**Original Research Article**

**Enhanced Bioremediation of Degreasers Polluted Wetland Soil using *Bacillus amyloliquefaciens* and *Pseudomonas putida***

**ABSTRACT**

This study aimed to evaluate the enhanced bioremediation of degreasers (designated as Aqua break and Teepol) polluted wetland soil using *Bacillus amyloliquefaciens* and *Pseudomonas putida*. It employs laboratory-scale experimental designs, statistical data and interpretation. The wetland soil samples were collected from Oguruama at latitudes 4o 4’45.8” N and Longitudes 6o 57’20.4” E in Degema Local Government Area, Rivers State, Nigeria. The *Pseudomonas* and *Bacillus* species used in this study were isolated from the wetland soil and identified using standard biochemical and molecular methods; the 16S rRNA extraction, amplification and sequencing were done. The bioremediation experimental set-up was carried out in clay pots with the two bacteria; *Bacillus amyloliquefaciens* (BAC) and *Pseudomonas putida* (PSD), the two types of degreaser; applied are Aquabreak (AQ) and Teepol (TE). The nine (9) experimental set-ups in this study were: CTL (Control), AQPS (Aquabreak Polluted Soil), TEPS (Teepol Polluted Soil), AQPS + PSD, AQPS + BAC, TEPS + PSD, TEPS+BAC, TEPS+PSD+BAC, AQPS+PSD+BAC. The Bioremediation potential of the respective test organisms were monitored for 28 days at an interval of 14 days using microbiological parameters such as; Total Heterotrophic Bacteria (THB) and Degreaser Utilizing Bacteria (DUB). At the same time, the physicochemical parameters monitored were: Nitrogen, Phosphorus, Potassium, and Total Hydrocarbon content (THC) using Spectrophotometer SPECVIS-720. Percentage (%) Bioremediation was also determined to ascertain the actual potential of treatment agents, singly and in combination. Assessment of Enhanced bioremediation of Aquabreak degreaser using THC values revealed the amount of degreaser remediated and Percentage (%) remediation. The Aquabreak setup from the initial contamination value of 1,535mg/kg decreased in this order: AQPS+BAC (1265mg/kg, 82.41%) > AQPS+PSD+BAC (1245mg/kg, 81.11%) > AQPS+PSD (1065mg/kg, 69.38%) > AQPS (without test organism)(565mg/kg, 38.81%). Changes in THC during bioremediation of the Teepol degreaser revealed that the amount of degreaser remediated and the percentage bioremediation from the initial contaminated value of 5,990mg/kg during the 28 days in decreasing order is; TEPS+PSD+BAC (4815mg/kg, 80.38%) >TEPS+BAC(3135, 53.17%) > TEPS+PSD (2165mg/kg,36.14%) >TEPS(without test organism) (1935mg/kg,32.30%). It was observed that *Bacillus amyloliquefaciens* had more degradability potential than *Pseudomonas putida* on the degreasers. In conclusion, Teepol degreaser is more biodegradable than the Aquabreak degreaser considering the amount of pollutant remediation. Hence, *Bacillus amyloliquefaciens*is is a better option for degreaser bioremediation. Therefore, Teepol degreaser is recommended for both industrial and domestic use.

**Keywords**: Enhanced Bioremediation, Degreaser, Aquabreak, Teepol, *Pseudomonas*, *Bacillus*, wetland soil

1. **INTRODUCTION**

Degreasers are solvent based chemical substances majorly used in dissolving or removing water insoluble substances such as grease, waxes, lubricants, paints, corrosive products or organic films from hard surfaces (Nrior and Odokuma, 2015). They are used to remove oil-borne soils or oils that have been welded, stamped and machined from objects. Degreasers may be oil or water-based and are usually used for both domestic and industrial purposes such as in nuclear power plants, optics automotive, transportation, aircraft as well as cleaning the floors and tiles, etc.(DEEP,2013)

According to the Department of Energy and Environmental Protection of the United States (DEEP) (2013), most oil-based degreasers easily evaporate and are typically harmful to humans and flammable, as tiny amounts reaching the surface or groundwater can lead to major pollution, in other words, contribute to the ground level zone or smog. Water-based degreasers are generally eco-friendly and safer for humans and the environment, when compared to oil-based degreasers, they are less toxic.

