



## Detection of Enteric Bacteria in Selbe River, Mongolia, with Infection Risk Estimation of the Selbe River, Ulaanbaatar

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### ABSTRACT

The indicator bacteria and pathogenic bacteria *Salmonella spp.* and *Shigella spp.* were tested in the laboratory with two different methods, the Petri-dish method, and the IDEXX tray method. The findings of this study reveal concerning levels of bacterial pollution in the Selbe River, illustrating the serious impact of unplanned urban growth along its banks. Laboratory tests using both the Colilert-18 IDEXX Tray and agar plate methods showed high levels of bacteria, with some samples even exceeding the limits of the tests. The average bacterial concentrations detected were 23.55 CFU/ml for *E. coli*, 2.1 CFU/ml for *Salmonella spp.*, and 225.7 CFU/ml for *Shigella spp.* all of which are significant indicators of contamination. The presence of these bacteria, particularly in such high concentrations, suggests fecal contamination and highlights the public health risks for people living nearby and using the river. This pollution is likely tied to untreated waste, poor sanitation facilities in densely populated ger areas, and urban runoff that worsens with seasonal rains. These results emphasize the need for better waste management and ongoing water quality monitoring to help restore the river's health. Improving sanitation infrastructure and implementing stronger urban planning along the river could reduce pollution and make the water safer for residents and the environment. This study reinforces the importance of taking immediate steps to protect the Selbe River, which ultimately supports the larger Tuul River Basin.

**Keywords:** indicator bacteria, *Salmonella spp.*, *Shigella spp.*, *E. coli*, Selbe river, Ulaanbaatar Mongolia

### 1. INTRODUCTION

Surface water is replenished by rainfall or snowfall that ends up as runoff, by groundwater, which discharges as baseflow, and by other sources. It is often the primary transport medium for soil pollutants entering stream systems. As a result, downstream areas are frequently the most affected by pollution. The detection of indicator bacteria in the Selbe River, Ulaanbaatar, Mongolia, indicates faecal contamination [1], most likely associated with pit latrines in nearby ger areas. This contamination suggests the potential presence of pathogenic microorganisms, raising significant concerns about the spread of waterborne diseases.

The population growth in Ulaanbaatar, the capital of Mongolia, has harmed the river that runs through the city. In 1990, the population was approximately 500,000; by 2023, it had grown to 1,500,000. Over 40 per cent of the population resides in apartments, while the remainder live in ger areas. The prevalence of open pit latrines in the Ger areas has annually increased by 5-10 percent of households. These latrines contribute to soil contamination, which is transported into the river through surface runoff during rainfall events. A total of 144,992 pit latrines in 203,548 households in Ger area were counted in Ulaanbaatar, with 9,443 pit latrines in Zone IV, 43,377 pit latrines in Zone III, 71150 pit latrines in Zone II, and 21,022 pit latrines in Zone I. In Figure 1, the

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impacted zones (II Zone yellow-moderate, III Zone orange-high, IV zone red-very high) of the open pit latrines [2].

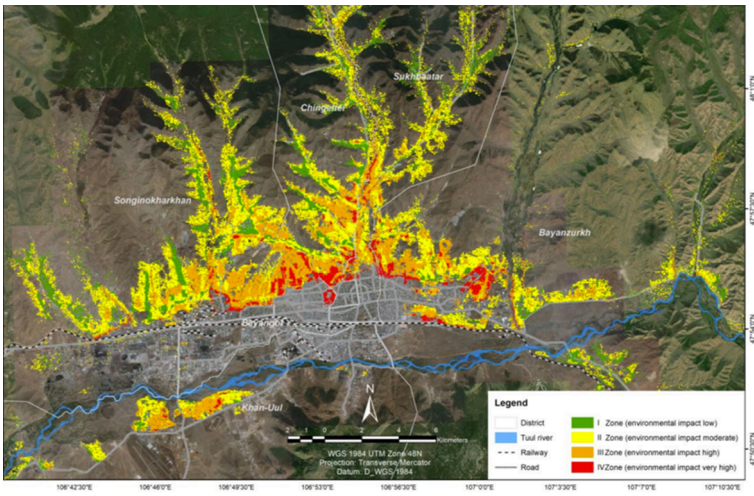


Figure 1. Open pit latrine impact by zones [2]

