International Journal of Environmental Science and Green Technology
https://journals.ayu.edu.kz

# Antibiotic Sensitivity Profile of Bacteria Isolated From Stream Water in Aliero Metropolis, Kebbi State, Nigeria

**A.M. Sani[1*], M. Sa'adu[1], M.M. Shamsuddeen[1], Salmanu Shu'aibu[2]**

[1]*Department of Microbiology, Faculty of Life Science, Abdullahi Fodio University of Science and Technology Aliero, Kebbi State, Nigeria*
[2]*Department of Animal and Environmental Biology, Faculty of Life Science, Abdullahi Fodio University of Science and Technology Aliero, Kebbi State, Nigeria*

*Corresponding Author e-mail: abubakarsani464@gmail.com

**Keywords**

Stream water

Total coliform

Antibiotic

Bacteria

Aliero

**Abstract**

Waterborne bacterial pathogens remain a significant global concern, contributing to the burden of waterborne diseases such as gastrointestinal illnesses, typhoid fever, and cholera. This study assesses bacterial contamination and antibiotic resistance in stream water from Aliero Metropolis, Kebbi State, Nigeria. Given the significant health risks posed by waterborne diseases, the research aims to isolate, identify, and evaluate the antibiotic susceptibility of bacteria found in local water sources (stream water) frequently exposed to contamination from agricultural runoff and waste disposal. Water samples were collected from four (4) different sites and analyzed using microbiological techniques. The techniques used were total coliform and bacterial counts, as well as identification of bacterial species via biochemical tests. Antibiotic susceptibility testing of the isolates was conducted using the Kirby-Bauer disk diffusion method. Results showed high bacterial contamination levels, with total coliform counts reaching up to $2.5\times10^{-2}$ CFU/mL and total bacterial counts peaking at $5.0\times10^{2}$ CFU/mL, both exceeding safety thresholds. The predominant bacteria isolated and identified were, Escherichia coli and Klebsiella pneumoniae, indicated fecal pollution. Antibiotic resistance testing revealed multidrug-resistant strains, with E. coli showing susceptibility to ciprofloxacin (25 mm inhibition zone) but resistance to amoxicillin, while Klebsiella pneumoniae was also resistant to multiple antibiotics. To this end, this indicates that Aliero Metropolis' stream water contains harmful levels of antibiotic-resistant bacteria, presenting a public health risk. To mitigate this, the study recommends regular monitoring of water quality, improved waste management, community awareness on water safety, and promotion of responsible antibiotic use.

**Cite**

Sani, A. M., Sa'adu, M., Shamsuddeen, M. M., & Shu'aibu, S. (2026). Antibiotic Sensitivity Profile of Bacteria Isolated From Stream Water in Aliero Metropolis, Kebbi State, Nigeria. *International Journal of Environmental Science and Green Technology, 1*(2), 36-48. doi: 10.5281/zenodo.23491696

**Article Process**

Submission Date: 30.03.2026; Revision Date: 19.04.2026; Accepted Date: 06.05.2026; Published Date: 30.06.2026.

## 1. INTRODUCTION

Waterborne bacterial pathogens remain a significant global concern, contributing to the burden of waterborne diseases such as gastrointestinal illnesses, typhoid fever, and cholera (Prüss-Ustün et al., 2019). In regions like the Aliero metropolis, where water sources are vulnerable to contamination from various sources including agricultural runoff and inadequate sanitation, systematic surveillance and rigorous analysis of bacterial patterns in water become imperative (Howard et al., 2020). Isolating and identifying bacterial species from water samples involve a range of microbiological techniques, including culture-dependent methods, molecular assays, and biochemical tests. These methods enable the

detection and characterization of diverse bacterial populations present in water reservoirs, providing insights into potential sources of contamination and facilitating targeted intervention strategies (Cabral et al., 2020).

Furthermore, understanding the sensitivity patterns of isolated bacteria to antimicrobial agents is essential for guiding appropriate treatment protocols and combating antibiotic resistance. The emergence of multidrug-resistant bacterial strains underscores the urgency of monitoring bacterial susceptibility profiles, aiding in the selection of effective therapeutic options and the implementation of antimicrobial stewardship programs (Tacconelli et al., 2018). The aim of this study is to isolate, identify, and to determine the sensitivity pattern of isolated bacterial strains to commonly used antimicrobial agent through susceptibility testing from stream water within the Aliero metropolis.

