Microbial and Physicochemical Evaluation of a Communal Piggery Wastewater and Its Bioremediation Using Autochthonous Bacterial Isolates

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Abstract: Piggery activities necessitate large amount of wastewater generation with high concentrations of organic matter and pathogens. This study characterized the microbial and physicochemical properties of discharged piggery wastewater and its bioremediation potential. Wastewater samples collected weekly from May to July, 2024 at piggery farm, Federal University of Technology Akure, were subjected to microbiological succession analysis and cultivated using pour plate technique. Isolates identified colonially by conventional methods were subjected to 16S rRNA sequencing and phylogeny. Samples' physicochemical parameters were assessed before and after treatment with dominant isolates using standard methods. Bioremediation was done in four batches; individual isolates, consortium and control. Bacterial growth reduced from 8.36×10^{-1} cfu/ml (day 1) to 1.29×10^{-5} cfu/ml (day 5) at 10^3 serial dilutions. Fungal growth was recorded only on day 1 (1.3×10^{-5} sfu/ml) at 10^3 serial dilutions, with no growth detected thereafter. At day 5, most dominant bacterial species were identified as *Proteus mirabilis* OLU (PX611816) and *Pseudomonas aeruginosa* OLU (PX614431). Samples bioremediated with *P. mirabilis* OLU and *P. aeruginosa* OLU consortium increased pH from 7.15±0.03 to 7.52±0.9, dissolved oxygen level from 4.61±0.02 to 5.81±0.01 mg/ml, and decreased biochemical oxygen demand from 206.42±0.05 to 121.83±0.33 mg/ml and chemical oxygen demand values from 386.94±0.04 to 192.02±0.03 mg/ml. Findings from the study revealed that autochthonous bacterial isolates from piggery wastewater samples has potential to remediate samples with poor microbiological and physicochemical qualities. This suggests a stakeholders' call for upscale of bioremediation strategies in wastewater treatment.

Key word: 16S rRNA gene sequencing, bioremediation, microbial composition, physicochemical properties, piggery wastewater

INTRODUCTION

A piggery is a facility where pigs are kept, or a place where pigs are reared. The piggery at Federal University of Technology, Akure (FUTA), like many others, generates significant amounts of wastewater rich in organic matter, nutrients, and potential pathogens. This wastewater, if left untreated, can lead to environmental degradation and pose risks to public health (Aleruchi *et al*., 2025). Piggery wastewater contains high concentrations of contaminants, such as suspended solids, organic matter, and nutrients, which can significantly weaken the quality of environments where they are discharged (Fischer *et al*., 2018). Traditionally, in developing countries, pig farms manage wastewater by flushing it directly into drainages which lead to water bodies. However, continuous effluent application can upshot in extreme nitrogen and phosphorus build-up in soils, leading to nutrient imbalances or contamination of surface and groundwater (Lei *et al.,* 2013). Though, pig slurry is known as a valued fertilizer that enhances crop efficiency and reduces the dependence on mineral fertilizers (Khaleel *et al.,* 2018), its inappropriate application can unfavourably affect the soil's physical, chemical, and biological properties. Of note are the biological impacts, as piggery wastewater contains a varied microbiota originating from the gastrointestinal tract of pigs. These microorganisms, including potential pathogens such as *Salmonella* spp., *Escherichia coli, Giardia lamblia* and *Cryptosporidium parvum* are discharged into the environment through faeces (McConnell *et al.,* 2012). Close contact with poorly treated wastewater was associated with increased risk of diarrheal disease in adults (Pham-Duc *et al.,* 2020).

