SSR Journal of Multidisciplinary (SSRJM)
Volume 2, Issue 3, 2025 Homepage: https://ssrpublisher.com/ssrjm/ ISSN: 3049-1304
Email: office.ssrpublisher@gmail.com

Antibiotic Resistance Patterns of Airborne Bacteria Isolated from Waste Dumpsites in Elele, Rivers State, Nigeria

Anele, B. C.[1], Okorite, George-West[2] & Ebulue, A.M.C.[1]

[1]Department of Microbiology, Madonna University, Nigeria Elele, Rivers State.
[2]Department of Science Laboratory Technology, Captain Elechi Amadi Polytechnic, Rumuola, Port Harcourt, Rivers State, Nigeria

Received: *19.05.2025* | ***Accepted:*** *27.06.2025* | ***Published:*** *30.06.2025*

***Corresponding Author:** Anele, B. C.

DOI: *10.5281/zenodo.15776903*

Abstract **Original Research Article**

Antibiotic resistance remains a critical global health concern, particularly in low- and middle-income countries where pharmaceutical misuse and inadequate waste management exacerbate the proliferation of resistant microorganisms. Environmental reservoirs such as open dumpsites are understudied sources of bioaerosol-borne pathogens with the potential to disseminate resistance genes. This study investigated the antibiotic resistance profiles of airborne bacterial isolates from waste dumpsites in Elele, Rivers State, Nigeria. Ten air samples were collected using the passive sedimentation method, including a control site located 10 meters from the dumpsites. Isolates were identified and subjected to antimicrobial susceptibility testing via the Kirby-Bauer disk diffusion method on Mueller-Hinton agar. *Micrococcus* spp. exhibited the highest susceptibility to chloramphenicol (36.00 mm) but displayed marked resistance to rifampicin (2.0 mm), levofloxacin (1.0 mm), and norfloxacin (9.0 mm). *Escherichia coli* were sensitive to gentamicin, streptomycin, and erythromycin (22.0 mm), but resistant to rifampicin, chloramphenicol, ampiclox, and levofloxacin (0–4 mm). *Pseudomonas aeruginosa* demonstrated extensive multidrug resistance, with susceptibility only to gentamicin and streptomycin (22.0 mm), and complete resistance to chloramphenicol and levofloxacin (0 mm). *Serratia marcescens* showed high susceptibility to ciprofloxacin, norfloxacin, gentamicin, amoxicillin, and streptomycin (22–26 mm), while exhibiting resistance to erythromycin, rifampicin, chloramphenicol, ampiclox, and levofloxacin (≤10 mm*). Pseudomonas oleovorans* was susceptible to ciprofloxacin, norfloxacin, gentamicin, amoxicillin, and streptomycin (20–25 mm), exhibited intermediate resistance to levofloxacin (13 mm), and was resistant to erythromycin, rifampicin, chloramphenicol, and ampiclox (0–12 mm). These findings highlight the significant presence of multidrug-resistant airborne bacteria in unmanaged waste sites, underscoring the environmental dimension of antimicrobial resistance and the need for strengthened surveillance and mitigation strategies.

Keywords: Antibiotic Resistance, Airborne Bacteria, Dumpsites, Antimicrobial Susceptibility, Multidrug Resistance, Elele, Environmental Reservoirs, Surveillance, Public Health.

Citation: Anele, B. C., Okorite, George-West, & Ebulue, A. M. C. (2025). Antibiotic resistance patterns of airborne bacteria isolated from waste dumpsites in Elele, Rivers State, Nigeria. *SSR Journal of Multidisciplinary (SSRJM)*, *2*(3), 139-144.

