

## Microbial Assessment of Piggery Effluents in Receiving Soil and Surface Water Environments in Rivers State, Nigeria

Ephraim-George, T. D. <sup>1\*</sup>, Douglas, S. I. <sup>2</sup>, Boisa N. <sup>1</sup>, Bull O. S. <sup>1</sup>, and P. M. Amaibi <sup>1</sup>

<sup>1</sup>Department of Chemistry, Faculty of Science, Rivers State University, Nkpolu-Oroworukwo, Port Harcourt, Rivers State, Nigeria. <sup>2</sup>Department of Microbiology, Faculty of Science, Rivers State University, Nkpolu-Oroworukwo, Port Harcourt, Rivers State, Nigeria.

**\*Corresponding Author:** tokoni.ephraim-george@ust.edu.ng

### ABSTRACT

This study assessed the microbiological characteristics of piggery effluents and receiving soil and surface water across five pig farms (Kono, NNPC Akpajo, Obeakpu, Omagwa, and Rivers State University) in Rivers State, Nigeria. Effluent, surface-water, and soil samples were collected aseptically and analyzed for total heterotrophic bacteria (THB), total coliform (TC), faecal coliform (FC), and fungal counts using standard spread plate techniques. Bacterial and fungal isolates were identified using morphological and biochemical characteristics. High microbial counts were observed across all samples, with THB counts ranging from  $5.0 \times 10^7$  to  $2.9 \times 10^8$  CFU/mL in effluents,  $1.6 \times 10^7$  to  $2.8 \times 10^8$  CFU/mL in surface-water, and  $1.5 \times 10^7$  to  $1.3 \times 10^8$  CFU/g in soil. Faecal coliform counts ranged from  $3.0 \times 10^3$  to  $3.2 \times 10^4$  CFU/mL for effluent, for surface water it ranged from  $6.0 \times 10^3$  to  $4.8 \times 10^4$  CFU/mL and for soil  $4.0 \times 10^3$  to  $2.3 \times 10^4$  CFU/g. These values exceeded the permissible limits for agro-industry effluent discharge into surface water of <400 MPN/100 mL for total coliforms and <200 MPN/100 mL for faecal coliforms. The dominant bacterial isolates include: *Bacillus* sp., *E. coli*, *Pseudomonas* sp., *Klebsiella* sp., *Serratia* sp., *Staphylococcus* sp., *Proteus* sp., *Enterobacter* sp., and *Micrococcus* sp. Fungal species identified includes: *Aspergillus* sp., *Candida* sp., *Mucor* sp., *Penicillium* sp., *Rhodotorula* sp., *Fusarium* sp. and *Alternaria* sp., with *Aspergillus* species being the most dominant. Isolate distribution varied across piggeries, reflecting farm-specific effluent characteristics. The presence of these potentially pathogenic and opportunistic microorganisms highlights the public health and environmental risks associated with untreated piggery effluents. Proper effluent treatment and management procedures are recommended to mitigate contamination receiving water bodies.

**Keywords:** Piggery Effluent, Soil, Faecal Coliform, Public Health, Water Environment, Fungi, Bacteria.

### Introduction

Improper disposal of effluents from piggeries (pig farms) can directly or indirectly affect the receiving environment by altering its microbiological composition, which can lead to serious air and waterborne diseases through inhalation of aerosols contaminated with microorganisms or consumption of contaminated water (Matjuda & Aiyegoro, 2016). Pigs are one of the most prevalent livestock species produced, and their gut microbiomes are remarkably comparable to those of humans, particularly because pigs share over 96% of the functional metabolic pathways found in the human gut microbiome (Han et al., 2023).

It has been documented that contaminants such as biological, chemical and mechanical (dust) are emitted during large-scale pig farming.

The contamination of the environment by microorganisms from pig effluents could pose serious environmental hazards to humans and animals around those environments (Trawińska et al., 2015).

Increasing demand for pork has contributed to the expansion of the pig-farm to meet this demand, which in turn has resulted in the production of higher volumes of effluents (Aleruchi et al., 2025). In addition to nutrients and organic matter, pig farm effluents may contain potential pathogens, heavy metals, and other contaminants that could alter soil and water ecosystems if the effluents are not properly treated before discharge (Nkoa, 2014). Moreover, the use of untreated pig effluents in agriculture could alter soil properties, including physical and chemical characteristics, thereby influencing the biogeochemical cycle, soil fertility, and overall soil health (Wang et al., 2014).

Additionally, microbial contaminants from pigs and pig effluents could directly or indirectly pose serious hazards to farmers (occupational health hazard) and people who live in the neighbourhood.

