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The Genetic Role of Escherichia Coli in Surface Water Quality Monitoring: A Molecular Review

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KEYWORDS

surface water; Escherichia coli; identification methods; marker genes

ABSTRACT

Surface water, including rivers, lakes, and waterfalls, which are closely linked to daily human activities, is highly vulnerable to microbial contamination, particularly by Escherichia coli. This article reviews the role of specific E. coli marker genes in surface waters, molecular detection methods, and target genes used for E. coli identification in such environments. The review was conducted by synthesizing recent literature on the genetic detection of E. coli in surface water environments, using keyword searches such as Escherichia coli, identification methods, surface water, molecular markers, virulence genes, PCR, and water contamination. E. coli exhibits remarkable genetic diversity, driven by exceptional adaptability and shaped by horizontal gene transfer and extensive genomic variation. Approaches to E. coli identification have evolved from traditional culture techniques to molecular and integrated methods. The presence and activity of E. coli in water are influenced by the expression of specific genes that enable accurate detection and identification. Detection of universal markers such as 16S rRNA is essential for rapidly confirming bacterial presence and identity before conducting more specific analyses. Molecular detection of E. coli pathotypes relies on genetic markers closely associated with their virulence traits, such as EHEC, ETEC, EPEC, EAEC, DAEC, and ExPEC, highlighting the role of surface waters as significant reservoirs for the dissemination of enteric pathogenic bacteria.

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INTRODUCTION

Water is a strategic natural resource that plays a vital role in sustaining life, ecosystems, and human activities. Water containing pathogenic microorganisms can cause disease transmission, which has become a global concern (Suzuki et al., 2023). Some surface water sources, such as rivers, lakes, and waterfalls, are highly susceptible to microbial contamination caused by inadequately treated domestic, agricultural, and industrial wastewater discharge (Debassi et al., 2025). One of the most common indicators used to assess biological contamination in surface water is the presence of Escherichia coli, a Gram-negative bacterium found in the normal intestinal flora of humans. The presence of E. coli in surface water is considered an indicator of contamination and a potential health hazard (Nuozzi et al., 2025).

Several previous studies have examined the role of Escherichia coli as an indicator of surface water quality and its genetic characterization. Zarić et al. (2023) and Tamsa and Nola (2023) emphasized the importance of E. coli detection in water monitoring systems, including

its use in microcosm experiments with plant extracts, demonstrating that E. coli remains a key marker for assessing microbiological contamination in various aquatic environments. Moussa et al. (2025) conducted field research showing that E. coli presence in the Niger River is significantly influenced by human activities and environmental factors such as rainfall and nutrient availability, highlighting the complex interactions between anthropogenic pressures and bacterial contamination. Cho (2019) investigated the persistence of E. coli in surface waters of mixed-use watersheds and found strong relationships with environmental factors, offering valuable insights into how E. coli dynamics are influenced by seasonal variations and land use patterns. Furthermore, McLarnan (2017) revealed that E. coli's ability to persist in sediment can complicate efforts to trace the exact source of contamination, suggesting that water quality monitoring should consider both the water column and sediment compartments. Gilfillan et al. (2018) applied Maxent modeling approaches to predict E. coli distribution based on environmental variables such as temperature and dissolved oxygen, demonstrating the utility of advanced statistical methods in understanding and predicting bacterial contamination patterns in surface waters. Studies conducted in urban environments by Dimpor et al. (2025) and Buckalew et al. (2015) showed almost universal detection rates of E. coli and a uniform distribution in the water column, further reinforcing its reliability as an indicator of fecal contamination across diverse aquatic settings.

Detection and quantification of E. coli in surface water are crucial for monitoring water quality, preventing waterborne diseases, mitigating bioterrorism risks, and supporting environmental risk assessments (Soheili et al., 2020). In recent years, the development of molecular-based techniques has become increasingly important for the identification of E. coli, particularly through the detection of specific marker genes in surface water such as uidA, lacZ, and fimH, as well as virulence genes including stx1, stx2, and eae (Arai et al., 2022). This genetic approach offers significant advantages in terms of speed, accuracy, and the ability to differentiate between pathogenic and non-pathogenic strains (Emurotu et al., 2024).