1. INTRODUCTION

The escalating issue of antibiotic resistance poses a significant public health threat, especially in low- and middle-income nations, where regulatory supervision of waste management and drug utilisation is frequently inadequate (WHO, 2020). Environmental sources, such as municipal and open dumpsites, represent underexplored reservoirs of antibiotic-resistant microorganisms. These garbage disposal sites frequently contain varied microbial populations, including potentially dangerous bacteria that may get airborne and contribute to bioaerosol pollution (Nwankwo et al., 2018). Bioaerosols, airborne particles originating from living entities, have been widely acknowledged as carriers of antibiotic-resistant microbes in both outdoor and indoor settings (Ghosh et al., 2015). Due to insufficient waste segregation and the widespread practice of open dumping, dumpsites in quickly urbanising areas like Elele, a town in Rivers State, Nigeria, pose a serious risk to the environment and public health. Trash from households, hospitals, farms, and factories frequently contaminates these dumpsites, which encourages the growth of bacteria and the dissemination of genes that cause antibiotic resistance in humans

(Akinbile & Yusoff, 2011). Thus, bacteria aerosolised from such circumstances may contribute to the broader transmission of resistance traits in the environment in addition to being dangerous to nearby residents and garbage workers (Zhai et al., 2018).

Many studies have shown that multidrug-resistant patterns are commonly seen in bacteria isolated from dumpsites, most likely due to the selection pressure imposed by antibiotics and other antimicrobial agents found in waste products (Adekanmbi & Falodun, 2015).

Therefore, the purpose of this work was to identify the antibiotic resistance profiles of bioaerosolic bacteria from Elele dumpsites and to isolate and characterise them. It is anticipated that the results will shed light on the possible health hazards associated with airborne resistant bacteria and guide public health initiatives focused on antibiotic stewardship and waste management in the area.

2. MATERIALS AND METHODS

2.1: Study Area and Sample Collection

This study was conducted at selected dumpsites in Elele, Rivers State, Nigeria, an area characterised by increasing waste generation due to urbanisation. Bioaerosol samples were collected during dry weather conditions to avoid dilution effects from rainfall. Sampling was carried out using a settle plate method and active air sampling technique in triplicates at each site, following standard protocols (Nevalainen et al., 1993; Lee et al., 2006).

Nutrient agar and MacConkey agar plates were exposed to ambient air for 15–30 minutes at approximately 1.5 metres above ground level to mimic the human breathing zone. The plates were then incubated at 37°C for 24 hours for bacterial growth.

2.2: Isolation and Identification of Bacteria

Pure isolates were obtained by subculturing colonies with different morphologies. Following Cheesbrough (2006), the following standard microbiological and biochemical methods were used to identify the bacteria: Gram staining, catalase, oxidase, indole, citrate utilisation, and triple sugar iron (TSI) agar tests (Cheesbrough, 2006).

2.3: Antibiotic Susceptibility Testing

The antibiotic resistance profile of the isolates was determined using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar, as recommended by the Clinical and Laboratory Standards Institute (CLSI, 2020). Commonly used antibiotics tested included ampicillin (10 µg), ciprofloxacin (5 µg), tetracycline (30 µg), gentamicin (10 µg), and ceftriaxone (30 µg). Zones of inhibition were measured in millimeters and interpreted as susceptible, intermediate, or resistant based on CLSI guidelines.

2.4: Data Analysis

All experiments were conducted in triplicates. Results were expressed as means ± standard deviation. Descriptive statistics were used to present the distribution and resistance patterns of isolates using Microsoft Excel 2019.

3. RESULTS

3.1: Antibiotics Sensitivity Pattern of Gram-Positive Bacterial Isolate Obtained from Air Dumpsites Samples from Elele, Rivers State, Nigeria

The *Micrococcus* isolate demonstrated a broad range of antibiotic susceptibility. It was highly susceptible to gentamicin (31.0 mm), streptomycin (35.0 mm), chloramphenicol (36.0 mm), ciprofloxacin (22.0 mm), amoxicillin (22.0 mm), erythromycin (22.0 mm), ampiclox (22.0 mm), and norfloxacin (22.0 mm). However, it showed resistance to rifampicin (2.0 mm) and levofloxacin (1.0 mm), and moderate resistance to norfloxacin (9.0 mm).

