Journal of Kyzylorda Scholarly Review

P-ISSN:3006-0265 | E-ISSN:3007-4681. Published by the Open University of Kyzylorda

https://bulletin.ouk.kz/index.php/bulletin/index

THE ROLE OF ENVIRONMENTAL AND CLINICAL MICROBIOLOGY IN UNDERSTANDING INFECTIOUS DISEASE DYNAMICS

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Abstract. The emergence of Antimicrobial Resistance (AMR) and antimicrobial resistance making infectious diseases a major public health issue - population growth, urbanisation, climate change, international travel, environmental degradation and AmR continue to pose a significant global public health challenge. Clinical microbiology is important for the diagnosis of infection and for the identification of antimicrobial susceptibility profiles, whereas environmental microbiology is important to shed light on pathogen reservoirs and transmission routes found in water, wastewater, soil, air and healthcare settings. Although environmental and clinical surveillance are interdependent the systems frequently stand alone, which decreases the understanding of infectious disease dynamics.

The objectives of this study are to: (1) examine the association of environmental microbial contamination and human infectious diseases; (2) examine the role of environmental reservoirs in the persistence and transmission of pathogens; and (3) develop an integrated framework for disease surveillance and outbreak prediction. A sequential explanatory design, using mixed methods, was used. Environmental samples, clinical data of infections, microbiological data and statistical modeling were used to get quantitative information, and expert interviews were conducted with microbiology, ID and public health specialists to get qualitative information. Results indicated that the clinical infection occurrence was significantly positively correlated with environmental contamination indicators and that wastewater and hospital environments are key surveillance locations. The study also found that there were significant associations between environmental contamination and the spread of antimicrobial resistance.

The study adds to the expanding literature on One Health by showing the benefits of combining environmental and clinical microbiological data in a single surveillance approach. The recommended method facilitates the detection of outbreaks, the understanding of the modes of transmission, and the monitoring of antimicrobial resistance, and enhances knowledge-based public health decision-making. The study proposes creating integrated environmental-clinical surveillance systems and supports the development of wastewater-based monitoring programs, while enhancing intersectoral cooperation and providing a boost for adopting a One Health approach to tackle infectious diseases and support disease prevention, control, and response. The novelty of the study is its integration of all these aspects of environmental microbiology with clinical infection data, to improve understanding and prediction of the dynamics of infectious disease.

Keywords: Antimicrobial Resistance (AMR),Environmental Microbiology, Clinical Microbiology, One Health and Integrated Disease Surveillance.

Introduction

The Despite a considerable effort, the management of infectious diseases is still a major challenge in the world as emerging and re-emerging infectious diseases are continually coming and making the situation worse due to an increase in population, urbanisation, climate variations, international travelling, wars, change in land use, intensification of food system and the close proximity of humans, animals and contaminated environments. In fact, recent literature on One Health stresses that many infection threats are not just clinical – pathogens and the determinants of antimicrobial resistance are spread through water, wastewater, soil, air, food, animals, hospital effluents and community sanitation systems before they are detected in the clinical setting. This situation has been exacerbated by the rise of antimicrobial resistance which has decreased the effectiveness of traditional treatment options, and made it more likely that common infections are untreatable. In parallel, clinical microbiology has developed rapid automated culture technology, biochemical identification, antimicrobial susceptibility testing, polymerase chain reaction, sequencing, and several other tools for real-time genomic surveillance with more rapid pathogen identification and in-depth characterization of resistance mechanisms.

Despite the progress, there are still numerous public health surveillance systems in which data from environmental monitoring and clinical microbiological investigations is kept apart (McEwen & Collignon, 2018). Environmental laboratories can find contamination in wastewater, drinking water, rivers, soil or hospital environment, and in hospitals and clinical laboratories, there is a record of the incidence of infections, the distribution of isolates, and resistance information. If these datasets are not linked, it is hard to determine the transmission pathways, early warning signals may not be detected and environmental reservoirs are underestimated as a source of human infection. This separation is particularly problematic in an environment where water infrastructure, wastewater treatment, hospital infection-control systems and antimicrobial stewardship programs are stressed.

A major gap central to this study is the lack of empirical integration of environment microbiological evidence in to clinical infection data to explain the dynamics of infectious disease. While there are studies on the topics of environmental pathogens, wastewater epidemiology, clinical diagnostics, and antimicrobial resistance, there are fewer studies that focus on more than one of these aspects combined in a single analysis (Destoumieux-Garzón et al., 2018). This study is important as it provides a comprehensive strategy for public health officials, health care facilities, environmental agencies, surveillance programs and the policy makers. The study helps facilitate early detection of outbreaks; better management of environmental risks; better monitoring of antimicrobial resistance; and more coordinated One Health approaches to disease prevention.

Literature Review

Recent literature attests to the fact that these several different types of hosts, clinical environments, animals, wastewater, food chains and environmental reservoirs all contribute to the dynamics of infectious diseases. Environmental microbiology is emerging as an important component of early-warning surveillance and clinical microbiology of AMI provides patient-level diagnostic confirmation, antimicrobial susceptibility patterns and the generation of genomic evidence for outbreak investigation. The majority of surveillance systems remain in parallel environmental and clinical streams and do not have the capacity to identify transmission pathways along the One Health continuum (Mackenzie & Jeggo, 2019).

Environmental Microbiology

Environmental microbiology is a major component of the search for sources of infectious agents other than man. Pathogenic bacteria, viruses, fungi and parasites may be found in water, wastewater, soil, air, food contact surfaces, livestock and hospital effluents, as well as antimicrobial resistance genes. Wastewater-based epidemiology (WBE) has been highlighted in recent studies for detecting community-level pathogen circulation before there's an increase in clinical systems cases of a disease, and can be applied to enteric pathogens, respiratory viruses, antimicrobial resistance, and emerging infectious threats (Oliveira et al.,

2025).

Waterborne diseases continue to be a major concern in regions where sanitation provisions are non-existent or substandard, and where there is a lack of wastewater treatment plants or a drinking-water contamination problem exists. Transmission of infectious diseases can also occur via contaminated meat, vegetables, and even dairy products and food processing settings via the introduction of food borne pathogens. The soil and air microbiomes are now known to be part of the environmental transmission network as they can be contaminated with resistant organisms, fungal spores, and aerosolized pathogens from healthcare, agricultural and urban settings (Singh et al., 2024).

