

Petroleum Hydrocarbon Effects on Soil Microbial Communities in K-Dere, Gokana Niger Delta

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Research Article

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Abstract

In Nigeria, Niger Delta is the region most affected by petroleum hydrocarbon pollution, which affects soil microbial communities. This study looked at the functional and structural responses of soil fungi and bacteria to hydrocarbon pollution in Gokana, Rivers State, Nigeria. Soil samples from polluted and control sites were analyzed for elemental composition, total petroleum hydrocarbons (TPH), microbial counts, and microbial identification. Polluted soils contained 78.3 mg/kg TPH, which exceeds the regulatory limit of 50 mg/kg, compared to 10.8 mg/kg in control soils. The polluted soil showed elevated sulfur (6.36 mg/kg vs. 0.20 mg/kg), chlorine (0.85 mg/kg vs. 0.30 mg/kg), and nickel (0.061 mg/kg vs. 0.043 mg/kg) contents, while phosphorus (0.068 mg/kg vs. 0.253 mg/kg) and calcium (0.526 mg/kg vs. 0.124 mg/kg) declined in the unpolluted soil. Microbial counts indicated comparable Total Heterotrophic Bacteria (THB) in polluted and control soils (5.0×10^3 cfu/g), while Hydrocarbon-Utilizing Bacteria (HUB) in polluted soils showed higher rates (5.3×10^3 cfu/g vs. 3.8×10^3 cfu/g). Hydrocarbon-Utilizing Fungi (HUF) maintained moderate populations (3.3×10^3 cfu/g) in both areas. This indicated fungal resilience and metabolic adaptation. Dominant bacterial genera included *Proteus*, *Klebsiella*, *Enterobacter*, *Citrobacter*, *Pseudomonas*, and *Bacillus*, while fungi were dominated by *Fusarium*, *Candida*, and *Penicillium* species exhibiting septate hyphae, conidial spores, and rapid growth indicative of stress tolerance. These results demonstrate that hydrocarbon contamination drives measurable shifts in microbial abundance and function, favoring hydrocarbon-degrading taxa. The integration of soil chemistry and microbial ecology provides a quantitative basis for natural attenuation and sustainable remediation strategies in hydrocarbon-impacted wetlands of the Niger Delta.

1.0 Introduction

The Niger Delta region of Nigeria has suffered decades of crude oil pollution. This is a result of continuous petroleum exploration, production, and transportation activities (Alao et al., 2025; Felix, 2024; Omokaro et al., 2025). As a result, it has led to the persistent contamination of soils, sediments, and water bodies across the region (Mohanta et al., 2024; O'Farrell et al., 2025). Areas such as K-Dere in Gokana Local Government Area, according to the United Nations Environment Programme (UNEP, 2011), remained one of the most severely affected. They are affected by high concentrations of petroleum hydrocarbons and heavy metals, still detectable years after spills occurred. Crude oil contamination affects the soil ecosystems. It alters the physicochemical balance by reducing aeration, increasing hydrophobicity, and limiting nutrient availability. These changes hinder plant growth and interfere with soil biological activity (Elijah, 2022; Hussien et al., 2022; Kakde & Sharma, 2024; Truskewycz et al., 2019). Yet, within this ecological disturbance lies a remarkable natural response to the adaptation and resilience of soil microbial communities (Chikere et al., 2012; Okonofua et al., 2023; Truskewycz et al., 2019).

Mekonnen et al. (2024) pointed out that microbial communities play important roles in mitigating hydrocarbon pollution through biodegradation- a natural process in which certain bacteria and fungi use hydrocarbons as their carbon and energy sources. Different studies have recorded the presence of hydrocarbon-degrading taxa such as *Pseudomonas*, *Bacillus*, *Acinetobacter*, *Candida*, *Fusarium*, and *Penicillium* as dominant species in polluted environments (Chicca et al., 2022; Chikere et al., 2012; Obayori et al., 2018). In the Niger Delta, Ehis-Eriakha et al. (2025) found that petroleum-contaminated soils had reduction in overall microbial diversity but an enrichment of specialized hydrocarbon degraders. This reflected adaptive ecological shifts. Ichor et al. (2016) observed elevated counts of *Pseudomonas* and *Micrococcus* species in oil-impacted soils of Ogoniland with selective pressure toward microbial taxa capable of hydrocarbon utilization.

