clay (%)</td>
<td>18.382</td>
<td>0.116</td>
</tr>
<tr>
<td>Cation Exchang Capacity (cmol/kg)</td>
<td>0.123</td>
<td>0.547</td>
</tr>
<tr>
<td>Ca (cmol/kg)</td>
<td>0.077</td>
<td>0.074</td>
</tr>
<tr>
<td>Mg (cmol/kg)</td>
<td>0.025</td>
<td>0.453</td>
</tr>
<tr>
<td>K (cmol/kg)</td>
<td>0.132</td>
<td>0.012</td>
</tr>
<tr>
<td>Na (cmol/kg)</td>
<td>0.0204</td>
<td>0.0201</td>
</tr>
</tbody>
</table>

*DSS = Dumpsite Soil sample, CSS = Control Soil Sample

3.2 Bioload status

The result of microbiological enumeration of the different soils enabled us tracked the bioload levels. The microbial count of the dumpsite soil was found to be higher than the control soil (agricultural soil) and maintained $5.4±0.11 \times 10^5$ CFU/g and $1.9±0.21 \times 10^5$ CFU/g respectively for bacteria and $9.0±0.31 \times 10^5$ CFU/g and $5.0±0.12 \times 10^5$ CFU/g respectively for fungi on the point of collection (week 1). A sharp decline was observed on the dumpsite soil sample while the experiment lasted on the sixth week to $1.1±0.41 \times 10^6$ CFU/g for bacteria and $4.0±0.33 \times 10^5$ CFU/g for fungi with temperature...
change from 66.71°C to 42.35°C and pH change from 8.113 to 6.251. There was no change in
temperature and pH in CSS though, total microbial decline was reported but this was not as drastic as
the DSS. The microbial counts on the sixth week were 1.6±0.23 × 10^6 CFU/g for bacteria and
4.0±0.34 × 10^5 CFU/g for the fungal isolates. We therefore, reported that changes in chemicals,
physical conditions (pH and dump pile temperature) and organic compositions of the soil microcosm
withdrawn from the dumpsite led to a significant cell mass loses. Isolated bacterial species conformed
to the works of previous investigators [12,13].

Table 2. Microbial counts of soils

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DSS</th>
<th>CSS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bacterial count on week one (CFU/g).</td>
<td>5.4±0.11 × 10^6</td>
<td>1.9±0.21 × 10^6</td>
</tr>
<tr>
<td>Fungal count on week one (CFU/g)</td>
<td>9.0±0.31 × 10^5</td>
<td>5.0±0.12 × 10^5</td>
</tr>
<tr>
<td>Bacterial count after 6 weeks (CFU/g)</td>
<td>1.1±0.41× 10^6</td>
<td>1.6±0.23 × 10^6</td>
</tr>
<tr>
<td>Fungal count after 6 weeks (CFU/g)</td>
<td>4.0±0.33 × 10^5</td>
<td>4.0±0.34 × 10^5</td>
</tr>
</tbody>
</table>

^b Values are mean of triplicate analyses ±SD, DSS = Dumpsite Soil sample, CSS = Control Soil Sample, CFU/g = colony Forming Unit per gram.

3.3 Molecular analysis

Tables 3 and 4 below show the microbial characterization of isolates before molecular identification.

DSS1 IMI 504614 identified as *Aspergillus candidus*. This sample was identified by ITS rDNA
sequencing analysis using the FASTA algorithm with the Fungus database from EBI and by
examination of morphology. The sequence obtained from this sample showed top matches at 100%
identity to multiple sequences of *Aspergillus candidus* including published sequences from reference
cultures collection strains e.g. sequence JN942868 from DAOM 216320 published in Schoch C.L. et
al. (2012). Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode
marker for Fungi. Proceedings of the National Academy of Sciences of the United States of America
109 (16):6241-6. Morphological features observed were consistent with published taxonomic
Centraal Bureau voor Schimmelcultures, Utrecht, Netherlands.

