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Article

Ecological risk of mercury pollution of the Bureya Reservoir after a major landslide

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Abstract. In December 2018, a giant landslide occurred for the first time in the Russian Far East at a temperature of −32 °C on the Bureya Reservoir. This landslide triggered a tsunami, destroyed forests on the opposite bank, and altered the hydrological regime. The resulting natural dam affected the dynamics of the biogeochemical cycles of C, N, S, and Hg in the reservoir ecosystem. Microbiological and spectral studies conducted in the summer of 2022 revealed significant changes in the organic matter composition of the water around the landslide. High numbers of culturable heterotrophic and sulfate-reducing bacteria (SRB) observed in the water of bays with increased humification among floating wood. Microbial communities from the bays and bottom water demonstrated high adaptive potential for utilizing readily available calcium lactate in the presence of mercury (II) nitrate at 5 MAC. Sixty-two bacterial strains from various habitats were isolated in the landslide-affected zone, approximately 50% of which grew on agar medium at a mercury concentration of 100 mg/L. Spectroscopic analysis showed that bacterial strains isolated from bottom water at a depth of 65 m exhibited the highest *in vitro* activity toward soluble sodium humate (HNa). They transformed the aromatic and aliphatic components of HNa in the presence of 10 and 100 mg/L $Hg(NO_3)_2$. Aromatic components can act as precursors of volatile compounds with methyl groups, which participate in mercury methylation, increasing its toxicity and bioavailability. Mercury-resistant SRBs isolated from the Bureya Reservoir bottom water layers and wood-filled bays serve as sensitive bioindicators for predicting the ecological risks of methylmercury formation in the landslide-affected zone.

Keywords: rockfall, aquatic ecosystem, mercury methylation, microbial complexes, ecological safety forecasting

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Научная статья

Экологический риск ртутного загрязнения Бурейского водохранилища после крупного оползня

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Аннотация. Впервые на Дальнем Востоке России в декабре 2018 г. при температуре −32 °С на Бурейском водохранилище произошел гигантский оползень, который спровоцировал цунами, уничтожение леса на противоположном берегу и изменил гидрологический режим. Возникшая природная дамба повлияла на динамику биогеохимических циклов C, N, S и Hg в экосистеме водохранилища. Согласно микробиологическому и спектральному исследованиям, проведенным в летний период 2022 г., состав органических веществ в воде вокруг оползня существенно изменился. В воде заливов с повышенной гумификацией среди плавающей древесины отмечена высокая численность культивируемых гетеротрофных и сульфатредуцирующих бактерий (СРБ). Микробные комплексы из заливов и придонной воды характеризовались высоким адаптационным потенциалом при утилизации легкодоступного лактата кальция в присутствии 5 ПДК нитрата ртути (II). В зоне влияния оползня выделено 62 штамма бактерий из разных местообитаний, среди них около 50% росли на агаризованных средах при концентрации 100 мг/л соли ртути. Спектральным методом показано, что максимальную активность *in vitro* по отношению к растворимому гумату натрия (ГNa) проявляли штаммы бактерий, выделенные из придонной воды с глубины 65 м. Они трансформировали ароматическую и алифатическую составляющую ГNa в присутствии 10 и 100 мг/л $Hg(NO_3)_2$. Ароматические компоненты могут выступать предшественниками летучих веществ с метильными группами, которые участвуют в метилировании ртути, повышая ее токсичность и биодоступность. Ртутьрезистентные СРБ, выделенные в Бурейском водохранилище из придонных слоев воды и заливов, заполненных древесиной, выступают в роли чувствительных биоиндикаторов для прогнозирования экологических рисков образования метилртути в зоне влияния оползня.

Ключевые слова: обвал горных пород, водная экосистема, метилирование ртути, микробные комплексы, прогнозирование экологической безопасности

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Introduction

Reservoirs are essential freshwater ecosystems, providing habitat for diverse groups of organisms and critical water resources that are subject to various anthropogenic impacts (Schofield et al., 2018; Zwahlen, 2022). The main factors affecting reservoir stability include hydromorphological changes, water level fluctuations, eutrophication, organic pollution, and land use changes in the region (Palma et al., 2021; Poikane et al., 2020; Xiao et al., 2023). Disruption of the ecological balance in reservoirs often accompanied by the loss of their self-purification capacity (Amusan et al., 2024).

Climate change, biodiversity and habitat loss, and the impact of various chemicals from anthropogenic sources are taken into account during assessing the ecological status of reservoirs (Kuehne et al., 2017; Poikane et al., 2020). Research into the responses of biota to habitat pollution aims to identify the root causes of the transformation and degradation of water body ecosystems (Lima et al., 2023; Suresh et al., 2023).

Climate change is driving transformations in the biosphere and cryosphere, including permafrost (Margesin and Collins, 2019). Studies of permafrost impacts across regions show that large-scale effects on our planet manifested through changes in biogeochemical activity at the microscopic level of observation (Zona, 2016). During assessing the ecological status of water bodies, one method that has proven successful in addressing general trends is bioindication with use of aquatic community structure. Phytoplankton, zooplankton, and benthic macroinvertebrates most commonly used as key bioindicators (Liu et al., 2023). Future research should preferably utilize more nuanced indicator organisms of water body ecological health, as well as introduce new physical traits and indicators of sustainability (Biney et al., 2025).

Microorganisms, with their use, decompose organic matter (OM) of variable origin and have great potential for eliminating ecological problems. However, their metabolism can result in secondary pollution with chemicals. Succession resulting from autochthonous microbial complexes in water content accompanied by changes in the fractional composition of OM in sediments, bottom, and surface water layers (Mazur et al., 2024).