3.2: Antibiotics Sensitivity Pattern of Gram-Negative Bacterial Isolates Obtained from Air Dumpsites Samples from Elele Rivers State, Nigeria

Escherichia coli exhibited intermediate susceptibility to ciprofloxacin, norfloxacin, amoxicillin, and ampicillin (15–18 mm), and were susceptible to gentamicin, streptomycin, and erythromycin (22 mm). It showed high resistance to rifampicin, chloramphenicol, ampiclox, and levofloxacin, with inhibition zones ranging from (0–4 mm). *Pseudomonas aeruginosa* demonstrated extensive multidrug resistance, with susceptibility observed only to gentamicin and streptomycin (22 mm). It was resistant to all other antibiotics, including complete resistance to chloramphenicol and levofloxacin (0 mm). *Serratia marcescens* was highly susceptible to ciprofloxacin, norfloxacin, gentamicin, amoxicillin, and streptomycin (22–26 mm). However, it showed resistance to erythromycin, rifampicin, chloramphenicol, ampiclox, and levofloxacin, with inhibition zones below (10 mm). *Pseudomonas oleovorans* showed susceptibility to ciprofloxacin, norfloxacin, gentamicin, amoxicillin, and streptomycin (20–25mm), while being resistant to erythromycin, rifampicin, chloramphenicol, and ampiclox (0–12 mm). It exhibited intermediate resistance to levofloxacin (13 mm).

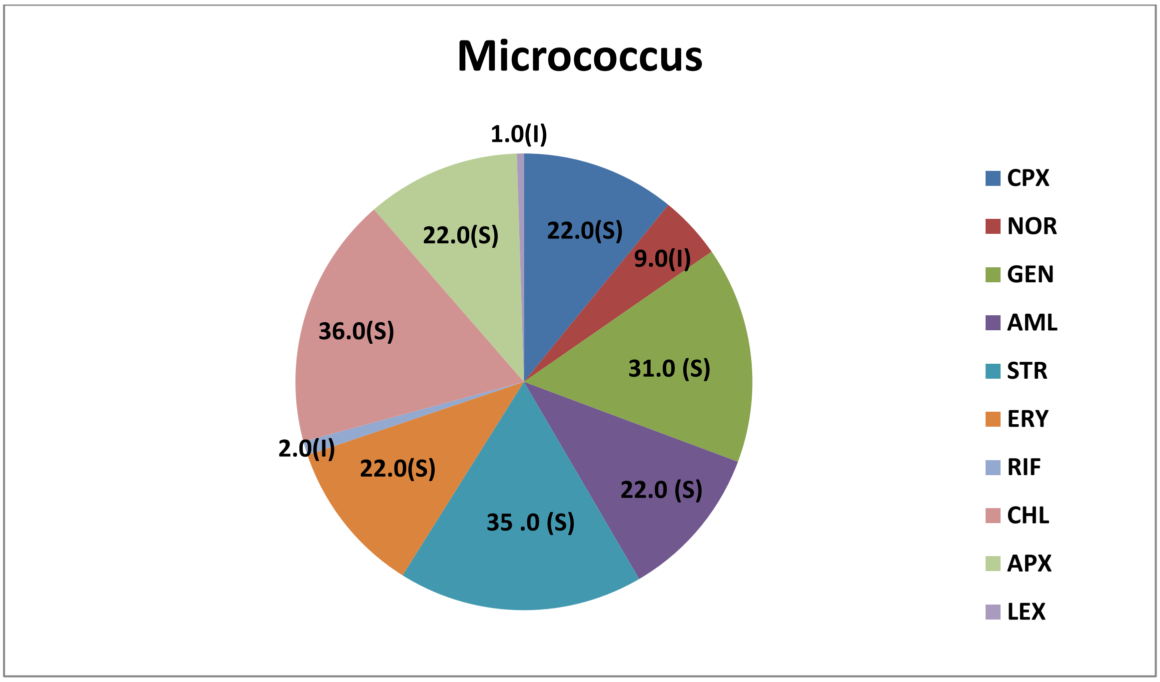

Fig.1: Antibiotics sensitivity pattern of Gram-positive bacterial isolates obtained from Air Dumpsites samples from Elele, Rivers State, Nigeria