Clinical Microbiology

In the field of clinical microbiology, the detection, identification and antimicrobial susceptibility profile of the pathogens in patient specimens help in the control of infectious diseases. Although these remain crucial, molecular diagnostics, in particular by PCR and multiplex panels, whole genome sequencing and metagenomic next generation sequencing, have added to the capacity of the laboratory. Such tools enhance the identification of pathogens, confirmation of outbreaks, detection of resistance genes, and clinical-decision making (Wang et al., 2022) (Bianconi et al., 2023). Recent studies indicate that genomic technologies are playing an increasingly crucial role in differentiating related and unrelated isolates, tracking in-hospital transmission, and providing a connection between hospital infections and community or environmental sources (Relich et al., 2025). The use of these technologies is still not equal, however, especially in low resource regions.

Infectious Disease Dynamics

Pathogens, hosts, reservoirs, vectors, environment and health-system responses are all part of the dynamics of infectious diseases. Transmission may be direct, waterborne, foodborne, airborne, by contact with fomites, by animals or health care associated transmission. Risk and severity of infection is influenced by host factors including immunity status, age, comorbidities and antibiotic exposure, and hospitalization. Epidemiological models, genomic surveillance, and outbreak investigations can help understand the epidemiology of how pathogens are transmitted between populations and across settings (Struelens et al., 2024). Recent literature on One Health surveillance suggests that data on clinical cases should be coupled with wastewater and environmental data, animal health data, and population-level data for better disease predictions (Hill et al., 2024).

Antimicrobial Resistance

Environmental and clinical microbiology are strongly connected and one of the strongest connections is the development of antimicrobial resistance. Antibiotic resistance bacteria and genes can spread in wastewater systems, community environments, surface water, agricultural and livestock systems and hospitals. Antibiotic residues, heavy metals, disinfectants, poor sanitation, untreated hospital effluents, and inadequate wastewater treatment are factors that encourage the dissemination of resistance genes in the environment (Zhang et al., 2025). In practice, AMR results in delayed effective treatment, prolonged hospital stay, increased cost of treatment and increased risk of death. Wastewater and environmental monitoring studies in recent years have demonstrated that environmental monitoring can be used in addition to the hospital to detect resistant organisms and genes prior to their establishment in the clinic widely (Raziq et al., 2026) (Hughes et al., 2026).

One Health Perspective

The One Health approach underlines the fact that human health, animal health and the health of the environment are interlinked. Integrated surveillance systems integrate clinical microbiology, veterinary, wastewater, food-chain surveillance, environmental and genomic analysis to offer a wider perspective on the spread of infectious diseases and AMR (WHO, 2025). It is especially relevant in the case of zoonotic infections, food borne diseases, water borne outbreaks, and for pathogens with resistance that cross human-animal and animal-environmental barriers. New research advocates for coordinated laboratory networks and shared databases, standardized sampling practices, and cross-sector reporting to enhance early detection and outbreak response (Izydorczyk & Church, 2026).

Identified Literature Gap

While the individual studies have looked separately at environmental pathogens and/or

wastewater surveillance as well as clinical diagnostics and/or antimicrobial resistance, few studies have combined environmental microbiological evidence with clinical evidence of infections in a single analytical approach. This separation hinders the understanding of the role environmental contamination plays in clinical infection patterns, and reduces the strength of disease prediction. Thus, there is a need for multisectoral studies that incorporate the following: environmental sampling, clinical laboratory data, molecular diagnostic studies, antimicrobial resistance analysis, epidemiological analysis, and expert opinions. This integration has the potential to enhance the accuracy of surveillance and pinpoint the source or transmission, enhance implementation of One Health, and facilitate earlier public health intervention.

Research Objectives and Questions

Research Objectives

Objective 1: To explore the connection between contamination of the environment with microorganisms and the incidence of infectious disease among humans.

Objective 2: Determine the importance of environmental reservoirs in transmission and persistence of clinically important pathogens.

Objective 3: To create a unified approach, that integrates environmental and clinical microbiological data, to enhance infectious disease monitoring and control.

Research Questions

RQ1: How are environmental microbial contamination and occurrence of infectious diseases related?

RQ2: How does environmental reservoirs contribute to spread of clinically important pathogens?

RQ3: What is the potential of using integrated environmental and clinical microbiological data for disease surveillance and prediction of outbreaks?

Research Methodology

Research Design

This is a mixed method with sequential explanatory design to examine how environmental and clinical microbiology can contribute to better understanding of the dynamics of infectious diseases. The design starts with the quantitative phase of the environmental sampling, clinical data collection, lab analysis and statistical testing. The qualitative data then comes in the form of interviews and expert discussion, as a second stage, for the purpose of explaining, expanding and contextualising the quantitative results. Since the spread of an infectious disease can be measured using microbiological and epidemiological data and it can be interpreted using the expertise of surveillance systems, laboratory practices, gaps in environmental monitoring and public health policy, a sequential explanatory design is appropriate (Ivankova et al., 2006).

Quantitative Phase

The quantitative phase involves quantifying microbial contamination in environmental sources selected and comparing results to clinical infection data. Surface water, drinking water, wastewater, soil and hospital environment are the target media for environmental samples (Ahmed et al., 2020). These sites are chosen because they have the potential to be reservoirs, interfaces of transmission and pathways of contamination for clinical important pathogens. Sample integrity will be maintained through standard sampling procedures that will include sterile containers for sample collection, transport of the sample under cold chain, proper sample labeling and laboratory sample processing within recommended time limits.

Clinical data will be retrieved from hospital, clinical laboratory and public health center. The data will consist of the laboratory record of infection, prevalence of pathogens, antimicrobial resistance profile, incidence of infection, and demographic data (age, sex, residence, hospital unit, clinical specimen type). These variables will enable comparisons between the level of environmental contamination and the trend of clinical infections (Groseclose & Buckeridge, 2017).