Humans have over the years, from their activities introduced substances with toxic properties into the environment. For instance, soil, air, and water bodies have been polluted via oil exploration, illegal bunkering, the release of wastes, etc. The toxicity and risk levels of these substances vary for both flora and fauna in the ecosystems as the effect of the toxic substances may be immediate or long-term, which may affect the chemical or genetic composition of the environment (Ogbonna *et al.,* 2020). As a result, toxic substances that have been introduced to the soil or groundwater must be removed, reduced, mitigated, or remedied by the activities of man through the introduction of microorganisms to detoxify contaminants via the process known as Bioremediation (Douglas *et al*., 2022)

“Bioremediation is a collective phenomenon involving processes that use biological systems to either restore or clean up contaminated sites” (Vimal and Vijai, 2020). This procedure reduces the pollutant levels to a non-toxic, undetectable, or acceptable level, that is, those that fall within regulatory agency-set boundaries. Most of the indigenous microbes can effectively take back the environment to its original form by immobilizing, oxidizing, or converting the pollutants (Douglas *et al*., 2020). According to Nrior and Wosa, (2016), the concept, of “bioremediation” involves processes such as biostimulation, bioaugmentation, and natural attenuation. Biostimulation occurs when the contaminated soils are enriched by the addition of nutrients and other materials to stimulate natural attenuation processes. Natural attenuation depends on the capacity of the naturally occurring soil microorganisms in the environment to use up the pollutant, which happens without human involvement other than monitoring. Bioaugmentation involves the addition of organisms (usually derived from outside that environment) that can detoxify a specific pollutant, occasionally using genetically modified microorganisms. Microorganisms are largely distributed in the biosphere due to their impressive metabolic activity and being able to grow easily in a variety of environmental situations. For the biodegradation of contaminants, the versatility of nutrition can be used. Thus, bioremediation and biodegradation terms are used interchangeably (Strong and Burgers, 2008).

According to the National Geographic Society (2022), a wetland is a part of land or an area which is partly covered by water. These water sources can come from surface water like rivers, lakes, creeks and even seawater which are affected by tidal actions. The area is usually covered by water for some periods of the year with varying time and depth. Wetland is also called transition zones, since they are not completely covered by water or dry, having both properties. These properties determine the vegetation cover of the area with their unique adaptation to the water logged environment. Seasonally dry wetlands or wetlands with slow-moving water can often support trees and other sturdy vegetation. Typically, treeless, is primarily made up of grasses and other herbaceous plants. This study aimed to evaluate the enhanced bioremediation of degreasers (designated as Aqua break and Teepol) polluted wetland soil using *Bacillus amyloliquefaciens* and *Pseudomonas putida*.

**2. Materials and Methods**

**2.1 Study Area and Sample Collection**

Wetland soil samples were collected from Oguruama at latitudes 4o4’45.8” N and Longitudes 6o57’20.4” E in Degema Local Government Area, Rivers State, Nigeria. Wetland soil samples were collected using a soil auger from the topsoil (0-15cm), at five different points, 1 metre apart and pulled together to form composite into a black sterile polythene bags and transported immediately to the Department of Microbiology Laboratory of the Rivers State University, Port Harcourt. The sample bags were transported in ice box. Degreasers used were Aquabreak and Teepol degreasers, purchased from PX offshore Chemicals Limited, Port Harcourt, Nigeria.