Mercury occupies a significant place among the most important atmospheric, soil, and water elements posing a risk to organisms at different trophic levels (O'Connor et al., 2019). Reservoirs can influence mercury biogeochemical cycling at both global and local scales (Feng et al., 2018). Mercury is present in the form of HgO, HgS, $HgCl_2$, and mercury-containing derivatives (Wang et al., 2012). The latter, especially methylmercury (MeHg), are more bioavailable than other mercury compounds (Fukuto et al., 2020). It shown that newly created reservoirs are hotbeds of methylmercury (MeHg). This substance is highly concentrated in the tissue of organic bodies and the effect of its impact enhanced during transmission to higher trophic levels, posing a risk to human health (Scheuhammer et al., 2007).

Organomercury compounds (in particular, methylmercury, dimethylmercury, ethylmercury, and phenylmercury) formed from inorganic forms with the participation of aquatic microorganisms and, less frequently, through abiotic processes. With the age of the reservoir, MeHg production gradually decreases (Feng et al., 2018). The resistance of microorganisms to mercury pollution determines the importance of their participation in various detoxification mechanisms. For example, the efficiency of mercury removal from the aquatic environment by a strain of *Citrobacter* sp. was 89% at pH 6.5 and a temperature of 30 °C due to its accumulation on the surface of bacterial cells (Singh et al., 2022). Enhancement of the activity of microbial detoxification of mercury pollution observed with the addition of S-containing co-substrates, in particular, compounds with sulfhydryl groups (SH) (Abraham et al., 2018). In addition to sulfur-containing functional groups, mercury is capable of forming strong bonds with carbonyl, amino, and cyano groups (Maia et al., 2019), which are formed during the metabolism of bacterial cells; this underlies the mechanisms of Hg bioaccumulation and biosorption. Using *Bacillus sphaericus* as an example, it has been shown that both living and inactivated microbial biomass participate in these processes (Velásquez and Dussan, 2009).

Sulfate-reducing bacteria (SRB) and iron-reducing bacteria (IRB) are the main players in mercury methylation in various habitats (Lin et al., 2021; Zhang et al., 2020). These microorganisms possess specialized genes responsible for mercury methylation. In particular, the ability of representatives of the genera *Desulfovibrio* and *Desulfomicrobium* to methylate mercury at concentrations of 10 mg/L demonstrated (Bakour et al., 2025; Regnell and Watras, 2019).

Many ecological factors influence the process of mercury methylation: oxidative (Lehnherr et al., 2011; Ullrich et al., 2001) and reducing conditions (Sonke et al., 2013); sulfate content (Yu et al., 2010); the presence of dissolved organic matter containing aromatic groups (Waples et al., 2005). It known that *Geobacter metallireducens* and *Geobacter sulforeducens* are capable of producing MeHg when grown on a medium containing Fe (III). Later, it shown that this process could occur without iron reduction – in the presence of fumarate or nitrate (Kerin et al., 2006).

Research into the mechanisms of microbial resistance to mercury contamination continues to generate considerable interest. Particular attention paid to mercury methylation processes, its active and passive transport into cells, and its accumulation on their surfaces. Equally important is the analysis of the role of microbial complexes and individual strains from different habitats in mercury migration, as well as the identification of their resistance to mercury contamination (Feng et al., 2018).

The aim of our research was to determine the localization of Hg-resistant bacteria in the zone of influence of a large landslide on the Bureya Reservoir, to assess their ability to decompose easily accessible (lactate, peptone) and difficult to mineralize humus-like organic matter (sodium humate) at different concentrations of mercury salt to identify metabolites that contribute to the formation of toxic methylmercury.

Objects and methods of researches

General characteristics of the landslide

The Bureya Reservoir (BR) catchment area located in an area with very complex permafrost and hydrogeological conditions (Kulakov et al., 2019). During the construction of the hydroelectric dam and the formation of the BR, some hydrogeologists predicted the intensification of exogenous geological processes in the form of landslides. A winter landslide with a volume of 24.5 million m^3 in December 2018 collapsed directly into the BR, blocking it from bank to bank, effectively creating a natural dam. The landslide generated a tsunami wave that struck the opposite bank, destroyed a significant portion of the forest, and completely eroded the soil cover down to bedrock. All organic and terrigenous material washed into the reservoir (Fig. 1). The area of destroyed soil was approximately 120 hectares, from which approximately 6000 tons of undecomposed organic matter (organogenic-sod, peaty-organogenic soils, and dispersed organic matter) washed away (Makhinov et al., 2020). According to calculations, the volume of the above-water portion of the landslide exceeded 4.5 million m^3, with the majority of it submerged. The depth of the reservoir at the landslide site is over 70 m. The landslide length is 800 m from end to end, and its height ranges from 7.5 to 46 m. Blasting operations carried out to restore water flow to the hydroelectric power station; an artificial channel created in the body of the landslide.Description of the geological, geomorphological, and geophysical features of the Bureya landslide presented in a series of publications (Kondratieva et al., 2020; Kulakov et al., 2019; Makhinov et al., 2019; Zerkal et al., 2019).

Water sampling

Water samples from the BR collected in the summer of 2022 from two bays (Pervyi and Sredniy Sandar), which received fragmented wood and the surface soil layer washed away by the river tsunami, as well as from the surface and bottom layers of water above and below the landslide body using a classic bathometer (Fig. 1).

