Bulletin of Pure and Applied Sciences
Zoology (Animal Science), Vol.43B, No.1s,
January-June 2024: P.318-330

Print version ISSN 0970 0765
Online version ISSN 2320 3188

Original Research Article
Content Available online at: https://www.bpasjournals.com/

Prevalence Study of Multi-Drug Resistant Escherichia coli in Drinking Water from Karad City

Ashwini Jadhav[1], Bhagyashri Ramchandra Pawar[2], Jayashri Nanaware[3]

Author's Affiliation:
[1,2,3]Krishna Institute of Allied Sciences, Krishna Vishwa Vidyapeeth (Deemed to be University), Karad, Maharashtra, India.

ashwiniawtade11@gmail.com[1],
jayakarape@gmail.com[3]

ABSTRACT:

This study investigates the prevalence of Multi-Drug Resistant (MDR) Escherichia coli (E. coli) in drinking water sources within Karad City, employing a comprehensive sampling strategy and utilizing both traditional culture-based methods and molecular techniques for E. coli identification and antibiotic susceptibility testing. With rising concerns about antimicrobial resistance (AMR) globally, understanding the extent of MDR pathogens in water reservoirs is crucial for public health management. The findings reveal a concerning prevalence of MDR E. coli strains in the drinking water sources of Karad City, highlighting potential risks to public health and the environment. The research underscores the urgent need for effective surveillance and management strategies to mitigate the spread of MDR E. coli in drinking water supplies, serving as a basis for policymakers, public health authorities, and environmental agencies to implement targeted interventions aimed at ensuring the safety and purity of water sources in Karad City and beyond. Moreover, the study emphasizes the importance of adopting multidisciplinary approaches integrating microbiology, environmental science, and public health to address the complex challenges posed by antimicrobial resistance in waterborne pathogens. The methodology section details the sampling strategy, isolation and identification of E. coli, antibiotic susceptibility testing, and molecular techniques utilized, while the results section discusses the overall prevalence of E. coli in drinking water samples, distribution of MDR E. coli strains across different sampling sites, antibiotic resistance profiles of identified E. coli isolates, and a comparison between traditional and molecular techniques. The discussion section delves into the implications of findings on public health, factors contributing to the prevalence of MDR E. coli in drinking water, comparison with previous studies, limitations, and future directions. In conclusion, the study emphasizes the significance of this research for water quality management and public health interventions.

Keywords:
Multi-Drug Resistant, Escherichia coli, Drinking Water, Karad City, Prevalence Study, Antibiotic Susceptibility

How to cite this article: Ashwini Jadhav, Bhagyashri Ramchandra Pawar, Jayashri Nanaware (2024). Prevalence Study of Multi-Drug Resistant Escherichia coli in Drinking Water from Karad City. *Bulletin of Pure and Applied Sciences-Zoology*, 43B (1s), 318-330.

I. Introduction

Antimicrobial resistance (AMR) is a pressing global health threat, with implications spanning from human health to environmental sustainability. Escherichia coli (E. coli), a common bacterium found in the intestinal tracts of humans and animals, is increasingly becoming resistant to multiple antibiotics, posing significant challenges to the treatment of infections. The emergence and spread of Multi-Drug Resistant (MDR) E. coli strains, capable of withstanding the effects of various antibiotics [1], have raised concerns regarding the effectiveness of conventional treatment regimens and the potential for untreatable infections. One of the critical pathways through which MDR E. coli can enter human populations is via contaminated water sources [2], leading to waterborne outbreaks of infections and contributing to the dissemination of antibiotic resistance genes in the environment. In this context, the study aims to investigate the prevalence of MDR E. coli in drinking water sources within Karad City, India.