The river passes through 27 khoroo, the smallest administrative units in Mongolia, distributed across five districts: Sukhbaatar (SBD) with 11 khoroo, Bayanzurkh (BZD) with 6, Khan Uul (HUD) with 4, Bayangol (BGD) with 4, and Chingeltei (CHD) with 2 khoroo. This study specifically focuses on the upstream section of the river, where Ger areas are located across 11 khoroo with 22478 households. In 2022, this area included 22,182 households, increasing to 25638 households by 2023; however, some governmental measures of air pollution as well as soil contamination have influenced the households of 22478 in the ger area, and it has decreased by 12 percent in the upstream area surrounding the Selbe River in 2024 (see Figure 2) [3]. The households are directly related to open latrines.

According to Mongolian health statistics, dysentery is the most prevalent acute enteric disease among communicable illnesses. The BZD district exhibits notably higher incidence rates of such diseases than other districts [3]. Importantly, the 29th khoroo of Bayanzurkh is situated upstream of the Selbe River, indicating a possible source of contamination contributing to downstream health risks, even though there is no information on dysentery disease of the khoroo unit.

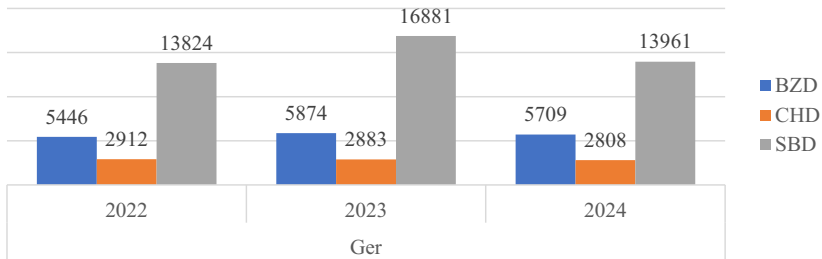


Figure 2. Households in upstream of the river

Several studies have documented waterborne diseases associated with drinking water, recreational water, and other types of water exposure [4–6]. These diseases can infect individuals through contaminated drinking water and accidental Figure 1. Households in the upstream area had contact with polluted water by swimming and eating lettuce, which acts as a passive carrier of infectious agents.

Coliform bacteria, including *Escherichia coli* (*E. coli*), are widely used as key indicators of surface water contamination and the potential presence of pathogenic microorganisms. The identification system for coliform bacteria typically employs enzymatic methods based on the activity of  $\beta$ -glucuronidase and  $\beta$ -galactosidase enzymes. Specifically,  $\beta$ -D-galactosidase catalyzes the hydrolysis of lactose into glucose and galactose, facilitating the detection of total coliforms. This enzyme activity is particularly associated with *E. coli*, a member of the Enterobacteriaceae family [9]. In 1988, Edberg and colleagues introduced a novel method for detecting coliforms and *E. coli* using chromogenic and fluorogenic substrates. These include O-nitrophenyl- $\beta$ -D-galactopyranoside (ONPG) for the detection of  $\beta$ -D-galactosidase activity (indicative of total coliforms) and 4-methylumbelliferyl- $\beta$ -D-glucuronide (MUGlu) for  $\beta$ -glucuronidase activity (specific to *E. coli*) [10]. This innovation led to the development of the Colilert®-18 system (IDEXX Laboratories, Westbrook, ME, USA), which has since become an internationally recognized standard for microbiological monitoring of both drinking and surface waters [10]. This innovation led to the first commercially available test of the Colilert®-18 system (IDEXX Laboratories, Westbrook, ME, USA), now an internationally recognised standard for microbiological monitoring of drinking and surface water [11]. This technique is reliable, with test results minimally influenced by background microbial flora. While it may occasionally underestimate microbial presence of other microbiological methods, Colilert® effectively enumerates coliforms in various water types, including drinking water, surface water, and wastewater.