The population of faecal bacteria in farmers could shift as a result of aerosolisation, which occurs when pig faecal microorganisms move from the upper respiratory system into the gastrointestinal system (Moor et al., 2021). Many factors, including dietary habits and the environment, influence the composition of gut microbes, which in turn affects physical health in a variety of ways (Shang et al., 2022; Martel et al., 2022; Yang et al., 2022). Pathogens and indicator organisms such as *Salmonella* spp., *Escherichia coli*, *Clostridium perfringens*, and *Erysipelothrix rhusiopathiae* have been isolated from the effluent generated from a small-scale swine farm (Cordero et al., 2010). Due to the hazards associated with pig effluents, it is necessary to ensure proper treatment before they are discharged into the environment. Pig farmers traditionally manage effluents by flushing them into anaerobic lagoons, with the effluent later sprayed onto agricultural fields (Lei et al., 2013). However, continuous effluent application can result in excessive nitrogen and phosphorus accumulation in soils, leading to nutrient imbalances or contamination of surface and groundwater (Lei et al., 2013). These reports necessitates the need for proper effluent handling and monitoring. However reports on the microbiological characteristics of pig-farm effluents and receiving environment in Rivers State is scarce. Thus, evaluating effluents from different pig-farms in Rivers State would be important for assessing their microbiological impact on the receiving environment. This study therefore assessed microbial populations in pig-farm effluents and receiving soil and surface-water across five pig-farms in Rivers State, Nigeria, and identified the dominant bacterial and fungal isolates using conventional techniques.

## Materials and Methods

### Study Area

The samples for this study were collected from Piggeries in five (5) different Local Government Areas (LGAs) of Rivers State which constituted the study area. The LGAs are; Eleme LGA, Ikwerre LGA, Port Harcourt LGA, Khana LGA, and Oyigbo LGA. The Piggeries in these LGAs were located in NNPC Akpajo, Omagwa, Rivers State University, Kono, and Obeakpu respectively. The five (5) sampling locations

and their corresponding geographical coordinates are; NNPC Estate Akpajo, Eleme LGA (4.808889°N; 7.095556°E); Omagwa, Ikwerre LGA (4.985278°N; 6.918056°E); Rivers State University farm, Port Harcourt LGA (4.803333°N; 6.976944°E); Kono, Khana LGA (4.604167°N; 7.498056°E); and Obeakpu (Enyi Farms), Oyigbo LGA (4.855556°N; 7.307778°E).

### Sample Collection

Piggery effluent, surface-water and soil samples from five pig farms were collected aseptically into sterile containers for surface water and effluent. Soil samples were collected using hand soil auger at a depth of 0 – 15 cm into sterile zip-lock bags and labeled properly. The soil samples were collected from four different points, approximately 1 m from the discharge point, and bulked to obtain a homogeneous composite sample. Effluent samples were collected directly from the discharge point into sterile bottles, while surface-water samples were collected from two points: the point of discharge into the receiving water body and approximately 1 m downstream of the discharge point. The surface-water samples were mixed to form a composite sample. All samples were properly labelled and transported immediately to the Microbiology Laboratory, Rivers State University, in ice-packed coolers for analysis.

### Enumeration and Isolation of Total Heterotrophic Bacteria

Using a sterile pipette, 1mL of the effluent and water samples were transferred aseptically into 9 mL of sterile normal saline. Ten-fold serial dilution was done, as described by Prescott et al. (2005). One milliliter of the dilution was then transferred into another test tube containing 9mL of normal saline, the serial dilution continued to  $10^{-5}$ . The soil samples were processed by adding 1g into 9 mL of sterile normal saline and diluted to  $10^{-5}$ . Spread plate technique was used, were 0.1mL of the diluted ( $10^{-4}$  to  $10^{-5}$ ) samples were inoculated on Nutrient agar plates, in duplicate and spread with flame sterilized hockey stick. The plates were incubated at 37°C for 24 hours. Discrete colonies that emerge from the plates after 24 hours were counted and the mean counts calculated as colony forming unit per milliliter (CFU/mL/g). Repeated sub-culturing was done to get pure culture that was stored on agar slant and refrigerated until it is required for further analyses (Iyerite et al., 2021).

### Total Coliform Bacteria Enumeration

Total coliform counts were achieved by inoculating 0.1mL aliquot from the  $10^{-3}$  to  $10^{-4}$  dilutions on MacConkey agar plates in duplicates, spread with sterile hockey stick. The plates were incubated at 37°C for 24 hours, the colonies were counted, the mean values calculated expressed as CFU/mL/g (Prescott et al., 2005).

### **Faecal Coliform Bacteria Enumeration**

Faecal coliform bacteria were enumerated using Eosin methylene blue agar as described by Prescott et al. (2005). Using a sterile pipette, 0.1 mL from  $10^{-1}$  to  $10^{-2}$  from the various dilution were inoculated in duplicate on the Eosin Methylene Blue (EMB) agar plates. Spread with sterile hockey stick and the plates incubated at a temperature of 44.5°C for 24 to 48 hours. After incubation, counts were taken and mean counts expressed in CFU/mL or CFU/g.

### **Enumeration of Fungi in the Samples**

This was carried out using Sabouraud Dextrose agar (SDA) supplemented with 0.05% (v/v) tetracycline to inhibit the growth of bacteria in the media. Using the spread plate technique, 0.1 mL from the various  $10^{-2}$  to  $10^{-3}$  dilutions were plated on the surface of the SDA plates, in duplicate and spread using sterile hockey stick. The inoculated plates were incubated at 25°C for 3 to 5 days. Colonies that develop were counted and the mean counts were expressed as CFU/mL or CFU/g (Prescott et al., 2005).