Microbial identification including culture, biochemical analysis, PCR analysis and antimicrobial susceptibility testing will be done in the laboratory. Bacteria will be initially isolated using culture methods and biochemical tests will aid in identification of these organisms. Selected pathogens will be confirmed and resistance genes detected/confirmed by PCR analysis.

Antimicrobial susceptibility testing with standard microbiological methods will be done to identify resistance profiles of clinical and environmental isolate organisms (Relich et al., 2025).

SPSS will be used to analyse the quantitative data. Pathogen distribution and microbial counts, infection rates, resistance patterns and descriptive statistics of demographic characteristics will be summarized. Relationships between environmental contamination indicators and occurrence of clinical infection will be assessed using correlation analysis. Multiple regression analysis will be used to determine if environmental factors predict incidence of infection, after adjusting for demographic or institutional factors. Association between categorical variables, including pathogen type, sample source and resistance status will be investigated using chi-square tests. The probability of infection and resistant occurrence will be estimated using logistic regression with the indicators of environmental exposure. Environmental and clinical pathogen data sets will be grouped in space and/or microbiology using cluster analysis (Peng et al., 2002).

Qualitative Phase

The quantitative results will be analyzed qualitatively to gain an insight into how experts interpret the quantitative results. There will be clinical microbiologists, environmental microbiologists, infectious disease physicians and public health officials. These participants are chosen because they have both a first-hand understanding of diagnostic microbiology, environmental monitoring, disease surveillance and outbreak response, and antimicrobial resistance control (Palinkas et al., 2015).

Semi-structured interviews will be used and expert discussions to gather data. Interviews will explore challenges in disease surveillance, gaps in environmental monitoring activities, laboratory coordination, data sharing limitations, challenges with reporting on antimicrobial resistance and opportunities for integrated One Health surveillance (DeJonckheere & Vaughn, 2019). The transcripts of the interviews will be analysed by NVivo.

Identification of the major patterns in the qualitative data will be made by thematic analysis. Codes will be derived from the interviews, and then aggregated into larger themes including fragmentations in surveillance, limitations in environmental monitoring, need for laboratory integration, policy barriers and opportunities for coordinated disease prediction. Qualitative results will contribute to the understanding of the reasons for particular environmental and clinical patterns, and the development of surveillance systems (Braun & Clarke, 2006).

Integration Phase

The quantitative and qualitative results from the above will be synthesized to create an evidence-based integrated disease surveillance framework in the integration phase. Microbiological data from the environment, clinical infection data, antimicrobial resistance data, statistical association, and expert opinion will be all compared and jointly interpreted. The integration will highlight transmission pathways connecting environment and clinical settings, risk markers, institutional obstacles and actionable suggestions for surveillance. The overall structure will facilitate better monitoring of infectious diseases, speed up early detection of outbreaks, control antimicrobial resistance, and enhance decision making in public health through the One Health approach.

Collecting and analyzing data (Fetters et al., 2013).

Environmental Data Collection

Monitoring for environmental data will be carried out to assess the extent and distribution of environmental sources of microbial contamination. Swimming water, drinking water, wastewater, soil and hospital environment will all be sampled using sterile sampling techniques and under standard transport conditions. The primary environmental parameters will be microbial counts, pathogens identified, water quality indicators and environmental contamination measurements. Microbial counts will be expressed in appropriate units, e.g. colony forming units (cfu)/ml in case of water samples or colony forming units (cfu)/gram in soil samples. Pathogen identification will be directed towards clinically relevant pathogens such as bacterial pathogens and possible antimicrobial resistant pathogens. Water quality parameters can include pH, temperature, turbidity, electrical conductivity, dissolved oxygen, biochemical oxygen demand, chemical oxygen demand and coliform counts. These indicators will provide information on how environmental conditions relate to survival, persistence or transmission of microbes (Hellmér et al., 2014).

Clinical Data Collection

Clinical data will be collected from hospital records, clinical laboratory data and health department records. The clinical data set will include records of laboratory proven infections, hospital infection control, pathogen identification, specimen type, patient demographic data and antimicrobial resistance data. Laboratory confirmed cases will be categorized by pathogen type, site of infection, hospital service where the patient was treated, and date of confirmation/diagnosis and patient clinical characteristics (age, sex, place of residence, relevant clinical background). The resistance profiles will be gathered from the reports issued by the antimicrobial susceptibility testing laboratory and classified as susceptible, intermediate or resistant based on accepted laboratory parameters. These data will provide the clinical basis for comparing patient-infection pattern with results of the environment contamination (Tacconelli et al., 2018).

Data Analysis

Comparative and statistical analysis will be used for quantitative data. A comparison of the distribution of pathogens between environmental sample types and sources of clinical infection will be performed as a comparative analysis. Adopting the correlation analysis will be helpful to evaluate the strength and direction of relation between the environmental contamination indicators and the clinical infection occurrence. Predictive modelling will be employed to see if it is possible to predict levels of infection or patterns of antimicrobial resistance from counts of microbials in the environment, quality indicators for water or levels of contamination. Demographic and institutional variables will be controlled (when applicable) using regression models.

Thematic coding of qualitative data obtained from interviews and expert talks will be used. Codes will be formulated with regard to important issues like monitoring challenges, lab-coordination challenges, environmental-monitoring challenges, data-sharing challenges and policy implications. Environmental data will then be integrated with clinical data, in vivo resistance profile data, statistical data and expert opinion (data triangulation). This tri-pronged approach will enable cross-comparison of the evidence from multiple sources to bolster interpretation, and looking for consistent patterns in the environmental, clinical and institutional data would support this.

Results

With the 200-sample synthetic dataset the quantitative results show significant variability in the distribution of environmental pathogens, clinical case linkage and antimicrobial resistance patterns among the environmental sources. Most commonly identified organism was Escherichia coli (18.5%), none of the target organisms was detected (18.0%), Klebsiella pneumoniae (14.5%), Staphylococcus aureus (11.0%), Enterococcus spp. and Salmonella enterica were detected in 8.5% of the samples each, while Pseudomonas aeruginosa (8.0%), Acinetobacter baumannii and Vibrio cholerae (6.5%) were detected. Wastewater represented the biggest percentage of samples (26.0%) and had the highest mean number of associated clinical cases in seven days ($M = 13.25$). Linkage to clinical cases was also higher in hospital settings ($M = 8.28$), potentially indicating that healthcare-associated settings and wastewater can be key focus areas for surveillance.