The potential of microbial bioremediation, which is the use of indigenous or introduced microorganisms to detoxify contaminated environments is a sustainable solution for oil-polluted ecosystems, is high. Studies show that bioremediation techniques, including bioaugmentation, biostimulation, and natural attenuation are effective, environmentally safe, and cost-efficient compared to physicochemical remediation methods (Ayilara et al., 2023; Dehnav et al., 2022; Lopes et al., 2022). For the Niger Delta, several studies have demonstrated that stimulating indigenous hydrocarbon-degrading microbes through nutrient amendment or aeration can significantly enhance the degradation of total petroleum hydrocarbons (TPH), thereby restoring soil functionality (Chikere et al., 2019; Yaman, 2020).

Despite chronic petroleum hydrocarbon exposure, ecological and socio-economic importance of K-Dere wetlands, there is limited information on the effect of crude oil pollution on soil microbial community. This study combines soil chemistry and microbial ecology by investigating the abundance, diversity, and adaptation of microbes found in the hydrocarbon-polluted soils.

2.0 Materials and Methods

2.1 Site description

Samples were collected from crude oil-polluted sites in K-Dere in Gokana Local Government area in the community of Ogoni land within April and June 2024. These sites have experienced prolonged pollution from oil industry facilities and exploration. Ogoni land covers over 1000 km² in Rivers State, South South, Niger Delta, Nigeria. The global positioning system (GPS) was used to compute the coordinates of the sample sites. The GPS coordinates is 4.64514826N, 7.23794585E.

2.2 Soil Sample Collection

Sampling was conducted at two depths: 0–15 cm (surface layer) and 15–30 cm (subsurface layer) to capture vertical variations in contamination. Samples were collected in triplicates from each depth using sterilized stainless-steel soil augers to prevent cross-contamination.

Control samples were collected from an unpolluted site located approximately 250 meters away from the visibly polluted area, ensuring similar soil type and vegetation characteristics. All collected samples were placed in sterile polyethylene bags, properly labelled, and transported in iceboxes to Production Chemistry laboratory, SPDC for immediate physicochemical and microbiological analyses. Upon arrival, samples were air-dried, homogenized, and sieved (2 mm mesh) before analysis.

2.3 Analysis of Soil Physicochemical Properties

Soil physicochemical parameters were analyzed following standard procedures. pH was measured using a Metrohm automated probe analyzer (Model 692, Herisau, Switzerland), while soil color was visually assessed. Moisture content was determined by oven-drying samples at 105 °C for 12 h. Concentrations of nitrate (NO_3^-) and phosphate (PO_4^{3-}) were analyzed using ASTM (2010) methods. Heavy metals including Pb, Ni, Cd, and Cr were quantified using X-ray fluorescence (XRF) spectrometry. All measurements were performed in triplicate, and results were compared with FMEnv/NUPRC regulatory limits to evaluate contamination levels.

2.4 Determination of Total Petroleum Hydrocarbons (TPHs)

Total petroleum hydrocarbons (TPH) were quantified using Gas Chromatography–Flame Ionization Detection (GC-FID) following the method of Chikere et al. (2019). One gram of soil was extracted with 20 mL n-pentane, ultrasonicated for 15 minutes, and allowed to separate at 30 °C for 60 minutes. The organic phase was analyzed using an HP 7673 GC-FID system with injector and detector temperatures set at 250 °C and 320 °C, respectively. The oven was programmed from 40 °C (3 min) to 300 °C, using helium as the carrier gas. Data were processed with Agilent ChemStation software, and TPH concentrations were determined from peak area integrations between n-C₆ and n-C₃₅.

2.5 Microbiological Analysis

2.5.1 Enumeration of Microbial Populations

Microbial populations were quantified using the serial dilution and spread plate technique.

- i. Total Heterotrophic Bacteria (THB) were enumerated on Nutrient Agar.
- ii. Hydrocarbon-Utilizing Bacteria (HUB) were enumerated on Bushnell–Haas Agar supplemented with crude oil as the sole carbon source.
- iii. Hydrocarbon-Utilizing Fungi (HUF) were cultured on Sabouraud Dextrose Agar (SDA) amended with chloramphenicol (50 mg/L) and crude oil vapor. Plates were incubated at 30 ± 2 °C for 24–72 h for bacteria and 28 °C for 5–7 days for fungi. Counts were expressed as colony-forming units per gram (cfu/g) of dry soil.