Determination of organic matter content in water

A spectrophotometric method used (Shimadzu UV-3600 spectrophotometer, Japan) to assess the OM content in the reservoir water in the landslide area. The total content of dissolved OM (OM254) was determined at a wavelength of λ = 254 nm, and the aromatic compounds (OM_{275}) at 275 nm (Kumar, 2006). The proportion of OM affecting water color due to water-soluble fractions of humic substances and their chromophoric groups was determined at wavelengths of 365 and 465 nm (Shirshova et al., 2015).

Microbiological research

The abundance of ecological-physiological groups of bacteria cultivated on different substrates used as microbiological indicators of the presence of various OM. Cultivated heterotrophic bacteria (CHB) determined on fish-peptone agar diluted tenfold (FPA:10); ammonifying bacteria (AMB) – on FPA; nitrifying bacteria (NB) – on starch-ammonia agar (Kuznetsov and Dubinina, 1989); sulfate-reducing bacteria (SRB) – on Postgate medium (Postgate, 1984); bacteria utilizing humic substances (HB) – on M9 medium with the addition of sodium humate (HNa) (Gerhard et al., 1983). The number of cultured bacteria was expressed in colony-forming units (CFU/mL), using the mean value with standard deviation for three replicates. Potential activity of microbial complexes (MC) towards various carbon sources, including calcium lactate and sodium humate, determined by culturing at 23 °C in liquid medium M9 of the following composition (g/L distilled water): 1.33 KH_2PO_4, 2.67 K_2HPO_4, 1 NH_4Cl, 2 Na_2SO_4, 2 KNO_3, 0.001 $FeSO_4{\cdot}7H_2O$, 0.1 $MgSO_4{\cdot}7H_2O$. Natural water served as the inoculum at a ratio of 1:10 (1 part inoculum to 10 parts nutrient medium). Carbon sources used in the following concentrations: calcium lactate – 2 g/L, HNa – 0.2 g/L. The growth of microorganisms (accumulation of biomass) on easily accessible substrates was determined on the 7th day with use of a photometric method based on the change in the optical density of the culture liquid (CL) on KFK-3-01 at a wavelength of 600 nm (Metris et al., 2006).

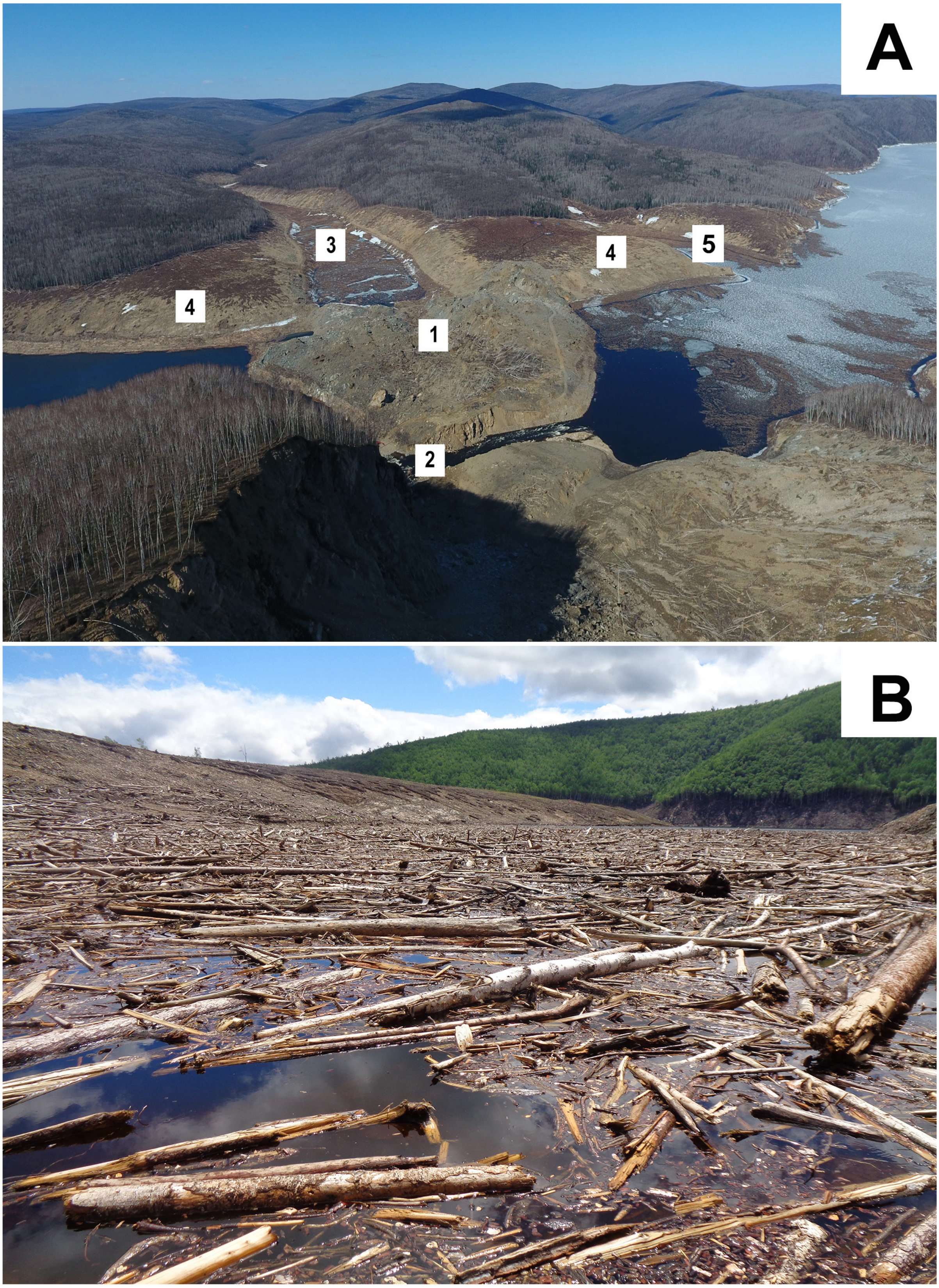

Fig. 1. General view of the Bureya Reservoir section with the landslide site: **A** – Drone photo of the general view of the landslide location: 1 – landslide body, 2 – artificial channel, 3 – Sredniy Sandar Bay filled with wood, 4 – areas with damaged soil cover and destroyed forest, 5 – Pervyi Bay; **B** – Sredniy Sandar Bay filled with wood (photo by A. Ostroukhov).