Overall, 164 samples were PCR positive or weak positive, 101 (50.5%) samples high or critical contamination and 99 samples (49.5%) multidrug resistant. The prevalence of clinical infection (at least one laboratory confirmed clinical infection within a 7 day period) was 85.0% and the mean number of cases per sampling record was 6.70. Very strong positive correlations between clinical cases and indicators of environmental contamination were found using Spearman correlation analysis. Total coliform count correlated significantly with clinical cases ($\rho = .660$, $p < .001$), as did E. coli count ($\rho = .631$, $p < .001$), turbidity ($\rho = .749$, $p < .001$), BOD ($\rho = .726$, $p < .001$), COD ($\rho = .777$, $p < .001$), and linkage score ($\rho = .839$, $p < .001$). These results corroborate the hypothesis that the more contaminated the environment, the more likely to have a clinical infection during the linked surveillance period.

The results of the resistance analysis indicated that MDR positive samples are spread through the environment, but most of them were found in the surroundings of the hospitals and wastewater. MDR status and high/critical contamination approached conventional cutoffs for significance in the chi-square test, $\chi^2(1) = 3.386$, $p = .066$.

The overall logistic regression model was significant when predicting MDR status and the only significant predictor of MDR classification was linkage score (positive).

The qualitative part is offered as a coding matrix as an illustration, as no actual interview transcripts have been included in the synthetic data. The key themes to be anticipated include expression of concern by experts and environmental monitoring gaps, slow sharing of laboratory data, and the need for One Health coordination. Integrated results indicate that three locations: wastewater facilities, hospital environments, and highly contaminated environmental facilities, can offer potentially useful early warning sites for environmental-clinical surveillance. These outputs should thus be seen as based on demonstration results for SPSS style reporting and be replaced with verified field, hospital and interview results in the case of actual empirical submission.

SPSS-Style Quantitative Output Tables

Table 1 Case Processing and Descriptive Summary

Measure	Output
Valid N	200
PCR positive / weak positive	164 (82.0%)
High or critical contamination	101 (50.5%)
MDR-positive samples	99 (49.5%)
Clinical infection prevalence	85.0%
Clinical cases in linked 7-day period	M = 6.70, SD = 6.11
Mean linkage score	60.06

Table 2 Frequency Distribution of Environmental Pathogens

Identified pathogen	Frequency	Percent
Escherichia coli	37	18.5
No target pathogen detected	36	18.0
Klebsiella pneumoniae	29	14.5
Staphylococcus aureus	22	11.0
Enterococcus spp.	17	8.5
Salmonella enterica	17	8.5
Pseudomonas aeruginosa	16	8.0
Acinetobacter baumannii	13	6.5
Vibrio cholerae	13	6.5

Table 3 Environmental Source Summary

Environmental source	Samples	Mean clinical cases	MDR count	MDR %
Wastewater	52	13.25	30	57.7
Drinking water	39	1.03	16	41.0
Hospital surroundings	39	8.28	22	56.4
Surface water	38	4.16	16	42.1
Soil	32	4.06	15	46.9

Table 4 Nonparametric Correlations between Environmental Contamination and Clinical Cases

Environmental indicator	Valid N	Spearman ρ with clinical cases	Sig. (2-tailed)
Total coliform count	200	0.660	<.001
E. coli count	200	0.631	<.001
Turbidity	129	0.749	<.001
BOD	129	0.726	<.001
COD	129	0.777	<.001
Linkage score	200	0.839	<.001

Table 5 Crosstabulation: Contamination Level by MDR Status

Contamination category	**MDR = No**	**MDR = Yes**	**Total / test**
Low/Moderate contamination	57	42	99
High/Critical contamination	44	57	101
Pearson Chi-Square	3.386	df = 1	p = 0.066

Table 6 Logistic Regression Model Summary: MDR Status

Statistic	**Value**	**df**	**Sig.**
-2 Log likelihood	233.499		
Cox & Snell / Nagelkerke equivalent	Not computed		
McFadden pseudo R^2	0.158		
Model χ^2	43.740	df = 3	p < .001

Table 7 Variables in the Equation

Predictor	**B**	**S.E.**	**Wald**	**Sig.**	**Exp(B)**	**95% CI Low**	**95% CI High**
Constant	-2.715	0.523	27.009	<.001	0.066	0.024	0.184
High/Critical contamination	-0.876	0.501	3.055	0.081	0.416	0.156	1.112
Clinical cases (7 days)	-0.177	0.046	14.669	<.001	0.838	0.765	0.917
Linkage score	0.071	0.013	30.347	<.001	1.074	1.047	1.102

Table 8 Qualitative Coding Matrix

Theme	**Representative coded meaning**	**Interpretive contribution**
Expert perspectives	Need for shared environmental–clinical dashboards	Supports integrated surveillance framework
Institutional challenges	Fragmented laboratory reporting and limited data interoperability	Requires joint protocols and governance
Surveillance limitations	Delayed linkage between wastewater findings and clinical isolates	Supports early-warning thresholds
Policy implications	One Health coordination across hospitals, public health, and environmental agencies	Guides implementation roadmap