This review aims to explore the role of specific marker genes of E. coli in surface water, discussing the relevance of molecular detection methods, commonly used gene targets, and the future prospects of molecular-based water quality monitoring. The article makes a theoretical contribution by advancing the understanding of Escherichia coli's genetic role in surface water ecosystems, particularly in relation to marker gene diversity and pathogenic potential. Academically, it serves as a comprehensive reference for students and researchers in microbiology, environmental science, and public health who are interested in molecular-based water quality monitoring. Practically, it provides environmental agencies with insights into the latest molecular methods for rapid and accurate detection of fecal contamination, supports public health policymakers in developing water safety plans and early warning systems for waterborne diseases, and underscores the importance of integrating molecular approaches into routine monitoring programs to detect emerging pathogenic strains and antimicrobial resistance genes—ultimately contributing to improved public health protection and environmental sustainability.

METHOD

This article review was conducted using a qualitative, literature-based approach to synthesize the latest information on genetic detection of E. coli in surface water environments. A comprehensive literature search and selection were conducted by collecting literature through trusted scientific databases such as PubMed, ScienceDirect, Scopus, SpringerLink, and Web of Science. Keywords used in the search process included Escherichia coli, identification methods, surface water, molecular markers of E. coli, virulence genes of E. coli, PCR, and water contaminations. From the article selection process, approximately 25 articles that met the criteria were reviewed in depth. Several selected articles were analyzed qualitatively and a summary table was created to compare various specific marker genes and molecular methods across various studies (Alimi et al., 2023).

RESULT AND DISCUSSION

E. coli as a Biological Indicator of Surface Water Quality

E. coli is an important biological indicator in assessing surface water quality because it reflects recent fecal contamination and potentially contains enteric pathogens. Various studies have identified E. coli as a key marker of microbiological contamination that can impact surface water quality. Studies by Zarić et al. (2023) and Tamsa & Nola (2023) emphasize the importance of E. coli detection in water monitoring systems, including its use in microcosm experiments with plant extracts. Field research, such as that of Moussa et al. (2025) and Lyautey, shows that the presence of E. coli in water is significantly influenced by human activities and environmental factors such as rainfall and nutrients. Research by McLarnan (2017) revealed that E. coli's ability to persist in sediment can make it difficult to trace the exact source of contamination. Modeling approaches such as Maxent (Gilfillan et al., 2018) have also been used to predict E. coli distribution based on environmental variables such as temperature and dissolved oxygen.

Meanwhile, studies in urban environments by Dimpor et al. (2025) and Buckalew et al. (2015) showed almost universal detection rates, as well as a uniform distribution in the water column, which strengthens its reliability as an indicator. However, the transport characteristics of E. coli, which differ from viruses, suggest that using a single indicator may not be sufficient to reflect all microbiological risks (Korajkic et al., 2020). Therefore, although E. coli is very useful as an early indicator, water quality monitoring approaches should be accompanied by complementary methods to improve the accuracy and sensitivity of contamination detection.

The presence and activity of E. coli in waters is influenced by the expression of certain genes that allow for specific detection and identification, such as the detection of the uidA gene (encoding the β-glucuronidase enzyme (Taskin et al., 2011), the lacZ gene (encoding β-galactosidase), 16S rRNA (housekeeping gene) (Heijnen et al., 2024). The presence of E. coli also acts as an indicator of fecal contamination and the risk of the presence of other pathogens such as Salmonella or Giardia (Chubaka et al., 2018). E. coli strains are also able to adapt in general waters that have genes supporting resistance to UV, low nutrients, and biofilms. For example, genes in the Pho or Rpos regulon (stress regulator) help them survive in extreme water conditions (Chen & Goulian, 2019). The genetics of E. coli also plays a role in the

detection of resistance genes such as bla_TEM, sul1, and intl1, in studies of AMR contamination in surface water, indicating that E. coli is not only an indicator of fecal contamination but also an indicator of genetic contamination due to pharmaceutical or hospital waste (Reichert et al., 2021).