Bioremediation is the use of living organisms, primarily microorganisms to degrade, detoxify, or remove pollutants from contaminated environments. Bioremediation offers several advantages over conventional physicochemical treatment methods. It is

often more moneymaking, environmentally approachable, and can be applied *in situ*, mitigating the need for extensive infrastructure (Atojunere and Ogedengbe, 2019). Microorganisms used in bioremediation can adapt to varying environmental conditions and can potentially degrade a wide range of pollutants simultaneously. The process of microbial succession in bioremediation typically begins with the colonization of easily degradable substrates by fast-growing, generalist microorganisms. These initial colonizers, often referred to as r-strategists, have high growth rates but may lack the specialized metabolic capabilities to break down more complex pollutants (Fierer *et al.,* 2010). As these readily available nutrients are depleted, the community composition shifts towards more specialized organisms, known as K-strategists, which can metabolize the remaining, often more recalcitrant, compounds (Dini-Andreote *et al.,* 2014). The study provided valuable insights into the composition of microbial communities and physicochemical properties of piggery wastewater in FUTA. Then, the potential of employing indigenous organisms for the remediation of these wastewaters.

MATERIALS AND METHODS

Study Area: The study area is at the Piggery Unit, Animal Research Farm, Department of Animal Production and Health, Federal University of Technology Akure, Ondo State, Nigeria. The geographical location of the FUTA Farm is approximately 7.25 °N latitude and 5.12 °E longitude (Ojo and Adebayo, 2020). The piggery unit in the research farm practices the intensive system of pig rearing. They have diverse kinds of pigs; such as boar, sow, litter, grower etc. The practice of supplying water to the piggery house for wallowing, drinking, and cleaning is manual (Olanrewaju and Olowoyeye, 2018). The Piggery is located on Malu road, Northgate area, Federal University of Technology, Akure, Ondo State.

Collection of Piggery Wastewater Samples: Piggery wastewater samples were collected from FUTA, Malu road Northgate, Akure using sterile 200 ml sample bottles for microbiological analysis according to standard methods described by Cheesbrough (2006). Two litres of wastewater samples were collected in clean plastic containers for physicochemical analysis. Collection of wastewater samples was carried out weekly from May to July, 2024. Samples were collected with the bottles facing upward and underneath, towards the flow of water to avoid contamination (Cheesbrough, 2006). Collection was carried out in the morning hours when slaughtering and washings are done, then a large quantity of wastewater is generated. Samples were transported to the laboratory within 2 to 4 hours of collection for analysis.

Microbiological Analysis of Piggery Wastewater Samples: The microbiological assay of collected wastewater samples was determined by pour plate technique described by Olusola-Makinde *et al.* (2022). Serial dilution was carried out to 10^4, then, 0.1 ml aliquot was assayed using nutrient agar (NA) and potato dextrose agar (PDA) as growth media. The NA and PDA inoculated plates were incubated for growth at 37°C for 24 hours and 25°C for 48 hours respectively. Numbers of colonies on the plates were counted. The negative control of each batch of the test medium was confirmed by incubating one uninoculated plate along with the inoculated plates.

Microbial Succession Analysis of Piggery Wastewater Samples: The piggery wastewater samples were stored in a refrigerator at 4 °C for a period of 5 days. Each day, from day 1 to day 5, an aliquot was analysed for microbial load. For each day's sample, a serial dilution was carried out to assess the microbial load. One milliliter of the piggery wastewater sample was added to the 9 mL of sterile distilled water, resulting in a 10^{-1} dilution up to a 10^{-5} dilution. The aliquot was incubated for growth as described in microbiological analysis section.

Distinct colonies at day 5 were selected based on morphological differences as dominant organisms. These selected colonies were streaked on fresh NA plates using the quadrant streak method, which helps to obtain pure cultures (Cheesbrough, 2006). The plates were incubated at 28 °C for 24 hours. Pure isolates were stored at 4 °C in refrigerator at for further analysis.

Phenotypic and Molecular Identification of Dominant Bacterial Isolates from Piggery Wastewater Samples

Phenotypic Identification of isolates: Pure culture from wastewater samples at day 5 were sub-cultured on sterile nutrient agar and subjected to morphological and biochemical tests as described by Cheesbrough (2006). Bergey's manual of systematic bacteriology was employed to suggest the phenotypic characteristics of the bacterial isolates. The identified bacteria were maintained on nutrient agar respectively, slanted at 4 °C in refrigerator for subsequent use.