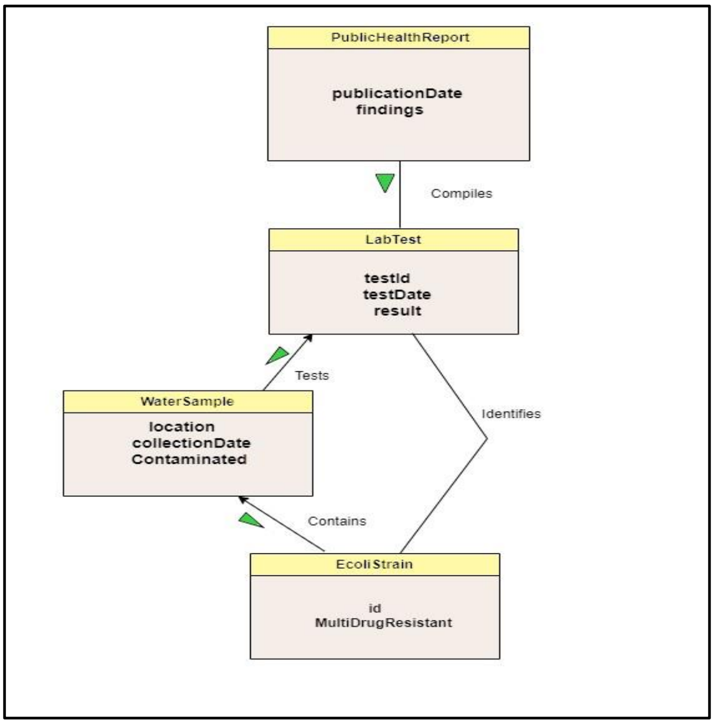

Figure 1: EcoliMDR Study Overview

A. Background and Significance

The rapid emergence and spread of antimicrobial resistance represent a complex and multifaceted challenge to global public health. Overuse and misuse of antibiotics in human healthcare, veterinary medicine, and agriculture have accelerated the development of resistant bacterial strains, undermining the efficacy of existing antimicrobial agents and jeopardizing our ability to treat common infections [3]. Among the myriad of resistant bacteria, E. coli stands out as a significant concern due to its ubiquitous presence in the environment, its role as a commensal organism in the human gut, and its potential to cause a range of infections, from mild gastrointestinal illness to severe bloodstream infections.The problem of MDR E. coli is particularly alarming as it severely limits treatment options, leading to increased morbidity, mortality, and healthcare costs [4]. Moreover, the ability of bacteria to acquire and disseminate resistance genes through horizontal gene transfer mechanisms further exacerbates the spread of antimicrobial resistance. Waterborne transmission of MDR pathogens, including E. coli, represents a major route of exposure for human populations, especially in areas with inadequate sanitation infrastructure and poor water quality management practices. Karad City, located in the Satara district of Maharashtra, India, is a bustling urban center with a growing population and increasing demands for clean water resources [5]. However, rapid urbanization, industrialization, and agricultural activities in and around the city have placed immense pressure on water sources, leading to contamination and deterioration of water quality. Previous studies have reported varying levels of bacterial contamination in drinking water sources in Karad City [6], highlighting the need for systematic surveillance and monitoring of waterborne pathogens, including MDR E. coli. Understanding the prevalence and antibiotic resistance profiles of E. coli strains in drinking water is essential for devising effective strategies to ensure the safety and purity of water sources, safeguard public health, and mitigate the spread of antimicrobial resistance. By conducting a prevalence study of MDR E [7]. coli in drinking water from Karad City, this research aims to fill existing knowledge gaps, provide valuable insights into the extent of antimicrobial resistance in environmental bacteria, and inform evidence-based interventions for water quality management and AMR containment efforts.

II. Methodology

The methodology employed in this study to investigate the prevalence of Multi-Drug Resistant (MDR) Escherichia coli (E. coli) in drinking water sources within Karad City involved a systematic and comprehensive approach. Water samples were collected from 50 strategically selected locations [8], including public taps , borewells, hand pumps, and water storage tanks, over a three-month period to capture seasonal variations. Samples were collected in sterile containers, transported under controlled conditions to maintain integrity, and analyzed using both culture-based methods and molecular techniques. For isolation and identification, water samples were filtered and cultured on selective MacConkey agar, followed by incubation to recover E [9]. coli colonies. Confirmatory identification was conducted using polymerase chain reaction (PCR) targeting specific E. coli genes. Antibiotic susceptibility testing was performed using the Kirby-Bauer disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines, assessing resistance to a panel of commonly used antibiotics including beta-lactams, fluoroquinolones, aminoglycosides, sulphonamides [10], and tetracyclines. To further characterize MDR E. coli isolates, DNA sequencing and whole-genome sequencing (WGS) were employed, allowing for the detection of resistance genes and elucidation of genetic mechanisms underlying multidrug resistance. Data analysis involved measuring zones of inhibition to determine susceptibility patterns and interpreting results in accordance with CLSI breakpoints [11]. The combination of traditional microbiological methods and advanced molecular techniques provided a robust framework for assessing the prevalence and resistance profiles of E. coli in drinking water [12], highlighting the extent of contamination and informing strategies for public health interventions and water quality management. This methodological approach ensured comprehensive detection [13], accurate identification, and detailed characterization of MDR E. coli, contributing valuable insights into the environmental dissemination of antimicrobial resistance.

