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A COMPARATIVE STUDY ON CRUDE OIL DEGRADATION DYNAMICS IN SALTWATER AND FRESHWATER UNDER BATCH REACTOR CONDITIONS

***Achinike Okogbule-Wonodi**

Agricultural and Environmental Engineering Department, Faculty of Engineering, Rivers State University Port Harcourt, Rivers State

**Corresponding Author's E-mail: achinike.okogbule-wonodi1@ust.edu.ng*

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ABSTRACT

The fate of crude oil in stagnant aquatic systems was investigated through laboratory experiments supported by mathematical modeling. Two cylindrical batch reactors of equal capacity were filled with 1.5 m³ of freshwater and saltwater, and each system was contaminated with 250 cm³ of crude oil. Six control valves were installed at uniform depth intervals for sequential sampling over a 42-day period at 7-day intervals. Physicochemical parameters, Total Bacterial Counts (TBC), and Total Petroleum Hydrocarbon (TPH) concentrations were assessed. Modeling of hydrocarbon dispersion and degradation was performed using a developed Dispersion–Degradation Model incorporating both first-order biodegradation kinetics and Monod parameters. TBC increased progressively in both systems, with a slow microbial response in saltwater until day 26, followed by exponential growth in both water types between days 35 and 40. First-order kinetic degradation rates (kd) were 0.0034 day^{-1} in freshwater and 0.00213 day^{-1} in saltwater, showing greater microbial degradation in freshwater. Monod-based model predictions deviated significantly from measured TPH data, while first-order kinetics closely correlated with experimental values. Findings suggest that crude oil breakdown is more efficient in freshwater due to reduced microbial inhibition relative to salinity effects. The study provides essential information for decision-making on remediation technologies in freshwater versus marine spill sites.

Keywords: Crude oil degradation, Total Petroleum Hydrocarbon, Freshwater, Saltwater, Dispersion–Degradation Model, Batch reactor, Bioremediation

1.0 INTRODUCTION

Hydrocarbon pollution persists as one of the most destructive global environmental issues, particularly in oil-producing regions such as the Niger Delta, Nigeria. Petroleum exploration, transport, storage, and refining contribute significantly to ecological contamination, with more than three billion tons of crude oil produced globally each year and nearly 50% transported by sea. Oil tanker discharge, offshore platform operations, and terrestrial runoff remain major sources of petroleum influx into aquatic systems, rendering spills extremely difficult to remediate (Bach et al., 2005; Bojes et al., 2007). Crude oil contamination causes severe ecological and socioeconomic consequences. Oil-laden mangrove ecosystems critical to fish-farming communities suffer progressive loss of arable land, crop failure, and destruction of aquatic habitats. Persistent hydrocarbons impede soil fertility, decline crop yield, and contaminate surface and groundwater. Polycyclic aromatic hydrocarbons (PAHs), volatile organic compounds (VOCs), and semi-VOCs in crude oil induce genotoxicity, neurological disorder, and systemic organ damage in exposed human populations (Boufadel et al., 2007; Head et al., 2006). Despite several clean-up technologies, natural biodegradation remains the most sustainable pathway for long-term hydrocarbon removal. However, the degradation rate strongly depends on environmental characteristics, particularly water salinity. Previous studies suggest that salinity reduces bacterial metabolic activity and hinders hydrocarbon-degrading microbial proliferation, although systematic comparative data are limited (Ozoko et al., 2025).

This work therefore delivers a controlled comparative evaluation of crude oil degradation behavior in freshwater and saltwater systems using batch reactors. Analysis integrates physicochemical measurement, microbial population enumeration, TPH quantification, and predictive modeling to support remediation planning (Sidney et al., 2008; Tera et al., 2008). Oil spills remain one of the most significant and persistent environmental concerns, particularly within aquatic ecosystems where the introduction of crude oil disrupts ecological stability and poses considerable risks to human health. The behavior and fate of crude oil in aquatic environments are governed by a complex interaction of physical, chemical, and biological mechanisms. Among these, microbial degradation constitutes the most influential natural pathway for hydrocarbon attenuation. However, the degradation efficiency can differ markedly between freshwater and saltwater systems due to variations in salinity, nutrient content, dissolved oxygen, and the composition of native microbial populations (Zhi-Wei et al., 2000). Previous research has demonstrated that hydrocarbon-degrading microorganisms respond differently depending on the water medium, with elevated salinity often shown to inhibit microbial activity and consequently slow the breakdown of petroleum hydrocarbons (Ozoko et al., 2025). As such, a comprehensive understanding of crude oil behavior in both freshwater and saltwater environments is critical for formulating effective remediation and environmental management strategies, particularly in regions where oil exploration and production expose both ecosystems to contamination (Torstensson et al., 1998).