Molecular Identification of isolates: A polymerase chain reaction-based characterization of the isolates was carried out. Genomic DNA of the isolates was extracted and purified according to Gurakan *et al.* (2008). DNA concentration was estimated as described by Olusola-Makinde *et al.* (2018). The 16S rRNA gene of the isolates was amplified as described by Sambrook *et al*. (2001) using the primer pair 27F-5′-AGAGT TTGATCCTGGCTCAG-3′ and 1492R 5′-GGTTACC TTGTTACGACTT-3′.

The 16S rRNA gene amplified products were purified with Exo sap and subjected to DNA Sanger sequencing. The sequence data were analysed using the ABI Sequencing Analysis software (version 5.2), and were subjected to the basic local alignment search tool on the NCBI Genbank website (www.ncbi.nlm.nih.gov). Nucleotide sequences generated from each amplified 16S rRNA gene were submitted to the Genbank Nucleotide Sequence Database (Olusola-Makinde *et al.,* 2018).

Determination of Physicochemical Parameters of Piggery Wastewater Samples: Physicochemical parameters of wastewater samples such as pH, temperature, dissolved oxygen, chemical oxygen demand, biochemical oxygen demand, turbidity, total suspended solids and cyanide level were determined using the methods of Ademoroti (1996) and APHA (APHA, 2021).

Degradation of Piggery Wastewater Samples

Inoculum Preparation: Bacterial cultures containing dominant bacterial isolates were inoculated in separate 25 ml of nutrient broth bottles and incubated with shaking overnight at 35 °C. Culture purity was ascertained by streaking on sterile nutrient agar plates and incubated with shaking at 35 °C overnight, again. These mother cultures were used for sub-culturing and batch degradation. One hundred microlitres of the mother culture was inoculated into 100 ml of nutrient media broth of pH 7.0 and incubated with shaking at 35 °C for a period of 16-18 hours and 200 rpm. Actively growing culture of each isolate was washed with sterile deionized water thrice and centrifuged at 12,000 pm for 10 minutes to get wet pellet of each isolate. The pellet was resuspended in sterile deionized water till turbidity reaches McFarland 0.5 standard using absorbance reading of 0.10 at 600 nm (Wayne, 2009).

Bioremediation of piggery farm wastewater samples using dominant bacterial isolates: One milliliter of standardized re-suspended pellets containing four batches of the bacterial isolates were inoculated in 50 ml of freshly collected piggery wastewater sample. The four batches comprise of Batch A: Piggery wastewater sample + *Pseudomonas aeruginosa*, Batch B: Piggery wastewater sample + *Proteus mirabilis*, Batch C: Piggery wastewater sample + *Proteus mirabilis* and *Pseudomonas aeruginosa* consortium, and Batch D: Piggery wastewater sample without inoculation (positive control). The set-up was incubated with shaking at 35 °C for 52 hours.

After incubation, the physicochemical parameters including temperature, chemical oxygen demand (COD), pH, biochemical oxygen demand (BOD), total suspended solids (TSS), total dissolved solids (TDS), salinity and turbidity were estimated and compared to the readings before inoculation according to the procedure discussed in standard methods (APHA, 2021).

Statistical Analysis: Data obtained in this study were subjected to one-way analysis of variance (ANOVA), and differences between means were compared by Duncan's New Multiple Range Test (DNMRT) at 95% confidence interval using Statistical Package for Social Sciences (SPSS) version 26.0. Data obtained from the study was also subjected to XY grouped data table on Graph pad prism version 8.0.5.

RESULTS

Table 1 showed the microbial load of the piggery wastewater samples. Bacterial growth on was highest compared to fungal growth. At dilution factor of 10^{-3}, mean bacterial colony counts were 2.24×10^{-2} cfu/ml and reduced to 2.0 cfu/ml at 10^{-5} dilution factor. The mean fungal counts were 1.3×10^{-1} sfu/ml at dilution 10^{-3}, with no growth observed at 10^{-5} dilution factor (Table 1).