2.6 Isolation and Purification of Microbial Isolates

Distinct colonies were sub-cultured onto fresh agar plates to obtain pure cultures. Pure bacterial isolates were maintained on Nutrient Agar slants, while fungal isolates were preserved on Potato Dextrose Agar (PDA) at 4 °C.

2.7 Identification of Microbial Isolates

Bacterial isolates were characterized using Gram staining, motility, and biochemical tests (catalase, citrate utilization, indole, methyl red, Voges–Proskauer, and starch hydrolysis) following the Bergey's Manual of Determinative Bacteriology (Holt et al., 1994).

Fungal isolates were identified based on macroscopic and microscopic morphology using Lactophenol Cotton Blue staining, with reference to Barnett and Hunter (1998).

2.8 Statistical Analysis

All experiments were conducted in triplicate, and results were expressed as mean $\pm$ standard deviation (SD). Statistical differences between polluted and control sites were determined using Student's t-test at a 95% confidence level ($p < 0.05$). Relationships between soil chemical parameters and microbial counts were analysed using Excel sheet.

3.0 Results

3.1 Total Petroleum Hydrocarbons and Elemental Composition

The concentration of total petroleum hydrocarbons (TPH) in the polluted soil (78.3 mg kg⁻¹) was markedly higher than that of the control soil (10.8 mg kg⁻¹), exceeding the permissible limit of 50 mg kg⁻¹ set by the Nigerian Upstream Petroleum Regulatory Commission (NUPRC). This confirms the presence of hydrocarbon contamination in the Gokana sampling site.

Elemental analysis revealed distinct variations between polluted and control soils (Table 1). Polluted soil exhibited elevated concentrations of sulfur (6.36 mg kg⁻¹ vs 0.20 mg kg⁻¹), chlorine (0.85 mg kg⁻¹ vs 0.30 mg kg⁻¹), nickel (0.061 mg kg⁻¹ vs 0.043 mg kg⁻¹), copper (0.04 mg kg⁻¹ vs 0.03 mg kg⁻¹), and silver (0.0105 mg kg⁻¹ vs 0.0064 mg kg⁻¹) relative to the control. In contrast, essential elements such as phosphorus (0.068 mg kg⁻¹ vs 0.253 mg kg⁻¹) and silicon (33.1 mg kg⁻¹ vs 43.4 mg kg⁻¹) were reduced in polluted soil. The increase in metallic and halogen elements suggests anthropogenic influence from hydrocarbon deposition, while nutrient depletion indicates impaired soil fertility.

Table 1: Physicochemical parameters of soil sample

Parameters	Polluted	Control	Fmnev/Nuprc Limit
Aluminum-Al	6.78	8.90	
Silicon-Si	33.1	43.4	
Phosphorus-P	0.0680	0.2527	
Sulphur-S	6.36	0.20	
Chlorine-CL	0.85	0.30	
Potassium-K	0.712	0.395	
Calcium-Ca	0.526	0.124	
Titanium-Ti	1.29	1.49	
Vanadium-V	0.0123	0.0173	50.0000
Chromium-Cr	0.02	0.02	100.00
Manganese-Mn	0.0161	0.0172	850.0000
Iron-Fe	4.0	2.4	4.7
Nickel-Ni	0.061	0.043	35.000
Copper-Cu	0.04	0.03	36.00
Zinc-Zn	0.024	0.016	140.000
Arsenic-As	0.0013	0	
Bromine-Br	0.00639	0.00103	
Silver-Ag	0.0105	0.0064	
Cadmium-Cd	0.0069	0.0041	0.8000
Tin-Sn	0.020	0.012	
Lead-Pb	0.0027	0.0028	85.0000
Barium-Ba	<0.0001	0	200
Mercury-Hg	<0.0002	0	0.3
Total petroleum hydrocarbon-TPH	78.3	10.8	50.0

3.2. Microbial Growth and Enumeration

The total heterotrophic bacterial (THB), hydrocarbon-utilizing bacterial (HUB), and hydrocarbon-utilizing fungal (HUF) counts varied between polluted and control samples (Figure 1).

- THB: 5.0×10^3 cfu g⁻¹ in both polluted and control soils.
- HUB: 5.2×10^3 cfu g⁻¹ in polluted soil compared to 4.0×10^3 cfu g⁻¹ in control soil.
- HUF: 3.4×10^3 cfu g⁻¹ in polluted soil and 3.3×10^3 cfu g⁻¹ in control soil.