*Salmonella spp.* are members of the g-subgroup of the Proteobacteria. Close genetic relatives include the genera *Escherichia*, *Shigella*, *Proteus* and *Enterobacter*, and the group is commonly referred to as enteric bacteria [7]. Depending on the source, 1000–2000 strains of *Salmonella spp.* have been known. The World Health Organisation considers all members of the genus *Salmonella* to be human pathogens. However, there are the most important species of *S. typhi*, *S. enteritidis* and *S. typhimurium*. The *S. typhi* is the cause of typhoid fever due to large outbreaks generally associated with water contamination [8]. *Shigella spp.* found in natural environments is often unable to initiate the disease. The species responsible for the more severe illness, *S. dysenteriae*, is more common in tropical regions [9, 10]. *Shigella dysenteriae* has shown a particular ability in this

regard and often develops resistance to a new antibiotic within 2 years. Thus, *Shigella* outbreaks are difficult to recover from, and problems increase where endemic conditions exist. In addition, it is biologically plausible that *S. dysenteriae* could be encountered in freshwaters used for recreation. This pathogenic bacteria detection uses membrane filtration (MF) and pour plating method.

Exposure assessment is set as part of a risk assessment. Furthermore, it can be a stand-alone process, such as when there is a lack of information presented to take on a dose-response or when the risk management question only concerns quantifying or searching for ways to minimise exposure. Exposure assessments are frequently very detailed for the building, processing and utilisation samples within a country or region. Quantitative assessment is divided into two categories, namely deterministic and stochastic, consistently and alluded to respectively as ‘point-source’ and ‘non-point source’ exposure assessments. The previous study [1, 11] built the land use of the target area with natural purification of hydraulic estimation and organic characteristics. We will use the data in Table 1 and 2.

Table 1. Exposure assessment

Scenarios	Exposure frequency, (EF)	Volume of water ingested	References
Swimming in surface water	7 days/year	50ml per hrs	[12, 13]
Eating lettuce from an irrigated field	48 days/year	15ml equals 100g of vegetables	[4]
Working in an irrigated field	163 days/year	100 ml equals 0.1-0.01 g of soil	[4]

Table 2. Dose-response parameters

Pathogens	Dose response		Reference	P <sub>ill/inf</sub>	Reference
	N <sub>50</sub> <sup>a</sup>	α <sup>c</sup>			
<i>Salmonella spp.</i>	23600	0.313	[12]	0.43	[14]
<i>Shigella spp.</i>	1120	0.21	[12]	0.3	[15]
<i>E. coli</i> O157:H7	596000	0.49	[16]	0.24	[17]

<sup>a</sup> the number of ingested microorganisms which survive 50 percentages of them to initiate illness

<sup>b</sup> dose response parameter

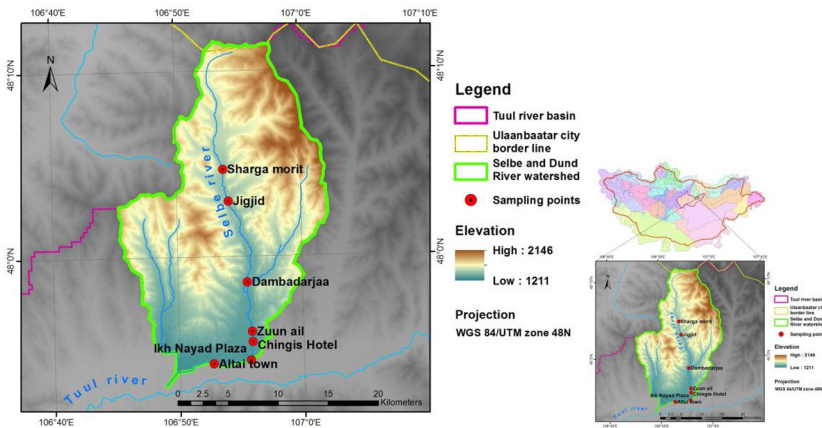
In this study, we assess the waterborne pathogens in the contaminated river and estimate the potential health risks based on measured data and assumed exposure scenarios. Risk assessment is a valuable tool for determining which waterborne pathogens pose the greatest threats when considering factors such as dose response relationships, disease severity, mortality rates, occurrence in water, and the effectiveness of treatment processes.