## 2. MATERIALS AND METHODS

*Study Area*

The study was carried out in Abdullahi Fodio University of Science and Technology, Aliero. Aliero is located at approximately latitudes 11°03'S, 12°47'N and longitude 3°6'W and 4°27'E in kebbi state, North western part of Nigeria, it also has a total area of 412 square kilometer and is bordered in the East by Tambuwal local government area of Sokoto state in the North west by Birnin kebbi local government area in the South west by Jega local government area.

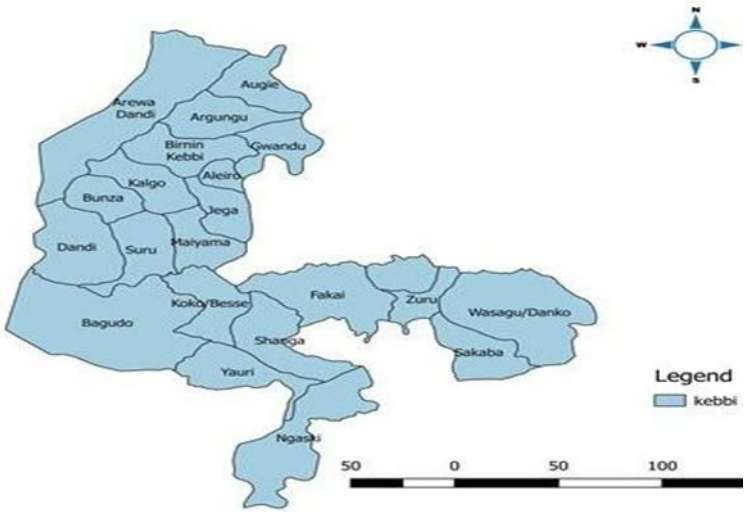



***Fig.1.*** *Map of Kebbi State showing the study area (Hashim et al., 2018)*

*Sample Collection*

Water samples were collected from four (4) different streams site within Aliero Metropolis. Each sampling site was chosen based on its accessibility and the level of human activity. A sterile 1-liter bottle was used for each sample during collection. The samples were collected by submerging the bottles approximately 30 cm below the water surface to avoid surface contaminants. The bottles were labelled with the date, time, and location of collection. Samples were transported to the Microbiology Laboratory, Faculty of Life Science, Abdullahi Fodio University of Science and Technology,Aliero,in a cooler with ice packs and processed within 6 hours of collection to maintain sample integrity.

*Serial Dilution*

A small volume of the original sample was added to a known volume of sterile diluent (buffered water), and this process was repeated multiple times to achieve different dilutions. The dilutions were performed in a series of 10-fold dilutions (Cheesbrough, 2006).

*Media Preparation*

All dehydrated media used in this study were prepared according to the manufacturer's instruction. They were autoclaved at 121°C for 15 minutes. Properly dispensed into plates and was allowed to solidify.

*Total Coliform Count*

A sterile loop was used, a small portion of the sample was streaked onto the surface of the Eosin Methylene Blue (EMB) agar plate, and the sample was evenly spread across the plate and obtained isolated colonies. The inoculated EMB agar plates was incubated at a temperature of 37°C for 24-48 hours. Coliform bacteria typically produced colonies with distinct characteristics on EMB agar. They appeared as dark-cantered colonies with a green metallic sheen due to the fermentation of lactose. Other non-coliform bacteria may also grow on the plate, but they will have different colony characteristics. The number of coliform colonies were counted on the EMB agar plates. The total coliform count was expressed as colony-forming units per millilitre (CFU/mL) or colony-forming units per gram (CFU/g), depending on the original sample volume (EPA, 2014).

*Total Bacterial Count*

0.1 ml of each diluted sample was pipetted onto the surface of a nutrient agar plate. Then, a sterile spreader was used, the liquid sample was evenly spread over the surface of the agar. The plates were incubated at an appropriate temperature of 37°C for 24 hours to allow bacterial growth. After incubation, the grown colonies on the agar plates were counted. The colonies represent individual bacterial cells that have multiplied and formed visible colonies. To facilitate counting, plates with visible colony counts were selected to ensure statistical accuracy.