Tables 2 – 4 showed the morphological and biochemical characteristics of bacterial and fungal isolates from piggery wastewater samples. The tentative bacterial isolates from the Onyearugbulem abattoir wastewater samples include *Alcaligenes faecalis, Streptococcus pyogenes*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella pneumoniae*, *Proteus mirabilis*, *Salmonella typhi*, *Bacillus subtilis* and *Serratia marcescens*, *Pseudomonas aeruginosa*. Fungal isolates from the wastewater samples include *Rhizopus stolonifer, Aspergillus fumigatus, Penicillium chrysogenum, Fusarium oxysporium* and *Saccharomyces cerevisiae.*

Table 5 showed the microbial succession (cfu/ml) of the piggery wastewater samples. On Nutrient Agar (NA), which supports bacterial growth, there was a continuous increase in colony forming units (CFU) from day 1 (2.24×10^{-2} cfu/ml) to day 4 (4.2×10^{-2} cfu/ml), followed by a decline on day 5 (3.4×10^{-2} cfu/ml) at dilution 10^{-3}. On potato dextrose agar (PDA), which supports fungal growth, growth was observed only at day 1 (1.3×10^{-1} sfu/ml) at dilution 10^{-3}, with no growth observed in subsequent days (Table 1).

By day 5, two bacterial isolates that became dominant from piggery wastewater samples were presumptively identified as *Proteus mirabilis* and *Pseudomonas aeruginosa* (Table 3). Molecular identity of the isolates after sequencing its DNA was *Proteus mirabilis* OLU and *Pseudomonas aeruginosa* OLU. The accession numbers from submission to GenBank are PX611816 and PX614431 for *Proteus mirabilis* OLU and *Pseudomonas aeruginosa* OLU respectively. *Proteus mirabilis* OLU has 97.67% similarities with *Proteus mirabilis* GD22 (KF928778.1) and *Proteus mirabilis* S74-3-3 (CP073245.1) (Plate 1 and Figure 1). *Pseudomonas aeruginosa* OLU has 100% similarities with *Pseudomonas aeruginosa* EH8 (GU339238.1) and *Pseudomonas aeruginosa* PpB3 (PV274339) (Plate 1 and Figures 1 and 2).

Table 6 revealed physicochemical characteristics of wastewater samples generated from piggery wastewater samples. It was slightly neutral in pH (7.15± 0.03), high biochemical oxygen demand (206.42 ± 0.05 mg/ml) and chemical oxygen demand values (386.94 ± 0.04 mg/ml), low dissolved oxygen level (4.61 ± 0.02 mg/ml) and high turbidity (170 ± 0.11 NTU). The total suspended solid was 0.07± 0.05 g/l and total dissolved solid was 0.23 ± 0.01 g/l.

Physicochemical characteristics of the piggery wastewater samples was altered after treatment with the dominant bacterial isolates; *Proteus mirabilis* and *Pseudomonas aeruginosa*. The batches containing *Proteus mirabilis* and *Pseudomonas aeruginosa* individually recorded increase in pH (7.53± 0.11 and 7.67± 0.2) and dissolved oxygen

level (4.71 ± 0.01 mg/ml and 4.77 ± 0.2 mg/ml), decreased biochemical oxygen demand (118.4± 0.04 mg/ml and 113.9± 0.01 mg/ml) and chemical oxygen demand values (189.06 ± 0.07 mg/ml and 187.02± 0.04 mg/ml).

In comparison with untreated wastewater sample, the batch containing consortium of *Proteus mirabilis* and *Pseudomonas aeruginosa* revealed increase in pH (7.52 ± 0.9) and dissolved oxygen level (5.81 ± 0.01 mg/ml), decreased biochemical oxygen demand (121.83 ± 0.33 mg/ml) and chemical oxygen demand values (192.02 ± 0.03 mg/ml).