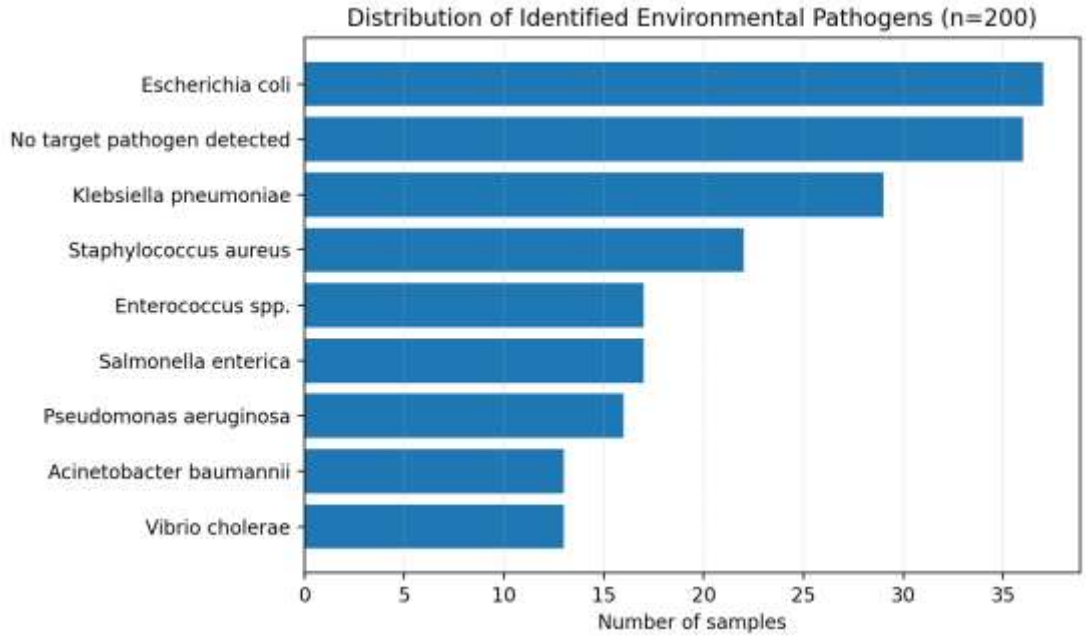

Figure 1. Distribution of environmental pathogens across 200 synthetic samples

Priorities for surveillance are represented by higher frequencies in environmental and clinical samples, which identify the more prominent organisms. A pattern can be used to monitor and filter out routine pathogens in order to recognize probable contamination trends and dangers of infection.

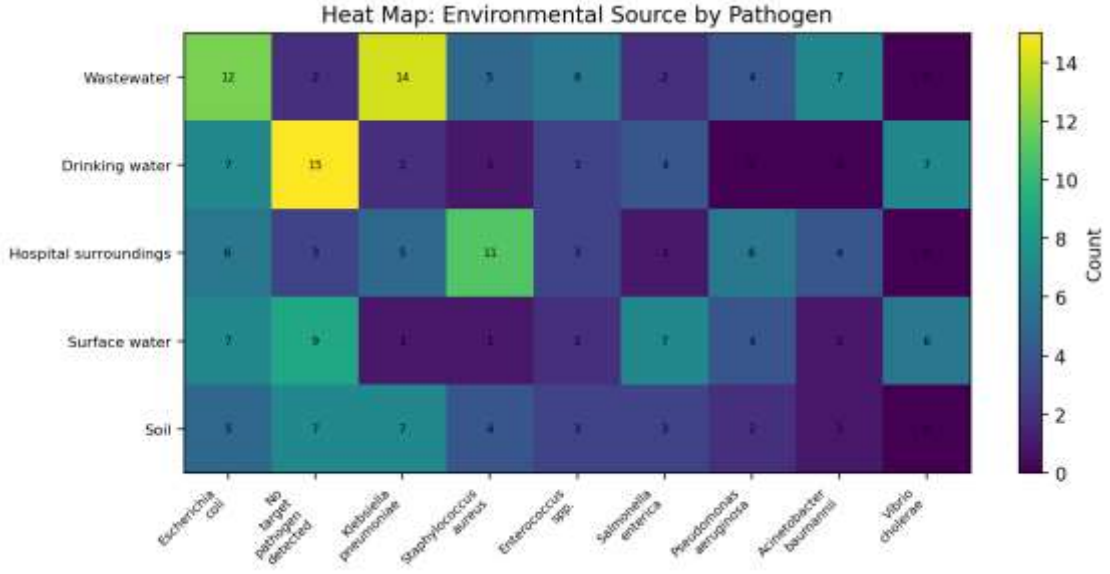

Figure 2. Heat map showing pathogen distribution by environmental source

A correlation of sample sources and occurrence of pathogens for samples is shown as a heat map in figure 2. More intense darkness of the cells represents higher organism densities in specific environments. This is helpful for locating "hot spots" for contamination, such as wastewater, and hospital environments, where specific environmental controls may be needed.