The higher bacterial counts in polluted soil indicate microbial adaptation to hydrocarbon stress, with bacteria displaying greater resilience and utilization capacity than fungi

3.3 Biochemical Characterization of Bacterial Isolates

Ten bacterial isolates (LL1–LL10) were obtained from the polluted soil and identified using standard biochemical assays. The isolates belonged to the genera *Proteus*, *Klebsiella*, *Enterobacter*, *Citrobacter*, *Micrococcus*, *Pseudomonas*, and *Bacillus*. Among these, *Pseudomonas* sp. and *Bacillus* sp. were the most frequently detected, both known for hydrocarbon degradation and biosurfactant production. The predominance of Gram-negative rods such as *Proteus*, *Klebsiella*, and *Enterobacter* further supports active participation in organic pollutant degradation.

Table 2: Biochemical test and identification of test microbes

Isolate ID	catalase	citrate	glucose	lactose	indole	MR	VP	motility	starch	TSI	H2S	Gram stain	Possible genera	Oxidase
LL1	+	+	+	-	+	-	-	-	+	A B G	+	- rod	<i>Proteus sp.</i>	-
LL2	+	+	+	+	-	-	-	+	+	A B G	-	- rod	<i>Klebsiella sp.</i>	-
LL3	+	+	+	+	-	+	+	+	-	A B G	-	- rod	<i>Enterobacter sp.</i>	-
LL4	+	+	+	-	-	-	-	+	-	A A G	+	- rod	<i>Citrobacter sp.</i>	-
LL5	+	+	+	-	-	-	-	-	-	B B -	-	+cocci	<i>Micrococcus sp.</i>	+
LL6	+	+	+	-	-	-	-	-	-	B B -	-	- rod	<i>Pseudomonas sp.</i>	-
LL7	+	+	+	-	-	-	-	+	-	B B -	-	- rod	<i>Pseudomonas sp.</i>	-
LL8	+	+	+	-	-	-	-	+	+	A B -	-	+ rod	<i>Bacillus sp.</i>	-
LL9	+	+	+	-	-	+	-	-	-	B B -	-	+cocci		-
LL10	+	+	+	-	-	-	+	+	+	A B -	-	+ rod	<i>Bacillus sp.</i>	-

3.4 Morphological and Microscopic Identification of Fungal Isolates

Three fungal isolates were recovered and identified as *Fusarium sp.*, *Candida sp.*, and *Penicillium sp.* based on macroscopic colony morphology and microscopic characteristics. *Fusarium sp.* formed fast-growing white cottony colonies with septate hyphae and macroconidia; *Candida sp.* produced cream, smooth colonies with oval budding cells; and *Penicillium sp.* exhibited green mycelia with brush-like conidiophores. The presence of these genera indicates fungal tolerance to petroleum hydrocarbons and potential for hydrocarbon degradation.

Table 4.4: Fungal Description

Isolate code	Macroscopy	Microscopy	Probable genera
LL1	White non-cracked reverse, fast-growing white colony with a cotton surface	Presence of septate hyphae, thin hyaline, and presence of macroconidia	<i>Fusarium sp.</i>
LL2	Cream, raised, opaque, smooth and shiny, circular, entire 0.4cm	Oval purple	<i>Candida sp.</i>
LL3	Domed-shaped rough dry mycelia..slow growing, cracked reverse...green mycelia with white margin	Presence of spore globose shaped, brush-like conidiophores bearing conidia Thin hyphae	<i>Penicillium sp.</i>

4.0 Discussion

The elevated concentration of total petroleum hydrocarbons (TPH) observed in the polluted soil (78.3 mg kg⁻¹) compared to the control (10.8 mg kg⁻¹) clearly demonstrates petroleum hydrocarbon contamination in the Gokana soil, exceeding the permissible limit of 50 mg kg⁻¹ set by the Nigerian Upstream Petroleum Regulatory Commission (NUPRC). This result agrees with previous findings by Chikere et al. (2019) who reported similar exceedances in oil-impacted soils of the Niger Delta. The differences in elemental composition between polluted and control soils, as presented in Table 1, reflect the direct influence of hydrocarbon deposition and associated heavy metals. The increase in sulfur (6.36 mg kg⁻¹), chlorine (0.85 mg kg⁻¹), and nickel (0.061 mg kg⁻¹) in polluted soil is consistent with Akhigbe et al. (2019), who found elevated Fe, Ni, and Cu concentrations in hydrocarbon-impacted soils. Such increases arise from crude-oil fractions and combustion residues that alter soil chemistry and pH, leading to heavy-metal accumulation and potential toxicity to sensitive microbial species. Conversely, the decline in phosphorus (0.068 mg kg⁻¹ versus 0.253 mg kg⁻¹ in the control) indicates nutrient depletion, a condition reported by Okafor et al. (2025) in Eleme, where crude-oil contamination reduced available macronutrients required for microbial metabolism. Figure 1 further supports this, showing that microbial populations, particularly hydrocarbon-utilizing bacteria, were more abundant in the polluted soil (5.3 × 10³ cfu g⁻¹) than in the control (4.0 × 10³ cfu g⁻¹), reflecting microbial adaptation to hydrocarbon stress. This agrees with Chikere et al. (2020), who noted enrichment of hydrocarbon-degrading populations in long-term contaminated soils. The