### **Identification of Isolates**

The representative colonies from the various media and samples were sub-cultured on freshly prepared nutrient and Sabouraud dextrose agar for bacteria and fungi, respectively using sterile wire loops. The isolates were carefully purified through streaking method until they were void of contaminants. They were further identified via morphology, biochemical and molecular methods. The morphological method was based on their appearance on respective culture media and microscopic examination. Biochemical tests employed were as follows: Tests for motility, citrate consumption, Oxidase, Catalase, Indole, Methyl Red, Voges-Proskauer, and Sugar fermentation. For the identification of bacteria, Bergey's Manual of Determinative Bacteriology was used (Holt et al., 1994).

The fungal isolates were identified using microscopic analysis and cultural morphology. The wet mount

technique as outlined by Cheesebrough (2006) was followed. Using a sterile inoculating loop, a tiny piece/ spores of the isolate was selected and put on a pristine, grease-free microscope slide. After adding and smearing a drop of lactophenol blue, it was covered with a cover slip and viewed under the microscope with the x10 and x40 objective lenses to see further distinguishing characteristics.

### **Statistical Analysis**

The obtained bacterial and fungal mean counts were presented in Microsoft Excel. The percentages of occurrence of the bacterial isolates were also determined using the statistical tool.

### **Results**

The results of the microbial counts for the surface water are shown in Table 1. Total heterotrophic bacterial counts (THBC) for the various pig farms ranged  $1.6 \times 10^7$  to  $2.8 \times 10^8$  CFU/mL, with the Omagwa farm having the highest and Kono farm having the least counts. The total coliform counts (TCC) ranged from  $2.6 \times 10^6$  to  $1.5 \times 10^7$  CFU/mL. Faecal coliform counts (FCC) for the surface-water ranged from  $6.0 \times 10^3$  to  $4.8 \times 10^4$  CFU/mL, with Omagwa having the highest and Kono having the least.

It was observed that Omagwa farm had the highest THBC, TCC and FCC for surface-water when compared to the other farms. While Kono had the least counts for THBC, TCC, and FCC. The Total Fungal counts (TFC) ranged from  $1.1 \times 10^4$  to  $9.0 \times 10^4$  CFU/mL. With NNPC Akpajo having the highest counts while Obeakpu farm had the least fungal counts.

Results of the microbial counts in the effluent samples of the various farms are displayed in Table 2. THB counts ranged from  $5.0 \times 10^7$  to  $2.9 \times 10^8$  CFU/mL. The TCC ranged from  $1.4 \times 10^6$  to  $1.8 \times 10^7$  CFU/mL. FC counts ranged from  $3.0 \times 10^3$  to  $3.2 \times 10^4$  CFU/mL with Obeakpu having the least and Omagwa farm with a count of  $3.2 \times 10^4$  CFU/mL as the highest. The fungal counts ranged from  $1.3 \times 10^4$  to  $9.5 \times 10^4$  CFU/mL. NNPC Akpajo had the highest counts of  $9.5 \times 10^4$  CFU/mL, while Obeakpu farm had the least counts of  $1.3 \times 10^4$  CFU/mL.

**Table 1: Microbial Counts for Surface-water Samples (CFU/mL)**

| Location    | Microbial Counts for Surface-water Samples (CFU/mL) |                   |                   |                   |
|-------------|-----------------------------------------------------|-------------------|-------------------|-------------------|
|             | Total Heterotrophic Bacteria                        | Total Coliform    | Faecal Coliform   | Total Fungi       |
| NNPC Akpajo | $1.8 \times 10^8$                                   | $8.1 \times 10^6$ | $3.4 \times 10^4$ | $9.0 \times 10^4$ |
| Omagwa      | $2.8 \times 10^8$                                   | $1.5 \times 10^7$ | $4.8 \times 10^4$ | $6.5 \times 10^4$ |
| RSU         | $1.9 \times 10^8$                                   | $8.9 \times 10^6$ | $3.5 \times 10^4$ | $1.9 \times 10^4$ |
| Kono        | $1.6 \times 10^7$                                   | $2.6 \times 10^6$ | $6.0 \times 10^3$ | $7.0 \times 10^4$ |
| Obeakpu     | $3.1 \times 10^7$                                   | $3.8 \times 10^6$ | $9.5 \times 10^3$ | $1.1 \times 10^4$ |

**Table 2: Microbial Counts for Piggery Effluent Samples**

| Location    | Microbial Counts for Piggery Effluent Samples (CFU/mL) |                   |                   |                   |
|-------------|--------------------------------------------------------|-------------------|-------------------|-------------------|
|             | Total Heterotrophic Bacteria                           | Total Coliform    | Faecal Coliform   | Total Fungi       |
| NNPC Akpajo | $2.9 \times 10^8$                                      | $1.8 \times 10^7$ | $3.8 \times 10^3$ | $9.5 \times 10^4$ |
| Omagwa      | $2.7 \times 10^8$                                      | $1.5 \times 10^7$ | $3.2 \times 10^4$ | $3.5 \times 10^4$ |
| RSU         | $2.2 \times 10^8$                                      | $6.0 \times 10^6$ | $2.9 \times 10^4$ | $5.5 \times 10^4$ |
| Kono        | $9.9 \times 10^7$                                      | $3.7 \times 10^6$ | $2.6 \times 10^4$ | $1.5 \times 10^4$ |
| Obeakpu     | $5.0 \times 10^7$                                      | $1.4 \times 10^6$ | $3.0 \times 10^3$ | $1.3 \times 10^4$ |

The results of the microbial populations in the soil samples are shown in Table 3 with the THB counts ranging from  $1.5 \times 10^7$  to  $1.3 \times 10^8$  CFU/g, with Obeakpu having the least and RSU having the highest. For TCC, ranged from  $2.0 \times 10^6$  to  $6.2 \times 10^6$  CFU/g.