Determination of Hg resistance in vitro

Two concentrations of $Hg(NO_3)_2$ used at the first stage of the study to determine the resistance of MC to mercury salts: 0.0005 and 0.001 mg/L, corresponding to 5 and 10 MACs[1] for standardizing water bodies for fishery purposes. According to recent studies (Ustiatik et al., 2022), many strains of microorganisms can survive in a wide range of mercury concentrations ranging from 10 to 250 mg/L. Strains with maximum resistance to mercury selected from different habitats to assess the activity of HNa transformation: *Bacillus* sp. 6 SS isolated from a water sample from Sredniy Sandar Bay; *Pseudomonas* sp. 42 BCB isolated from the bottom water below the channel; *Arthrobacter* sp. 59 ACB – from the bottom water above the channel. Identification of strains to the genus level carried out by cultural and morphological characteristics and Gram staining (Opredelitel bakterii Berdzhi, 1997). At the second stage of Hg resistance of individual strains studying, $Hg(NO_3)_2$ used at concentrations of 1, 10 and 100 mg/L. Features of microbial transformation of HNa in the presence of mercury salt determined by the change in the absorption values of the culture liquid on the 30th day (after its filtration through membrane filters with a pore diameter of 0.45 µm) at different wavelengths with use of a SHIMADZU UV-3600 spectrophotometer. Changes in the total content of OM were assessed at λ = 254 nm; the presence of aromatic groups – at 275 nm (Kumar, 2006); transformation of chromophore groups – at 436 and 465 nm (Chen et al., 2002; Shirshova et al., 2015). A nutrient medium with HNa without inoculum used as a control.

Results and discussion

The combination of multiple landslide-related events (river tsunami, shoreline erosion, soil erosion, and coastal forest destruction) significantly affected water quality in the Bureya Reservoir. These changes recorded during the winter with use of microbiological parameters before and after blasting, both above and below the landslide body (Kondratyeva et al., 2021). All the organic-terrigenous material that entered the reservoir after the landslide subsequently significantly affected the organic matter composition, particularly in the bottom water layers.

The content of OM and the number of cultivated physiological groups of bacteria in the summer period of 2022

In the summer of 2022, the maximum total dissolved organic matter and aromatic compounds in the bottom water recorded in the bottom water above the landslide body (Table 1). In surface water, the content of various OM was half as high. The minimum OM content in the surface layer observed in Pervyi and Sredniy Sandar Bays. Such differences may be due to the presence of colloidal OM fractions in the water, products of plant residue decomposition, which filtered out before spectrophotometry. Watercolor depended on the presence of water-soluble chromophoric groups (λ = 365, 465 nm): their content was highest in the bottom water above the channel at a depth of 65 m. Second place occupied by surface water below the landslide body, where water flow decreased, and the OM content increased after water drainage through the collapsed mass of rocks, soils, and vegetation.

The spectral composition of OM in the water around the landslide influenced the microbial composition and the abundance of culturable physiological groups of bacteria (CPGB) (Table 2). The maximum abundance of CHB and SRB founded in water samples from Pervyi and Sredniy Sandar Bays. Moreover, the SRB abundance in Sredniy Sandar Bay, with its large wood accumulation (Fig. 1**B**), was twice that of Pervyi Bay. Furthermore, a high abundance of microorganisms involved in the nitrogen cycle – ammonifying and nitrifying bacteria – observed here. A bottom water sample collected above the landslide body with the maximum content of dissolved OM_{254} and OM_{275} revealed high abundance of CHB and SRB, but it was significantly lower than in the bays. This may be due to the presence of OM that is difficult for bacterial metabolism. In water samples collected below the landslide body, differences in the abundance of CPGB in surface and bottom waters were insignificant, likely due to the hydrodynamic mixing of water layers after passing through a narrow channel. Low CPGB abundance detected in surface waters above the landslide body, comparable to data obtained in this area earlier, before the landslide. Although the group of bacteria growing on agar medium containing hard-to-reach humic substances (HB) was low in number, a slight increase in their abundance recorded in the bays and in the bottom water at a depth of 65 meters.

[1] Order of the Federal Agency for Fisheries dated May 26, 2025 No. 296 "On approval of water quality standards for water bodies of fishery importance, including standards for maximum permissible concentrations of pollutants in the waters of water bodies of fishery importance".

Table 1. Spectral characteristics of the organic matter composition in water samples in the landslide-affected zone (August 2022).