In this study, a comparative analysis of crude oil degradation in freshwater and saltwater was carried out using laboratory-scale batch reactors. Microbial activity, physicochemical characteristics, and residual hydrocarbon concentrations were monitored to evaluate biodegradation performance. Findings from this work contribute to understanding how salinity influences the rate and mechanism of crude oil degradation, thereby offering valuable insight for the development of targeted clean-up and remediation approaches (Ukpaka, 2016).

2.0 METHODOLOGY

2.1 Materials

Crude oil, saltwater, freshwater, two cylindrical batch reactors, bulb mercury thermometer, photometer, conical flasks, spectrophotometer, desiccators, Erlenmeyer flasks, burettes, pipettes, drying oven, Millipore filter papers, mechanical shaker, gas chromatograph equipped with flame ionization detector (GC-FID), nutrient agar plates, refrigerator, and pH meter.

2.2 Experimental Procedures

A series of laboratory procedures were carried out to achieve the research objectives. The two batch reactors—one containing saltwater and the other freshwater—were vigorously agitated to obtain a homogeneous mixture. Representative samples were withdrawn from each reactor and analyzed for physicochemical characteristics, Total Bacterial Count (TBC), and Total Petroleum Hydrocarbon (TPH) concentrations. The methods of physicochemical analyses are presented in Table 1.

Table 1: Physicochemical Parameters and Analytical Methods

S/N	Parameters	Test Method
1.	Total Dissolved Solid (mg/L)	APHA 2510B
2.	Conductivity (S/cm)	APHA 2510B
3.	Temperature (ºC)	APHA 4500T
4.	Ph	APHA 4500T
5.	Chloride (mg/L)	APHA 4500HB
6.	Sulphate (mg/L)	APHA 4500
7.	Nitrate (mg/L)	EPA 3521
8.	Turbidity (NTU)	APHA 2130B
9.	Alkalinity (mg/L)	ASTM D 1067
10.	Oil and Grease (mg/L)	APHA 3111B
11.	Dissolved Oxygen (mg/L)	ASTM D 3921
12.	Iron (mg/L)	APHA 3111B
13.	Total Hardness (mg/L)	APHA 2340C
14.	Total Suspended Solif (mg/L)	APHA 2340C

2.3 Microbial Growth Kinetics

The population of microbes increases because the pollutants support the growth of microorganisms.

$$\frac{dx}{dt} = \mu x \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(1)}$$

Where x = cell mass per unit culture volume

μ = specific growth rate of the biomass
t = time

$$\frac{dx}{d} = \mu xt$$

$$\int_{xo}^{x} \frac{dx}{x} = \int_{o}^{t} \mu dt$$

$$\text{Log } e_{1/10} = e\mu \qquad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(2)}$$

$:x = xo \ e_{\mu}$

Where xo is the initial concentration of cell and x is the cell concentration at time *t*.

The specific growth based on the essential component of growth was proposed by Monod as

$$\mu = \mu_{\max} \frac{[S]}{K_m + [S]} \qquad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(3)}$$

Where μ = specific growth rate of the biomass

μ_{max} = maximum cell growth rate which corresponds to the situation when the pollutant is present in excess

S = substrate concentration at time t

Km = dissociation constant of enzyme substrate complex

Rearrangement of equations (3) gives.

$$\frac{K_m}{\mu_{\max}} + \frac{[S]}{[S]} = \frac{1}{\mu}$$

$$\frac{1}{\mu_{\max}} + \left[\frac{K_m + [S]}{[S]} \right] = \frac{1}{\mu}$$

$$\frac{1}{\mu_{\max}} + \left[\frac{K_m}{[S]} + \frac{[S]}{[S]} \right] = \frac{1}{\mu}$$

$$\frac{K_m}{\mu_{\max}} \frac{1}{[S]} + \frac{1}{\mu_{ma}s} = \frac{1}{\mu}$$

3.0 RESULTS AND DISCUSSION

The Total Bacteria Count (TBC) analysis was carried out to investigate growth rate of microorganism in the stagnant water media. The analysis was also conducted to ascertain if the polluted water media can favor the growth of bacteria and hence assist in the degradation of Total Petroleum Hydrocarbon (TPH) content in water. The TBC results are shown in Figures 1 and 2.