CSS IMI 504615 identified as *Aspergillus flavus*. This sample was identified by ITS rDNA
sequence analysis using the FASTA algorithm with the Fungus database from EBI and by
examination of morphology. The sequence obtained from this sample showed 100% identity to ITS
sequences described from multiple strains of *Aspergillus flavus* and several strains of *A. oryzae*.
These included sequences from strains reported in peer-reviewed literature e.g. *A. flavus* sequence
JX502758 published in Hadrich I. et al. (2013) Microsatellite typing of *Aspergillus flavus* in patients with
observed were consistent with published taxonomic descriptions of *A. flavus* e.g. Klich M. (2002)
Identification of Common *Aspergillus* Species pp 46-47. Centraal Bureau voor Schimmelcultures,
Utrecht, Netherlands. This species can be distinguished from *A. oryzae* based on conidial size.
*A. flavus* has smaller conidia up to 6μm, whereas those of *A. oryzae* are larger, up to 8μm.

DSSb IMI 504618 identified as *Bacillus subtilis*. This sample was identified by 16S rDNA
sequence analysis using the FASTA algorithm with the Prokaryote database from EBI. The top 750
results gave matches of >99% to members of this species group which includes *B. subtilis*, *B.
amyloliquefaciens, B. mojavensis etc. The validated type strain sequence of B. subtilis gave a match of 99.8% (AJ276351). Members of this species group are difficult to differentiate using this method.

DSSd IMI 504619 also identified as Bacillus subtilis: This sample was identified by 16S rDNA sequence analysis using the FASTA algorithm with the Prokaryote database from EBI. The top 750 results gave matches of >99% to members of this species group which includes B. subtilis, B. amyloliquefaciens, B. mojavensis etc. The validated type strain sequence of B. subtilis gave a match of 99.8% (AJ276351), and B. mojavensis (AB021191) gave a match of 99.6%. Members of this species group are difficult to differentiate using this method.

**Table 3. Biochemical identities of bacterial isolates**

<table>
<thead>
<tr>
<th>S/n</th>
<th>Isolate</th>
<th>Gram reaction</th>
<th>Motility</th>
<th>Citrate</th>
<th>Indole</th>
<th>Voges-Proskauer</th>
<th>Hydrolys. Starch</th>
<th>Oxidase</th>
<th>Urea</th>
<th>Glucose</th>
<th>Lactose</th>
<th>Sucrose</th>
<th>Maltose</th>
<th>Xylose</th>
<th>Arabinose</th>
<th>Identity of Bacterial Species</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>DSSb</td>
<td>Rods +</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>Bacillus subtilis</td>
</tr>
<tr>
<td>2</td>
<td>DSSd</td>
<td>Rods+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>Bacillus subtilis</td>
</tr>
</tbody>
</table>

*DSSb and DSSd = Designation of bacterial isolates on plates, - = negative, + = positive
without gas production

**Table 4. Identities of fungal isolates**

<table>
<thead>
<tr>
<th>S/no</th>
<th>Isolates</th>
<th>Culture Characteristics</th>
<th>Microscopic Characteristics</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>DSS1</td>
<td>Thick, dark brown and</td>
<td>Septate and branched</td>
</tr>
<tr>
<td></td>
<td></td>
<td>scattered surface of</td>
<td>hypha, conidia in chains</td>
</tr>
<tr>
<td></td>
<td></td>
<td>solid media.</td>
<td></td>
</tr>
<tr>
<td>2.</td>
<td>CSS</td>
<td>Thick and flatty with</td>
<td>Multi-segmented</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pure green surface</td>
<td>canoe-shaped and</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Reverse yellow</td>
<td>branched conidiophores</td>
</tr>
</tbody>
</table>

Aspergillus candidus.

Aspergillus flavus.

*DSS1, DSS3 and CSS = designation of fungi isolates on plate
3.4 Heavy metals and mineral quantification

The heavy metal and mineral quantification of the soil (Table 5) enabled us to reveal the heavy metal status of the soils. Result showed that the overall concentration of the heavy metals was noticeably higher in the dumpsite soil especially the four potentially toxic ones including mercury, chromium, lead and cadmium which were quantified 12.49 ppm, 9.871 ppm, 11.30 ppm, and 6.207 ppm respectively in the dumpsite and 0.00 ppm, 0.065 ppm, 0.970 ppm and 0.140 ppm respectively in the control soil.