Sample code	Sample place	Temperature, °C	Wavelength, nm			
			254	275	365	465
			Spectral characteristics of water, absorption units			
PB	Pervyi Bay	19.7	0.260	0.207	0.049	0.007
TSSB	Tributary to the Sredniy Sandar Bay	8.2	0.285	0.229	0.055	0.008
SSB	Sredniy Sandar Bay	18.5	0.163	0.130	0.030	0.003
ACS	Above the channel, surface	16.5	0.274	0.219	0.051	0.006
BCS	Below the channel, surface	17.1	0.343	0.277	0.071	0.012
ACB	Above the channel, bottom (65 m)	11.2	0.415	0.337	0.090	0.022
BCB	Below the channel, bottom (33 м)	14.8	0.297	0.239	0.063	0.015

Табл. 2. The abundance of cultivated successive groups preserved in the water around the landslide (August 2022).

Sample code	Sample place	Abundance, CFU/mL				
		CHB	AMB	NB	SRB	HB
PB	Pervyi Bay	141 ± 2	82 ± 5	60 ± 1	140 ± 4	46 ± 3
TSSB	Tributary to the Sredniy Sandar Bay	57 ± 14	9 ± 3	< 10	24 ± 2	–
SSB	Sredniy Sandar Bay	151 ± 12	82 ± 4	82 ± 3	282 ± 4	49 ± 3
ACS	Above the channel, surface	63 ± 14	40 ± 6	22 ± 1	34 ± 2	47 ± 2
BCS	Below the channel, surface	100 ± 11	25 ± 3	13 ± 1	74 ± 5	31 ± 3
ACB	Above the channel, bottom (65 m)	75 ± 4	36 ± 1	28 ± 1	80 ± 3	42 ± 3
BCB	Below the channel, bottom (33 м)	85 ± 3	28 ± 1	29 ± 1	66 ± 3	25 ± 2

Adaptation potential of microbial complexes to mercury pollution

In the first stage of the study, to assess the potential ability of MC from different habitats to utilize calcium lactate as the sole carbon source in the presence of $Hg(NO_3)_2$, natural water collected around the landslide served as the inoculum (Table 3). In the second stage, the CL used after 7 days of adaptation to the concentration of $Hg(NO_3)_2$ at 5 MAC, fisheries. As shown in Table 3, MC from the bays showed virtually no response to the used mercury salt concentrations. Weak growth inhibition by lactate observed for MC from an underground spring flowing into Sredniy Sandar Bay. Growth stimulation for MC from surface waters upstream of the channel observed as the mercury concentration increased fivefold. Other MC did not show significant responses to the presence of $Hg(NO_3)_2$ compared to the control.

During the second stage of adaptation to mercury concentrations of 5 MAC, a clear stimulation of growth observed in microorganisms from bays and bottom waters. A decrease in activity, compared to the first stage of adaptation, observed in microorganisms from surface waters. Considering the significant contribution of SRB to the community structure (Table 2) of microorganisms from bays, it assumed that they act as the main mercury methylators in wood debris accumulations.

It has been shown that the combined growth of SRB (*D. desulfuricans*) and methanogens (*Methanococcus maripaludis*), which decompose plant residues, activates mercury methylation when grown on lactate and without sulfate. Individually, these bacteria were unable to grow on this carbon source or methylate mercury in monoculture (Yu et al., 2010). Experimental studies assessing the ecological risk of mercury pollution in the Three Gorges Reservoir (China) under different oxygen concentrations also confirmed that under facultative anaerobic conditions, SRB growth was accompanied by active mercury methylation (Cao et al., 2021). Thus, sedimentation of plant residues in bottom water layers creates the preconditions for methane formation and mercury methylation.

Table 3. Indicators of two-stage adaptation of microbial communities around the landslide to mercury pollution.

Sample code	Stage 1 (initial MC, mercury salt in concentrations of 1 and 5 MAC for fisheries)			Stage 2 (inoculate of the LC after stage 1 of adaptation to mercury pollution at 5 MAC)	
	Lactate (control)	Lactate + Hg 1 MAC	Lactate + Hg 5 MAC	Lactate (control)	Lactate + Hg 5 MAC
PB	0.044 ± 0.001	0.044 ± 0.001	0.046 ± 0.001	0.061 ± 0.001	0.079 ± 0.001
TSSB	0.050 ± 0.001	0.046 ± 0.001	0.037 ± 0.001	0.079 ± 0.001	0.088 ± 0.001
SSB	0.028 ± 0.001	0.028 ± 0.001	0.027 ± 0.001	0.049 ± 0.001	0.080 ± 0.001
ACS	0.032 ± 0.001	0.047 ± 0.002	0.051 ± 0.002	0.028 ± 0.001	0.022 ± 0.001
BCS	0.030 ± 0.001	0.024 ± 0.001	0.039 ± 0.001	0.092 ± 0.001	0.059 ± 0.001
ACB	0.050 ± 0.003	0.046 ± 0.002	0.044 ± 0.001	0.038 ± 0.002	0.072 ± 0.001
BCB	0.048 ± 0.001	0.031 ± 0.001	0.046 ± 0.001	0.095 ± 0.001	0.089 ± 0.001

Resistance of individual strains to mercury contamination

Sixty-two microbial strains isolated from water samples collected from various sections of the BR around the landslide. These strains grew vigorously on agar nutrient media containing nitrogen-containing organic matter in the presence of 10 mg/L of mercury salt ($Hg(NO_3)_2$). Approximately 50% of these strains were resistant to 100 mg/L of this salt. The largest number of mercury-resistant strains were isolated from bottom waters collected at a depth of 65 m (ACB), where active sedimentation of suspended matter from upstream sections of the ACB and soils and rocks washed away.

Ten strains isolated on selective SRB media with lactate from Pervy and Sredny Sandar Bays, where submerged wood accumulated, as well as from bottom water layers above and below the landslide body, exhibited high mercury resistance (up to 10 mg/L). Strains isolated from surface water layers, which are potentially capable of sulfate reduction, were less tolerant to elevated mercury concentrations.