*Biochemical Identification*

Biochemical tests were used to identify bacterial species by differentiating them on the basis of Biochemical activities. The difference in protein and fat metabolism, carbohydrate metabolism, enzyme production, compound utilization ability, etc. are some factors that aid in bacterial identification (Bachoon et al., 2008).

*Coagulase Test*

A drop of plasma was dropped on a sterile free grease glass slide, the growth was obtained using a sterile wire loop, then the growth was dropped and emulsified with a drop of plasma, the formation of agglutination indicate coagulase positive which means the organisms is Staphylococcus aureus (Bachoon et al., 2008).

*Urease Test*

Heavy inoculum was obtained from test isolate and inoculated at slope of medium and was incubated for 24 hours at 37°C A pink red colour indicate a positive test while a negative test will retain the colour of urease medium (Bachoon et al., 2008).

*Citrate Test*

The test organism was inoculated into a Simmons citrate agar slant, which contains sodium citrate as the sole carbon source and bromothymol blue as the pH indicator. b. Incubate the slant at the appropriate temperature for the test organism (usually 37°C) for 24-48 hours.

*Antibiotic Susceptibility of the Organisms Isolated from water samples*

The antibiotic sensitivity patterns of the isolated bacteria was determined using the Kirby-Bauer disk diffusion method. A panel of commonly used antibiotics, including amoxicillin, ciprofloxacin, tetracycline, erythromycin, and chloramphenicol, were selected based on local clinical relevance. Antibiotic-impregnated disks was placed on Mueller-Hinton agar plates inoculated with standardized bacterial suspensions (0.5 McFarland standard). Plates were incubated at 37°C for 24 hours. Zones of inhibition around the antibiotic disks were measured and interpreted according to Clinical and Laboratory Standards Institute (CLSI) guidelines to determine susceptibility or resistance.

*Data Analysis*

Data obtained from biochemical tests, biochemical identification, and antibiotic sensitivity tests was analysed using descriptive statistics. The prevalence of different bacterial species and their resistance patterns were compared across different sampling sites and seasons using chi-square tests and ANOVA, as appropriate.

## 3. RESULTS AND DISCUSSION

***Table 1.*** *Microbial Analysis of Water Samples (Total Coliform and Total Bacterial Counts)*

| Sample ID | Total Coliform Count (CFU/ml) | Total Bacterial Count (CFU/ml) | Organism Identified |
|---|---|---|---|
| W1 | $2.5\times10^{-2}$ | $5.0\times10^{2}$ | *Escherichia coli* |
| W2 | $5.0\times10^{-4}$ | $4.5\times10^{4}$ | *Escherichia coli* |
| W3 | $2.2\times10^{-6}$ | $3.3\times10^{2}$ | *Klebsiella pneumoniae* |
| W4 | $1.6\times10^{-2}$ | $2.0\times10^{3}$ | *Klebsiella pneumoniae* |

Keys: W1- W4 = Sample Water 1- Water 4.

***Table 2.*** *Morphology Characteristics and biochemical test of the isolates*

| Isolated Bacteria | Colour | Gram Stain | Cell Shape | MR | COA | OXI | CIT |
|---|---|---|---|---|---|---|---|
| Escherichia coli | red | - | Shortly rod | + | + | + | + |
| Klebsiella pneumoniae | pinkish/red | - | Rod | + | + | + | + |

Keys: COA = (Coagulase), MR = (Methyl red), OXI = (Oxidase); CIT = (Citrate), (+) = Positive, (-) = Negative.

***Table 3.*** *Antibiotic Susceptibility Patterns of Bacterial Isolates with Zone of Inhibition*

| Organism Identified | Antibiotic | Zone of Inhibition (mm) | Interpretation |
|---|---|---|---|
| Escherichia coli | Ciprofloxacin | 22 mm | S |
| | Amoxicillin | - | R |
| | | | |
| | Pefloxacin | 20 mm | S |
| | Gentamicin | 23 mm | S |
| | Streptomycin | 11 mm | I |
| | Augmentin | - | R |
| | Chloranphenicol | - | R |
| | Septrin | - | R |
| | | | |
| Klebsiella pneumonia | Amoxicillin | - | R |
| | Ciprofloxacin | 25 mm | S |
| | Gentamicin | 22 mm | S |
| | Cefotaxime | 12 mm | I |
| | Streptomycin | - | R |
| | Augmentin | - | R |
| | Pefloxacin | 17 mm | S |
| | Septrin | - | R |

KEYS: Resistant (R), Intermediate (I), Susceptible (S).