KEYS: *CPX= Ciprofloxacin, NOR= Norfloxacin, GEN=Gentamycin, AML=Amoxil, STR= Streptomycin, ERY= Erythromycin, RIF= Rifampicin, CHL= Chloramphenicol, APX= Ampiclox, LEV=Levofloxacin.*
Clinical and Laboratory Standard Institute (CLSI) Guidelines 2024: 31st Edition: Sensitive (S)= > 20.0, Intermediate (I)=15-19, Resistant (R)= < 14.

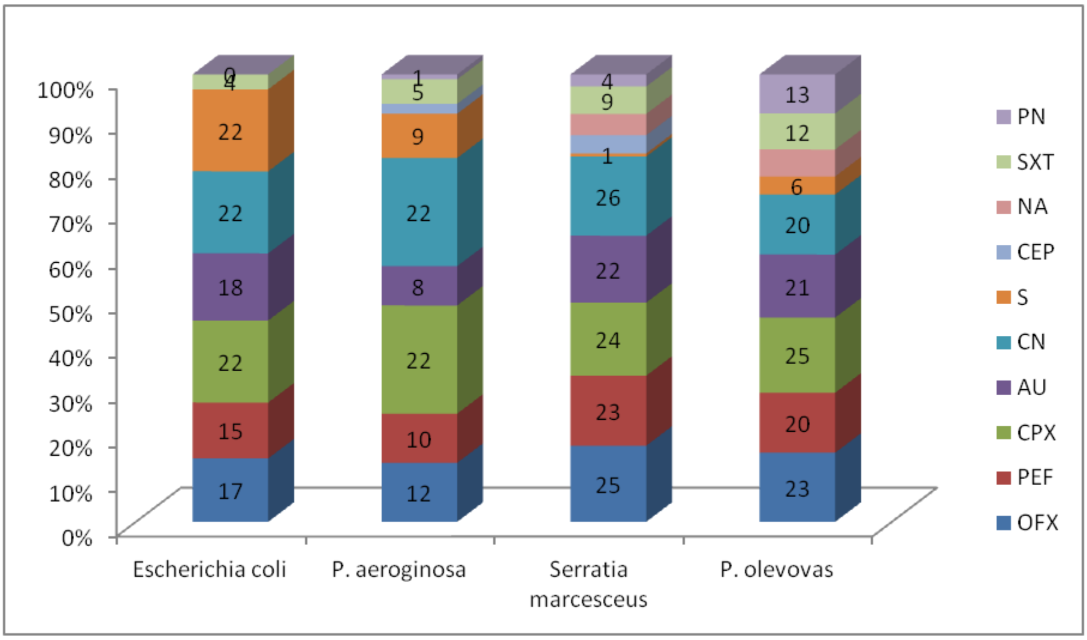

Fig.2: Antibiotics sensitivity pattern of Gram-negative bacterial isolates obtained from Air Dumpsites samples from Elele, Rivers State, Nigeria

3.2: Discussion

The *Micrococcus* isolate from bioaerosols at the dumpsite in Elele, Rivers State, Nigeria, exhibited a largely susceptible profile to a broad range of antibiotics, including gentamicin (31.0 mm), streptomycin (35.0 mm), and chloramphenicol (36.0 mm). These findings suggest that the strain remains vulnerable to aminoglycosides and phenicols, which are known to be effective against Gram-positive cocci like *Micrococcus* (Ryan & Ray, 2004). The high susceptibility to these antibiotics is consistent with prior reports indicating that environmental *Micrococcus* species tend to maintain sensitivity to first-line and broad-spectrum antibiotics, particularly when isolated from non-clinical settings (Madigan et al., 2015). This suggests that despite being exposed to the waste-rich environment of the dumpsite, the isolate may not have acquired significant resistance mechanisms to these drug classes.