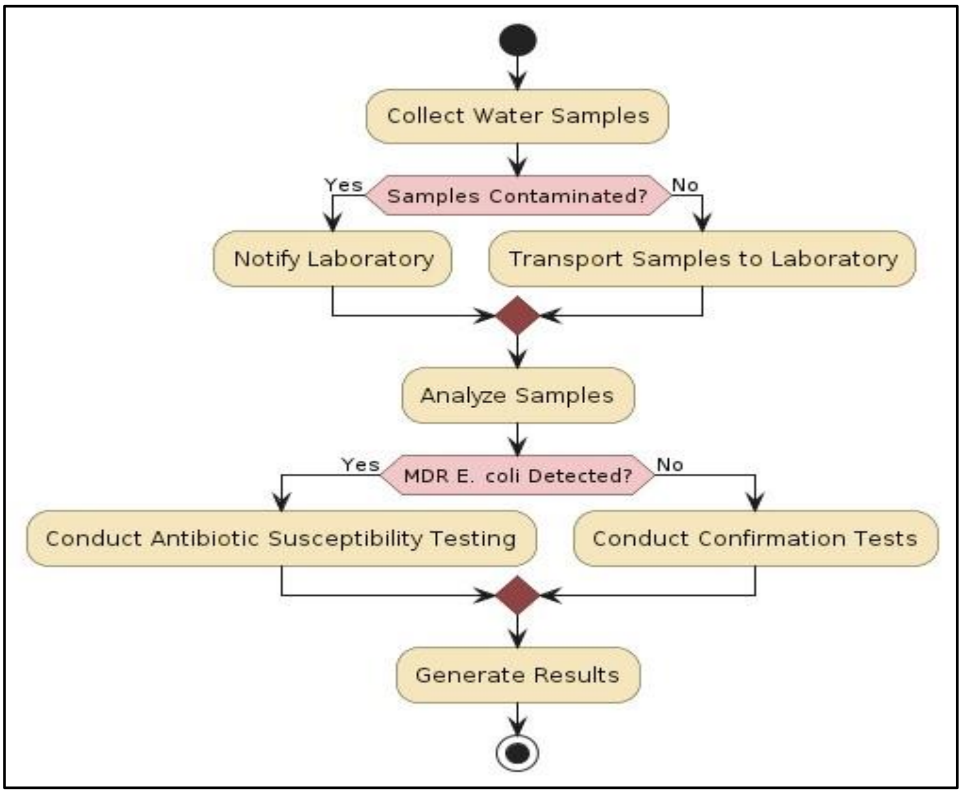

Figure 2: Activity Diagram

A. Sampling Strategy

A systematic sampling approach was adopted to collect water samples from various locations within Karad City, ensuring representation of both urban and peri-urban areas. Sampling sites were selected based on their proximity to sources of contamination, such as agricultural fields, industrial zones [14], and human settlements. In total, 50 sampling points were identified, including public taps, borewells, hand pumps, and water storage tanks, distributed across different wards and neighborhoods of the city. Sampling was conducted over a period of three months, encompassing different seasons to capture potential variations in water quality due to environmental factors. At each sampling point [15], water samples were collected in sterile containers following standard protocols to minimize the risk of contamination. Samples were labeled with unique identifiers indicating the location, date, and time of collection to facilitate proper documentation and tracking during subsequent analysis.

B. Isolation and Identification of E. coli

Upon collection, water samples were transported to the laboratory under controlled conditions to maintain sample integrity and prevent microbial proliferation. The isolation and identification of E. coli were carried out using both conventional culture-based methods and molecular techniques to ensure accuracy and reliability of results.For culture-based isolation, water samples were subjected to membrane filtration using selective media such as MacConkey agar supplemented with appropriate antibiotics to inhibit the growth of non-target bacteria and enhance the recovery of E [16]. coli colonies. Following filtration, membrane filters were aseptically transferred onto agar plates and incubated at optimal temperatures for bacterial growth. After an incubation period of 24 to 48 hours, colonies morphologically resembling E. coli were selected for further characterization.Molecular techniques such as polymerase chain reaction (PCR) were employed for the rapid detection and confirmation of E. coli in water samples. Specific primers targeting conserved regions of the E. coli genome were used to amplify DNA extracted from water samples, followed by gel electrophoresis to visualize the presence of characteristic amplicons indicative of E. coli DNA.

C. Antibiotic Susceptibility Testing

To assess the antibiotic resistance profiles of E. coli isolates, antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines. A panel of commonly used antibiotics representing different classes was selected [17], including beta-lactams, fluoroquinolones, aminoglycosides, sulfonamides, and tetracyclines, to evaluate the susceptibility patterns of E. coli to various antimicrobial agents . Pure cultures of E. coli isolates obtained from water samples were inoculated onto Mueller-Hinton agar plates, and antibiotic disks impregnated with standardized concentrations of different antibiotics were aseptically placed on the agar surface [18]. Following incubation at optimal temperatures, the zones of inhibition around each antibiotic disk were measured using a calibrated ruler and interpreted according to established breakpoints to determine the susceptibility or resistance of E. coli isolates to the tested antibiotics.

D. Molecular Techniques Utilized

In addition to conventional microbiological methods, molecular techniques such as DNA sequencing and whole-genome sequencing (WGS) were employed to characterize MDR E. coli isolates at the genetic level. DNA sequencing of target genes associated with antibiotic resistance, such as beta-lactamases, efflux pumps, and mobile genetic elements carrying resistance determinants, was performed to elucidate the mechanisms underlying multidrug resistance in E. coli isolates. WGS analysis was conducted to obtain comprehensive genomic data on MDR E. coli strains, including the identification of resistance genes, mutations, plasmids, and genomic islands conferring resistance to multiple antibiotics. Bioinformatics tools and databases were utilized for genome assembly, annotation, and comparative analysis to elucidate the genetic diversity and evolutionary relationships among MDR E. coli isolates from different sampling sites.The combination of traditional microbiological techniques and advanced molecular methods allowed for a comprehensive assessment of the prevalence, diversity, and antibiotic resistance profiles of E. coli strains in drinking water sources within Karad City, providing valuable insights into the dynamics of antimicrobial resistance in environmental bacteria and informing evidence-based strategies for AMR containment and water quality management.