dominance of *Pseudomonas*, *Bacillus*, *Proteus*, *Klebsiella*, and *Enterobacter* observed in Table 4.3 corresponds with previous studies by Unimke et al. (2025), which identified these genera as efficient hydrocarbon degraders due to their ability to produce biosurfactants and hydrocarbon-oxidizing enzymes such as monooxygenases and dehydrogenases. The presence of *Pseudomonas* and *Bacillus* in both polluted and control soils suggests their dual ecological role as opportunistic saprophytes and active degraders in oil-polluted environments. Fungal isolates identified microscopically (*Fusarium sp.*, *Candida sp.*, and *Penicillium sp.*) showed morphological features typical of hydrocarbon-tolerant fungi, with *Fusarium sp.* displaying abundant septate hyphae and macroconidia (Fig. 2). These fungi have been previously reported by Okpokwasili et al. (2013) in crude-oil-polluted soils for their ability to secrete extracellular oxidative enzymes, including laccases and peroxidases, which degrade aromatic hydrocarbons. Although bacterial counts were generally higher than fungal counts, the coexistence of both microbial groups suggests complementary degradation pathways, where fungi assist in breaking down complex hydrocarbons while bacteria mineralize simpler fractions. This observation is supported by Rezaei & Moghimi (2024), who demonstrated that bacterial–fungal consortia accelerate TPH degradation more effectively than single species. The combined results from Tables 1 and 4.3 and Figs. 1–2 indicate that hydrocarbon contamination significantly modifies soil chemistry and microbial community structure, favoring hydrocarbonoclastic species capable of surviving under toxic conditions. The persistence of these native microorganisms highlights the soil’s potential for natural attenuation and suggests that targeted bio-stimulation or bioaugmentation could enhance remediation of petroleum-contaminated soils in the Niger Delta region.

Conclusion

This study found that petroleum hydrocarbon contamination significantly alters the physicochemical characteristics and microbial community structure of wetland soils in K-Dere, Rivers State. The polluted soils exhibited elevated concentrations of total petroleum hydrocarbons (78.3 mg/kg) and toxic elements: sulfur, chlorine, and nickel, which exceeded recommended environmental limits. These chemical imbalances corresponded with distinct differences in microbial composition, notably the enrichment of hydrocarbon-tolerant bacteria (*Proteus*, *Klebsiella*, *Enterobacter*, *Citrobacter*, *Pseudomonas*, and *Bacillus*) and resilient fungi (*Fusarium*, *Candida*, and *Penicillium*). The observed microbial adaptations suggest an active ecological response to pollution. This highlights the potential of native microbes as indicators of contamination and agents of natural attenuation, especially for sustainable remediation strategies in the Niger Delta.

Declarations

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Declaration of Funding Sources

Non

Funding

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Conflict of interest statement