After preliminary adaptation of the strains to a mercury concentration of 10 mg/L in a liquid nutrient medium, changes in their cultural and morphological characteristics recorded. Cultivating strains isolated from bays and bottom water in an agar medium with a high mercury concentration of 100 mg/L have pigments – the fawn color changed to brown. When removing a colony of biomass from the substrate surface, an intense coloration from dark red to violet observed. These changes may be associated with the formation of mercuric sulfide (HgS): this is possibly how mercury released into the environment after its bioaccumulation in microbial biomass. Recent studies have shown that mercuric sulfide is widely distributed in nature in the form of nanoparticles, which methylated to form neurotoxic methylmercury (Cai et al., 2025). This effect is associated with bacterial sulfate reduction and the formation of hydrogen sulfide (H_2S).H_2S is known to be an important and endogenously generated signaling molecule, similar to other small molecular weight signaling agents (nitric oxide, carbon monoxide) that produced by many organisms (Fukuto et al., 2020).

Mercury sulfide long considered a highly inert compound and the largest reservoir of Hg in the lithosphere (Lei et al., 2022). However, with the development of analytical methods, HgS nanoparticles detected in various environmental matrices and organisms. The formation, presence, and methylation of HgS nanoparticles closely connected to environmental factors, particularly dissolved organic matter. Initial *in vitro* studies demonstrated the high bioavailability of HgS nanoparticles, which act as precursors of methylmercury (Cai et al., 2025).

In our studies, a rich diversity of strains isolated from bottom water layers at a depth of 65 m on agar medium for SRB: among them, pigmented, slimy, and wrinkled colonies found, some forming with substrate mycelium. Some strains induced fluorescence in the nutrient medium with mercury salt. Fluorescence of medium containing mercury ions observed during interaction with certain polymer gels containing thiol and benzene groups, as well as certain naphthoamide arenes (Abraham et al., 2018; Lin et al., 2017). It is likely that the strains we isolated from bottom water layers produced slimy polymers with these functional groups, which diffused into the agar medium and interacted with mercury. In fact, this fluorescence effect in the environment can serve as an identification feature for some representatives of the SRB.

Studies of the genetic, evolutionary, and biochemical aspects of mercury methylation have expanded the range of habitats with the potential to produce MeHg, including thawing permafrost soils, coastal zones of water bodies, agricultural soils, and extreme anaerobic environments (Gilmour et al., 2013; Hsu-Kim et al., 2013). It established that Hg methylators are primarily heterotrophic bacteria that use sulfate, iron, and carbon dioxide (CO_2) as terminal electron acceptors.

Features of metabolism of Hg-resistant strains

Five strains of Hg-resistant heterotrophic bacteria isolated from BR water from different habitats selected as inoculum to assess the role of individual MC in the transformation of readily available substrates (lactate, peptone) and difficult-to-mineralize humic substance derivatives (HNa) under mercury pollution conditions (Table 4). These strains exhibit resistance to 10 mg/L $Hg(NO_3)_2$, but differed in their resistance to 100 mg/L.

The effect of mercury salt on the metabolism of microorganisms studied for two groups of strains with use of readily available calcium lactate and peptone and difficult to mineralize HNa. The first group consisted of three strains from different habitats: *Bacillus* sp. 6 SS from Sredniy Sandar Bay; *Pseudomonas* sp. 42 BCB from bottom waters below the channel; *Arthrobacter* sp. 59 ACB from bottom waters above the channel. They grew on an agar medium for sulfate-reducing bacteria in the presence of 10 and 100 mg/L $Hg(NO_3)_2$. The second group consisted of two strains with lower Hg-resistance, isolated from bottom water at a depth of 65 m above the artificial channel: *Actinomyces* sp. 45 ACB and

Table 4. General characteristics of microbial strains involved in the in vitro transformation of sodium humate in the presence of different mercury concentrations. Colony growth on agar medium: "+++" – intensive growth, as in the mercury-free control; "++" – weak growth; "–" – no growth.

Strain	Sample place	Nutrient medium	Colony morphotype	Hg resistance	
				10 mg/L	100 mg/L
Bacillus sp. 6 SS	Sredniy Sandar Bay	Postgate	Fawn, slimy	+++	++
Pseudomonas sp. 42 BCB	Below the channel, bottom water, 33 m	Postgate	Fawn, slimy	+++	++
Actinomyces sp. 45 ACB	Below the channel, bottom water, 65 m	FPA	Gray, folded	+++	–
Bacillus sp. 48 ACB	Below the channel, bottom water, 65 m	FPA	Yellow, slimy	+++	+++
Arthrobacter sp. 59 ACB	Below the channel, bottom water, 65 m	Postgate	Orange, slimy	+++	++

Arthrobacter sp. 59 ACB, which were tested at lower concentrations of mercury salt (1 and 10 mg/L) on the same carbon sources.

The most active strain in utilizing lactate as a carbon source was *Pseudomonas* sp. 42 BCB, which exhibited maximum Hg resistance at a concentration of 100 mg/L (Table 5). *Bacillus* sp. 6 SS also exhibited fairly high resistance. *Arthrobacter* sp. 59 ACB did not utilize lactate.

The results of the study of strains of the second group (*Actinomyces* sp. 45 ACB and *Bacillus* sp. 48 ACB) with low mercury resistance on two easily accessible substrates (lactate, peptone) are presented in Table 6.