Table 1: Mean microbial load of piggery wastewater samples

Organism	Dilution 10^{-3}	Dilution 10^{-4}	Dilution 10^{-5}
Bacteria (cfu/ml)	2.24×10^{-2}	2.5×10^{-1}	2.0
Fungi (sfu/ml)	1.3×10^{-1}	1.0	0

Table 2: Morphological characteristics of bacterial isolates from piggery wastewater samples

Isolates	Form	Elevation	Margin	Surface	Colour
1	Circular	Raised	Entire	Smooth	Red
2	Irregular	Flat	Rhizoid	Rough	White
3	Circular	Flat	Lobate	Rough	Creamy
4	Circular	Convex	Entire	Smooth	Mucoid white
5	Circular	Flat	Entire	Rough	Creamy
6	Circular	Raised	Entire	Smooth	Pale yellow
7	Circular	Flat	Entire	Smooth	Creamy
8	Circular	Flat	Entire	Smooth	Creamy
9	Irregular	Convex	Entire	Smooth	Milky
10	Circular	Flat	Curled	Smooth	Creamy
11	Oval	Umbonate	Entire	Smooth	Green

Table 3: Biochemical characterization of probable bacterial isolates from piggery wastewater samples

Isolates	Gram reaction	Methyl Red	Voges-Proskauer	Catalase	Lactose	Mannitol	Sucrose	Glucose	Galactose	Citrate	Urease	Gas production	Probable Organism
1	-	-	+	+	+	+	+	+	-	+	+	+	*Serratia marcescens*
2	+	-	+	+	+	+	+	+	+	+	-	-	*Bacillus subtilis*
3	-	+	-	+	-	+	+	+	-	-	-	-	*Salmonella typhi*
4	-	+	-	+	+	+	+	+	+	+		+	*Klebsiella pneumoniae*
5	-	+	-	+	+	+	+	+	+	-	-	+	*Escherichia coli*
6	+	+	+	+	+	+	+	+	+	+	+	-	*Staphylococcus aureus*
7	+	-	-	-	+	-	+	+	+	-	-	+	*Streptococcus pneumoniae*
8	+	-	-	+	+	-	+	+	+	-	-	+	*Streptococcus pyogenes*
9	-	-	+	+	-	-	-	-	-	-	-	-	*Alcaligenes faecalis*
10	-	+	-	+	+	+	+	+	+	+	+	+	*Proteus mirabilis*
11	-	-	-	+	+	+	+	+	+	+	+	+	*Pseudomonas aeruginosa*

Keys: + = Positive, - = Negative

Table 4: Characteristics of fungal isolates from piggery wastewater samples

Cultural characteristics	Microscopic observation	Tentative identity
Blue-green with a narrow white border. Powdery surface.	Conidiophores are short, smooth walled and have conical shaped terminal vesicles. Septate hyphae	*Aspergillus fumigatus*
Flat, smooth, moist, glistering cream	Blastoconidia are unicellular, globuse and ellipsoid to elongate in shape	*Saccharomyces cerevisiae*
Blue-green growth	Septate mycelium bearing single conidiophores which are branched near the apex ending in phialides that carry conidia	*Penicillium chrysogenum*
Cotton-like mycelia at 24 hours that turned dirty with development of black spores on mycelium	Non-septate hyphae thin sporangiophore with a sporangium in umbrella-like form	*Rhizopus* spp.
White cotton-like mycelia spreads round whole plate	Mycelium extensive in a cottonwool-like form. It had phialides that is bearing a bean pod-like microconidia borne singly or in chain	*Fusarium oxysporium*

Table 5: Microbial succession of the piggery wastewater samples

Day	Medium	Dilution 10^{-3}	Dilution 10^{-4}	Dilution 10^{-5}
1	Bacteria (cfu/ml)	2.24×10^{-2}	2.5×10^{-1}	2.0
	Fungi (sfu/ml)	1.3×10^{-1}	1.0	0
2	Bacteria (cfu/ml)	2.8×10^{-2}	3×10^{-1}	3.0
	Fungi (sfu/ml)	0	0	0
3	Bacteria (cfu/ml)	3.5×10^{-2}	4×10^{-1}	4.0
	Fungi (sfu/ml)	0	0	0
4	Bacteria (cfu/ml)	4.2×10^{-2}	3.3×10^{-1}	5.0
	Fungi (sfu/ml)	0	0	0
5	Bacteria (cfu/ml)	3.4×10^{-2}	4.6×10^{-1}	2.0
	Fungi (sfu/ml)	0	0	0