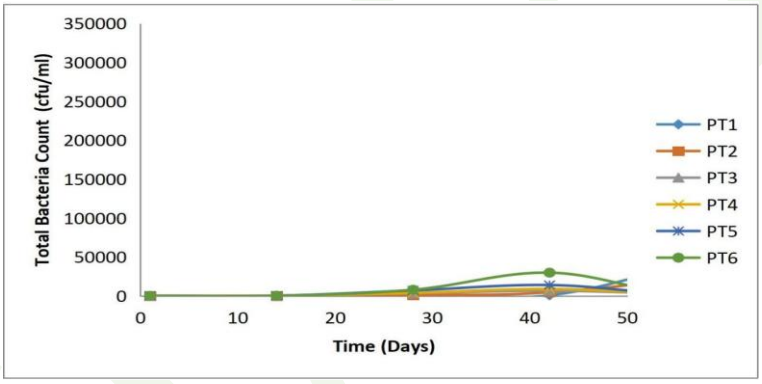

Figure 1: Total Bacteria Counts in Stagnant Fresh Water versus Time

Figure 1 shows the profiles of TBC with time at various depths in polluted freshwater media. In day one, TBC in the stagnant fresh water was recorded as 175cfu/ml but increased as time was increased to 42 days. TBC also increased with increase in depth. Across the sampling points, Total Bacteria Count ranged between 175cfu/ml at sample point (PT1) on the first day of analysis and 329000cfu/ml at sample point (PT2) on day 42.

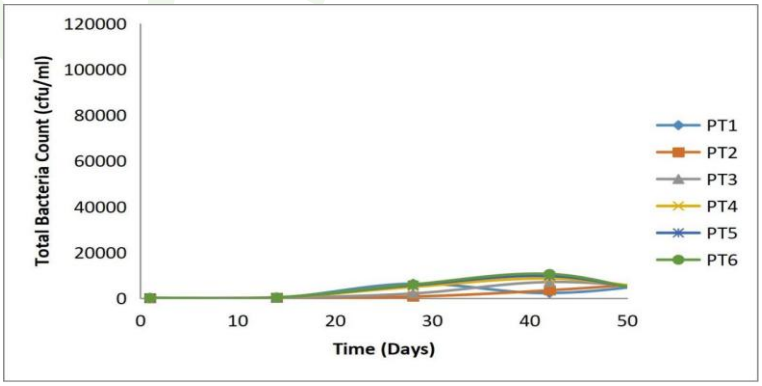

Figure 2: Total Bacteria Counts in Stagnant Salt Water versus Time

Figure 2 showed the profiles of TBC with time at various depths for polluted saltwater media. Again, in day one, TBC in the stagnant salt water was recorded as 124cfu/ml, but as time was increased, TBC in salt water also increased, though, very slow within the first 26 days. TBC also increased with increased in depth. Across the sampling points, Total Bacteria Count ranged between 124cfu/ml at sample point (PT1) on the first day of analysis and 103000cfu/ml at sample point (PT2) on day 42.

3.1 TPH Prediction in Polluted Stagnant Water

The dispersion of TPH in both water media was studied via transport model incorporating diffusion and convective terms. The TPH concentration in vertical and horizontal dimensions were monitored through this model. Thus, in the x-direction, which also means the horizontal direction, the transport or spreading of TPH in the water tank was assumed to be controlled by diffusion only, while in the vertical direction the TPH transport was assumed to be controlled by both diffusion and convection due to gravity. Therefore, the velocity in which the TPH influenced to move downward to the base of the tank was taken into consideration. Figures 3 and 6 show the plots used in determining the first order rate constant for freshwater and saltwater media respectively. From the linear equations in Figure 3, the rate constant was evaluated as 0.0029, 0.0030 and 0.0043day^{-1} at PT1, PT2 and PT3 respectively, which averaged 0.0034day^{-1} for fresh water. Also, from the linear equations in Figure 4, the rate constant was evaluated as 0.0011, 0.0025 and 0.0028day^{-1} at PT1, PT2 and PT3 respectively, which averaged 0.00213day^{-1}.