The organism also demonstrated complete susceptibility to ciprofloxacin, amoxicillin, erythromycin, and ampiclox, with inhibition zones of 22.0 mm across these antibiotics. Ciprofloxacin, a fluoroquinolone, targets bacterial DNA gyrase, while amoxicillin and ampiclox act on bacterial cell wall synthesis, and erythromycin inhibits protein synthesis (Levy & Marshall, 2004). The observed sensitivity suggests that these antibiotics remain effective treatment options against *Micrococcus* strains in environmental bioaerosols. These results align with previous studies that reported strong efficacy of these agents against Gram-positive cocci in both environmental and clinical isolates (Cheesbrough, 2006). However, the uniformity of the inhibition zone diameters (22.0 mm) across different antibiotics may also suggest a baseline susceptibility threshold rather than a measure of potent bactericidal activity, which warrants further minimum inhibitory concentration (MIC) analysis.

Despite the generally favorable susceptibility pattern, resistance was observed against rifampicin (2.0 mm), norfloxacin (9.0 mm), and levofloxacin (1.0 mm). Resistance to rifampicin, which targets RNA polymerase, is particularly concerning, as it may indicate the presence of mutations in the rpoB gene, a known resistance mechanism (Goldstein, 2014). The resistance to fluoroquinolones such as norfloxacin and levofloxacin is also notable, considering that these antibiotics are widely used and are increasingly detected in environmental matrices due to improper disposal and overuse (Martínez, 2009). These findings are supported by previous environmental microbiology research which suggests that selective pressure from residual antibiotics in waste dumpsites can contribute to the emergence of resistant bacterial populations (Baquero et al., 2008).

The presence of both susceptible and resistant phenotypes in the same Micrococcus isolate highlights the complex nature of antibiotic resistance evolution in environmental settings. Dumpsites serve as ecological reservoirs for genetic exchange and horizontal gene transfer among bacteria, including plasmid-mediated resistance genes (Allen et al., 2010). Although *Micrococcus* is generally considered non-pathogenic, its capacity to harbor and potentially transfer resistance genes to pathogenic bacteria in the environment poses a latent public health risk. The airborne nature of the isolate further amplifies its potential to spread resistant traits across human populations, especially among individuals living or working near unmanaged dumpsites (Ghosh et al., 2015).

Escherichia coli exhibited intermediate susceptibility to fluoroquinolones such as ciprofloxacin and norfloxacin, as well as to β-lactams including amoxicillin and ampicillin, with inhibition zones measuring between 15 and 18 mm. This intermediate susceptibility may indicate emerging resistance mechanisms, possibly mediated by mutations in DNA gyrase or efflux pump overexpression, consistent with trends reported in recent studies (Wang et al., 2023). Conversely, *E. coli* exhibited marked susceptibility to aminoglycosides (gentamicin, streptomycin) and erythromycin, as demonstrated by inhibition zones of 22 mm, which aligns with prior findings that these antibiotics remain effective against certain *E. coli* strains (Zhou et al., 2022).

Notably, *E. coli* displayed profound resistance to rifampicin, chloramphenicol, ampiclox, and levofloxacin, evidenced by negligible inhibition zones (0–4 mm), reflecting potential plasmid-mediated resistance and the presence of multidrug efflux systems, corroborating observations by (Zhou et al., 2022).

Pseudomonas aeruginosa exhibited extensive multidrug resistance, retaining susceptibility solely to gentamicin and streptomycin (22 mm). This phenotype underscores the notorious adaptability of *P. aeruginosa* and its intrinsic and acquired resistance mechanisms, including low outer membrane permeability and robust efflux pump activity, as documented extensively. Complete resistance to chloramphenicol and levofloxacin (0 mm inhibition) further exemplifies this bacterium's resilience, which poses significant therapeutic challenges in clinical settings (Poole, 2001; Li & Plésiat, 2016).