**2.2 Baseline Microbiological and Physicochemical Analysis of the Soil Samples**

The following Microbiological analysis were carried out; Total Heterotrophic Bacteria (THB) and Degreaser Utilizing Bacteria (DUB), This was achieved by adding 1g of the soil sample to 9ml of sterile normal saline which was serially diluted to 10-8. An aliquot of 0.1ml was placed on nutrient agar and mineral salt agar, supplemented with degreaser using the vapour phase transfer method for degreaser utilizers. The composition of the mineral salt medium used is as follows:K2HPO4(0.5g), MgSO4.7H2O(0.3g), NaNO3(0.03g), ZnCl2(0.3g), NaCl (0.3g), MnSO4.H2O (0.2g), FeSO4.6H2O(0.02g), Agar(15g) into 1000ml of distilled Water (Douglas *et al*., 2022). Soil Samples were also analyzed for pH, using a pH metre (H -19811-5, Romania). Temperature was determined using mercury-in-glass thermometer, Nitrogen, Phosphorous, Potassium, and the Total Hydrocarbon Content (THC), using the Standard procedures as described by APHA, (2005).

**2.3 Isolation of the Test Organisms**

The organisms used in this investigation were the bacteria: *Bacillus amyloliquefaciens* and *Pseudomonas putida*. These organisms were isolated from the wetland soil samples. The method described by Akani *et al*., (2020) was adopted. Pure cultures were obtained by repeated sub-culturing on Nutrient Agar using standard microbiological methods (spread plate method) as described by Prescott *et al*., (2005).

**2.4 Biochemical and Molecular Characterization of Test Organisms**

Bacterial isolates were characterized on the basis of their colonial morphology, microscopic features, and biochemical properties, including Gram’s reaction and motility. The following biochemical tests were carried out: catalase, oxidase, citrate, indole, methyl red, Voges Proskauer, starch hydrolysis, coagulase, urease, triple sugar iron agar test and sugar fermentation (Cheesebough, 2006). Molecular identification was done by DNA extraction, quantification, amplification and sequencing (Morange and Michel, 2016).

**2.5 Preparation of Broth Culture and Standardization of Inoculums**

The broth is prepared for the proliferation of the test organisms. To prepare the nutrient broth, 13grams were dissolved in 1000ml of distilled water according to the manufacturer’s specification, and then divided into 500ml Erlenmeyer flask where pure cultures of both bacteria were inoculated into and loosely plugged with sterile cotton wool for the growth of the augmenting test organisms (Ogbonna *et al*., 2019)

**2.6Screening for Biodegradability Potential of Test Organisms**

Bacterial isolates were screened using overnight pure cultures. The broth of the organisms was first prepared by transferring the pure cultures into properly labeled test tubes containing nutrient broth (that has been autoclaved and allowed to cool and agitated). Crude oil (0.1ml) was added into test tubes containing 9ml of 1% peptone water. After capping, all the test tubes were autoclaved at 121oC at 15psi for 15 minutes, then allowed to cool and labeled, 0.5ml of the broth (standardized bacterial suspension of the respective bacterial isolate) was transferred into labeled test tubes containing crude oil. The test tubes that served as controls were not inoculated. All test tubes were incubated for 7 days and their potential to utilize degreaser was determined for turbidity. The turbidimetry method adopted involves Spectrophotometric determination of each suspension’s turbidity at 660nm. The absorbance and concentration in reading were used to assay the degradation potential of the test organism (the higher the turbidity concentration, the higher the degradation potential) (Nrior and Otuagha, 2019).

**2.7 Bioremediation Set-up**

The experimental setup was conducted in nine (9) clay pots with 2000g of wetland soil each, two species of bacteria (*Bacillus amyloliquefaciens* and *Pseudomonas putida)*, the total volume of test organisms in each pot was 100 ml, the soil samples were deliberately contaminated with two types of degreasers (Aquabreak and Teepol), total volume of degreasers in pot is 40ml as shown in Table 1. This setup was monitored for 28 days (that is days 1, 14 and 28) for microbiological and physicochemical analyses according to Nrior *et al*., (2017).