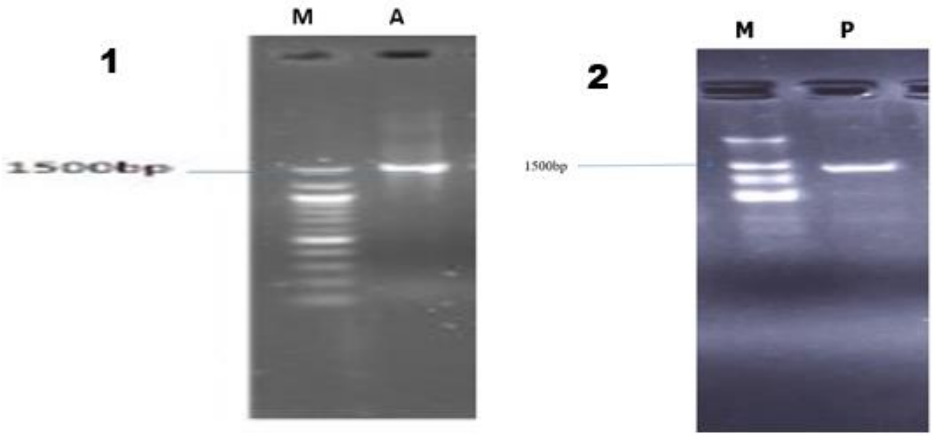

Plate 1: Agarose gel electrophoresis of 16S rRNA amplicons of dominant bacterial isolates from piggery wastewater samples
Keys: Lane M: 100 bp DNA ladder; Lane A: *Proteus mirabilis*, Lane P: *Pseudomonas aeruginosa*; 1500 bp = amplicon size

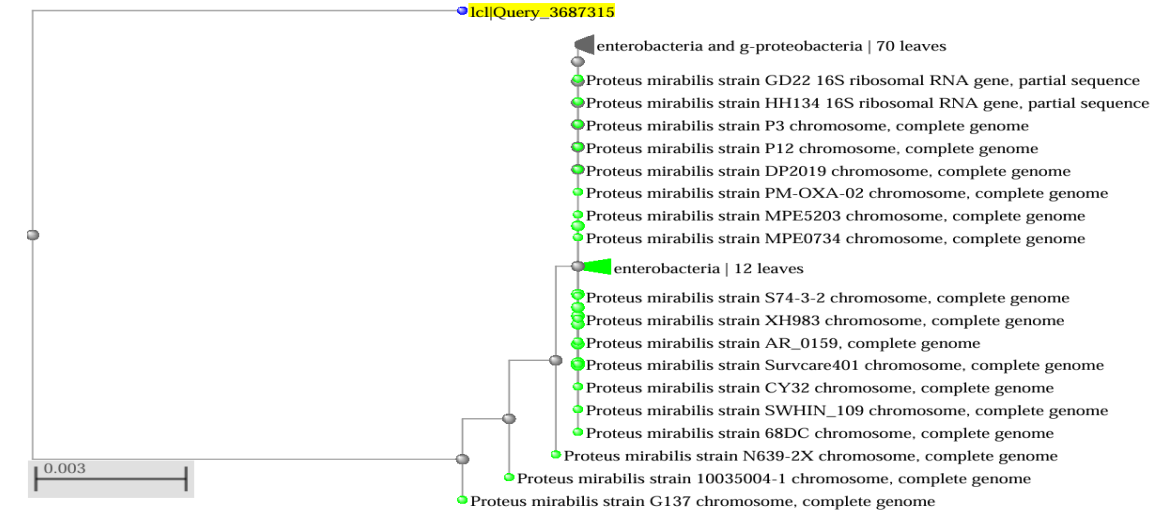

Figure 1: Unrooted phylogenetic tree construct showing the relationship of *Proteus mirabilis* OLU with other strains of *Pseudomonas* sp.
The scale bar indicates the number of substitutions per site