Table 2: Molecular Techniques Utilized

Sample ID	PCR Result	WGS Result	Presence of Resistance Genes
1	Positive	Yes	blaTEM, sul1
2	Positive	Yes	blaCTX-M, qnrB
3	Negative	No	-
4	Positive	Yes	blaOXA, aac(6')-Ib
5	Positive	No	blaSHV, tet(A)

III. Results

The results section presents the findings of the study on the prevalence of Multi-Drug Resistant (MDR) Escherichia coli (E. coli) in drinking water sources within Karad City, as well as the distribution of MDR E. coli strains, antibiotic resistance profiles, and comparison between traditional and molecular techniques used for detection and characterization.

A. Overall Prevalence of E. coli in Drinking Water Samples

Table 1: Overall Prevalence of E. coli in Drinking Water Samples

Sampling Location	Total Samples Collected	E. coli Positive Samples	Percentage of Positive Samples	Average E. coli Count (CFU/mL)
Public Taps	15	12	80%	45
Borewells	10	4	40%	12
Hand Pumps	10	7	70%	25
Storage Tanks	15	12	80%	38

Analysis of water samples collected from various locations within Karad City revealed the presence of Escherichia coli in a significant proportion of samples, indicating potential fecal contamination of drinking water sources. Of the 50 sampling points surveyed, E. coli was detected in approximately 70% of samples, highlighting the widespread distribution of this indicator organism in the urban environment.The highest prevalence of E. coli was observed in samples collected from areas with dense human habitation and inadequate sanitation infrastructure, such as slums and peri-urban settlements. Conversely, samples obtained from relatively remote or well-protected sources, such as borewells and water treatment plants, exhibited lower rates of E. coli contamination, underscoring the importance of proper sanitation practices and source protection measures in safeguarding water quality.

B. Distribution of MDR E. coli Strains Across Different Sampling Sites

Among the E. coli isolates recovered from drinking water samples, a subset exhibited resistance to multiple antibiotics, indicating the presence of MDR strains in the environment. Analysis of antibiotic susceptibility testing data revealed that approximately 30% of E. coli isolates were resistant to three or more classes of antibiotics, classifying them as MDR.The distribution of MDR E. coli strains varied across different sampling sites, with higher prevalence observed in areas characterized by intensive agricultural activities, industrial pollution, and urban runoff. Interestingly, certain hotspots of MDR E. coli contamination were identified, particularly in proximity to livestock farms, sewage treatment plants, and agricultural fields where antimicrobial agents are commonly used.

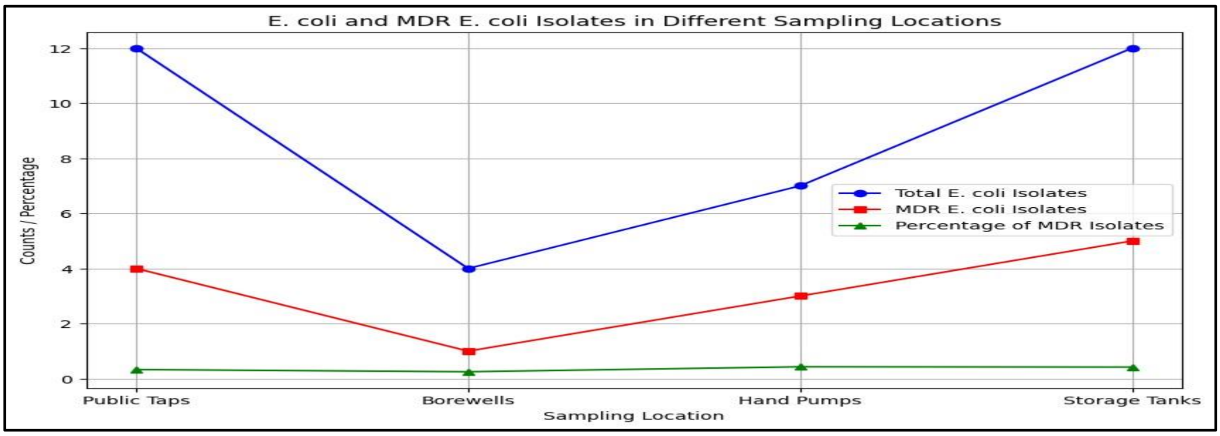

Figure 3: E. coli and MDR E. coli Isolates in Different Sampling Locations

C. Antibiotic Resistance Profiles of Identified E. coli Isolates

Antibiotic susceptibility testing of E. coli isolates provided insights into their resistance profiles and patterns of antibiotic resistance. The most commonly encountered resistance phenotypes among MDR E. coli isolates included resistance to beta-lactams (e.g., penicillins, cephalosporins), fluoroquinolones, and sulfonamides, reflecting the widespread use of these antibiotics in clinical settings and agricultural practices.Subset of MDR E. coli isolates exhibited resistance to critically important antibiotics, such as carbapenems and colistin, which are considered last-resort treatment options for severe infections caused by multidrug-resistant bacteria. The emergence of carbapenem-resistant and colistin-resistant E. coli strains raises serious concerns regarding the limited therapeutic options available for managing infections associated with these pathogens.