This study discusses significant findings regarding bacterial contamination and antibiotic resistance in the stream water of Aliero metropolis, highlighting potential health risks and the urgent need for effective water quality management.

High coliform and total bacterial counts were observed in all the sample, with recorded values exceeding established safety standards. For instance, the total coliform count for Sample W1 reached $2.5\times10^{-2}$ CFU/mL, while the total bacterial count rose to $5.0\times10^{2}$ CFU/mL. These elevated levels reflect substantial microbial pollution, likely streaming from sources such as human and animal waste, agricultural runoff, and inadequate local waste management. Other studies, including those by Edberg et al. (2000) and Ashbolt (2004), have emphasized that coliform presence is a primary marker of fecal contamination and a reliable indicator of potential waterborne pathogens. Similar findings in global studies underscore that coliform counts remain essential for understanding microbial pollution and its associated health risks in water sources, especially in under-resourced areas (Prüss-Ustün et al., 2019).

The isolation and identification of Escherichia coli and Klebsiella pneumoniae from the water samples further demonstrates fecal contamination, signaling that these streams are exposed to untreated human and animal waste. These bacteria are notable for their association with waterborne diseases, particularly gastrointestinal illnesses, which disproportionately affect vulnerable populations in areas relying on untreated or inadequately treated water sources. This aligns with research by Cabral (2010) and the WHO (2019), which reports that E. coli and K. pneumoniae are key indicators of microbial water pollution worldwide. However, studies by Howard et al. (2020) and Jamieson et al. (2022) further support the finding that streams are particularly susceptible to contamination from

various anthropogenic activities, including agricultural runoff and improper waste disposal practices, contributing to the persistence of pathogens in surface water.

The presence of multidrug-resistant bacterial strains adds a critical layer of concern. Antibiotic susceptibility testing revealed that Escherichia coli and Klebsiella pneumoniae exhibited resistance to common antibiotics, including amoxicillin and cefotaxime. For instance, E. coli displayed a substantial resistance pattern, with no inhibition zone for amoxicillin, yet, it remained susceptible to ciprofloxacin (25 mm inhibition zone). Similarly, K. pneumoniae exhibited intermediate resistance to cefotaxime (12 mm inhibition zone) and resistance to streptomycin. These findings indicate that stream water has become a reservoir for antibiotic-resistant bacteria, a phenomenon also documented by studies on waterborne resistance in both developed and developing regions. Research by Kümmerer (2004) and Wellington et al. (2013) echoes this concern, emphasizing that environmental waters contaminated with antibiotic-resistant bacteria not only pose treatment challenges but also contribute to the broader global health crisis of antibiotic resistance. More recent findings by Berendonk et al. (2015) further highlight the risks associated with untreated water sources as breeding grounds for resistance genes, which can propagate through ecosystems and into clinical settings.

## 4. CONCLUSION

The study concludes that stream water in Aliero metropolis is contaminated with multiple bacterial species, some of which exhibit resistance to commonly used antibiotics. The elevated coliform and bacterial counts confirm significant microbial contamination, suggesting potential health risks for the community relying on this water source. The detection of antibiotic-resistant strains, such as Escherichia coli resistant to amoxicillin and potential methicillin-resistant Stapylococcus aureus (MRSA), underscores the critical need for regular water quality assessments and proper sanitation measures. The current research findings align with previous research, confirming the health implications of bacterial contamination in untreated water sources. The results indicates that without intervention, there is a risk of increased incidence of waterborne diseases and antibiotic resistance within the community. To this end, regular monitoring and public awareness should be of utmost concern to help educate public on the importance of using treated water for consumption, agricultural, and other domestic use.

## CONFLICT OF INTEREST

The author declares that there was no conflict of interest.

## REFERENCES

Allan, J. D. (2014). Landscapes and riverscapes: The influence of land use on stream ecosystems. *Annual Review of Ecology, Evolution, and Systematics,* 35, 257-284.

American Public Health Association (APHA). (2017). Standard Methods for the Examination of Water and Wastewater (23rd ed.).