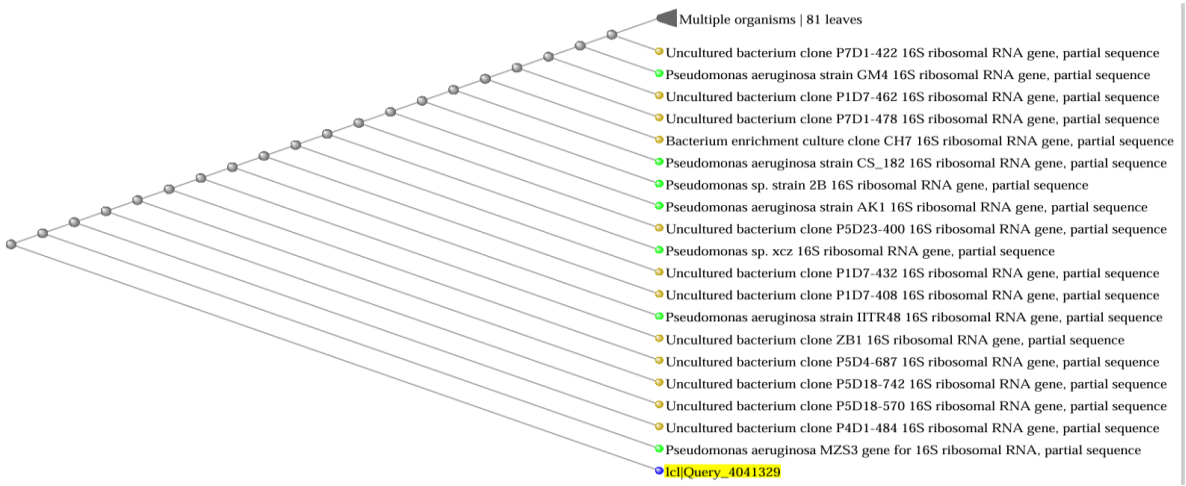

Figure 2: Unrooted phylogenetic tree construct showing the relationship of *Pseudomonas aeruginosa* OLU with other strains of *Pseudomonas* sp. The scale bar indicates the number of substitutions per site

Table 6: Physicochemical properties of piggery wastewater samples before and after treatment

S/N	Source	Temp. (°C)	pH	DO mg/ml	BOD mg/ml	COD mg/ml	Turbidity NTU	Salinity ppt	TSS g/L	TDS g/L
Before Bioremediation										
1.	Piggery Wastewater	27.60	7.15	4.61	206.42	386.94	170.00	0.22	0.07	0.23
After Bioremediation										
1.	Piggery Wastewater (consortium)	26.40	7.52	5.81	121.83	192.02	490.00	0.49	0.08	0.18
2.	Organism 1	26.35	7.53	4.71	118.46	189.06	501.01	0.54	0.09	0.15
3.	Organism 2	26.25	7.67	4.77	113.92	187.02	510.00	0.63	0.1	0.11

Keys: DO – Dissolved Oxygen, BOD – Biochemical Oxygen Demand, COD – Chemical Oxygen demand, TSS – Total Suspended solids, TDS – Total Dissolved Solids, Temp – Temperature

DISCUSSION

Piggery wastewater has been associated with significant load of pathogenic microorganisms. The study revealed bacterial and fungal counts in a communal piggery wastewater and bioremediation potentials. The microbial load of the piggery wastewater for 5-days revealed trends in bacterial and fungal successional population. This growth pattern aligns with typical bacterial growth curves, showing lag, exponential, stationary, and decline phases (Rolfe *et al.,* 2012). The initial increase in the bacterial population could be attributed to the high organic content of piggery wastewater, which provides ample nutrients for microbial growth. Similar growth patterns have been observed in studies on other starch-rich wastewaters (Rajasimman and Karthikeyan, 2007). This suggests that the piggery wastewater environment may not be conducive to fungal growth under given conditions. The presence of antibiotics or other inhibitory chemicals used in animal husbandry may prevent dominance of fungal development. Adebisi *et al.* (2025) also reported dominance of bacterial population in piggery wastewater.