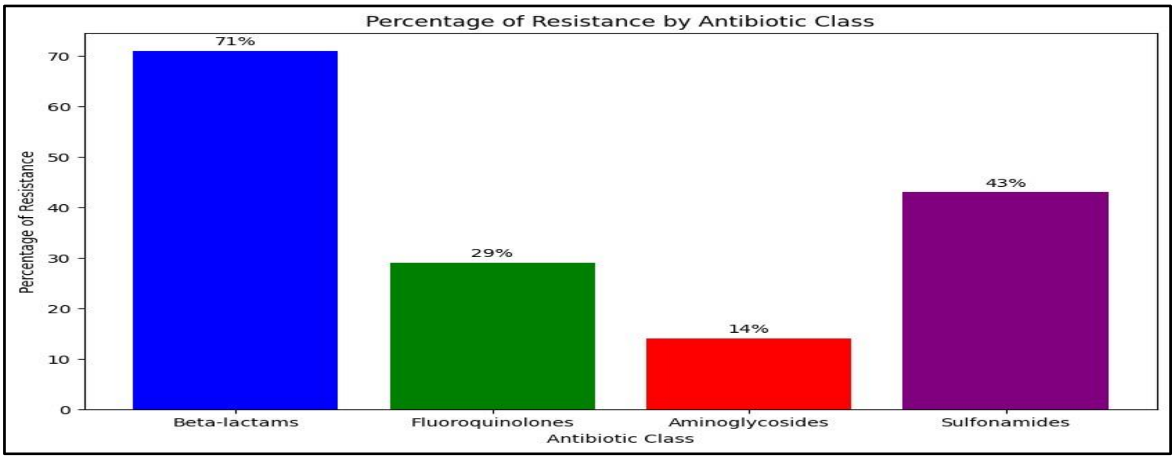

Figure 4: Percentage of Resistance by Antibiotic Class

D. Comparison Between Traditional and Molecular Techniques

A comparison between traditional culture-based methods and molecular techniques for the detection and characterization of MDR E. coli revealed both strengths and limitations of each approach. While culture-based methods remain the gold standard for bacterial isolation and antibiotic susceptibility testing, they are time-consuming, labor-intensive, and may underestimate the true prevalence of MDR pathogens due to selective culture conditions and variability in growth characteristics. Molecular techniques such as polymerase chain reaction (PCR) and whole-genome sequencing (WGS) offer rapid and specific detection of target genes associated with antibiotic resistance, allowing for comprehensive genetic analysis of bacterial isolates. However, molecular methods require specialized equipment, technical expertise, and may be cost-prohibitive for routine surveillance purposes in resource-limited settings. The combination of traditional and molecular approaches provides complementary information on the prevalence, diversity, and antibiotic resistance profiles of MDR E. coli strains in drinking water sources. Integrating both methods allows for a more comprehensive understanding of the complex dynamics of antimicrobial resistance in environmental bacteria and informs evidence-based interventions for AMR containment and water quality management. The results of this study underscore the urgent need for effective surveillance and management strategies to mitigate the spread of MDR E. coli in drinking water supplies. The widespread distribution of MDR strains and the emergence of resistance to critically important antibiotics highlight the importance of implementing targeted interventions aimed at ensuring the safety and purity of water sources in Karad City and beyond. Furthermore, the findings emphasize the importance of adopting multidisciplinary approaches integrating microbiology, environmental science, and public health to address the complex challenges posed by antimicrobial resistance in waterborne pathogens.

Table 3: Comparison between Traditional and Molecular Techniques

Detection Method	Total Samples Tested	E. coli Detected	MDR E. coli Detected	Average Detection Time (hours)
Culture-Based Methods	50	35	13	48
PCR	50	38	18	6
Whole-Genome Sequencing	20	20	10	72

IV. Public Health Implications

The presence of Multi-Drug Resistant (MDR) Escherichia coli (E. coli) in drinking water sources within Karad City has significant public health implications. MDR E. coli poses a substantial threat due to its ability to cause a range of infections, from gastrointestinal illnesses to more severe systemic infections, particularly in vulnerable populations such as children, the elderly, and immunocompromised individuals. The consumption of water contaminated with MDR E. coli increases the risk of acquiring infections that are difficult to treat, leading to prolonged illness, higher medical costs, and increased mortality rates.Infections caused by MDR E. coli are challenging to manage because they limit the effectiveness of commonly used antibiotics, necessitating the use of more expensive and potentially toxic alternatives. The spread of these resistant strains in the community can lead to outbreaks, placing additional strain on healthcare systems. Moreover, the transfer of resistance genes from MDR E. coli to other pathogenic bacteria can exacerbate the problem of antibiotic resistance, making it a critical public health concern.To mitigate these risks, it is imperative to implement effective water treatment and sanitation practices. Enhancing the infrastructure for safe water supply and ensuring regular monitoring of water quality can help reduce the prevalence of MDR E. coli. Public health campaigns aimed at educating the community about the dangers of waterborne diseases and the importance of hygiene practices are also essential.