When using readily available organic matter as a carbon source without adding mercury, the most active strain was *Bacillus* sp. 48 ACB. This same strain exhibited maximum resistance when adding 1 mg/L and 10 mg/L of mercury salt. Furthermore, increasing the mercury concentration to 10 mg/L increased the growth activity of this strain.

Completely different responses to the presence of mercury observed in these strains when they were cultivated on NH_4. At a mercury concentration of 10 mg/L, no differences observed between the strains, the greatest differences in the spectral characteristics of the CL observed at a mercury concentration of 100 mg/L (Fig. 2).

The *Bacillus* sp. 6 SS strain from Sredniy Sandar Bay was less active than the control without mercury salt. Two other strains isolated from bottom waters (*Pseudomonas* sp. 42 BCB – below the channel, *Arthrobacter* sp. 59 ACB – above the channel) differed in their activity towards different components of HNa. Thus, *Pseudomonas* sp. 42 BCB actively consumed aliphatic and aromatic components, as well as chromophoric groups of the HNa molecule. According to the spectral characteristics, the peculiarity of *Arthrobacter* sp. 59 ACB metabolism consisted of accumulation of these components in the nutrient medium. It assumed that with the participation of *Pseudomonas* sp. 42 BCB in bottom waters during the transformation of humic compounds, their aromatic component involved in mercury methylation processes; this was a manifestation of the response to the stress of mercury pollution. In this case, humic-like organic matter not only stimulated microbial activity but could also act as methyl donors and promote mercury methylation.

Recent studies (Cao et al., 2021) using two strains of the *Pseudomonas* genus (*P. fluorescens* and *P. putida*) demonstrated that mercury methylation followed by demethylation and a reduction in MeHg levels. The authors interpret this microbial mercury transformation as a passive stress response, dependent on the mercury content and the bacterial tolerance threshold for MeHg. Aerobic mercury methylation shown to be less efficient than a similar process under sulfate reduction conditions.

During the transformation of HNa, the response modes of the *Actinomyces* sp. 45 ACB and *Bacillus* sp. 48 ACB strains also detected depending on the mercury content in the nutrient medium.

Table 5. Use of lactate by *Bacillus* sp. 6 SS, *Pseudomonas* sp. 42 BCB, *Arthrobacter* sp. 59 ACB strains at mercury contamination

Strain	Lactate	Lactate + Hg 10 mg/L	Lactate + Hg 100 mg/L
Control	0.045	0.047	0.050
Bacillus sp. 6 SS	0.059 ± 0.001	0.062 ± 0.001	0.065 ± 0.001
Pseudomonas sp. 42 BCB	0.072 ± 0.002	0.083 ± 0.002	0.087 ± 0.002
Arthrobacter sp. 59 ACB	0.045 ± 0.001	0.047 ± 0.001	0.051 ± 0.001

Table 6. Utilization of lactate and peptone by strains from different habitats under mercury contamination conditions.

Strain	Lactate			Peptone		
	Without Hg	+ 1 mg/L Hg	+ 10 mg/L Hg	Without Hg	+ 1 mg/L Hg	+ 10 mg/L Hg
Контроль	0.040	0.042	0.043	0.041	0.043	0.043
45 ACB	0.065 ± 0.002	0.068 ± 0.002	0.072 ± 0.002	0.075 ± 0.002	0.078 ± 0.002	0.076 ± 0.002
48 ACB	0.078 ± 0.003	0.086 ± 0.003	0.096 ± 0.003	0.086 ± 0.003	0.101 ± 0.004	0.112 ± 0.005