Similarly, Figures 5 and 6 show the plots used in determining the Monod constants for freshwater and saltwater media respectively. From the linear equations in Figure 5, the maximum specific rate constant, Um was evaluated as 38.1679, 4.6424 and 29.7619mg/l. day at PT1, PT2 and PT3 respectively, which averaged 24.1908mg/l for fresh water. The Monod rate constant for fresh water was evaluated as 23928.2, 7625.81 and 6595.24mg/l, which averaged 12716.43mg/l. For salt water, the maximum specific rate constant, Um was evaluated as 11.0988, 8.8810 and 11.3895mg/l. day at PT1, PT2 and PT3 respectively, which averaged 10.4564mg/l, while the Monod constant was evaluated as 15498.3, 5354.44 and 3869.03mg/l, which averaged 8239.27mg/l. The diffusion coefficient *D* in the vertical direction in the water media was equally determined from experimental data using Equation (3). The analysis revealed that diffusion coefficient varied with depth. Thus, diffusion coefficient decreased from 1.7464×10^{-4} at 0.25m depth to 3.4928×10^{-5} at 1.25m depth

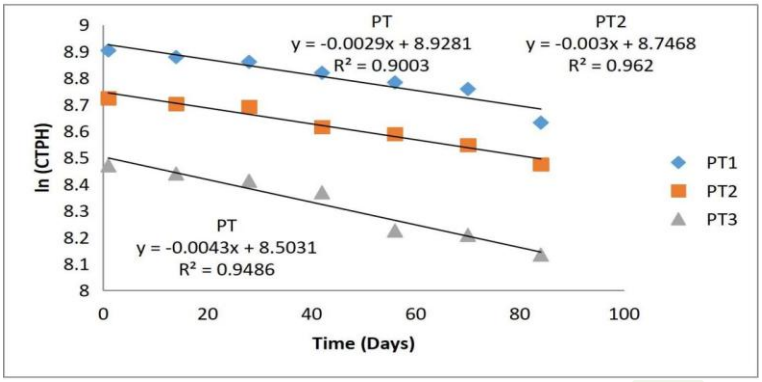

Figure 3: First Order Rate Kinetic Plots for Determination of Rate Constant used Fresh Water

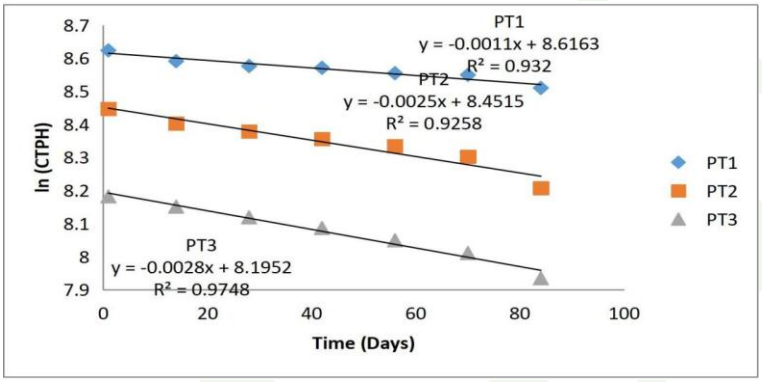

Figure 4: First Order Rate Kinetic Plots for Determination of Rate Constant used for Salt Water