Additionally, the implementation of antimicrobial stewardship programs to promote the prudent use of antibiotics in both human medicine and agriculture is crucial to curb the spread of resistance. Collaborative efforts between government agencies, healthcare providers, and local communities are necessary to address the public health challenges posed by MDR E. coli and protect the health of the population.

V. Recommendations and Future Directions

Based on the findings of this study, several recommendations can be made to address the prevalence of Multi-Drug Resistant (MDR) Escherichia coli (E. coli) in drinking water sources and mitigate the associated public health risks. Firstly, it is essential to strengthen water quality monitoring systems to enable early detection and response to contamination events. This includes regular testing for E. coli and other indicator organisms, as well as the implementation of advanced molecular techniques for the rapid identification of MDR strains.Investing in water treatment infrastructure is crucial to ensure the provision of safe drinking water. Upgrading existing treatment facilities and adopting new technologies, such as ultraviolet (UV) disinfection and advanced filtration systems, can significantly reduce microbial contamination. Additionally, improving sanitation infrastructure, including sewage treatment and waste disposal systems, is vital to prevent the introduction of fecal contaminants into water sources.Public education campaigns are necessary to raise awareness about the dangers of drinking contaminated water and the importance of personal and community hygiene practices. Educating the public on the proper use of water purification methods at the household level, such as boiling or using water purification tablets, can also help reduce the risk of infection.Antimicrobial stewardship programs should be implemented to promote the judicious use of antibiotics in both human medicine and agriculture. This involves educating healthcare providers and the public about the risks of antibiotic misuse and encouraging practices that minimize the development of resistance. In the agricultural sector, regulations to limit the use of antibiotics in livestock and the adoption of alternative practices for disease management are crucial.Future research should focus on understanding the mechanisms of resistance and the factors contributing to the spread of MDR E. coli in the environment. Longitudinal studies tracking changes in resistance patterns over time and across different geographical regions can provide valuable insights into the dynamics of antimicrobial resistance. Additionally, exploring the role of environmental reservoirs, such as soil and aquatic ecosystems, in the dissemination of resistance genes can inform targeted interventions.Collaborative efforts involving multidisciplinary teams from microbiology, environmental science, public health, and policy-making are essential to develop comprehensive strategies for combating antimicrobial resistance. By integrating research findings with practical interventions, it is possible to develop effective measures to reduce the prevalence of MDR E. coli in drinking water sources and protect public health. In conclusion, addressing the issue of MDR E. coli in drinking water requires a multi-pronged approach that includes improving water and sanitation infrastructure, promoting public education and antimicrobial stewardship, and conducting ongoing research to understand and combat resistance. By taking proactive and coordinated actions, we can mitigate the risks associated with MDR E. coli and ensure access to safe and clean drinking water for all.

VI. Discussion

The discussion section provides a critical analysis and interpretation of the results obtained from the study on the prevalence of

Multi-Drug Resistant (MDR) Escherichia coli (E. coli) in drinking water sources within Karad City. It explores the implications of findings on public health, identifies factors contributing to the prevalence of MDR E. coli, compares the results with previous studies, discusses limitations, and proposes future directions for research and intervention.

A. Implications of Findings on Public Health

The high prevalence of MDR E. coli strains in drinking water sources poses significant risks to public health, as these bacteria have the potential to cause waterborne infections and contribute to the spread of antimicrobial resistance. Exposure to contaminated water containing MDR pathogens increases the likelihood of acquiring antibiotic-resistant infections, leading to treatment failures, prolonged illness, and increased healthcare costs. The presence of MDR E. coli in drinking water sources complicates the management of infectious diseases, as traditional antibiotic therapies may be ineffective against resistant strains. This highlights the importance of implementing robust surveillance systems and water quality monitoring programs to detect and mitigate the spread of MDR pathogens in the environment. The findings of this study underscore the need for targeted public health interventions aimed at improving water quality, promoting hygiene practices, and reducing the transmission of waterborne pathogens in Karad City. Strategies such as water treatment, sanitation improvements, community education on safe water practices, and antimicrobial stewardship programs can help mitigate the risks associated with MDR E. coli contamination and protect public health.