The most predominant bacteria in this study; *Proteus mirabilis* and *Pseudomonas aeruginosa* are Gram-negative. Silhavy *et al.* (2010) reported that Gram-negative bacteria often exhibit higher resistance to environmental stressors and antibiotics, which may be advantageous in the harsh conditions of piggery wastewater. These biochemical characteristics often demonstrate specific metabolic capabilities, indicating their potential roles in various environments. These capabilities enable organisms to thrive in diverse environments and play crucial roles in ecosystems and industrial applications. The ability to metabolize diverse carbohydrates has been linked to enhanced bioremediation potential in previous studies on industrial effluents (de Souza *et al*., 2024).

Sugitha and Abirami (2025) reported efficient bioremediation potential of *Proteus mirabilis* isolated from Buckingham canal, Chennai. Pseudomonads are ubiquitous Gram-negative bacteria characterized by their highly versatile metabolism, aerobic respiration and motility. The key to the ubiquitous distribution of these bacteria is their genomic plasticity and the use of highly sophisticated regulatory mechanisms to adapt to changes in the local environment (Wu and Mittal, 2011). Zhang *et al.* (2024) also reported bioremediation activities of *Pseudomonas* spp. for of soils contaminated with organic pollutants. The neutral pH values (7.15 to 7.53) are within the typical safe discharge range (6.5-8.5) recommended by many environment protection agencies (EPA, 2021). This indicates a shift toward a more alkaline (basic) environment. Slightly higher pH levels can indicate reduced acidity, which may be beneficial in certain contexts, like preventing metal leaching. The low dissolved oxygen (DO) levels (4.61 and 4.07 ppm) indicated a high organic load and potential for rapid oxygen depletion in receiving water bodies, underscoring the need for aeration or other oxygen-enhancing treatments before discharge, which is a common challenge in high-strength wastewater treatment (Olusola-Makinde, 2023).

High turbidity (170 and 490 NTU) and significant levels of total suspended solids (TSS) and total dissolved solids (TDS) suggest a substantial rise in suspended solids, which can impact light penetration and aquatic ecosystems. This level of turbidity can indicate contamination from runoff, sediment disturbance, or algal blooms. A major concern is the effects on water quality, aquatic life and potential treatment processes. The finding is consistent with Okunade and Adekalu, (2013) on evaluation of piggery processing effluents. This indicates the need for effective clarification and filtration processes in the treatment system.

Improvement on physicochemical qualities of studied wastewater samples after treatment suggests the capacity of consortium to remediate piggery wastewater. Bioremediation using autochthonous

microorganisms offers a sustainable and environmentally friendly method for treating piggery wastewater, addressing a wide range of pollutants. By improving the physicochemical parameters, such as BOD, COD, nitrogen, phosphorus, and heavy metal levels, this process reduces the environmental risks associated with piggery farming, making it a viable option for wastewater management (Sugitha and Abirami, 2025).

CONCLUSION

This study provided valuable insights into the microbial composition and physicochemical properties of wastewater generated from piggery farm. The wastewater is categorised as neutral pH, high organic load (as indicated by high BOD and COD values), low dissolved oxygen, and high turbidity. These properties, if left unattended, could pose grave threats to water milieu and human health. Microbial succession in studied wastewater samples revealed *Proteus mirabilis* OLU and *Pseudomonas aeruginosa* OLU as most dominant bacterial species. Treatment of wastewater samples with these isolates suggests that native microbial community displays a vital role in the natural degradation processes of the waste. The presence of bacterium proficient in employing various organic compounds indicates potential for biological treatment approaches. Regulatory bodies should develop and enforce translational guidelines for organic remediation of piggery wastewater, promoting cleaner production techniques and safer environment.

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