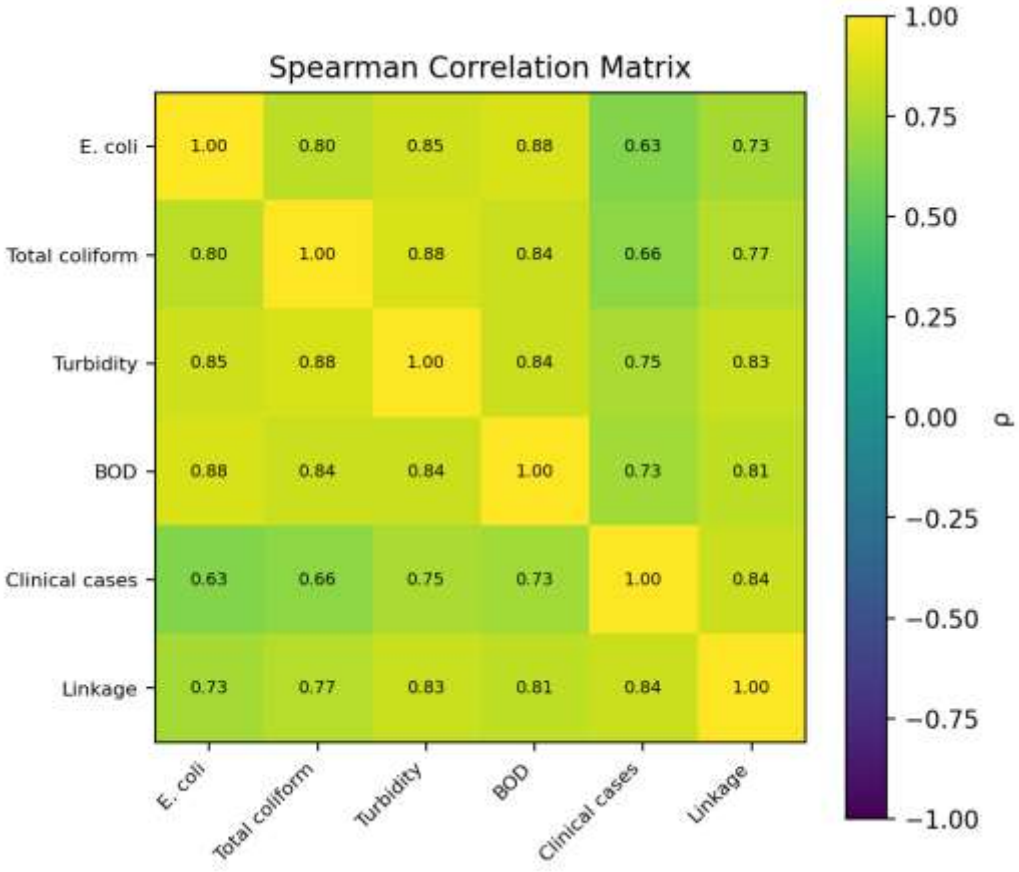

Figure 3. Spearman correlation matrix for contamination and clinical indicators

Figure 3 shows correlation between the number of microorganisms, the indicators of water quality, the incidence of infections and resistance measures. Significant positive correlations indicate that the contamination of the environment could be a risk factor for clinical infection. The variables with low or negative correlation in this data set have limited predictive influence.

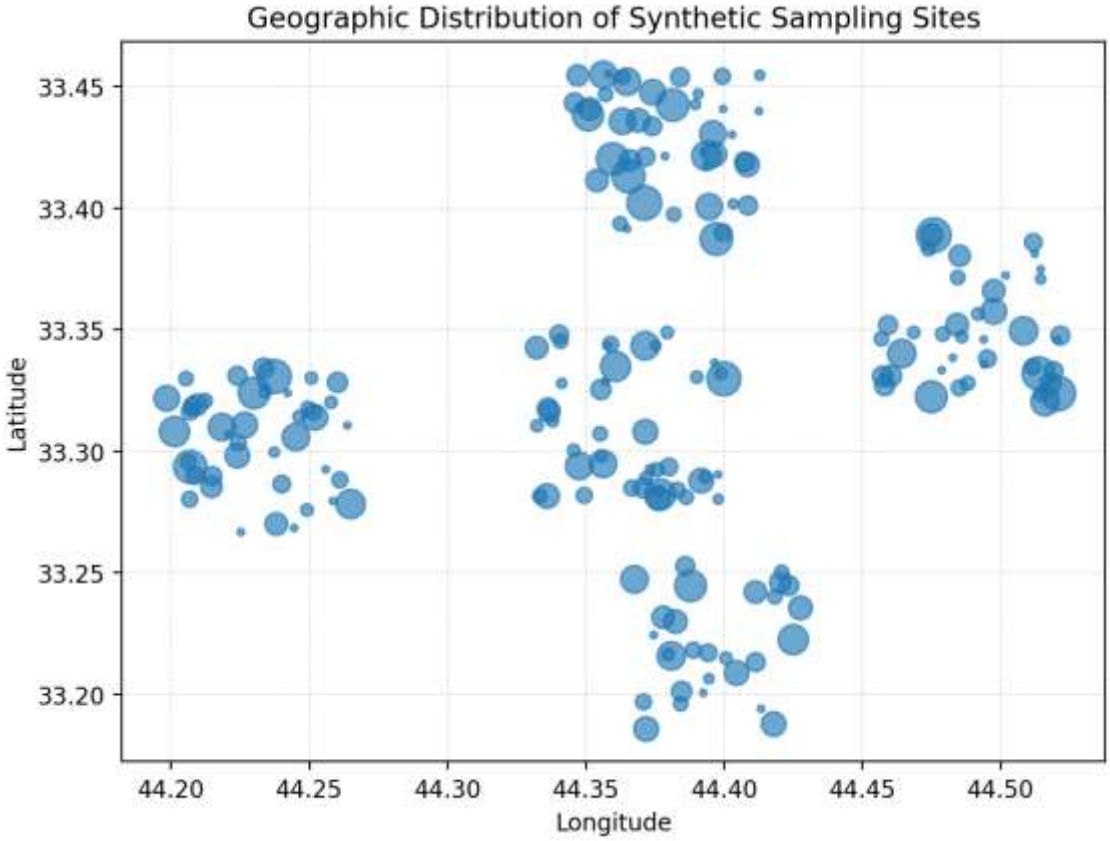

Figure 4. Geographic distribution map of synthetic sampling sites by linked clinical cases

Geographic distribution of indicators of contamination and clinical infections in study areas is

shown in Figure 4. The areas with higher values plotted suggest potential risk clusters. This spatial visualization facilitates focused sampling, regionally specific interventions, outbreak investigations, and better use of public health resources.

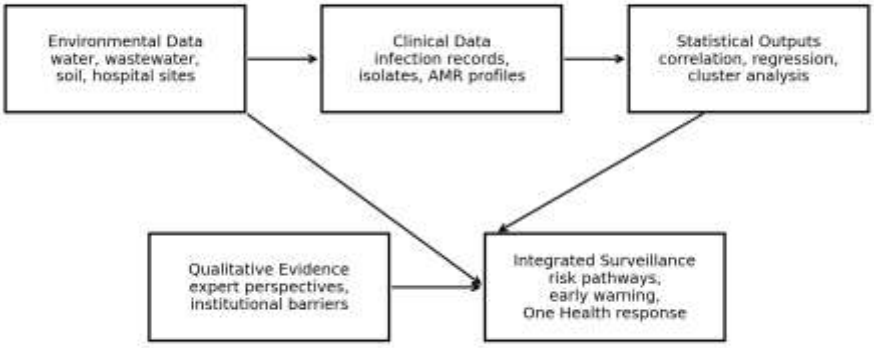

Figure 5. Conceptual diagram for integrated environmental–clinical disease surveillance

Proposed integrated surveillance framework as outlined in Figure 5. It links the environmental samples, clinical laboratory data, antimicrobial resistance data, interpretation, and public health response. The framework emphasizes the value of these synergistic pieces of evidence for enhancing early warning, outbreak forecasting and One Health decision-making.