None

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Figures

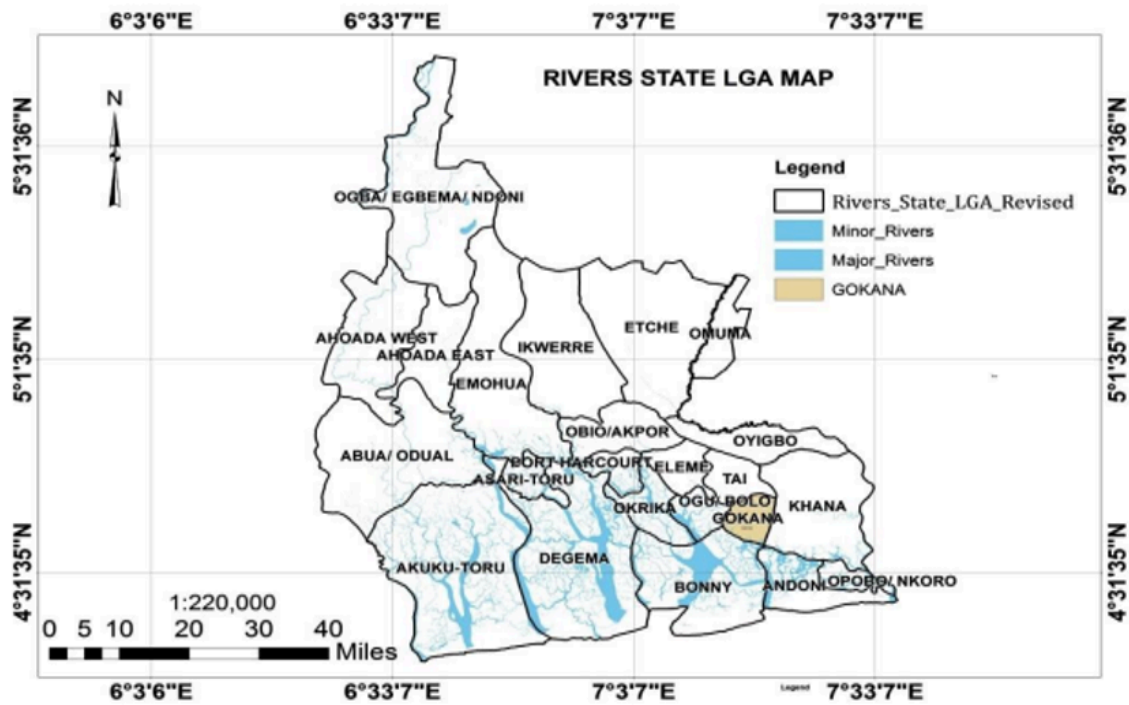


Figure 1

Rivers state map showing Gokana LGA

Source: (Emmanuel, 2022)

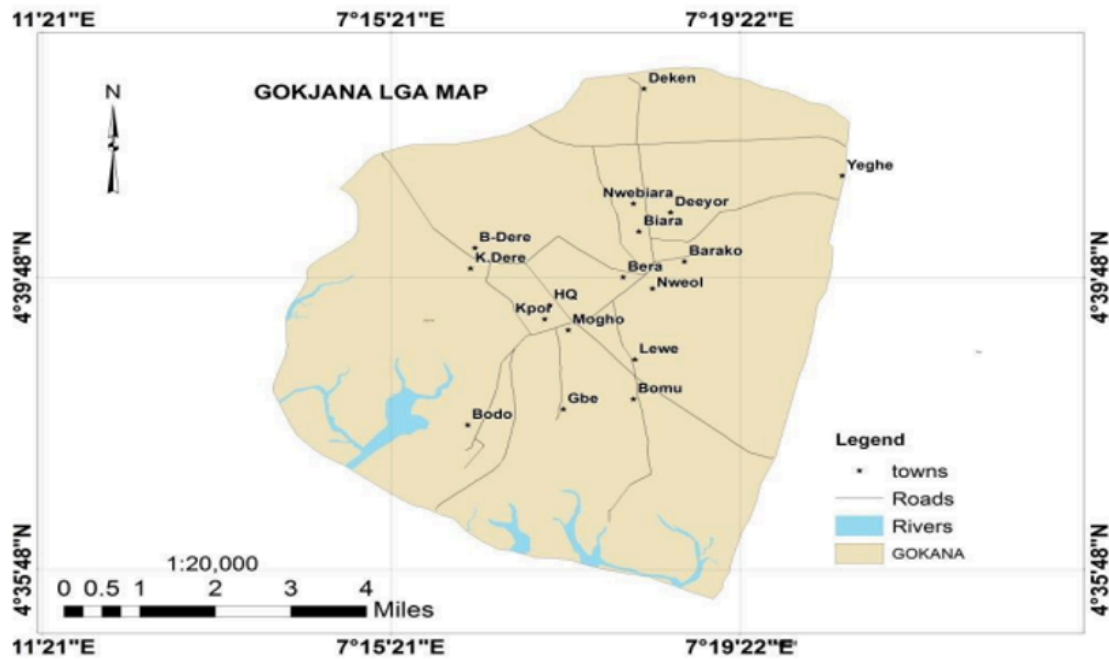


Figure 2

Map of Gokana LGA adopted

Source: (Emmanuel, 2022)