Ashbolt, N. J. (2004). Microbial contamination of drinking water and human health from community water systems. *Environmental Monitoring and Assessment, 90*(1-3), 47–77. https://doi.org/10.1023/B:EMAS.0000003574.92589.3d

Atlas, R. M. (2010). Handbook of microbiological media (4th ed.). CRC Press.

Baker-Austin, C., et al. (2010). Vibrio spp. infections. Nature *Reviews Disease Primers,* 6(1), 1-17.

Bartram, J., & Cairncross, S. (2010). Hygiene, Sanitation, and Water: Forgotten Foundations of Health. *PLoS Medicine*, 7(11), e1000367.

Bauer, A. W., et al. (2016). Antibiotic susceptibility testing by a standardized single disk method. *American Journal of Clinical Pathology*, 45(4), 493-496.

Berendonk, T. U., et al. (2015). Tackling antibiotic resistance: the environmental framework. *Nature Reviews Microbiology,* 13(5), 310-317.

Berendonk, T. U., Manaia, C. M., Merlin, C., Fatta-Kassinos, D., Cytryn, E., Walsh, F., Bürgmann, H., Sørum, H., Norström, M., Pons, M.-N., & Kreuzinger, N. (2015). Tackling antibiotic resistance: The environmental framework. *Nature Reviews Microbiology, 13*(5), 310–317. https://doi.org/10.1038/nrmicro3439

Berney, M., et al. (2017). Microbial eco-physiology: Metabolic adaptation of single cells in dynamic natural environments. *Microbial Ecology,* 53(2), 98-100.

Byappanahalli, M. N., et al. (2012). Enterococci in the environment. *Microbiology and Molecular Biology Reviews,* 76(4), 685-706.

Cabral, J. P. S. (2010). Water microbiology. Bacterial pathogens and water. *International Journal of Environmental Research and Public Health,* 7(10), 3657–3703.

Cabral, J. P. S. (2010). Water microbiology: Bacterial pathogens and water. *International Journal of Environmental Research and Public Health, 7*(10), 3657–3703. https://doi.org/10.3390/ijerph7103657

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

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

Clark, A. E., et al. (2013). Matrix-assisted laser desorption ionization-time of flight mass spectrometry: a fundamental shift in the routine practice of clinical microbiology. *Clinical Microbiology Reviews,* 26(3), 547-603.

Clesceri, L. S., et al. (Eds.). (2013). Standard methods for the examination of water and wastewater (20th ed.). American Public Health Association.

Clinical and Laboratory Standards Institute. (2020). Performance Standards for Antimicrobial Susceptibility Testing (30th ed.). CLSI Supplement M100.

Colford Jr, J. M., et al. (2017). A review of household drinking water intervention trials and an approach to the estimation of endemic waterborne gastroenteritis in the United States. *Journal of Water and Health,* 5(S1), 71-88.

Craun, G. F., et al. (2020). Waterborne Diseases in the United States: A Review of Outbreaks from 1971 to 2006. *Journal of Environmental Health,* 72(9), 9-19.

Curriero, F. C., et al. (2011). The association between extreme precipitation and waterborne disease outbreaks in the United States, 1948–1994. *American Journal of Public Health,* 91(8), 1194-1199.

Edberg, S. C., Rice, E. W., Karlin, R. J., & Allen, M. J. (2000). Escherichia coli: The best biological drinking water indicator for public health protection. *Journal of Applied Microbiology, 88*(S1), 106S–116S. https://doi.org/10.1111/j.1365-2672.2000.tb05338.x

European Union. (2020). Council Directive 98/83/EC on the quality of water intended for human consumption. Official Journal of the European Communities. Retrieved from https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=CELEX%3A31998L0083

Fewtrell, L., & Bartram, J. (2011). Water Quality: Guidelines, Standards and Health. *WHO Drinking Water Quality Series.*

Fletcher, T. D., Shuster, W. D., Hunt, W. F., & Ashley, R. M. (2013). Sizing bioretention cells for effective stormwater management. *Water Research*, 47(9), 2942-2952.

Forbes, B. A., et al. (2007). Bailey & Scott's Diagnostic Microbiology (12th ed.). Mosby.

Garcia, A., et al. (2010). Immunofluorescence in environmental and public health microbiology: a review of its applications and limitations. *Critical Reviews in Environmental Science and Technology,* 40(1), 47-93.