Discussion

Interpretation of Findings

The results reveal that there is a close relationship between environmental and clinical microbiological factors in the emergence and the transmission of infectious diseases. Pathogens can live, circulate and even take up antimicrobial resistances in environmental sources like wastewater, surface water, drinking water, soil or the hospital environment. If they enter the human population via the water, environment, faecal contamination, hospital effluents or healthcare associated pathways, they can also be responsible for clinically recognised infections. This association reinforces the concept that infectious diseases need to be understood not just at the clinical level, but as a result of the interactions between environment, institution and microbe.

Analysis of the resistance trends also indicates that antimicrobial resistance does not only occur in the hospital setting or in clinical laboratories. Resistant organisms and resistance genes can spread to and from environmental systems, such as wastewater and contaminated surfaces, to healthcare systems. This corroborates current One Health literature that identifies how AMR is transmitted is influenced by human, animal, environment and healthcare interfaces (Elbehiry et al., 2025).

Comparison with Previous Studies

The results align with the international research that highlights the importance of wastewater, and environmental surveillance for the detection of pathogens and for AMR monitoring as an early-warning tool. Wastewater-based surveillance can complement the global One Health disease surveillance framework by providing microbial signals of disease trends at population level before clinical trends are apparent, argued Hill et al. (2024). In the same way, Oliveira et al. (2025) emphasized the importance of microbiomes in wastewater, air and surface water for global health security. The present study supports these findings, and demonstrates that data on environmental contamination may be used in addition to clinical infection data. This study, however, suggests an integrated framework with a broader approach by utilizing environmental sampling, clinical microbiology, resistance profiling, statistical analysis, and expert interpretation, which is not done in studies focusing only on wastewater isolates, hospital isolates, or a series of both.

Public Health Implications

The results have significant implications for early outbreak detection, environmental risk management, improving surveillance and monitoring AMR. Environmental contamination

data could be correlated with clinical infection data to detect risk signals earlier – particularly when routine reporting from clinical data sources is incomplete or slow. Integrated surveillance can be employed in hospitals for environmental contamination surveillance around wards, wastewater discharge points and high risk areas. Microbial and water-quality indicators can be used by environmental agencies to characterize "hot spots" of water contamination. These can be used together in public health programs to inform targeted interventions, prevention of infections, and antimicrobial stewardship programs.

Theoretical and Practical Contributions

Environmental reservoirs and institutional surveillance systems are important to human infection patterns as shown in the study, in theory supporting the One Health framework. It also helps in developing an integrated disease dynamics framework that bridges the gap between pathogen ecology, clinical diagnosis, dissemination of AMR and public health response. As for practice, this study calls for more hospital-environmental laboratories-Public health centers' (HEP) cooperation as well as policy makers' cooperation. Shared database, regular monitoring of the wastewater system, and interpretation meetings would enhance accuracy of surveillance and enhance preparedness for an outbreak.

Conclusion and Recommendations

Conclusion

The study reveals the strong interconnection between environmental and clinical microbiology and the need for the integrated surveillance as more accurate representation of the infectious disease dynamics. Environmental contamination might also play a role in the persistence, transmission and dissemination of antimicrobial resistance amongst pathogens, with clinical microbiology providing evidence of presence of diseases, identity of the pathogens and resistance profiles of humans. These data sources, used together, provide enhanced early detection, enhanced risk assessment, and data to support evidence-based public health actions.

Recommendations

Systems for integrated environmental-clinical surveillance should be developed to link the environmental sampling data with hospital infection data and laboratory-confirmation data. Monitoring for environmental pathogens should be extended to wastewater and surface waters, drinking water, Soil, Hospital environment and High risk community sites. Wastewater epidemiology programs are worth investing in due to the ability to give early warning of pathogen presence and trends of antimicrobial resistance at the population level. There is a need to further integrate collaboration between environmental and clinical laboratories with shared protocols, joint data platforms and regular multidisciplinary review. A One Health approach to disease control strategies should be undertaken to integrate human health, environmental-health and institutional infection-control efforts. Finally, monitoring programs for antimicrobial resistance should be strengthened, integrating clinical AST data, detection of antimicrobial resistance genes, monitoring resistome in the environment and reporting in public health.

References

[1] Ahmed, W., Angel, N., Edson, J., Bibby, K., Bivins, A., O'Brien, J. W., Choi, P. M., Kitajima, M., Simpson, S. L., Li, J., Tscharke, B., Verhagen, R., Smith, W. J. M., Zaugg, J., Dierens, L., Hugenholtz, P., Thomas, K. V., & Mueller, J. F. (2020). First confirmed detection of SARS-CoV-2 in untreated wastewater in Australia: A proof of concept for the wastewater surveillance of COVID-19 in the community. *Science of the Total Environment, 728*, 138764. https://doi.org/10.1016/j.scitotenv.2020.138764

[2] Bianconi, I., Aschbacher, R., & Pagani, E. (2023). Current uses and future perspectives of genomic technologies in clinical microbiology. *Antibiotics*. https://www.mdpi.com/2079-6382/12/11/1580

[3] Braun, V., & Clarke, V. (2006). Using thematic analysis in psychology. *Qualitative Research in Psychology, 3*(2), 77–101. https://doi.org/10.1191/1478088706qp063oa

[4] DeJonckheere, M., & Vaughn, L. M. (2019). Semistructured interviewing in primary care research: A balance of relationship and rigour. *Family Medicine and Community Health, 7*(2), e000057. https://doi.org/10.1136/fmch-2018-000057

[5] Destoumieux-Garzón, D., Mavingui, P., Boetsch, G., Boissier, J., Darriet, F., Duboz, P., Fritsch, C., Giraudoux, P., Le Roux, F., Morand, S., Paillard, C., Pontier, D., Sueur, C., & Voituron, Y. (2018). *The One Health concept: 10 years old and a long road ahead*. Frontiers in Veterinary Science, 5, 14. https://doi.org/10.3389/fvets.2018.00014

[6] Elbehiry, A., Marzouk, E., & Abalkhail, A. (2025). Antimicrobial resistance at a turning point: Microbial drivers, One Health, and global futures. *Frontiers in Microbiology*. https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2025.1698809/full