RSU farm has the highest counts of  $6.2 \times 10^6$  CFU/g. FC counts ranged from  $4.0 \times 10^3$  to  $2.3 \times 10^4$  CFU/g. Soil fungal counts, ranged from  $2.5 \times 10^4$  to  $1.5 \times 10^5$  CFU/g, with Obeakpu farm having the least and Kono farm having the highest counts.

**Table 3: Microbial Counts for Soil Samples**

| Location    | Microbial Counts for Piggery Effluent Samples (CFU/g) |                   |                   |                   |
|-------------|-------------------------------------------------------|-------------------|-------------------|-------------------|
|             | Total Heterotrophic Bacteria                          | Total Coliform    | Faecal Coliform   | Total Fungi       |
| NNPC Akpajo | $1.2 \times 10^8$                                     | $2.5 \times 10^6$ | $5.0 \times 10^3$ | $5.5 \times 10^4$ |
| Omagwa      | $6.8 \times 10^7$                                     | $2.2 \times 10^6$ | $7.0 \times 10^3$ | $3.0 \times 10^4$ |
| RSU         | $1.3 \times 10^8$                                     | $6.2 \times 10^6$ | $2.3 \times 10^4$ | $6.0 \times 10^4$ |
| Kono        | $1.6 \times 10^7$                                     | $2.0 \times 10^6$ | $6.0 \times 10^3$ | $1.5 \times 10^5$ |
| Obeakpu     | $1.5 \times 10^7$                                     | $3.1 \times 10^6$ | $4.0 \times 10^3$ | $2.5 \times 10^4$ |

The biochemical and morphological characteristics of the isolates revealed that the following bacterial isolates were recovered from the samples from the various farms: *Bacillus* sp, *Serratia* sp, *Pseudomonas* sp, *Micrococcus* sp, *E. coli*, *Klebsiella* sp, *Proteus* sp, *Enterobacter* sp, and *Staphylococcus* sp.

Furthermore, the fungal isolates associated with the various samples were *Aspergillus niger*, *Rhizopus stolonifer*, *Aspergillus flavus*, *Mucor* sp, *Fusarium* sp., *Candida* sp, *Penicillium* sp, *Rhodotorula* sp, *Aspergillus terreus*, *Aspergillus fumigatus* and *Alternaria* sp.

The results of the distribution of the bacterial and fungal isolates of the surface water, effluent and soil samples are presented in Tables 4a to 4c, respectively.

Results of the percentage occurrence of the bacterial and fungal isolates of the water, effluent and soil samples are presented in Figures 1 to 6, respectively. Results showed that *E. coli* with 27.5% was the most isolated bacteria, followed by *Bacillus* sp., 20.9% while *Enterobacter* sp. with 2.2% was the least isolated from the water samples (Figure 1).

Table 4a: Microbial Distribution across the Surface Water samples

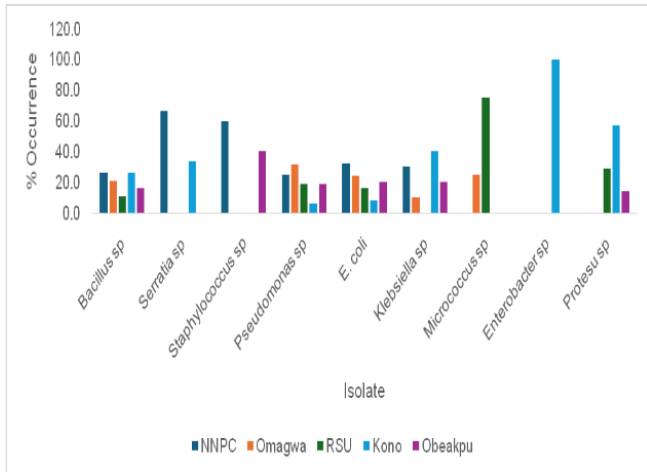
| Location    | Bacteria                                                                                                                                                       | Fungi                                           |
|-------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------|
| NNPC estate | <i>Bacillus</i> sp, <i>Serratia</i> sp., <i>Staphylococcus</i> sp, <i>Pseudomonas</i> sp, <i>Klebsiella</i> sp., <i>E. coli</i> .                              | <i>Aspergillus niger</i> , <i>Candida</i> sp    |
| Omagwa      | <i>Bacillus</i> sp, <i>Pseudomonas</i> sp, <i>Micrococcus</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i>                                              | <i>Aspergillus niger</i> , <i>Alternaria</i> sp |
| RSU         | <i>Proteus</i> sp., <i>Pseudomonas</i> sp, <i>Bacillus</i> sp., <i>Micrococcus</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i>                         | <i>Penicillium</i> sp, <i>A.niger</i>           |
| Kono        | <i>Serratia</i> sp., <i>Pseudomonas</i> sp, <i>Proteus</i> sp., <i>Bacillus</i> sp., <i>Enterobacter</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i> . | <i>Candida</i> sp, <i>Aspergillus niger</i>     |
| Obeakpu     | <i>Bacillus</i> sp, <i>Pseudomonas</i> sp, <i>Staphylococcus</i> sp, <i>Proteus</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i> .                      | <i>Rhodotorula</i> sp, <i>Candida</i> sp        |