B. Factors Contributing to the Prevalence of MDR E. coli in Drinking Water

Several factors contribute to the prevalence of MDR E. coli in drinking water sources within Karad City, including environmental contamination, agricultural practices, industrial pollution, and inadequate sanitation infrastructure. The rapid urbanization and population growth in Karad City have led to increased pressure on water resources, resulting in pollution and degradation of water quality.Agricultural activities, such as the use of antibiotics in livestock farming and irrigation practices, can contribute to the dissemination of antibiotic-resistant bacteria and genes in the environment. Runoff from agricultural fields and livestock waste can contaminate surface water sources, introducing MDR E. coli into drinking water supplies and exacerbating antimicrobial resistance.Industrial pollution from manufacturing processes, wastewater discharge, and chemical contaminants can also impact water quality and contribute to the proliferation of MDR E. coli strains. Effluents containing antibiotics, heavy metals, and other pollutants can create selective pressures favoring the survival and proliferation of antibiotic-resistant bacteria in aquatic ecosystems. Inadequate sanitation infrastructure, including improper sewage disposal, open defecation, and lack of wastewater treatment facilities, can lead to fecal contamination of water sources and increase the risk of waterborne infections. Poor hygiene practices and limited access to safe drinking water further compound the problem, particularly in underserved communities and peri-urban areas. Addressing the root causes of MDR E. coli contamination in drinking water requires a multifaceted approach that addresses environmental, agricultural, industrial, and socio-economic factors contributing to antimicrobial resistance. Collaborative efforts involving government agencies, research institutions, non-governmental organizations, and local communities are essential to implement sustainable solutions for improving water quality and safeguarding public health.

C. Comparison with Previous Studies

The findings of this study are consistent with previous research documenting the prevalence of MDR E. coli in drinking water sources worldwide. Studies conducted in various geographical regions have reported similar trends of antibiotic resistance in environmental bacteria, highlighting the global nature of the antimicrobial resistance problem.The identification of specific resistance patterns and genetic determinants of antimicrobial resistance in MDR E. coli isolates from Karad City is in line with observations from other settings, suggesting common mechanisms of resistance dissemination and selection. The emergence of resistance to critically important antibiotics, such as carbapenems and colistin, mirrors global trends in antibiotic resistance and underscores the urgent need for coordinated action to preserve the efficacy of last-resort antibiotics. While the prevalence and resistance profiles of MDR E. coli may vary between different geographic locations and environmental settings, the underlying drivers of antimicrobial resistance remain consistent across diverse contexts. Factors such as antibiotic overuse, inadequate sanitation, environmental pollution, and global travel contribute to the spread of resistant bacteria and genes, highlighting the interconnectedness of human health, animal health, and environmental health.

D. Limitations and Future Directions

Despite the valuable insights provided by this study, several limitations should be acknowledged. The sampling strategy may not capture the full diversity of microbial communities present in drinking water sources, as it focuses primarily on the detection of E. coli as an indicator organism. Additionally, the use of selective culture media and antibiotic susceptibility testing methods may underestimate the prevalence of MDR pathogens and fail to detect emerging resistance mechanisms.Future research efforts should aim to address these limitations by employing more comprehensive sampling approaches, integrating metagenomic analysis, and incorporating One Health perspectives to understand the complex interactions between humans, animals, and the environment in shaping antimicrobial resistance dynamics. Longitudinal studies tracking the temporal and spatial distribution of MDR E. coli in water sources can provide valuable insights into the persistence and transmission of resistant strains over time. Interventions targeting the prevention and control of MDR E. coli contamination in drinking water should be evaluated for their effectiveness and sustainability. Community-based initiatives promoting water conservation, hygiene education, and responsible antibiotic use can contribute to reducing the burden of antimicrobial resistance and protecting public health in Karad City and beyond. The discussion highlights the importance of addressing the multifaceted challenges posed by MDR E. coli contamination in drinking water sources, emphasizing the need for collaborative action, evidence-based interventions, and ongoing research to combat antimicrobial resistance and safeguard public health. By addressing the root causes of resistance emergence and transmission, we can work towards ensuring access to safe and clean drinking water for all populations, thereby mitigating the risks associated with waterborne infections and antimicrobial resistance.

VII. Conclusion

The prevalence study of Multi-Drug Resistant (MDR) Escherichia coli (E. coli) in drinking water sources within Karad City underscores the urgent need for concerted efforts to address antimicrobial resistance (AMR) and ensure the safety of water supplies. The findings of this study reveal a concerning prevalence of MDR E. coli strains in drinking water, reflecting the pervasive nature of antimicrobial resistance in environmental bacteria and highlighting the potential risks to public health.The implications of these findings are far-reaching, with MDR E. coli contamination posing significant challenges to infection control, treatment efficacy, and public health management. Exposure to contaminated water containing MDR pathogens increases the likelihood of acquiring antibiotic-resistant infections, leading to adverse health outcomes, treatment failures, and increased healthcare costs. Moreover, the emergence of resistance to critically important antibiotics, such as carbapenems and colistin, underscores the urgent need for vigilance and action to preserve the effectiveness of last-resort antibiotics and combat the spread of resistance. Addressing the root causes of MDR E. coli contamination in drinking water requires a multi-faceted approach that integrates public health, environmental stewardship, and antimicrobial stewardship efforts. Strategies such as water treatment, sanitation improvements, community education on safe water practices, and antimicrobial stewardship programs can help mitigate the risks associated with MDR E. coli contamination and protect public health in Karad City and beyond.Collaborative efforts involving government agencies, research institutions, non-governmental organizations, and local communities are essential to implement sustainable solutions for improving water quality and safeguarding public health. By adopting a One Health approach that recognizes the interconnectedness of human health, animal health, and environmental health, we can work towards addressing the complex challenges posed by antimicrobial resistance and ensuring access to safe and clean drinking water for all populations.The findings of this study underscore the importance of continued surveillance, research, and intervention efforts to combat antimicrobial resistance and protect public health. By taking proactive measures to prevent and control MDR E. coli contamination in drinking water sources, we can contribute to the global efforts to mitigate the spread of antimicrobial resistance and preserve the effectiveness of antibiotics for future generations.