## 2. METHODOLOGY

### Study area and sampling

The first water sampling campaigns were conducted in mid-November 2021, April and May 2022 [18], and late April 2023 [1]. These periods typically coincide with seasonal transitions when the

river functions as a shallow, high-energy stream due to snowmelt runoff from surrounding mountains. Mongolia experiences a temperate climate, with winter extending from late November to mid-March. In April 2023, hydraulic data were collected alongside observations of the river's



**Figure 3.** Study land area Selbe River Catchment area with sampling points (See Table 1)

natural purification processes and organic characteristics, including coliform bacteria levels.

To investigate the presence of pathogens in the river, additional water sampling was conducted during the warmer months of June and August [19]. The first set of samples was collected on June 19, 2024, from five designated sampling points: Dambadarjaa (DD, upstream), Zuun Ail (ZA, post-upstream), Chinggis Khan Hotel (CH, mid-point), Ikh Nayad Plaza (IN, pre-downstream), and Altai Town (AT, downstream) (Table 4). The weather was sunny and favourable for sampling and measurements during midday. However, a brief afternoon rainfall temporarily interrupted the process, and sampling at the final location (ZA) was completed once the rain had subsided.

The second sampling campaign took place on August 23, 2024, covering all five locations (AT, IN, CH, ZA, and DD). Conditions were sunny, enabling the measurement of pH, dissolved oxygen, and river temperature. However, changes in the river basin, particularly at AT and IN, presented some challenges. These included the relocation of vegetation (trees and shrubs) and the removal of sludge and sediment from the riverbed.

All samples in Figure 1 were collected in sterile, single-use plastic bottles, sealed immediately after collection, and transported to the laboratory in a cooled container. The transport duration did not exceed four hours to preserve sample integrity.

### Detection methods

In April 2023, the membrane filtration (MF), 45 µm HAWP04700 Merck Millipore Ltd, method [20] was used for detecting and quantifying *E. coli* in media of Endo agar, HIMEDIA® M029-500G, *Shigella spp.* and *Salmonella spp.* in media of Salmonella–Shigella (SS) agar media, HIMEDIA® M108-500G. Typically, a series of dilutions was prepared to prevent colony overcrowding and to ensure that at least one agar plate contained a countable number of colonies. Pathogenic bacteria, specifically *Salmonella spp.* and *Shigella spp.*, were enumerated using the standard method. For these analyses, water samples were tested using two dilutions: a 1:1 dilution and an undiluted (neat) sample. Various culture media and incubation conditions have been followed for the isolation of coliforms from water samples using this method. We used for

analysing surface water using MF method Endo (m-Endo) media [21] for *E. coli* and SS agar media for *Shigella spp.* and *Salmonella spp.*

In Jun and Aug 2024, detecting pathogenic microorganisms, various selective and differential agar media are utilized, including SS agar, Endo agar, and Xylose Lysine Deoxycholate (XLD) agar, BIOLAB Zrt XLD20500, using plate pour method. SS agar (Salmonella-Shigella agar) is selective for enteric Gram-negative bacteria, the isolation of *Salmonella* and *Shigella* species while inhibiting the growth of non-pathogenic organisms. Endo agar is designed for the detection of *E. coli* and other coliforms, characterized by its reddish coloration in the presence of lactose fermentation, which is indicative of coliform growth. XLD agar (Xylose Lysine Deoxycholate agar) is another selective medium that helps distinguish between *Salmonella* and *Shigella*, utilizing xylose fermentation and lysine decarboxylation as key metabolic indicators.

Static quantitative microbial risk assessment (QMRA) [8] was used to evaluate the likelihood of infection and disease burden among individuals whom the surface water serve as an essential means of livelihood. Stochastic data such as the fluctuating pathogen concentrations in the surface water were compiled during the present 14-month surveillance work, and susceptible fractions of exposed populations were obtained from random reconnaissance survey (see Table -3).