E. coli Genetics

E. coli is a Gram-negative, rod-shaped, facultative anaerobic bacterium belonging to the Enterobacteriaceae family (Riley, 2020). This bacterium has a relatively small but highly plastic genome, consisting of a core genome of approximately 2,398 genes and an accessory genome of 5,182 genes (Chauhan et al., 2024). The overall E. coli pangenome can encompass approximately 25,000 gene families (GFs), reflecting its high adaptability to a wide range of environmental conditions (Tantoso et al., 2022). E. coli exhibits high levels of horizontal gene transfer, recombination, and genome rearrangement, resulting in genetic diversity and a wide variety of pathotypes (D. Yu et al., 2021).

E. coli possesses extremely high genetic diversity, supported by its remarkable adaptability and evolution through horizontal gene transfer and extensive genomic variation. Horesh et al. (2021) showed that a collection of more than 10,000 E. coli genomes contains comprehensive information regarding its virulence profile, resistance, and genetic diversity, strengthening the evidence that this species is highly genomically plastic. E. coli can acquire virulence and resistance genes through mobile genetic elements such as plasmids, phages, and genomic islands (Saini et al., 2024), which allow it to adapt to various environments, including human and animal habitats.

The genome of multiresistant strains such as LCT-EC001 (Zhang et al., 2019) contains dozens of resistance genes, including those against last-line antibiotics. In addition, genetic variation also influences pathogenicity, as shown by Burgaya et al. (2023), who significantly distinguished between isolates causing bloodstream infections and those that are commensal. Research by Tiwari et al. (2023) also shows that E. coli has host-specific genes, indicating a high level of adaptation to humans, cattle, and poultry. With the ability to interact genetically as described by the eSGA method (Gagarinova et al., 2021), as well as its wide phylogenetic distribution (Salman, 2024), E. coli is an ideal model for understanding bacterial evolution and its clinical risks.

E. coli plays a dual role in human health, not only as a gut commensal contributing to intestinal homeostasis but also as a cause of various diseases, including gastroenteritis, urinary tract infections, neonatal meningitis, and sepsis.

Marker Genes for Molecular Detection of E. coli

Molecular detection of E. coli can begin with the detection of universal markers such as 16S rRNA to quickly confirm the presence and type of bacteria before proceeding to more specific further tests (Moorlag et al., 2023). Research by Paisan et al. (2025) demonstrated the isolation of dye-degrading bacteria from waters with varying levels of pollution. 16S rRNA gene sequencing confirmed the presence of E. coli along with other species such as Aeromonas and Shewanella. This study confirms the role of 16S rRNA as the gold standard for taxonomic identification of environmental bacteria. The study of Yu et al. (2025) focused on the molecular mechanisms in E. coli cells, showing that the signaling molecule s-di-GMP can inhibit the

activity of Rlml methyltransferase on rRNA, thereby disrupting ribosome assembly, while strengthening the relevance of rRNA analysis, including 16S, in the study of structural biology and bacterial stress responses. Another study by Dawood & Abdullah (2025) applied 16S rRNA-based PCR for the rapid identification of pathogenic bacteria such as K. pneumoniae; this study proved the flexibility of this method in detecting pathogens with a high level of accuracy. Meanwhile, the study of Sheet et al. (2025) developed a LAMP method for the rapid detection of Staphylococcus aureus, which has the potential to be adapted to target the 16S rRNA gene of E. coli due to its advantages in speed, sensitivity, and efficiency.

Molecular detection of E. coli pathotypes relies on specific genetic markers closely related to their virulence. For example, ETEC strains can be identified by the presence of genes encoding heat-labile (LT) and/or heat-stable (ST) enterotoxins, while EHEC and STEC are detected by the presence of stx1 and stx2 (Shiga toxins) (García & Fox, 2021). EPEC is characterized by the eae (intimin) and bfp (bundle-forming pilus) genes found in typical strains (Balière et al., 2015). Molecular detection of ExPEC is more challenging due to the lack of specific genetics. However, a widely accepted gene panel for identifying ExPEC includes papA/H and papC (P fimbriae), sfa/focDE (S and F1C fimbriae), afa/dra (Dr adhesin), iutA (aerobactin receptor), and kpsMII (group 2 capsule) (Zhu et al., 2017). These markers are commonly used in PCR-based assays to differentiate E. coli strains in clinical diagnostics and epidemiological surveillance (Wang et al., 2013).