In contrast, *Serratia marcescens* demonstrated high susceptibility to ciprofloxacin, norfloxacin, gentamicin, amoxicillin, and streptomycin, with inhibition zones ranging from 22 to 26 mm. This profile suggests a lower prevalence of resistance determinants within the tested isolates, aligning with reports indicating that fluoroquinolones and aminoglycosides remain efficacious against many *S. marcescens* strains. However, resistance to erythromycin, rifampicin, chloramphenicol, ampiclox, and levofloxacin, with inhibition zones below 10 mm, indicates selective pressure and potential resistance gene acquisition, paralleling findings in nosocomial outbreaks (Tavares-Carreon et al., 2023; Ferreira et al., 2023).

Pseudomonas oleovorans exhibited susceptibility to ciprofloxacin, norfloxacin, gentamicin, amoxicillin, and streptomycin (20–25 mm), suggesting that these agents may retain clinical utility against this species. However, resistance to erythromycin, rifampicin, chloramphenicol, and ampiclox (0–12 mm) coupled with intermediate resistance to levofloxacin (13 mm) points to an evolving resistance pattern that warrants continuous surveillance, as previously highlighted in environmental isolates of *Pseudomonas* spp (Zhou et al., 2022; Wang et al., 2023).

Overall, the antimicrobial resistance profiles observed herein underscore the imperative for judicious antibiotic use and the integration of molecular diagnostics to elucidate resistance mechanisms. These findings resonate with global concerns regarding the escalation of multidrug-resistant pathogens and highlight the necessity for sustained antimicrobial stewardship and novel therapeutic strategies (World Health Organization, 2023).

4. CONCLUSION

In conclusion, the airborne bacterial isolates from waste dumpsites in Elele, Rivers State, exhibit diverse and concerning antibiotic resistance patterns, underscoring the environmental reservoir potential for multidrug-resistant pathogens. The prevalence of resistance, particularly to critical antimicrobials, accentuates the public health risks posed by unmanaged waste and necessitates stringent surveillance alongside targeted antimicrobial stewardship. These findings advocate for urgent interventions to mitigate the dissemination of resistant bacteria within the community and to safeguard both environmental and human health.

5. RECOMMENDATIONS

We therefore, recommend the following:

1. Authorities should enforce comprehensive waste segregation, treatment, and disposal protocols to minimize the proliferation of antibiotic-resistant airborne bacteria from open dumpsites.

2. There should be a periodic monitoring of airborne microbial populations and their resistance profiles, which are essential to detect emerging threats early and to inform public health interventions.

3. Community-based education and healthcare provider training should be intensified to curb the indiscriminate use of antibiotics, thereby reducing selective pressure for resistance in environmental reservoirs.

REFERENCES

Adekanmbi, A. O., & Falodun, O. I. (2015). Antibiotic resistance profile of bacterial isolates from dumpsites in Ado-Ekiti, Nigeria. *International Journal of Environmental Bioremediation & Biodegradation, 3*(3), 59–63.

Akinbile, C. O., & Yusoff, M. S. (2011). Environmental impact of leachate pollution on groundwater supplies in Akure, Nigeria. *International Journal of Environmental Science and Development, 2*(1), 81–86.

Allen, H. K., Donato, J., Wang, H. H., Cloud-Hansen, K. A., Davies, J., & Handelsman, J. (2010). Call of the wild: antibiotic resistance genes in natural environments. *Nature Reviews Microbiology*, 8(4), 251–259.

Baquero, F., Martínez, J. L., & Cantón, R. (2008). Antibiotics and antibiotic resistance in water environments. *Current Opinion in Biotechnology*, 19(3), 260–265.

Cheesbrough, M. (2006). *District Laboratory Practice in Tropical Countries, Part 2*. Cambridge University Press.