Table 3. Simplified procedure for risk illness

Parameter	Findings
Surface water, pathogens per litre (C <sub>i</sub> )	Calculation from the quantification procedure
Accidental ingestion in selected scenarios (V <sub>s</sub> )	Monte Carlo assumptions from the literature
Exposure by ingestion in selected scenarios (E)	$E = C_i \times V_s$
Dose response (r, N <sub>50</sub> , α)	From literature (see Table 2)
Risk infection per day (P <sub>inf/d</sub> )	$P_{inf/d} = 1 - \left[ 1 + \frac{E}{N_{50}} \left( 2^{\frac{1}{\alpha}} - 1 \right) \right]^{-\alpha}$
Risk infection per year (P <sub>inf/y</sub> )	$P_{inf/y} = 1 - (1 - P_{inf/d})^{EF}$
Exposure frequency (EF) selected exposure	From the literature (see Table 1.)
Risk of illness or disease given infection (P <sub>ill,inf</sub> )	From literature (see Table 2.)
Risk of illness (P <sub>ill</sub> )	$P_{ill} = P_{ill,inf} \times P_{inf/y}$

Risks of illness or disease per infection, P (ill,inf), by 0.24 [17, 22] of *E. coli* O157:H7, 0.43 [14] of *Salmonella spp.*, and 0.3 [15] of *Shigella spp.* are constants. This data is mostly from tropical countries.

### 3 RESULT AND DISCUSSION

A preliminary test was conducted using the IDEXX Colilert method, and the results are presented in Table 4. The upstream sampling point at Dambadarjaa showed higher levels of total coliforms at the beginning of the warm season in April 2023 [1]. During this time, melting snow from the surrounding mountains contributes to the river through overland and subsurface flow. It was anticipated that the highest contamination would occur at the upstream point, likely due to the presence of pit latrines in the nearby ger area. The test results support this expectation. The fecal coliform concentration at the post upstream was lower compared to the upstream location. This reduction may be attributed to the increased river width at the mid-point, which likely enhanced dilution capacity. Additionally, higher flow velocity and shallower depth at this location may have contributed to the dispersion and reduction of microbial contamination. The concentration of fecal

coliform increased at the mid-point, which may be associated with the narrowing of the riverbank and an increase in river depth. These morphological changes can reduce flow velocity and dilution capacity, potentially leading to the accumulation of microbial contaminants. However, the distribution of *E. coli* concentrations showed a different pattern. It did not follow the expected trend based on hydraulic flow or anticipated contamination sources. This irregularity suggests that *E. coli* presence may be more closely associated with localized inputs or disease-related shedding rather than hydrodynamic factors alone.

Table 4. Result of IDEXX Colilert®

District, no. khoroo, West/North and East/South side	Sampling point location	The most probable number (MPN) in the 100 ml sample		
		Total Coliform	Fecal Coliform	<i>E. coli</i>
SBD, 14 <sup>th</sup> and SBD 15 <sup>th</sup>	Dambadarjaa, DD, Upstream	164.0	13.7	32.4
SBD 12 <sup>th</sup> and BZD 27 <sup>th</sup>	Zuun Ail, ZA, Post upstream	137.0	7.5	40.6
SBD 7 <sup>th</sup> and BZD 1 <sup>st</sup>	Chinggis Khan Hotel, CH, mid-point	64.0	16.4	65.9
HUD 15 <sup>th</sup> and BZD 26 <sup>th</sup>	lkh Nayad Plaza, IN, pre-downstream	99.0	5.3	22.2
BGD 24 <sup>th</sup> and HUD 3 <sup>rd</sup>	Altai Town, AT, downstream	42.0	4.2	50.4

The *E. coli* results were considered validated, as the values obtained from the two different methods, colony-forming units (CFU) and most probable number (MPN), were closely aligned, with CFU values averaging 28 units higher than MPN values (see Figure 4) through 4 points. An exception was observed at the ZA (post-upstream) sampling point, where the results differed notably (see Tables 4 and 5). At the CH (mid-point) sampling location, an increase in *E. coli* concentration was observed. This may be attributed to potential illegal discharges or the accumulation of pollution in that section of the river.