**2.8 Microbiological Parameters**

**2.8.1 Total Heterotrophic Bacterial Counts (THBC)**

 One gram of soil was introduced into 9 ml of normal saline. A tenfold serial dilution was done as described by Prescott *et al*. (2005). An aliquot of 0.1ml from 10-1 and 10-5 dilutions were spread in duplicate into sterile solidified nutrient agar and incubated at 37oC for 24 hours; the bacterial colonies that grew on the plates were counted. Discrete colonies on the plates were aseptically subcultured and pure culture was transferred into 10% (v/v) glycerol suspension, well-labeled and stored as stock cultures for preservation and identification.

**2.8.2 Enumeration of Degreaser Utilizing Bacteria (DUB)**

Degreaser Utilizing Bacteria (DUB) was enumerated as adopted by Ezekoye *et al*., (2015) using Mineral salts agar (MSA) with crude oil supplied as a source of carbon by the vapour phase transfer method by aseptically inserting sterile Whatman filter paper that has been saturated with crude oil on the cover of the Petri dish, then incubating the plates at 37°C for 5 to 6 days. The colonies on the plate were counted. The formula below was used to convert the colonies counted into Colony Forming Units (CFU) per gram of soil:

**Cfu/g =** no. of colonies equation ……………………. 1

 Aliquot x volume plated

**2.9 Determination of Total Hydrocarbon Content**

Total Hydrocarbon Content (THC) was analysed using the Spectrophotometric method. The soil samples were dried and lumps were gently crushed in a mortar. Thereafter, 5grams of the sample was weighed and transferred into a glass bottle for extraction and 20ml of extractant (organic solvent - xylene) was added to the bottle and extracted by shaking in a shaking bath for 1 hour. The solids were allowed to settle and filtered into a clean bottle using a glass funnel stuffed with little cotton wool and anhydrous Sodium sulphate at the aperture of the funnel to absorb water (Joel and Amajuoyi, 2010). The absorbance of the extract was measured at 420 nm (Ikeogu *et al*., 2017).

**2.10 Percentage (%) Bioremediation Evaluation**

The percentage (%) bioremediation rate was calculated from the formula adopted as follows.

**Step i:** The amount of the pollutant remediated equals to initial concentration of the pollutant (day 1) minus the final concentration of the pollutant at the end of the experiment (day 28)

**Step ii:** The percentage (%) Bioremediation equals the amount of pollutant divided by the initial concentration of the pollutant (at day 1), multiplied by 100

Bc = Ic – Fc…………………………………...Equation 2

Where

Bc = Amount of the pollutant remediated

Ic = Initial concentration of the pollutant (day 1)

Fc = Final concentration of the pollutant (day 28)

% Bioremediation =Bc /Ic x 100…………………Equation 3

**Table 1: Experimental Setup for Bioremediation Test**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  | **Volume of Pollutant(ml)** | **Volume of Test organism (ml)** |
| **S/N** | **Set-Up Code** | **Soil Quantity**  |  **Aquabreak** | **Teepol** |  **Pseud.** | **Bac.** |
| **1** | **CTL** | 2000g | - | - | - | - |
| **2** | **AQPS** | 2000g | 40 | - | - | - |
| **3** | **TEPS** | 2000g | - | 40 | - | - |
| **4** | **AQPS+PSD** | 2000g | 40 | - | 100 | - |
| **5** | **AQPS+BAC** | 2000g | 40 | - | - | 100 |
| **6** | **TEPS+PSD** | 2000g | - | 40 | 100 | - |
| **7** | **TEPS+BAC** | 2000g | - | 40 | - | 100 |
| **8** | **AQPS+PSD+BAC** | 2000g | 40 | - | 50 | 50 |
| **9** | **TEPS+PSD+BAC** | 2000g | - | 40 | 50 | 50 |

**Key: CTL=Control, AQPS=Aquabreak Polluted Soil, TEPS=Teepol Polluted soil, Psd =*Pseudomonas putida*, Bac. = *Bacillus amyloliquefaciens***

**2.11 Statistical Analysis**

Statistical analysis was carried out using Statistical Package for Social Science (SPSS) from the data that was obtained. To determine whether there is a significant difference in mean value between different treatment options and research data, analysis of variance (ANOVA) and a P-value test of significance was performed at a 95% level of confidence.