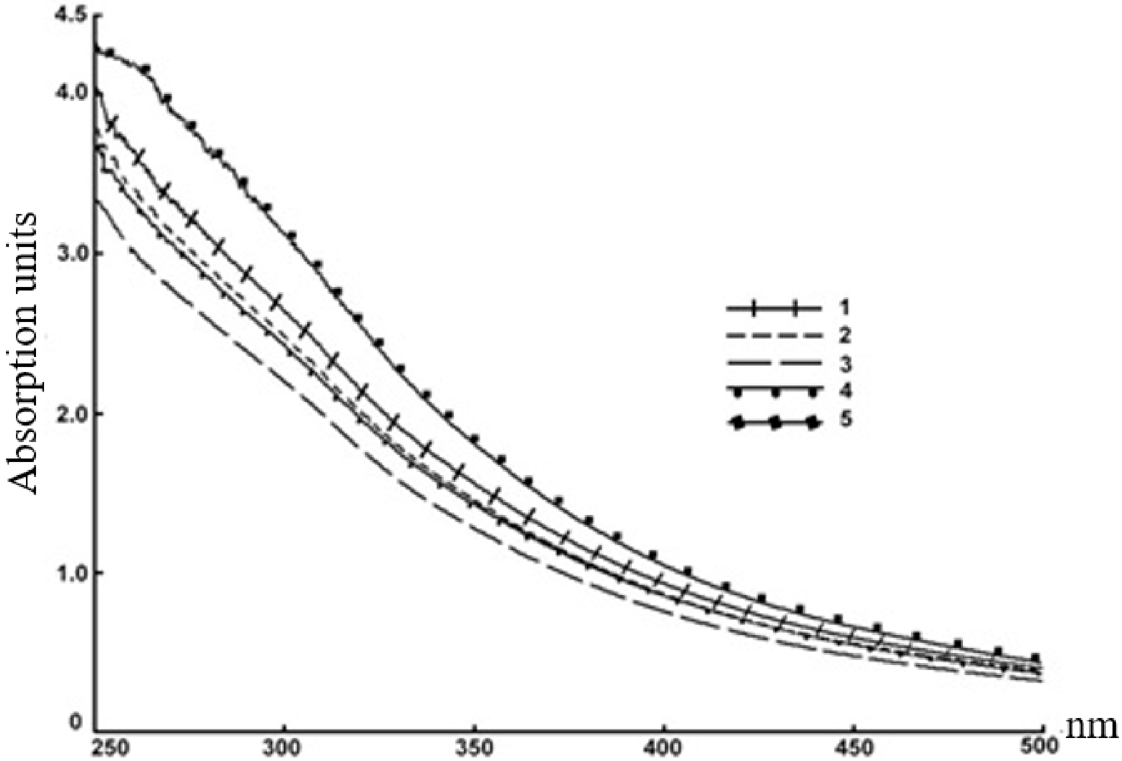

Fig. 2. Spectral characteristics of microbial transformation of sodium humate in the presence of 100 mg/L $Hg(NO_3)_2$: 1 – strain *Arthrobacter* sp. 59 ACB; 2 – strain *Bacillus* sp. 6 SS; 3 – strain *Pseudomonas* sp. 42 BCB; 4, 5 – control (sodium humate with a mercury salt concentration of 100 mg/L and without mercury salt, respectively).

Minor changes in the spectral characteristics of the CL in both strains observed as a result of monitoring in the area of the total content of OM and their aromatic activity at a concentration of 1 mg/L. A decrease in the content of chromophore groups in this regard recorded only with the inclusion of *Bacillus* sp. 48 ACB. The geometrical growth of the *Actinomyces* sp. 45 ACB strain at a mercury content of 10 mg/L was absent, and a change in the strain of the *Bacillus* sp. 48 ACB observed in all wavelength range of the CL. In an aquatic environment, when using supports with substances measured as the HNa *Actinomyces* sp. 45 ACB also turned out to be less stable, as recorded in the first tests in agar medium (Table 4).

Studies have shown that, under the same conditions, strains isolated from the same habitat differed in their Hg resistance. Furthermore, the *Actinomyces* sp. 45 ACB strain demonstrated the ability to form biofilms on the surface of rock particles and leach various chemical elements, including Al, Ca, Mg, and Mn, into aqueous solutions (Kondratyeva et al., 2024). Its functional activity was comparable to the intensity of element leaching in vitro from nonsterile rock using a natural microbial consortium.

Rock failure on slopes often considered a result of chemical erosion (Qu et al., 2018; Zhang et al., 2017). However, evidence has recently emerged of a relationship between microbial communities and landslide failure (Błońska et al., 2018). Thus, as a result of reservoir water level fluctuations and biogeochemical processes, the landslide body will actively deteriorate, and rock transformation products and metabolites of biofilms developing in the pore space may enter the aquatic environment. These metabolites may include precursors of methyl radicals. Some microorganisms that are part of natural consortia, involved in mercury methylation, while other representatives supply the aquatic environment with elements that ensure the activity of enzymes of the complete mercury cycle.

Thus, complex biogeochemical processes involving various groups of microorganisms occur around the landslide body. Predicting their behavior under such conditions is a very difficult task. However, studies have shown that there are numerous factors contributing to the ecological risk of mercury methylation in the bottom sediments of the Bureya Reservoir at the landslide site.

Conclusion

Studies of the functional activity of aquatic microbial communities in the Bureya landslide zone revealed that sulfate-reducing bacteria present in bays containing submerged wood and in the bottom water layers above the landslide body at a depth of 65 m act as sensitive indicators of mercury pollution. The half of the 62 bacterial strains isolated from various habitats were resistant to mercury at a concentration of 100 mg/L. Five strains with varying degrees of resistance to mercury (II) nitrate were shown to utilize readily available carbon sources (lactate, peptone). The most active strains were isolated from the bottom water layers on a selective medium for sulfate-reducing bacteria. It is hypothesized that active mercury migration from crushed rocks and its conversion to a dissolved state may occur in sedimentation areas around the landslide with the participation of active mercury methylators – sulfate-reducing bacteria. Hg-resistance of individual strains serves as an indicator of the resistance of microorganisms to new conditions formed in the landslide-influenced zone and allows one to assess the degree of ecological risk during the transformation of humic substances due to the formation of metabolites with a methyl group and subsequent methylation of mercury.

Differences in sodium humate metabolism by strains isolated from bottom water layers above and below the landslide body experimentally demonstrated. Spectral characteristics revealed that the metabolism of *Arthrobacter* sp. 59 ACB consisted of the accumulation of aliphatic, aromatic, and chromophoric groups in the aquatic environment during the transformation of HNa in the presence of a mercury salt. Under similar conditions, the *Pseudomonas* sp. 42 BCB strain actively consumed the aliphatic and aromatic components of HNa, as well as the chromophoric groups of the molecule. It hypothesized that with the participation of *Pseudomonas* sp. 42 BCB, the aromatic component of humic compounds is involved in mercury methylation processes as a response to mercury pollution stress.

Isolating strains from specific habitats, combined with spectral methods for studying the transformation products of persistent humic substances, makes it possible to assess the growth and metabolism of microorganisms in the presence of mercury migrating from rocks and to predict the risk of accumulation of volatile aromatic compounds and chromophore group carriers for a more comprehensive assessment of the reservoir's environmental status after a major landslide. The release of difficult-to-decompose plant-derived organic matter into bottom sediments from the catchment area and the limited oxygen content in the water-bottom contact zone contribute to the creation of conditions conducive to the activation of mercury methylation processes, increasing its mobility and toxicity. Sulfate-reducing bacteria with increased Hg resistance serve as indicators of the ecological risk of mercury pollution in the Bureya landslide zone.

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