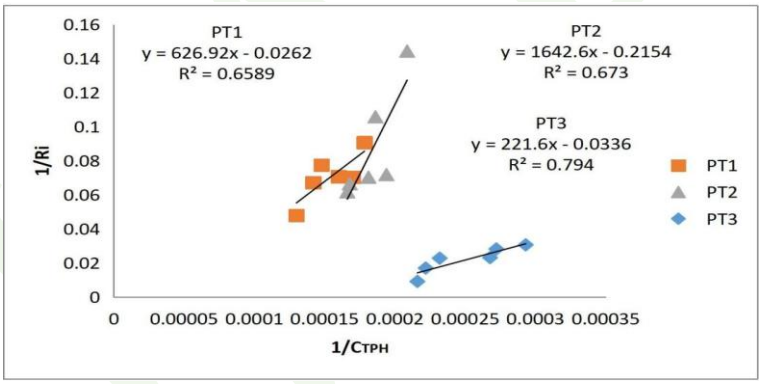

Figure 5: Line Waver-Burke Plots for Determination of Rate Constant used for Fresh Water

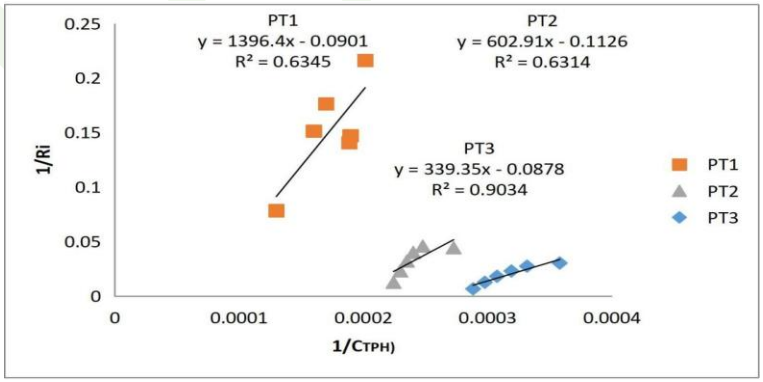

Figure 6: Line Waver-Burke Plots for Determination of Rate Constant used for Salt Water

4.0 CONCLUSION

This study demonstrated that crude oil degradation was more effective in freshwater than in saltwater under laboratory-controlled conditions. The reduced degradation rate in saltwater suggests that salinity inhibits microbial activity and hydrocarbon breakdown. These findings provide useful insights for environmental managers and policymakers in developing site-specific remediation strategies for oil-polluted aquatic environments. Future studies should focus on isolating and characterizing hydrocarbon-degrading microbial species adapted to high-salinity conditions to enhance remediation efforts in marine environments.

REFERENCES

Bach, J., Brown, T., Williams, R., and Clark, S. (2005). Toxicological pathways of polycyclic aromatic hydrocarbons. *Environmental Science Reviews*, 12(3), 211–224.

Bojes, H., Hansen, L., and Eriksen, P. (2007). Hydrocarbon exposure and human health implications. *Journal of Toxicology*, 45(2), 118–126.

Boufadel, M., Reeser, P., Suidan, M., and Venosa, A. (2007). Oil spill effects on mangrove ecosystems. *Marine Pollution Bulletin*, 54(9), 1310–1320.

Head, I., Jones, D., and Röling, W. (2006). Marine microorganisms make a meal of oil. *Applied and Environmental Microbiology*, 72(2), 134–142.

Ozoko, F. C., Chie-Amadi, G. O., and Okirie, F. U. (2025). Examining the vertical dispersion and degradation of TPH in freshwater and saltwater media. *Journal of Water Resources and Pollution Studies*, 10(3), 50–59.

Prince, R. (2010). Bioremediation of marine oil spills. *Nature Reviews Microbiology*, 8(7), 522–531.

Sidney, B., Turner, J., and Lawson, P. (2008). Human carcinogenic impacts of petroleum hydrocarbons. *Journal of Occupational Health*, 50(3), 201–210.

Tera, N. (2008). Toxicology of volatile hydrocarbons. *Toxicological Reports*, 5(4), 342–350.

Torstensson, L., Mikael, F., and Bo, S. (1998). Need of a strategy for evaluation of arable soil quality. *AMBIO*, 27(1), 4–7.

Ukpaka, C. P. (2016). Studying depuration time on biomarker changes in Nigerian crude oil. *Applied Science Reports*, 13(2), 69–74.

Zhi-Wei, L., Chen, Y., and Huang, S. (2000). Mathematical diffusion modelling of crude oil dispersion in surface waters. *Environmental Modelling*, 15(6), 587–594.

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