**3. Results and Discussion**

The baseline results for Total Heterotrophic Bacteria (THB) and Degreaser Utilizing Bacterial (DUB) counts were 2.75±1.06x107 and 2.40±0.71x103 cfu/g, respectively.

The results from screening the test organisms for the Biodegradability Potential show that isolates that had the highest growth on MSA (H3 and H4) also had higher absorbance and concentration than isolates on Nutrient Agar thus were sent for molecular identification. Results of the molecular identification showed the organisms (H3 and H4) to be *Pseudomonas putida* and *Bacillus amyloliquefaciens* and with absorbance and concentrations of 1.003, 12.61mg/l and 1.216, 14.91mg/l, respectively as shown in Table 2. These organisms were now used to carry out the bioremediation experiment.

The results of the bacterial counts of wetland soil contaminated with Aquabreak and Teepol, bioaugmented with *Bacillus amyloliquefaciens* and *Pseudomonas putida* for enhanced remediation and unenhanced wetland soil which served as control are presented in Tables 2 and 3 and Figures 1 - 4. The Total Heterotrophic Bacterial counts for Aquabreak polluted soil showed the individual strain of *Bacillus amyloliquefaciens* had a higher mean value of 10.21±0.25 CFU/g than the *Pseudomonas putida* with the lower mean value of 9.63±0.80 CFU/g after 28 days. Also, the consortium of *Pseudomonas putida* and *Bacillus amyloliquefaciens* had the highest mean value of 10.35±0.15 CFU/g after 28 days. Roberts *et al*., (2020) research on environmental consortium containing *Pseudomonas* and *Bacillus* species synergistically degrading polyethylene Terephthalate plastic.

Meanwhile, for Total Heterotrophic Bacterial counts in Tee polluted soil, *Bacillus amyloliquefaciens* showed the highest mean counts of 9.88±0.19 CFU/g, compared to *Pseudomonas putida* with the lowest mean counts of 9.49±1.06 CFU/g. This result also agrees with the research work carried out by Nrior and Otuogha, (2019), which stated that in freshwater, *Bacillus* species have the potential to accelerate the degradation of both Rigwash and Aquabreak degreaser*s*, when compared to *Pseudomonas* species and a consortium of both bio-augmenting bacteria used as biodegradation enhancers.

The results of the total hydrocarbon content (THC) in the respective wetland soils contaminated with Aqua and Tee degreasers as well as the uncontaminated wetland soils are presented in Figures 5 - 8. The amount of THC remediated indicates the enhanced degradation potential of the test organisms (*Pseudomonas putida* and *Bacillus amyloliquefaciens*). These results are in agreement with Nrior and Otuogha, (2019).

**Table 2: Biodegradability Potential of the Test Organism Using Turbidometry Method**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **S/N** | **Isolates** |  **1% Peptone Water** | **Vol. Of Degreaser** | **Volumeof Organism** | **Total Vol (Ml)** | **Absorbance****(420nm)**  | **Concentration****(Mg/l)** |
| 1 | CONTROL | 9 | 0.1 | - | 9.1 |  - | - |
| 2 | IS 1 | 9 | 0.1 | 0.5 | 9.6 | 0.382 | 5.93 |
| 3 | IS 2 | 9 | 0.1 | 0.5 | 9.6 | 0.443 | 6.58 |
| 4 | IS 3 | 9 | 0.1 | 0.5 | 9.6 | 0.582 | 8.08 |
| 5 | IS 4 | 9 | 0.1 | 0.5 | 9.6 | 0.591 | 8.18 |
| 6 | IS 5  | 9 | 0.1 | 0.5 | 9.6 | 0.571 | 7.96 |
| 7 | IS 6 | 9 | 0.1 | 0.5 | 9.6 | 0.528 | 7.50 |
| 8 | IS 7 | 9 | 0.1 | 0.5 | 9.6 | 0.581 | 8.07 |
| 9 | IS 8  | 9 | 0.1 | 0.5 | 9.6 | 0.548 | 7.71 |
| 10 | IS 9 | 9 | 0.1 | 0.5 | 9.6 | 0.565 | 7.90 |
| 11 | H3 | 9 | 0.1 | 0.5 | 9.6 | 1.003 | 12.61 |
| 12 | H4 | 9 | 0.1 | 0.5 | 9.6 | 1.216 | 14.91 |