Table 4b: Microbial Distribution across the Effluent samples

| Location    | Bacteria                                                                                                                                                                                | Fungi                                                              |
|-------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------|
| NNPC estate | <i>Bacillus</i> sp, <i>Serratia</i> sp., <i>Pseudomonas</i> sp, <i>Staphylococcus</i> sp, <i>Proteus</i> sp., <i>Enterobacter</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i> . | <i>Aspergillus niger</i> , <i>Candida</i> sp, <i>Alternaria</i> sp |
| Omagwa      | <i>Bacillus</i> sp, <i>Serratia</i> sp., <i>Staphylococcus</i> sp, <i>Pseudomonas</i> sp, <i>Bacillus</i> sp., <i>Micrococcus</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i>   | <i>A. niger</i> , <i>A. fumigatus</i>                              |
| RSU         | <i>Bacillus</i> sp, <i>Serratia</i> sp., <i>Staphylococcus</i> sp, <i>Pseudomonas</i> sp, <i>Escherichia coli</i>                                                                       | <i>A. terreus</i> , <i>A. niger</i> , <i>Penicillium</i> sp        |
| Kono        | <i>Bacillus</i> sp, <i>Pseudomonas</i> sp, <i>Micrococcus</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i> .                                                                     | <i>Candida</i> sp.                                                 |
| Obeakpu     | <i>Staphylococcus</i> sp, <i>Bacillus</i> sp., <i>Pseudomonas</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i> .                                                                 | <i>Alternaria</i> sp, <i>Penicillium</i> sp                        |

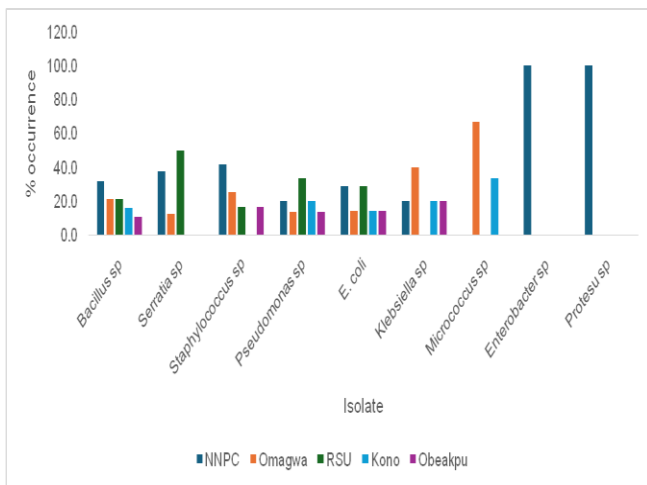
Table 4c: Microbial Distribution across the Soil Samples

| Location    | Bacteria                                                                                                                                    | Fungi                                                           |
|-------------|---------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------|
| NNPC estate | <i>Bacillus</i> sp, <i>Serratia</i> sp., <i>Staphylococcus</i> sp, <i>Pseudomonas</i> sp., <i>Escherichia coli</i> .                        | <i>Fusarium</i> sp, <i>Mucor</i> sp, <i>Aspergillus niger</i> , |
| Omagwa      | <i>Pseudomonas</i> sp, <i>Bacillus</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i>                                                  | <i>Fusarium</i> sp, <i>Candida</i> sp                           |
| RSU         | <i>Bacillus</i> sp, <i>Proteus</i> sp., <i>Micrococcus</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i>                              | <i>A. niger</i> , <i>A. flavus</i>                              |
| Kono        | <i>Bacillus</i> sp, <i>Pseudomonas</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i> .                                                | <i>Candida</i> sp, <i>Alternaria</i> sp, <i>Penicillium</i> sp  |
| Obeakpu     | <i>Bacillus</i> sp, <i>Staphylococcus</i> sp, <i>Bacillus</i> sp., <i>Pseudomonas</i> sp., <i>Klebsiella</i> sp., <i>Escherichia coli</i> . | <i>A. niger</i> , <i>Penicillium</i> sp.                        |



**Fig. 1: Percentage occurrence of bacterial isolates in the Surface Water samples**

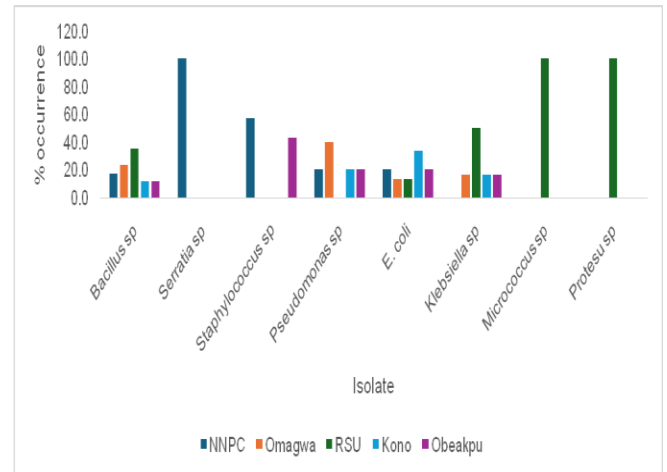
In the effluent samples, results showed that *Bacillus* sp with 23.5% was the most isolated followed by *Pseudomonas* sp (18.5%) while the least was *Proteus* sp, with 2.5% (Figure 2).