Various studies have identified various E. coli virulence genes detected in surface water samples from different regions of the world. The eagg gene, specific for Enteroaggregative E. coli (EAEC), was found to be the dominant gene in E. coli isolates from Bangladeshi surface water, although only 11% of isolates carried the virulence gene (Mou et al., 2024). In a study in Iran, the VT2 (43%), eltB (19%), lal (15%), PCVD (13%), and VT1 (3%) genes were detected with significant frequency, indicating the presence of EHEC, ETEC, and EIEC strains (Ranjbar & Khamesipour, 2017). Studies in Canada and Australia showed a high prevalence of stx2, eae, and astA genes, associated with STEC, EPEC, and EAEC, respectively. In Argentina, an E. coli O157:H7 strain from livestock surface water carried a combination of virulence genes such as stx2a, stx2c, eae, and ehxA, belonging to the high-virulence clade.

Other findings include the aggR, rfbO157, fliCH7, and flicH7 genes, which strengthen the evidence of the presence of potential pathogenic strains in aquatic environments (Abia et al., 2017). In general, these genes reflect the diversity of E. coli pathotypes such as EHEC, ETEC, EPEC, EAEC, DAEC, and ExPEC, which indicate that surface water can be an important reservoir for the spread of enteric pathogenic bacteria (García & Fox, 2021).

E. coli Detection Methods

E. coli identification approaches have evolved through the application of culture, molecular, and a combination of both methods. Culture methods, such as those used by Calarco and Dikobe, remain the basis for initial identification, using selective media such as TBX and mTEC agar, which demonstrate high specificity for E. coli. PCR-based molecular techniques are becoming increasingly dominant, as demonstrated in the studies of Adekanmbi et al. (2024) targeting the uidA gene, and by Ranjbar et al. (2017) using ERIC-PCR for genetic diversity analysis. Combination approaches have also emerged as more comprehensive strategies, such

as those employed by Janezic and Osińska, who combined phenotypic assays (API 20E, culture) with PCR to detect specific genes such as eaeA, uspA, and yaiO. Furthermore, new technologies such as biosensors are also beginning to be used, as reported in a study by Deshmukh & Roy (2023), which can rapidly detect very low colony counts. E. coli detection methods continue to evolve toward more sensitive, specific, and efficient approaches through the latest technological developments.

Future Challenges of E. coli in Surface Water

Surface water contamination by E. coli creates selective pressure that can drive antimicrobial resistance (Asif et al., 2024). Aquatic environments can be a primary reservoir for the evolution and spread of antimicrobial resistance genes (ARGs) such as blaCTX-M, blaTEM, qnrB19, and qnrS1 (Cutrupi et al., 2024). Antimicrobial resistance in surface water can develop into multidrug resistance (MDR) to various antibiotics such as ampicillin, cefotaxime, and ciprofloxacin (Magaña-Lizárraga et al., 2022).

Surface water contaminated with antimicrobial-resistant E. coli can become a source of human infection through various exposure routes, including drinking water consumption, recreational activities, and agricultural irrigation (Cho et al., 2023). Studies have shown that up to 61 CFU of ESBL-containing E. coli can be ingested during a single swim (Van Heijnsbergen et al., 2022). Studies on the interaction between environmental factors and resistance gene expression are still limited. Further research is needed to understand the molecular mechanisms underlying the development and spread of antimicrobial resistance in E. coli in aquatic environments (Asif et al., 2024).

CONCLUSION

The genetic role of E. coli as a surface water indicator lies in its ability to harbor and express molecularly detectable genes, representing the presence of potential fecal contamination, and reflecting environmental health risks through the monitoring of virulence and resistance genes. Genetic analysis is crucial for accurately distinguishing between fecal-derived strains and those adapted to aquatic environments. Future research should focus on developing sensitive molecular markers for emerging E. coli pathotypes and antimicrobial resistance genes in surface waters, supported by longitudinal studies on seasonal dynamics. Environmental agencies are encouraged to integrate molecular methods into routine monitoring programs alongside culture-based techniques and establish standardized protocols for data comparability. Public health authorities should develop early warning systems based on genetic detection to predict waterborne disease outbreaks, while fostering collaboration between researchers, agencies, and institutions to translate findings into effective water safety policies. Public education on protecting water sources and health risks is also essential. The application of emerging technologies such as next-generation sequencing and biosensors for real-time pathogen monitoring will further enhance water quality management and public health protection.

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