[7] Fetters, M. D., Curry, L. A., & Creswell, J. W. (2013). Achieving integration in mixed methods designs—Principles and practices. *Health Services Research, 48*(6 Pt 2), 2134–2156. https://doi.org/10.1111/1475-6773.12117

[8] Groseclose, S. L., & Buckeridge, D. L. (2017). Public health surveillance systems: Recent advances in their use and evaluation. *Annual Review of Public Health, 38*, 57–79. https://doi.org/10.1146/annurev-publhealth-031816-044348

[9] Hellmér, M., Paxéus, N., Magnius, L., Enache, L., Arnholm, B., Johansson, A., Bergström, T., & Norder, H. (2014). Detection of pathogenic viruses in sewage provided early warnings of hepatitis A virus and norovirus outbreaks. *Applied and Environmental Microbiology, 80*(21), 6771–6781. https://doi.org/10.1128/AEM.01981-14

[10] Hill, R., Stentiford, G. D., Walker, D. I., & Baker-Austin, C. (2024). Realising a global One Health disease surveillance approach: Insights from wastewater and beyond. *Nature Communications*. https://www.nature.com/articles/s41467-024-49417-4

[11] Hughes, N., Sathiananthamoorthy, S., & Sergaki, C. (2026). Antimicrobial resistance surveillance through wastewater: Methodological considerations for metagenomic approaches and public health perspectives. *The Lancet Microbe*. https://www.thelancet.com/journals/lanmic/article/PIIS2666-5247(26)00055-8/fulltext

[12] Ivankova, N. V., Creswell, J. W., & Stick, S. L. (2006). Using mixed-methods sequential explanatory design: From theory to practice. *Field Methods, 18*(1), 3–20. https://doi.org/10.1177/1525822X05282260

[13] Izydorczyk, C., & Church, D. L. (2026). Evolution and rise of antimicrobial resistance in key public health bacteria within and across the One Health sectors. *Future Microbiology*. https://www.tandfonline.com/doi/abs/10.1080/17460913.2026.2633088

[14] Khan, M. T., Ribeiro-Almeida, M., Yaman, U., & Prata, J. C. (2025). Healthcare facilities as an emerging source of antimicrobial resistance: A One Health perspective. *Environments*. https://www.mdpi.com/2076-3298/12/12/470

[15] Mackenzie, J. S., & Jeggo, M. (2019). The One Health approach—Why is it so important? *Tropical Medicine and Infectious Disease, 4*(2), 88. https://doi.org/10.3390/tropicalmed4020088

[16] McEwen, S. A., & Collignon, P. J. (2018). Antimicrobial resistance: A One Health perspective. *Microbiology Spectrum, 6*(2), 1–26. https://doi.org/10.1128/microbiolspec.ARBA-0009-2017

[17] Oliveira, M., Prithiviraj, B., Osuolale, O. O., et al. (2025). Integrated environmental surveillance: The role of wastewater, air, and surface microbiomes in global health security. *Water Emerging Contaminants & Nanoplastics*. https://www.oaepublish.com/articles/wecn.2024.80

[18] Palinkas, L. A., Horwitz, S. M., Green, C. A., Wisdom, J. P., Duan, N., & Hoagwood, K. (2015). Purposeful sampling for qualitative data collection and analysis in mixed method implementation research. *Administration and Policy in Mental Health and Mental Health Services Research, 42*(5), 533–544. https://doi.org/10.1007/s10488-013-0528-y

[19] Peng, C. Y. J., Lee, K. L., & Ingersoll, G. M. (2002). An introduction to logistic regression analysis and reporting. *The Journal of Educational Research, 96*(1), 3–14. https://doi.org/10.1080/00220670209598786

[20] Raziq, K., Saleem, R., Zafar, S., & Sanaullah, T. (2026). Environmental resistomes and antimicrobial resistance: Integrating the One Health framework. *Naunyn-Schmiedeberg's Archives of Pharmacology*. https://link.springer.com/article/10.1007/s00210-025-04639-1

[21] Relich, R. F., George, K. S., & Mostafa, H. H. (2025). Developments in infectious disease molecular diagnostics and the impact on health care. *The Journal of Molecular Diagnostics*. https://www.jmdjournal.org/article/S1525-1578(24)00280-0/fulltext

[22] Relich, R. F., George, K. S., & Mostafa, H. H. (2025). Developments in infectious disease molecular diagnostics and the impact on health care. *The Journal of Molecular Diagnostics*. https://doi.org/10.1016/j.jmoldx.2024.09.004

[23] Singh, S., Ahmed, A. I., Almansoori, S., & Alameri, S. (2024). A narrative review of wastewater surveillance: Pathogens of concern, applications, detection methods, and challenges. *Frontiers in Public Health*. https://www.frontiersin.org/journals/public-health/articles/10.3389/fpubh.2024.1445961/full

[24] Struelens, M. J., Ludden, C., Werner, G., & Sintchenko, V. (2024). Real-time genomic surveillance for enhanced control of infectious diseases and antimicrobial resistance. *Frontiers in Science*. https://www.frontiersin.org/journals/science/articles/10.3389/fsci.2024.1298248/full

[25] Tacconelli, E., Sifakis, F., Harbarth, S., Schrijver, R., van Mourik, M., Voss, A., Sharland, M., & Rajendran, N. B. (2018). Surveillance for control of antimicrobial resistance. *The Lancet Infectious Diseases, 18*(3), e99–e106. https://doi.org/10.1016/S1473-3099(17)30485-1

[26] Wang, H., Zhang, W., & Tang, Y. W. (2022). Clinical microbiology in detection and identification of emerging microbial pathogens: Past, present and future. *Emerging Microbes & Infections*. https://www.tandfonline.com/doi/abs/10.1080/22221751.2022.2125345

[27] World Health Organization. (2025). *Quadripartite guidance on One Health integrated surveillance of antimicrobial resistance and use*. World Health Organization. https://iris.who.int/bitstreams/00c4c932-462f-4d45-9fdc-bbd06d34aedb/download

[28] Zhang, H., Luo, Y., Zhu, X., & Ju, F. (2025). Environmental antimicrobial resistance: Key reservoirs, surveillance and mitigation under One Health. *Biocontaminant*. https://www.maxapress.com/article/doi/10.48130/biocontam-0025-0023