**Key: IS 1-9=Isolates from Nutrient Agar (NA), H3 and 4=Isolates from MSA**

**Table 3: Changes in Total Heterotrophic Bacteria (Log10CFU/g) during Enhanced Bioremediation of Degreasers Polluted Wetland Soil Using Selected Bacteria**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S/N** | **SET-UP CODE** | **DAY 1** | **DAY 14** | **DAY 28** | **MEAN±SD** |
| **1** | **CTL** | 9.57 | 9.62  | 9.45 | 9.55±0.09 |
| **2** | **AQPS** | 9.76 | 9.95 | 9.45 | 9.72±0.26 |
| **3** | **TEPS** | 9.87 | 9.49 | 9.65 | 9.67±0.19 |
| **4** | **AQPS+PSD** | 8.72 | 9.91 | 10.26 | 9.63±0.80 |
| **5** | **AQPS+BAC** | 9.94 | 10.43 | 10.28 | 10.21±0.25 |
| **6** | **TEPS+PSD** | 9.85 | 10.33 | 8.30 | 9.49±1.06 |
| **7** | **TEPS+BAC** | 9.86 | 10.07 | 9.70 | 9.88±0.19 |
| **8** | **AQPS+PSD+BAC** | 10.18 | 10.42 | 10.46 | 10.35±0.15 |
| **9** | **TEPS+PSD+BAC** | 9.34 | 9.93 | 9.74 | 9.67±0.30 |

key: CTL =Control, AQPS=Aquabreak Polluted Soil, TEPS=Teepol Polluted soil, Psd=*Pseudomonas putida*, Bac = *Bacillus amyloliquefaciens*

 **Fig 1:** **Changes in Total Heterotrophic Bacteria (Log10CFU/g) During Bioremediation of Tee Degreasers Polluted Wetland Soil using *Pseudomonas putida* and *Bacillus amyloliquefaciens***

 **Fig 2: Changes in Total Heterotrophic Bacteria (Log10CFU/g) During Bioremediation of Aquabreak Degreasers Polluted Wetland Soil using *Pseudomonas putida* and *Bacillus amyloliquefaciens***

 key: CTL=Control, AQPS=Aqua break Polluted Soil, Psd=*Pseudomonas putida*, Bac=*Bacillus amyloliquefaciens*

**Fig. 3: Changes in Aqua Utilizing Bacteria (AQUB)(log10Cfu/g) during Enhanced Bioremediation of Degreasers Polluted Wetland Soil using *Pseudomonas putida* and *Bacillus amyloliquefaciens***

key: CTL=Control, AQPS=Aquabreak Polluted Soil, Psd=*Pseudomonas putida*, Bac=*Bacillus amyloliquefaciens*

**Fig 4: Changes in Tee Utilizing Bacteria (TUB)(log10Cfu/g) during Enhanced Bioremediation of Degreasers Polluted Wetland Soil using *Pseudomonas putida* and *Bacillus amyloliquefaciens***

key: CTL=Control, TEPS=Tee Polluted soil, Psd=*Pseudomonas putida*, Bac=*Bacillus amyloliquefaciens*