Table 5. Heavy metal and mineral of the soil samples

<table>
<thead>
<tr>
<th>Heavy Metal (ppm)</th>
<th>DSS</th>
<th>CSS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mercury</td>
<td>12.49</td>
<td>0.00</td>
</tr>
<tr>
<td>Aluminium</td>
<td>5.605</td>
<td>5.103</td>
</tr>
<tr>
<td>Calcium</td>
<td>30.999</td>
<td>29.518</td>
</tr>
<tr>
<td>Potassium</td>
<td>20.598</td>
<td>9.532</td>
</tr>
<tr>
<td>Sodium</td>
<td>5.909</td>
<td>9.255</td>
</tr>
<tr>
<td>Magnesium</td>
<td>5.909</td>
<td>6.520</td>
</tr>
<tr>
<td>Arsenic</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>Chromium</td>
<td>9.871</td>
<td>0.065</td>
</tr>
<tr>
<td>Lead</td>
<td>11.30</td>
<td>0.970</td>
</tr>
<tr>
<td>Zinc</td>
<td>4.844</td>
<td>5.125</td>
</tr>
<tr>
<td>Iron</td>
<td>56.406</td>
<td>57.696</td>
</tr>
<tr>
<td>Cadmium</td>
<td>6.207</td>
<td>0.140</td>
</tr>
<tr>
<td>Manganese</td>
<td>4.194</td>
<td>7.890</td>
</tr>
</tbody>
</table>

DSS = Dumpsite Soil sample, CSS = Control Soil Sample

The heavy metal concentration in the leaves of pawpaw (Carica papaya) plucked from the dumpsite was found to be far much higher than the leaves of pawpaw plucked 1.1 km away from the dumpsite (Table 6). Significant mobility of heavy metal to the surrounding agricultural plants was reported. The result of percentage seed germination (Table 7) was generally low in the dumpsite soil relative to the control soil for both Vicia faba and Zea mays. The modified soil type (1:2 ratio DSS : CSS) gave the best result in both plant materials thus, indicated that the heavy metals at these concentrations lost its phytotoxic effect and acted as trace elements. The germination index was 51.2 % and 89.7 % for Vicia faba and Zea mays respectively.
Table 6. Heavy metal bioaccumulation of selected plants

<table>
<thead>
<tr>
<th>Heavy metal/minerals (ppm)</th>
<th>A₁</th>
<th>A₂</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mercury</td>
<td>6.430</td>
<td>2.120</td>
</tr>
<tr>
<td>Lead</td>
<td>5.160</td>
<td>3.060</td>
</tr>
<tr>
<td>Arsenic</td>
<td>3.890</td>
<td>1.620</td>
</tr>
<tr>
<td>Iron</td>
<td>10.517</td>
<td>3.145</td>
</tr>
<tr>
<td>Copper</td>
<td>2.162</td>
<td>0.296</td>
</tr>
<tr>
<td>Chromium</td>
<td>13.213</td>
<td>6.022</td>
</tr>
<tr>
<td>Cadmium</td>
<td>7.212</td>
<td>2.723</td>
</tr>
</tbody>
</table>

Key: A₁ = Pawpaw leaves collected at the dumpsites, A₂ = Pawpaw leaves collected away (1.1 km) from the dumpsites

Table 7. Percentage seed germination (%EG)

<table>
<thead>
<tr>
<th>Sample</th>
<th>Vicia faba</th>
<th>Zea mays</th>
</tr>
</thead>
<tbody>
<tr>
<td>DSS</td>
<td>10±0.03</td>
<td>50±0.14</td>
</tr>
<tr>
<td>CSS</td>
<td>70±0.11</td>
<td>70±0.32</td>
</tr>
<tr>
<td>1:1</td>
<td>30±0.22</td>
<td>80±0.44</td>
</tr>
<tr>
<td>1:2</td>
<td>50±0.13</td>
<td>90±0.12</td>
</tr>
<tr>
<td>Germination index (%IG)</td>
<td>51±0.25</td>
<td>89±0.46</td>
</tr>
</tbody>
</table>

Values are mean of triplicate analyses ±SD. DSS = Dumpsite soil sample, CSS = Control Soil Sample, 1:1 = one part of DSS to one part of CSS, 1:2 = one part of DSS to two parts of CSS

CONCLUSION

The result of the present study has proven that Obosi dumpsite, Anambra state is polluted with heavy metals especially mercury, lead, chromium and cadmium. It is also observed that continuous indiscriminate waste disposal would lead to increased pollution and affect the surrounding agricultural lands in the dumpsite environment to a point that would result to total sterilization of the arable lands therein. The phytotoxicity assay also proved that the dumpsite soil itself at present has been rendered agriculturally irrelevant and most agricultural plants can no longer grow on it.

REFERENCES