Clinical and Laboratory Standards Institute (CLSI). (2020). *Performance Standards for Antimicrobial Susceptibility Testing* (30th ed.). CLSI supplement M100. Wayne, PA: CLSI.

Ghosh, B., Lal, H., & Srivastava, A. (2015). Review of bioaerosols in indoor environment with special reference to sampling, analysis and control mechanisms. *Environment International, 85*, 254–272.

Goldstein, B. P. (2014). Resistance to rifampicin: a review. *The Journal of Antibiotics*, 67(9), 625–630.

Ferreira, A., Rezende, E., & Damas, M. (2023). Outbreak of extensively drug-resistant *Serratia marcescens* in an intensive care unit. *Antimicrobial Stewardship & Healthcare Epidemiology*, 3(1), e200.

Tavares-Carreon, F., De Anda-Mora, K., Rojas-Barrera, I. C., & Andrade, A. (2023). *Serratia marcescens* antibiotic resistance mechanisms of an opportunistic pathogen: a literature review. *PeerJ*, 11, e14399.

Li, X. Z., & Plésiat, P. (2016). Increased efflux pump expression and reduced outer membrane permeability: two mechanisms for the intrinsic resistance of *Pseudomonas aeruginosa* to β-lactams. *Antimicrobial Agents and Chemotherapy, 60*(1), 71–78.

Levy, S. B., & Marshall, B. (2004). Antibacterial resistance worldwide: causes, challenges and responses. *Nature Medicine*, 10(12s), S122–S129.

Lee, B. U., Yermakov, M., & Grinshpun, S. A. (2006). Removal of fine and ultrafine particles from indoor air environments by the unipolar ion emission. *Atmospheric Environment*, 38(29), 4815–4823.

Madigan, M. T., Martinko, J. M., Bender, K., Buckley, D., & Stahl, D. (2015). *Brock Biology of Microorganisms* (14th ed.). Pearson Education.

Martínez, J. L. (2009). Environmental pollution by antibiotics and by antibiotic resistance determinants. *Environmental Pollution*, 157(11), 2893–2902.

Nwankwo, C. D., Eze, M. O., & Anozie, M. C. (2018). Microbial quality and antibiotic resistance profile of airborne bacteria from waste dumpsites in Enugu, Nigeria. *African Journal of Clinical and Experimental Microbiology, 19*(4), 311–319.

Nevalainen, A., Willeke, K., & Liebhaber, F. (1993). Bioaerosols. In: *Aerosol Measurement: Principles, Techniques, and Applications*. Wiley-Interscience.

Poole, K. (2001). Multidrug efflux pumps and antimicrobial resistance in *Pseudomonas aeruginosa* and related organisms. *Journal of Molecular Microbiology andBiotechnology*, *3*(2), 255–264.

Ryan, K. J., & Ray, C. G. (2004). *Sherris Medical Microbiology* (4th ed.). McGraw-Hill.

World Health Organization (WHO). (2020). *Antimicrobial resistance*. Retrieved from https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance

Wang, J., Zhang, H., Zhang, X., Yang, Y., & Zhang, Y. (2023). Draft Genome Sequence of *Pseudomonas oleovorans* Isolated from Industrial Wastewater. *Microbiology Resource Announcements, 12*(8), e00336-23.

Zhai, Y., Li, X., Wang, T., Wang, B., Li, C., & Zeng, G. (2018). A review on airborne microorganisms in particulate matters: Composition, characteristics and influence factors. *Environment International, 113*, 74–90.

Zhou, Q., Liu, Z., Li, Y., & Zhao, Y. (2022). Occurrence and Characteristics of Antibiotic Resistance Genes in Airborne Particulate Matter from a Wastewater Treatment Plant. *Science of The Total Environment, 806*, 151251.

Zhou, Q., Liu, Z., Li, Y., & Zhao, Y. (2022). Occurrence and Characteristics of Antibiotic Resistance Genes in Airborne Particulate Matter from a Wastewater Treatment Plant. Science of The Total Environment, 806, 151251.