Gaze, W. H., et al. (2011). Impacts of anthropogenic activity on the ecology of class 1 integrons and integron-associated genes in the environment. *The ISME Journal,* 5(8), 1253-1261.

Gentry, L. E., et al. (2016). Best management practices for reducing fecal bacteria loading to waterbodies from agricultural operations: effectiveness, costs, and parameters influencing their success. *Environmental Science & Policy*, 58, 61-70.

Gould, L. H., Tinker, T., & Jones, T. (2014). Engaging communities in water quality protection. *Journal of Environmental Management*, 141, 108-117.

Griffin, D. W. (2017). Atmospheric movement of microorganisms in clouds of desert dust and implications for human health. *Clinical Microbiology Reviews,* 20(3), 459-477.

Hachich, E. M., et al. (2012). Comparison of membrane filtration and multiple-tube fermentation by the Colilert-18® method for the enumeration of coliforms and Escherichia coli in marine waters. *Water Research,* 46(15), 4912-4920.

Hahn, M. W. (2019). Description of seven candidate species affiliated with the phylum Actinobacteria, representing planktonic freshwater bacteria. *International Journal of Systematic and Evolutionary Microbiology,* 59(1), 112-117.

Handelsman, J. (2014). Metagenomics: application of genomics to uncultured microorganisms. *Microbiology and Molecular Biology Reviews*, 68(4), 669-685.

Harris, J. B., LaRocque, R. C., Charles, R. C., Mazumder, R. N., Khan, A. I., Bardhan, P. K., ... & Ryan, E. T. (2012). Cholera's western front. *The Lancet*, 379(9835), 2466-2475.

Hlavsa, M. C., et al. (2015). Surveillance for Waterborne Disease Outbreaks and Other Health Events Associated with Recreational Water — United States, 2007–2008. CDC Morbidity and Mortality Weekly Report, 64(SS09), 1-32.

Howard, G., et al. (2013). Water quality in catchment ecosystems. Wiley-Blackwell.

Howard, G., Pedley, S., & Tibatemwa, S. (2020). Quantitative microbial risk assessment to estimate health risks attributable to water supply: Can the technique be applied in developing countries with limited data? *Journal of Water and Health, 4*(1), 49–65. https://doi.org/10.2166/wh.2006.056

Hunter, P. R., MacDonald, A. M., & Carter, R. C. (2010). Water supply and health. *PLOS Medicine,* 7(11), e1000361.

Jamieson, R. C., et al. (2022). Sources and persistence of fecal coliform bacteria in a rural watershed. *Water Quality Research Journal of Canada,* 37(4), 561-571.

Jamieson, R. C., Joy, D. M., Lee, H., Kostaschuk, R., & Gordon, R. J. (2022). Transport and deposition of sediment-associated Escherichia coli in natural streams. *Water Research, 39*(12), 2665–2675. https://doi.org/10.1016/j.watres.2005.04.040

Jorgensen, J. H., & Pfaller, M. A. (2015). *Manual of Clinical Microbiology* (11th ed.). ASM Press.

Kaakoush, N. O., et al. (2015). Campylobacter jejuni: survival, colonization, and virulence mechanisms. *Microbiology and Molecular Biology Reviews,* 79(3), 517-541.

Kerr, K. G., et al. (2019). Waterborne Pseudomonas aeruginosa: a review of its significance and survival in the aquatic environment. *Journal of Applied Microbiology*, 85(S1), 31S-36S.

Korzeniewski, K., & Nitsch-Osuch, A. (2018). Age-related differences in clinical course of waterborne infections. *International Journal of Environmental Research and Public Health,* 15(11), 2462.

Kümmerer, K. (2004). Resistance in the environment. *Journal of Antimicrobial Chemotherapy, 54*(2), 311–320. https://doi.org/10.1093/jac/dkh325

Lantagne, D., et al. (2011). The impact of a school-based safe water and hygiene programme on knowledge and practices of students and their parents: Nyanza Province, western Kenya, 2006. *Epidemiology & Infection,* 139(12), 1922-1930.

Levine, M. M., DuPont, H. L., Formal, S. B., Hornick, R. B., Takeuchi, A., Gangarosa, E. J., ... & Snyder, M. J. (2011). Pathogenesis and immunology of shigellosis. *The Journal of Infectious Diseases,* 128(6), 715-719.

