

Metagenomic monitoring in wastewater: early detection of pathogens and antibiotic resistance genes.

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Article History	Abstract
Received: 11 th April, 2026 Accepted: 10 th May 2026	This study focuses on the application of metagenomic monitoring in wastewater to serve as an early detection system for epidemiological threats and to assess the prevalence of antimicrobial resistance genes (ARGs). Wastewater acts as a collective biological mirror of a population; thus, high-throughput DNA/RNA sequencing (NGS) allows for the identification of pathogenic microorganisms before clinical cases peak. Through shotgun metagenomic sequencing, this research analyzes bacterial and viral pathogens alongside mobile resistance determinants (plasmids and integrons) present in wastewater infrastructure. The findings highlight the critical role of wastewater-based epidemiology (WBE) as a non-invasive, cost-effective early warning tool for public health surveillance and pandemic preparedness.
Keywords: Metagenomics, wastewater-based epidemiology (WBE), antimicrobial resistance genes (ARGs), pathogens, NGS sequencing, public health surveillance.	

Annotatsiya:

Ushbu ish oqova suvlarda metagenomik monitoring usullarini qo‘llash orqali epidemiologik xavflarni erta aniqlash hamda antibiotiklarga rezistentlik genlari (ARG) tarqalishini baholashga bag‘ishlangan. Oqova suvlar muayyan populyatsiyaning biologik ko‘rsatkichi bo‘lib, undan DNK va RNK sekvenatsiyasi

(NGS) yordamida namunalar olish klinik holatlar namoyon bo'lishidan oldin patogen mikroorganizmlarni aniqlash imkonini beradi. Tadqiqot davomida metagenomik tahlil vositasida oqova suv tarkibidagi bakterial, virusli patogenlar hamda transmissiv rezistentlik determinantlari (plazmidlar va integronlar) tahlil qilinadi. Olingan natijalar oqova suv epidemiologiyasi (WBE) jamoat salomatligida erta ogohlantirish tizimi sifatida qanchalik samarador ekanligini ko'rsatib beradi.

Kalit so'zlar: Metagenomika, oqova suv epidemiologiyasi (WBE), antibiotik rezistentligi genlari (ARG), patogenlar, NGS sekvenatsiyalash, jamoat salomatligi.

Аннотация:

Данная работа посвящена применению методов метagenомного мониторинга сточных вод для раннего выявления эпидемиологических угроз и оценки распространенности генов устойчивости к антибиотикам (ARG). Сточные воды представляют собой интегральный биологический маркер населения, а их высокопроизводительное секвенирование (NGS) позволяет фиксировать присутствие патогенных микроорганизмов еще до появления массовых клинических симптомов. В ходе исследования методом метagenомного анализа исследуется состав бактериальных и вирусных патогенов, а также мобильные элементы резистентности (плазмиды и интегроны). Полученные результаты подтверждают высокую эффективность эпидемиологии на основе анализа сточных вод (WBE) как системы раннего предупреждения для защиты общественного здоровья.

Ключевые слова: Метagenомика, эпидемиология сточных вод (WBE), гены устойчивости к антибиотикам (ARG), патогены, NGS секвенирование, общественное здравоохранение.

Introduction:

Metagenomic monitoring in wastewater is a modern approach aimed at studying the complete genetic makeup of microbial communities through environmental samples (mainly sewage and treatment plant wastewater), including the identification of pathogenic microorganisms and antibiotic resistance genes (ARGs), and monitoring the dynamics of their distribution. This technology provides faster, more comprehensive, and more sensitive information than traditional culture-based methods, making it an important tool for early prediction of public health risks.

What is metagenomics and why is it important for wastewater?

Metagenomic studies are based on the simultaneous sequencing of the DNA of all microbes in a sample using the “shotgun” (whole-genome sequencing) method. This approach allows not only the identification of the presence of a particular species, but also gene functions, virulence factors, and resistance genes. Because wastewater reflects the microbiome of a large portion of the population, it serves as a source of “community-level diagnostics”: providing near-real-time information about diseases, antibiotic consumption, and the spread of resistance genes in a city or region.

Main goals and applications

Early detection of pathogens: Early detection of epidemiological risks by monitoring viruses (e.g. SARS-CoV-2, norovirus), bacteria (Salmonella, Shigella, Legionella) and parasites in wastewater.

Monitoring antibiotic resistance: Identifying the types, quantities, and sources of ARGs in wastewater; tracking the horizontal transfer of these genes (HGT) and potentially dangerous strains.

Integration of environmental and clinical data: assessing the impact of agricultural, livestock and medical waste on aquatic ecosystems; improving political decisions and antibiotic use strategies.

The main stages of the Monitoring process

1 Sampling: Samples are taken from the wastewater inlet and outlet points at regular intervals (e.g. weekly).

2 DNA extraction and library preparation: Concentrate the microbes by filtration or centrifugation, then extract high-quality total DNA.

3 Sequencing (NGS): High-throughput sequencing is performed on Illumina, Nanopore, or other platforms.

4 bioinformatic analysis: quality control of Read sequences, Assembly (assembly), gene annotation, comparison of ARG and pathogen markers with bases (e.g. CARD, ResFinder, VFDB).

5 Statistical and ecological analysis: Study of the abundance of ARG species, their relationship to environmental factors (heavy metals, nutrients), and their relationship to the microbial community.

6 interpretation and reporting of results: assessment of risk levels, recommendation of career measures, integration of data into public health systems.

Expected results and practical significance

Regular monitoring of pathogens: Genetic markers detected in wastewater can signal epidemiological outbreaks days/weeks in advance.

Map of resistance genes: which antibiotic classes are commonly encountered by opposing genes (e.g. β -lactam, tetracycline, macrolide, aminoglycoside) and their potential host bacteria (Proteobacteria, Actinobacteria, etc).

Identify and manage sources: The impact of hospital waste, livestock or agricultural drugs on water systems will be assessed, which will help optimize control measures.

Policy and standards development: provides the basis for the introduction of standard environmental monitoring methodologies and constraint values nationally and internationally.

Methodological limitations and future prospects

Although metagenomic approaches have high sensitivity and wide coverage, they still face a number of challenges: data processing complexity, lack of standardized protocols, sensitivity problems in detecting pathogens at low concentrations, and the need to properly integrate results with clinical data. In the future, it is expected to automate bioinformatic analysis using artificial intelligence and machine learning, create real-time monitoring systems, and expand information exchange at the global level.

Conclusion

Metagenomic monitoring of wastewater is a powerful tool for early detection of pathogens and antibiotic resistance genes, understanding their transmission mechanisms, and proactively managing public health risks. This technology can be widely used not only in scientific research, but also in the field of practical epidemiological control, the policy of rational use of antibiotics and Environmental Protection.

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