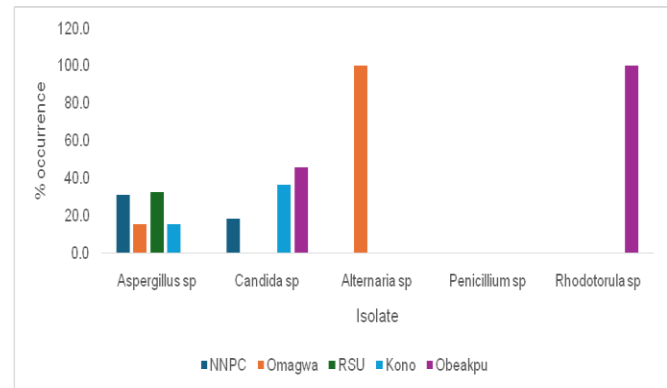
**Fig. 2: Percentage Occurrence of the bacterial Isolates across the Effluent samples**

On the other hand, *Bacillus* sp (28.3%) was the most dominant bacterial isolates in the soil samples followed by *E. coli* (25.0%), while *Proteus* and *Serratia* sp were the least with 1.7% (Figure 3).

The fungal isolates identified includes *Aspergillus* species, with 41.9%, were the most dominant, followed by *Candida* sp (35.5%), while *Penicillium* and *Rhodotorula* species were the least is 6.5% (Figure 4).

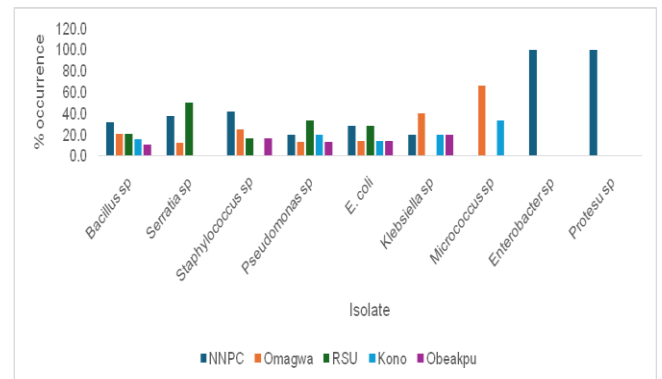


**Fig. 3: Percentage occurrence of the bacterial isolates across the soil samples**



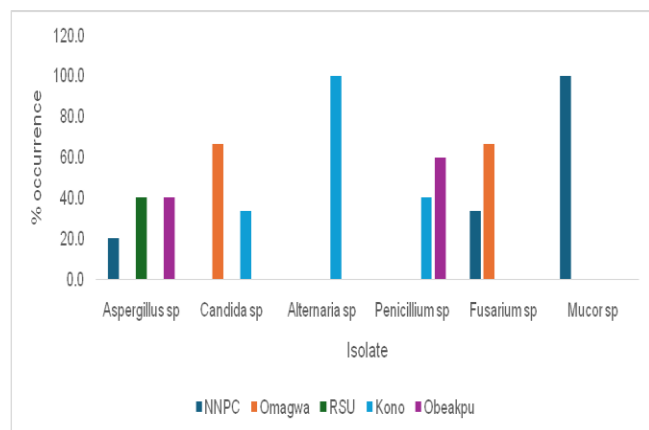
**Fig. 4: Percentage occurrence of fungal isolates in the Surface Water samples**

In Figure 5, *Aspergillus* sp (36.8%) were the most dominant, while *Alternaria* sp. (15.8%) were the least identified.



**Fig. 5: Percentage Occurrence of the fungal Isolates across the Effluent samples**

Moreover, *Aspergillus* sp. (41.7%) was the most dominant in the soil samples (Figure 6). While *Fusarium* and *Mucor* species were the least dominant (12.5%).



**Fig. 6: Percentage occurrence of the fungal isolates across the soil samples**

## Discussion

This present study assessed the microbial populations and microbial isolate identities of pig-farm effluents and their surrounding surface-water and soil environments at five different locations in Rivers State. High microbial loads were observed across the sampled matrices. In surface water, the highest THB count was recorded at Omagwa ( $1.4 \times 10^8$  CFU/mL), followed by Rivers State University ( $9.6 \times 10^7$  CFU/mL) and NNPC Akpajo ( $9.2 \times 10^7$  CFU/mL).

The study showed that the microbiological quality of the receiving environment, varied from one location to another. For instance, the surface water around NNPC Akpajo pig-farm showed the highest total heterotrophic bacterial load ( $2.9 \times 10^8$  CFU/mL) followed by the Omagwa ( $2.7 \times 10^8$  CFU/mL) and RSU ( $2.2 \times 10^8$  CFU/mL). Highest faecal coliform counts of  $4.8 \times 10^4$  CFU/mL were observed in the surface-water from the Omagwa pig-farm.