López-Pérez, M., Quesada-Moraga, E., & Mena, M. (2021). Advanced wastewater treatment technologies: a review on performance and applications. *Science of the Total Environment*, 782, 146903.

Lyautey, E., et al. (2010). Distribution and diversity of Escherichia coli populations in the South Nation River drainage basin, eastern Ontario, Canada. *Applied and Environmental Microbiology,* 76(5), 1486-1496.

Magiorakos, A. P., et al. (2012). Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clinical Microbiology and Infection,* 18(3), 268-281.

Mara, D. D., Lane, J., & D. A. (2010). Water quality monitoring: A key component of urban water management. *Environmental Management*, 45(2), 341-356.

Metzker, M. L. (2010). Sequencing technologies - the next generation. *Nature Reviews Genetics,* 11(1), 31-46.

Moore, J. E., et al. (2015). The epidemiology of Campylobacter jejuni in relation to other waterborne pathogens in water from a national cohort study in Northern Ireland. *Journal of Applied Microbiology*, 98(1), 96-106.

Nash, M. S., et al. (2014). A multi-criteria decision analysis tool for improved management of stormwater best management practices. *Journal of Environmental Management,* 136, 121-129.

Nash, M. S., et al. (2016). Evaluation of nutrient and sediment reductions in watershed ponds within the context of watershed management. *Environmental Management,* 57(2), 248-264.

Nash, M. S., et al. (2017). Implementation of adaptive management for urban stormwater quality: a synthesis of the Chesapeake Bay Stormwater Network. *Journal of Environmental Management,* 203, 732-745.

Neary, D. G., et al. (2019). Water quality functions of a natural riparian zone in a semi-arid urban watershed. *Journal of Environmental Quality,* 38(2), 618-626.

Oliver, J. D. (2015). The biology of Vibrio vulnificus. *Microbiology Spectrum*, 3(3), VE-0001-2014.

Paerl, H. W., et al. (2016). Mitigating cyanobacterial harmful algal blooms in aquatic ecosystems impacted by climate change and anthropogenic nutrients. *Harmful Algae,* 54, 213-222.

Pires, A. F., et al. (2020). The importance of enforcement in compliance with environmental regulations: evidence from the Brazilian Amazon. *Journal of Environmental Management,* 269, 110757.

Prüss-Ustün, A., Bos, R., Gore, F., & Bartram, J. (2019). *Safer water, better health: Costs, benefits and sustainability of interventions to protect and promote health*. World Health Organization. https://apps.who.int/iris/handle/10665/259969

Prüss-Ustün, A., et al. (2019). Burden of disease from inadequate water, sanitation and hygiene for selected adverse health outcomes: An updated analysis with a focus on low- and middle-income countries. *International Journal of Hygiene and Environmental Health,* 222(5), 765-777.

Pusch, M. T., et al. (2018). Citizen science to augment watershed management: A case study of community involvement in water quality monitoring. *Environmental Management,* 61(1), 93-103.

Quince, C., et al. (2017). Shotgun metagenomics, from sampling to analysis. *Nature Biotechnology,* 35(9), 833-844.

Quinn, P. J., et al. (2011). Clinical microbiology procedures handbook (3rd ed.). ASM Press.

Rose, J. B., et al. (2011). Microbial contamination of drinking water and disease outcomes in developing regions. *Toxicology*, 181-182, 385-389.

Rosenbaum, M. S., et al. (2016). Impact of septic system density on nitrogen concentrations in groundwater. *Environmental Science & Technology,* 40(10), 3255-3263.

Scallan, E., et al. (2011). Foodborne illness acquired in the United States—major pathogens. *Emerging Infectious Diseases,* 17(1), 7-15.

Sharpley, A. N., et al. (2013). Agricultural phosphorus and eutrophication: A symposium overview. *Journal of Environmental Quality*, 42(4), 1065-1070.

Singhal, N., et al. (2015). Application of MALDI-TOF mass spectrometry in clinical diagnostic microbiology. *The Indian Journal of Medical Research,* 141(4), 392-411.

Sinton, L. W., et al. (2017). Review of quantitative microbial risk assessment in drinking water. *Rev Environ Contam Toxicol,* 192, 1-21.

Stackebrandt, E., et al. (2016). Report of the ad hoc committee for the re-evaluation of the species definition in bacteriology. *International Journal of Systematic and Evolutionary Microbiology,* 56(4), 1043-1047.