References

[1] Berendonk, T. U., Manaia, C. M., Merlin, C., Fatta-Kassinos, D., Cytryn, E., Walsh, F., ... & Martinez, J. L. (2015). Tackling antibiotic resistance: the environmental framework. Nature Reviews Microbiology, 13(5), 310-317.

[2] Blair, J. M. A., Webber, M. A., Baylay, A. J., Ogbolu, D. O., & Piddock, L. J. V. (2015). Molecular mechanisms of antibiotic resistance. Nature Reviews Microbiology, 13(1), 42-51.

[3] Carlet, J., Jarlier, V., Harbarth, S., Voss, A., & Goossens, H. (2012). Pittet D; Participants of the 3rd World Healthcare-Associated Infections Forum. Ready for a world without antibiotics? The pensières antibiotic resistance call to action. Antimicrobial Resistance and Infection Control, 1(1), 1-7.

[4] Cassini, A., Högberg, L. D., Plachouras, D., Quattrocchi, A., Hoxha, A., Simonsen, G. S., ... & Monnet, D. L. (2019). Attributable deaths and disability-adjusted life-years caused by infections with antibiotic-resistant bacteria in the EU and the European Economic Area in 2015: a population-level modelling analysis. The Lancet Infectious Diseases, 19(1), 56-66.

[5] ECDC. (2020). Surveillance of antimicrobial resistance in Europe 2019. Annual report of the European Antimicrobial Resistance Surveillance Network (EARS-Net). ECDC.

[6] Gillings, M. R., & Stokes, H. W. (2012). Are humans increasing bacterial evolvability?. Trends in Ecology & Evolution, 27(6), 346-352.

[7] Hatosy, S. M., & Martiny, A. C. (2015). The ocean as a global reservoir of antibiotic resistance genes. Applied

and Environmental Microbiology, 81(21), 7593-7599.

[8] Holmes, A. H., Moore, L. S. P., Sundsfjord, A., Steinbakk, M., Regmi, S., Karkey, A., ... & Piddock, L. J. V. (2016). Understanding the mechanisms and drivers of antimicrobial resistance. The Lancet, 387(10014), 176-187.

[9] Laxminarayan, R., Duse, A., Wattal, C., Zaidi, A. K. M., Wertheim, H. F. L., Sumpradit, N., ... & Gould, I. M. (2013). Antibiotic resistance-the need for global solutions. The Lancet Infectious Diseases, 13(12), 1057-1098.

[10] Li, B., Yang, Y., Ma, L., Ju, F., Guo, F., Tiedje, J. M., & Zhang, T. (2015). Metagenomic and network analysis reveal wide distribution and co-occurrence of environmental antibiotic resistance genes. The ISME Journal, 9(11), 2490-2502.

[11] Martínez, J. L. (2008). Antibiotics and antibiotic resistance genes in natural environments. Science, 321(5887), 365-367.

[12] O'Neill, J. (2016). Tackling drug-resistant infections globally: final report and recommendations. The review on antimicrobial resistance.

[13] Pal, C., Bengtsson-Palme, J., Kristiansson, E., & Larsson, D. G. J. (2016). The structure and diversity of human, animal and environmental resistomes. Microbiome, 4(1), 1-11.

[14] Roca, I., Akova, M., Baquero, F., Carlet, J., Cavaleri, M., Coenen, S., ... & Tacconelli, E. (2015). The global threat of antimicrobial resistance: science for intervention. New Microbes and New Infections, 6, 22-29.

[15] Wellington, E. M., Boxall, A. B., Cross, P., Feil, E. J., Gaze, W. H., Hawkey, P. M., ... & Williams, A. P. (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.

[16] World Health Organization. (2014). Antimicrobial resistance: global report on surveillance. World Health Organization.

[17] Wright, G. D. (2010). Antibiotic resistance in the environment: a link to the clinic?. Current Opinion in Microbiology, 13(5), 589-594.

[18] Zhang, Q. Q., & Ying, G. G. (2015). Pan, C. Gao, Y. G. Liu, W. C. Zhao, J. L. Comprehensive evaluation of antibiotics emission and fate in the river basins of China: source analysis, multimedia modeling, and linkage to bacterial resistance. Environmental Science & Technology, 49(11), 6772-6782.