According to FEPA (Federal Environmental Protection Agency, 1991), the maximum permissible limits for total coliforms discharged from agro-industry effluent (such as pig-farm, slaughter and food processing activities) into surface water should be less than 400 MPN/100mL and faecal coliform measured as *E. coli* is strictly less than 200MPN/100mL.

Values obtained in this study, exceeded the permissible limits for total and faecal coliforms, which calls for concerns due to the possible risk. The total heterotrophic bacterial counts in the present study for both effluent, surface water, and soil environments were lower than the values of  $1.33 \times 10^{10}$  CFU/mL reported by (Matjuda & Aiyegoro, 2016). Cook *et al.*, (2010) reported higher counts within the range of  $2.58 \times 10^{10}$  to  $1.49 \times 10^{11}$  CFU/mL in a farrowing facility at a pig-farm.

Additionally, most of the microbial counts recorded in the soil and surface water were higher than those recorded in the effluent, which could imply that effluents discharged into these environments influenced the microbial loads recorded. Soil acts as reservoir, accumulates over time. This corroborates previous studies, which have opined that effluents from livestock, including pig farms, contained microorganisms amongst other substances, and their discharge into another environment could alter the microbiological state of that environment (Aleruchi *et al.*, 2025; Cao *et al.*, 2021; Han *et al.*, 2023).

The bacterial isolates characterized in the present study showed that they belonged to 9 different genera such as *Bacillus* sp, *Serratia* sp, *Pseudomonas* sp, *Micrococcus* sp, *E. coli*, *Klebsiella* sp, *Proteus* sp, *Enterobacter* sp, and *Staphylococcus* sp while six genera of fungi such as *Aspergillus* sp, *Mucor* sp, *Candida* sp, *Penicillium* sp, *Rhodotorula* sp and *Alternaria* sp were isolated in this study. Bacterial and fungal isolates in the respective samples varied across locations, with some locations showing the presence of isolates not found in the other areas. This disparity in bacterial and fungal profiles may be due to the composition of the effluents, which varies with farm practices, population of the pigs, waste-handling practices, environmental conditions, and other farm specific factors (Monger *et al.*, 2021).

Also, previous studies have also established that bacterial and fungal communities across livestock manures, including pig-farms, exhibit farm-specific microbial patterns in the effluent, which could drive location-specific contamination (Marin *et al.*, 2024; Nalini, 2019; Wan *et al.*, 2021).

The presence of these bacterial and fungal pathogens in soils and surface-water samples in the pig-farms is attributed to the high loads of faecal matter in the Pig-Farm seepage and could serve as an indicator of possible microbiological pollution and which could

have an effect on both the soil ecological balance and aquatic life (Matjuda & Aiyegoro, 2016). Similar bacterial and fungal isolates have been reported from soil, water, and effluents in previous study (Cao et al., 2021; Han et al., 2023; Monger et al., 2021; Nalini, 2019; Wan et al., 2021). The public health implications of these bacterial isolates range from complications in gastroenteritis and urinary tract infections (*E. coli*, *Klebsiella*, *Proteus*, sp) to respiratory and wound infections (*Pseudomonas*, *Serratia*, and *Staphylococcus* sp) (Sarnino et al., 2025). While the fungal isolate, such as *Aspergillus* sp have been implicated in aspergillosis, and may have environmental and occupational-health importance, even though the identification of these microbes does not prove that they are pathogenic. Other fungal isolates including *Aspergillus* sp in the present study, has potentials to produce mycotoxins that could become allergens (Rodrigues & Teiga-teixeira, 2025).

## Conclusion

This study has shown that the effluents from pig-farms and the receiving environments were associated with elevated microbial loads and the presence of faecal indicator and potential opportunistic microorganisms in receiving soil and surface-water. The high microbial loads including, the presence of potentially pathogenic bacteria such as *E. coli*, *Pseudomonas* sp, *Klebsiella* sp, *Proteus* sp, etc and fungi, such as *Aspergillus* sp, *Candida* sp, etc across the sampled sites highlights the risks of improper effluent treatment and disposal, which could pose great public health danger to individuals within such a vicinity. The variations in microbial distributions are a reflection of different management practices. Thus, urgent implementation of effective waste treatment practices and regulatory monitoring is essential to safeguard environmental and human health in these environments.