Table 5. MF technique result

Location	Endo media <i>E. coli</i> CFU in 100 ml sample			SS agar media <i>Salmonella spp.</i> CFU in 100 ml Sample		
	1:1 dilution	No dilution	Mean	1:1 dilution	No dilution	Mean
DD, upstream	60	60	60.0	0	10	5
ZA, post unstream	20	30	25.0	0	0	0
CH, mid point	100	80	90.0	60	70	65
IN, pre-downstream	80	40	60.0	0	20	10
AT, downstream	80	70	75.0	0	0	0

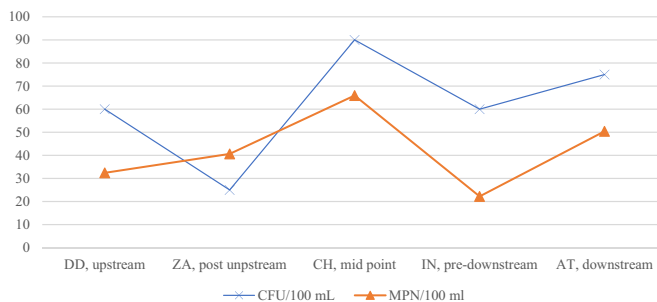


Figure 4. *E. coli* for result for different methods

In the subsequent step conducted in 2024, *Shigella spp.* and *Salmonella spp.* were isolated using two different selective media: SS agar and XLD agar. At each sampling point, three replicate tests were conducted at 37°C for 24 hrs to 48 hrs, and the mean values were used for data analysis. As shown in Table 6, the concentration of *Shigella spp.* was significantly higher than that of *Salmonella spp.* This finding aligns with national statistics on communicable diseases, particularly the prevalence of dysentery, caused by *Shigella spp.*, discussed in the Introduction. The presence of *Shigella spp.* appears to be correlated with the river’s hydrodynamic conditions, particularly the natural purification processes observed along the sampling points, as well as the environmental sanitation conditions in the surrounding ger areas, especially at the first three sampling locations. Based on the results, it can be concluded that both selective media, SS agar and XLD agar, are reliable for the detection of *Shigella spp.*. However, SS agar proved to be more suitable for the isolation of *Salmonella spp.*.

Table 6. Data analysis of pathogenic bacteria in two media, CFU/mL

Sampling point	SS agar		XLD agar	
	<i>Salmonella spp.</i>	<i>Shigella spp.</i>	<i>Salmonella spp.</i>	<i>Shigella spp.</i>
Upstream	6.7	413.3	0	497.8
Post upstream	6.7	266.7	1.1	763.3
Mid point	6.7	126.7	0	242.2
Pre-downstream	6.7	86.7	0	381.1
Downstream	6.7	186.7	1.1	463.3

Single-exposure infection risks,  $P_{inf/d}$ , values per pathogen were averaged for the relevant surface water, with typical values around  $P_{inf/d} \approx 10^{-4}$  [23]. As shown in Table 7, the values indicate that the river is highly contaminated and poses a significant risk for the transmission of communicable diseases, particularly through activities such as swimming or consuming lettuce irrigated with this water. Annual risk of infection,  $P_{inf/ys}$ , the value falls between 0 and 1, where a value of 1 represents the certainty of infection. The internationally accepted threshold for annual infection risk is  $P_{inf/y} \approx 10^{-3}$  [8]. However, it is important to note that Quantitative Microbial Risk Assessment (QMRA) does not account for the likelihood of multiple infections per individual within a year unless supported by epidemiological studies [4]. Although people may not typically swim in or consume crops irrigated with river water in this context, national statistical data supports the reliability of the risk assessment findings (see Figure 6).