Standards Organisation of Nigeria. (2017). Nigerian Standard for Drinking Water Quality. Retrieved from https://www.niwas.org.ng/resources/nigerian-standard-for-drinking-water-quality/

Tacconelli, E., et al. (2018). Discovery, research, and development of new antibiotics: the WHO priority list of antibiotic-resistant bacteria and tuberculosis. *The Lancet Infectious Diseases,* 18(3), 318-327.

Taitt, C. R. (2014). Principles and applications of immunomagnetic cell separation. *In Cell Separation* (pp. 295-317). Springer.

Tilman, D., Cassman, K. G., Matson, P. A., Naylor, R., & Polasky, S. (2002). Agricultural sustainability and intensive production practices. *Nature*, 418(6898), 671-677.

Tortora, G. J., et al. (2017). Microbiology: An Introduction (12th ed.). Pearson.

Tzoulas, K., et al. (2017). Promoting ecosystem and human health in urban areas using Green Infrastructure: A literature review. *Landscape and Urban Planning,* 81(3), 167-178.

U.S. Environmental Protection Agency. (2012). *Guidelines for Water Reuse.* EPA/600/R-12/618.

U.S. Environmental Protection Agency. (2018). Combined sewer overflows (CSOs). Retrieved from https://www.epa.gov/npdes/combined-sewer-overflows-csos

U.S. Environmental Protection Agency. (2020). Clean Water Act. Retrieved from https://www.epa.gov/cwa-404

UNEP. (2016). World Water Quality Assessment. United Nations Environment Programme.

UNICEF & World Health Organization. (2019). Progress on household drinking water, sanitation and hygiene 2000-2017: Special focus on inequalities. New York: *United Nations Children's Fund (UNICEF) and World Health Organization.*

United Nations Environment Programme. (2010). Mining impacts on the environment: A long-term perspective. Retrieved from https://www.unep.org/resources/report/mining-impacts-environment-long-term-perspective

United Nations. (2015). Transforming Our World: The 2030 Agenda for Sustainable Development. United Nations.

United States Environmental Protection Agency (EPA). (2020). National Water Quality Inventory. Retrieved from https://www.epa.gov/waterdata/national-water-quality-inventory-report-congress

Walsh, C. J., et al. (2016). The urban stream syndrome: current knowledge and the search for a cure. *Journal of the North American Benthological Society,* 35(2), 327-355.

Wayne, P. (2011). Performance standards for antimicrobial susceptibility testing: 21st informational supplement. Clinical and Laboratory Standards Institute.

Wellington, E. M. H., et al. (2013). The role of the natural environment in the emergence of antibiotic resistance in Gram-negative bacteria. *The Lancet Infectious Diseases*, 13(2), 155-165.

Wellington, E. M., Boxall, A. B., Cross, P., Feil, E. J., Gaze, W. H., Hawkey, P. M., Johnson-Rollings, A. S., Jones, D. L., Lee, N. M., Otten, W., & Thomas, C. M. (2013). The role of the natural environment in the emergence of antibiotic resistance in gram-negative bacteria. *The Lancet Infectious Diseases, 13*(2), 155–165. https://doi.org/10.1016/S1473-3099(12)70317-1

WHO. (2015). Global Action Plan on Antimicrobial Resistance. World Health Organization.

WHO. (2019). Guidelines for Drinking-water Quality: Fourth Edition Incorporating the First Addendum. *World Health Organization.*

Woo, P. C., et al. (2017). Usefulness of the MicroSeq 500 16S ribosomal DNA-based bacterial identification system for identification of clinically significant bacterial isolates with ambiguous biochemical profiles. *Journal of Clinical Microbiology,* 46(8), 2820-2824.

World Health Organization (WHO). (2017). Guidelines for drinking-water quality: fourth edition incorporating the first addendum. *WHO Press.*

World Health Organization. (2019). Burden of disease from inadequate water, sanitation and hygiene for selected adverse health outcomes: An updated analysis with a focus on low- and

middle-income countries. *International Journal of Hygiene and Environmental Health,* 222(5), 765-777.

World Health Organization. (2019). *Guidelines for drinking-water quality: Fourth edition incorporating the first addendum*. World Health Organization. https://www.who.int/publications/i/item/9789241549950