## References

- Aleruchi, O., Nengi-Benwari, A. O., & Okparaekke, C. C. (2025). Impact of Different Concentrations of Swine Wastewater on Bacterial Population and Physicochemical Properties of Soil. *International Journal of Microbiology and Applied Sciences*, 4(1), 73–81.
- Cao, S. T., Tran, H. P., Thi, H., Le, T., Phung, H., Bui, K., Thi, G., & Nguyen, H. (2021). Impacts of effluent from different livestock farm types (pig, cow, and poultry) on surrounding water quality: a comprehensive assessment using individual parameter evaluation method and water quality indices. *Environmental Science and Pollution Research*, 1–14.
- Cheesbrough M. District Laboratory Practice in Tropical Countries, 2nd ed., Part 2, Cambridge University Press, 2006.
- Cook, K., Rothrock Jr., M. J., Lonanh, N., Sorrell, J. K. & Loughring, J. H. (2010). Spatial and temporal changes in the microbial community in an anaerobic swine waste treatment. *Anaerobe*, 16(2), 74-82.
- Cordero, A., García, M., Herradora, M., Ramírez, G., & Martínez, R. (2010). Bacteriological characterisation of wastewater samples obtained from a primary treatment system on a small scale swine farm. *Bioresource Technology*, 101(9), 2938-2944.
- Federal Environmental Protection Agency (FEPA). National Interim Guidelines and Standards for Environmental Pollution in Nigeria, 1991.
- Han, J., Li, M., Li, X., Liu, C., Li, X. L., Wang, K., Qiao, R., & Yang, F. (2023). Effects of microbes in pig farms on occupational exposed persons and the environment. *AMB Express*, 13, 136.
- Holt, J. G., Krieg, N. R., Sneath, P. H. A., Staley, J. T., & Williams, S. T. (1994). *Bergey's Manual of Determinative Bacteriology* (9th edition). Baltimore: Williams & Wilkins
- Iyerite, F. V., Obire, O. and Douglas, S. I. (2021) Effect of Anthropenic Activities on the Microbiological Quantity of Lobia Creek in Southern Ijaw of Bayelsa State, Nigeria. *Acta Scientific Microbiology*. 4(8), 95 - 103.
- Lei, X. G., Ku, P. K., Miller, E. R. & Yokoyama, T. K. (2013). Supplementing corn-soybean meal diets with microbial phytase linearly improves phytate phosphorus utilization by weanling pigs. *Journal of Animal Science*, 71, 3359–3367.
- Marin, C., Rodríguez, J. C., Ventero, M., Pérez-gracia, M. T., Vega, S., Tort-miró, C., Marco-fuertes, A., Lorenzo-rebenaque, L., & Montoro-dasi, L. (2024). Swine farm environmental microbiome: exploring

microbial ecology and functionality across farms with high and low sanitary status. *Front. Vet. Sci*, 1–13.

Martel, J., Chang, S. H., Ko, Y. F., Hwang, T. L., Young, J. D. & Ojcius, D. M. (2022). Gut barrier disruption and chronic disease. *Trends Endocrinol Metab*, 33(4), 247–265.

Matjuda, D. S., & Aiyegoro, O. A. (2016). Soil bacteriological pollution in pig farm vicinity: Assessment of bacterial dynamics and detection of antimicrobial resistance gene. *African Journal of Microbiology Research*, 10(38), 1625–1636.

Monger, X. C., Gilbert, A., Saucier, L., & Vincent, A. T. (2021). Antibiotic Resistance: From Pig to Meat. *Antibiotics*, 10(1209), 1–20.

Moor, J., Wüthrich, T., Aebi, S., Mostaccia, N., Overesch, G., Oppliger, A., & Hilty, M. (2021). Influence of pig farming on human Gut Microbiota: role of airborne microbial communities. *Gut Microbes*, 13(1), 1927634.

Nkoa, R. (2014). Agricultural benefits and environmental risks of soil fertilization with anaerobic digestates: a review. *Agronomy for Sustainable Development*, 34(2), 473–492.

Prescott LM, Harley JP, Klein DA. Microbiology, 6th ed., McGraw-Hill Publishing Company, UK, 2005.

Rodrigues, M. A., & Teiga-teixeira, P. (2025). Occurrence of Moulds and Yeasts in the Slaughterhouse: The Underestimated Role of Fungi in Meat Safety and Occupational Health. *Foods*, 14(1320), 1–23.

Sarnino, N., Basak, S., Collineau, L., & Merle, R. (2025). Pathways of Escherichia coli transfer from animal manure: risks and mitigation in agriculture. *Frontiers in Public Health*, 13(6), 1–10.

Shang, P., Dong, S., Han, Y., Bo, S., Ye, Y., Duan, M., & Chamba, Y. (2022). Environmental exposure to swine farms reshapes human gut microbiota. *Chemosphere*, 307, 135558.

Trawińska, B., Józwik, M., Nowakowicz-Dębek, B., Chmielowiec-Korzeniowska, A., Lechowski, J., Tymczyna, L., & Pyrz, M. (2015). Effect of pig farm on microbial contamination of soil. *Annals of Animal Science*, 15(1), 165–175.

Wan, J., Wang, X., Yang, T., Wei, Z., & Banerjee, S. (2021). Livestock Manure Type Affects Microbial Community Composition and Assembly During Composting. *Frontiers in Microbiology*, 12, 621126.

Wang, Q., Guo, M., Yates, S. R., & Shelton, D. R. (2014). Degradation kinetics of swines manure-borne tetracyclines in soil. *Environmental Science & Technology*, 48(2), 1679–1686.

Yang, H., Wu, J., Huang, X., Zhou, Y., Zhang, Y., Liu, M., Liu, Q., Ke, S., He, M., Fu, H., Fang, S., Xiong, X., Jiang, H., Chen, Z., Wu, Z., Gong, H., Tong, X., Huang, Y., Ma, J., Gao, J., Charlier, C., Coppieters, W., Shagam, L., Zhang, Z., Ai, H., Yang, B., Georges, M., Chen, C. & Huang, L. (2022). ABO genotype alters the gut microbiota by regulating GalNAc levels in pigs. *Nature*, 606(7913), 358–367.