**Figure 5: Changes in THC (mg/kg) Removal during bioremediation of Aquabreak Degreasers Polluted Wetland Soil using *Pseudomonas putida* and *Bacillus amyloliquefaciens***

key: CTL=Control, AQPS=Aqua Polluted Soil, TEPS=Teepol Polluted soil, Psd=*Pseudomonas putida*, Bac=*Bacillus amyloliquefaciens*

**Fig 6: Percentage (%) Bioremediation of THC during bioremediation of Aqua Degreasers Polluted Wetland Soil using *Pseudomonas putida* and *Bacillus amyloliquefaciens***

**Fig 7: Changes in THC (mg/kg) during bioremediation of Teepol Degreasers Polluted Wetland Soil using *Pseudomonas putida* and *Bacillus amyloliquefaciens***

key: CTL= Control, AQPS = Aquabreak Polluted Soil, TEPS = Teepol Polluted soil, Psd = *Pseudomonas putida*, Bac = *Bacillus amyloliquefaciens*

**Fig 8: Percentage (%) Bioremediation of THC during bioremediation of Teepol Degreasers Polluted Wetland Soil using *Pseudomonas putida* and *Bacillus amyloliquefaciens***

key: CTL=Control, AQPS=Aqua Polluted Soil, TEPS=Tee Polluted soil, Psd=*Pseudomonas putida*, Bac=*Bacillus amyloliquefaciens*

Enhanced bioremediation of Aquabreak degreaser evaluation for THC revealed the amount of degreaser remediated and its percentage value from the initial contamination value of 1535mg/kg during the period of 28 days in decreasing order as AQPS+BAC (1265mg/kg, 82.41%) > AQPS+PSD+BAC (1245mg/kg, 81.11%) > AQPS+PSD (1065mg/kg, 69.38%) > AQPS (without test organism)(565mg/kg, 38.81%). Changes in THC during bioremediation of Teepol degreaser revealed that the amount of degreaser remediated and its percentage value from the initial contaminated value of 5990mg/kg during the period of 28 days in decreasing order as TEPS+PSD+BAC (4815mg/kg, 80.38%) > TEPS+BAC(3135,53.17%) > TEPS+PSD (2165mg/kg,36.14%) >TEPS(without test organism) (1935mg/kg,32.30%).

The Figures show that *Bacillus amyloliquefaciens* has a high potential to enhance the bioremediation of Aquabreak and Teepol polluted soil when compared to *Pseudomonas putida*. In a research conducted by Nrior and Odokuma, (2015) on the Ultimate Biodegradability Potential of Trichloroethylene (TCE) used as degreaser in Marine, Brackish and Fresh water, the following degreaser degrading-bacterial genera were identified; *Pseudomonas*, *Bacillus*, *Micrococcus* and *Enterobacter* with *Pseudomonas* occurring most frequently, followed by *Bacillus*, then *Micrococcus* and *Enterobacter*. The relative occurrence of specific genera of bacteria could be used as an index of the pollution status or biodegradation of the environment. This fact clearly state that the significance occurrence may be due to the fact that *Bacillus amyloliquefaciens* and *Pseudomonas putida* are more adapted to survival and bioremediating capabilities in wetland polluted soil.

**4. Conclusion and Recommendations**

This study has revealed that bioaugmenting bacteria *Bacillus amyloliquefaciens* has a higher potential to enhance degradation of both Aquabreak and Teepol Polluted wetland soils when compared to *Pseudomonas putida* and the consortium of both bioaugmenting bacteria used as bioremediation enhancers. Furthermore, the results indicate that Teepol degreaser is more biodegradable than Aquabreak degreaser considering the amount of pollutant remediated.

Therefore, Teepol degreaser is recommended for both industrial and domestic use. Also, in a wetland area polluted with either Aquabreak or Teepol, *Bacillus amyloliquefaciens* should be considered the organism of choice for the bioremediation.

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