Table 7. Probability of infection per day,  $P_{inf/d}$

Sampling point	SS agar media				XLD agar media			
	<i>Salmonella spp.</i>		<i>Shigella spp.</i>		<i>Salmonella spp.</i>		<i>Shigella spp.</i>	
	Swim	Eating lettuce	Swim	Eating lettuce	Swim	Eating lettuce	Swim	Eating lettuce
Upstream	0.0337	0.0106	0.7192	0.6430	0.0000	0.0000	0.7295	0.6560
Post upstream	0.0337	0.0106	0.6935	0.6106	0.0059	0.0018	0.7516	0.6841
Mid point	0.0337	0.0106	0.6445	0.5490	0.0000	0.0000	0.6876	0.6031
Pre-downstream	0.0337	0.0106	0.6167	0.5143	0.0000	0.0000	0.7146	0.6373
Downstream	0.0337	0.0106	0.6709	0.5821	0.0059	0.0018	0.7255	0.6511

The risk of dysentery from ingested water in Scenario 1, swimming in the river (see Table 1 in the Introduction), was estimated for *Shigella spp.* using a Monte Carlo simulation based on the data presented in Table 6, which is formulated by Table 3. The results indicate that the upstream sampling point is highly contaminated, likely due to subsurface runoff from open pit latrines in the surrounding area (see Figures 5 and 6). Figure 6 presents supporting data from the National Statistics Office of Mongolia, which shows a high in reported dysentery cases in Bayanzürkh District (BZD), further corroborating the public health risk associated with river water contamination.

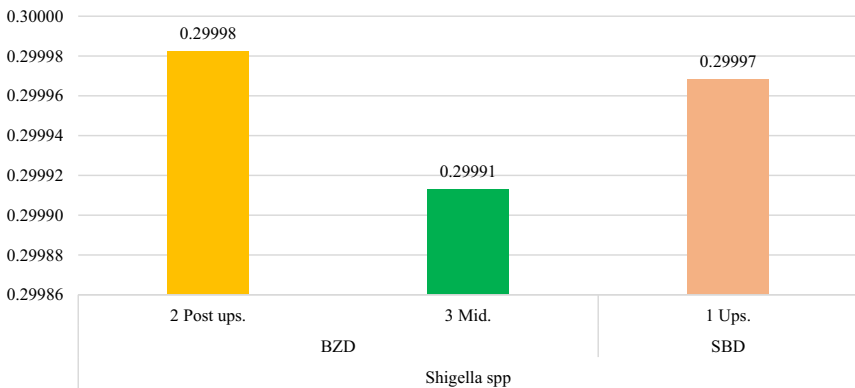


Figure 5. Probability of risk of illness,  $P_{ill}$ , for *Shigella spp.* in swimming scenario-1

Even though the differences in risk values are small, post-upstream point has the highest illness probability, suggesting a contamination source exists shortly after the upstream point due to river natural purification process. This pattern is important for identifying pollution sources and managing recreational water safety.

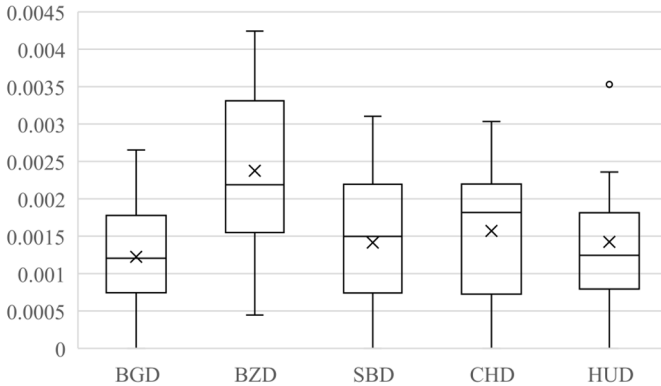


Figure 6. Dysentery disease case per 10000 people 2010-2023

#### 4 CONCLUSIONS

This study assessed the microbial contamination of a river system in Ulaanbaatar, Mongolia, focusing on the presence of *Escherichia coli*, *Shigella spp.*, and *Salmonella spp.* through multiple sampling campaigns and analytical methods. *E. coli* concentrations measured by CFU and MPN methods were closely aligned, validating the reliability of the data, except at the post-upstream (ZA) point. Notably, elevated *E. coli* levels at the CH (mid-point) sampling location suggest possible illegal discharges or pollutant accumulation.

Isolation of *Shigella spp.* and *Salmonella spp.* using SS and XLD agar confirmed the predominance of *Shigella spp.*, particularly at the first three sampling points. This aligns with national health statistics showing a rising trend of dysentery cases, especially in Bayanzürkh District, and suggests a strong link between river contamination and inadequate sanitation in nearby ger areas. Both agar media were effective for *Shigella spp.* detection, while SS agar was more suitable for isolating *Salmonella spp.*

Quantitative Microbial Risk Assessment (QMRA) revealed that the river poses a high infection risk, particularly in swimming and irrigation scenarios. Single-exposure infection risks per day for *Shigella spp.* reached values around  $10^{-4}$ , exceeding the acceptable annual risk threshold ( $P_{inf/y} \approx 10^{-3}$ ). Although direct exposure (e.g., swimming or consuming river-irrigated crops) is uncommon, national epidemiological data validate the modelled health risks.

Overall, the study highlights the urgent need for improved sanitation infrastructure, regular microbial monitoring, and public health interventions to mitigate the risk of waterborne diseases in urban river systems.

#### AUTHORS' CONTRIBUTIONS

Conceptualization, A.T.; methodology, U.P. B.L. and A.T.; software, A.T.; validation, B.L., A.T., and G.D.; formal analysis, U.P. and A.T.; writing original draft preparation, U.P. and B.L.; writing-review and editing, A.T. and B.L.; visualization, A.T. All authors declare no conflict of interest. The funders had no role in the design.

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## Annex

Table A1. The river bordering districts with khoroods

Districts	Area	Khoroo No	Population		Households	
			2022	2023	2022	2023
Bayanzurkh	Apartment	1	9754	10957	2769	3085
Bayanzurkh	Apartment	3	8914	8752	2182	2456
Bayanzurkh	Apartment	6	10304	10925	2638	2868
Bayanzurkh	Apartment	43	14604	15872	4177	4626
Bayanzurkh	Apartment	36	14379	16769	4323	5163
Sukhbaatar	Apartment	7	9046	9076	2444	2513
Sukhbaatar	Apartment	8	7113	7043	1848	1831
Sukhbaatar	Apartment	1	9042	9419	2490	2476
Khan-Uul	Apartment	15	16721	19430	4892	6164
Khan-Uul	Apartment	1	11605	10516	2452	2448
Khan-Uul	Apartment	2	13575	12794	3157	3250
Bayangol	Apartment	26	14420	16747	3762	4494
<b>Total</b>			<b>139477</b>	<b>148300</b>	<b>37134</b>	<b>41374</b>
Chingeltei	Ger	19	7456	6954	2014	1972
Chingeltei	Ger	24	2782	2670	898	911
Bayanzurkh	Ger	29, 2	6565	6693	2101	2255
Sukhbaatar	Ger	11	16395	16733	4514	4662
Sukhbaatar	Ger	12	6210	5648	1586	1541
Sukhbaatar	Ger	13	8193	7419	2099	2042
Sukhbaatar	Ger	14	4800	4496	1288	1300
Sukhbaatar	Ger	15	6485	6551	1851	1888
Sukhbaatar	Ger	16	3243	11028	2972	2969
Sukhbaatar	Ger	17	5716	5221	1644	1590
Sukhbaatar	Ger	19	2190	2170	842	889
<b>Total</b>			<b>70035</b>	<b>75583</b>	<b>21809</b>	<b>22019</b>
Khan-Uul	Industrial	3	15285	15452	3956	4307
Bayangol	Industrial	20	4053	3670	1136	1086
Bayangol	Industrial	25	7038	7336	1991	2119
Bayangol	Industrial	24	9211	13318	2719	4016
<b>Total</b>			<b>35587</b>	<b>39776</b>	<b>9802</b>	<b>11528</b>
<b>All Total</b>			<b>245099</b>	<b>263659</b>	<b>68745</b>	<b>74921</b>

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