ISSN 2658-3518

LIMNOLOGY & FRESHWATER BIOLOGY

2019, № 4

> abiotic and biotic water components;
> ecosystem-level studies;
> systematics and aquatic ecology;
> paleolimnology and environmental histories;
> laboratory experiments and modeling

Limnology and Freshwater Biology 2019 (4): 259-265 DOI:10.31951/2658-3518-2019-A-4-259

Original Article

ISSN 2658-3518

LIMNOLOGY FRESHWATER BIOLOGY

www.limnolfwbiol.com

Microbial communities in the estuarine water areas of the rivers in the southeastern part of Lake Baikal

Zemskaya T.I., Bukin S.V.*, Zakharenko A.S., Chernitsyna C.M., Shubenkova O.V.

Limnological Institute of the Siberian Branch of the Russian Academy of Sciences, Ulan-Batorskaya 3, 664 033 Irkutsk, Russia.

ABSTRACT. Using the Illumina MiSeq platform, we have studied the diversity of bacteria and archaea in three rivers of the southeastern end of Lake Baikal in the under-ice period of 2018. In analysed 16S rRNA gene libraries of all rivers, we have identified sequences of 12 bacterial phyla: *Actinobacteria*, *Bacteroidetes*, *Cyanobacteria*, *Elusimicrobia*, *Epsilonbacteraeota*, *Fibrobacteres*, *Firmicutes*, *Omnitrophicaeota*, *Patescibacteria*, *Planctomycetes*, *Proteobacteria*, and *Verrucomicrobia*. The contribution of minor taxa to the microbiomes from the estuaries of the rivers Solzan and Bolshaya Osinovka is more significant. Three phyla (*Thaumarchaeota*, *Euryarchaeota* and *Crenarchaeota*) and one superphylum (DPANN) represent archaea. The diversity of bacteria and archaea in the investigated ecotopes has its specifics and is different to that found in the pelagic zone of Southern Baikal. Bacteria show phylogenetic diversity at the level of families and genera, whereas archaea – at the level of phyla. In the microbiomes, we have identified microorganisms involved in various stages of transformation of organic and inorganic substances.

Keywords: small tributaries of Lake Baikal, microbial communities, diversity and structure, 16S rRNA gene, Illumina MiSeq

1. Introduction

Rivers and their estuarine water areas are zones, where transformation and accumulation of various substances from shores and river waters take place (Newton et al., 2013; 2015; Cloutier et al., 2015). The depth of information acquired by using advanced molecular genetic approaches provides a means to characterize the microbial composition, distribution, and transportation pathways in the environment and to relate them to understand pollution mechanisms (Newton et al., 2013; Halliday et al., 2014). There was the active destruction of various substances in the estuarine water areas of large tributaries of Lake Baikal: the rivers Selenga and Upper Angara (Maksimenko et al., 2008; 2012; Sorokovikova et al., 2012), and to a lesser extent – in water areas small inflowing tributaries (Maksimov, 1995). There were practically no studies concerning the diversity of microbial communities in these areas; only the taxa ratio at the phylum level were investigated in rivers and estuarine water areas of the rivers Selenga and Upper Angara. At the same time, some works state that precipitation (Khodzher et al., 2002; Sorokovikova et al., 2002; Tomberg et al., 2016) as well as domestic sewage (Drucker et al., 1993; Shtykova et al., 2016) and groundwater runoff from sludge and lignin storage pits of the closed Baikalsk Pulp and Paper Mill (State Report…, 2017) influence the chemical composition in the rivers of Southern Baikal.

In the under-ice period of 2018, we conducted comprehensive studies at estuaries and estuarine water areas of small rivers in the southeastern part of Lake Baikal (Zemskaya et al., 2019). We found that acidity of snow cover and waters of the Pereyomnaya River did not adversely affect the abundance of microorganisms and their productiveness. The high values of dark carbon dioxide fixation in the water of the estuaries of the rivers in comparison with the estuarine zone were a distinctive feature of these water areas, and the high P/B coefficients (specific bacterioplankton production) with a significantly lower total microbial count indicated a high percentage of metabolically active cells that ensure the inclusion of carbon not only in the bacterioplankton biomass but also other organic compounds. Therefore, we were interested in the study of the diversity and structure of microbial communities at the estuary and an estuarine water area of the Pereyomnaya River as well as estuaries of the rivers Solzan and Bolshaya Osinovka having the acidity of snow cover and inflow of wastewater from sludge and lignin storage pits, using the Illumina MiSeq platform.

---

*Corresponding author.
E-mail address: sergeibukin@lin.irk.ru (S.V. Bukin)

2. Material and methods

2.1. Study areas and sampling

The water studies were carried out in March 2018 at estuaries and an estuarine water area of the Pereyomnaya River as well as the estuaries of the rivers Solzan and Bolshaya Osinovka (Southern Baikal). Water was sampled using a Niskin bottle at the estuaries of the rivers and a distance of 100 and 200 m from the estuaries. A description of the stations, methods for studying chemical parameters and pH are shown in (Zemskaya et al., 2019).

2.2. DNA extraction

We obtained five DNA samples from the surface water. Water samples (5 L) were filtered on nitrocellulose filters (25 mm diameter, 0.2 micron pore size; "Millipore", Germany) using a diaphragm pump. The filter was then placed in a TE buffer (10 mM Tris-HCl, pH 7.4; 1 mM EDTA, pH 8.0) and frozen at -20°C. Then, it was transported to the laboratory. DNA was extracted according to the modified method of phenol-chloroform extraction (Sambrook et al., 1989). The extracted DNA was kept at -70°C for further use. The universal primers U341F (5'-CCTACGGGRSGCAGCAG-3') and U785R (5'- GACTACHVGGGTATCTAATCC -3') as well as a program: 96°C for 3 min; 96°C for 30 s; 55°C for 30 s; 72°C for 40 s (25 cycles); and 72°C for 10 min, were used for PCR amplification of 16S rRNA gene fragments of bacteria, including the variable region V3–V4. The primers that included the variable region V2–V3: A113F (5'-ACKGCTSAGTAACACGTGG-3') and A520R (5'-TACGGCGGCKGCTGGCA-3') (Whitehead and Cotta, 1999; Kim et al., 2011), as well as a program: 96°C for 2 min; 96°C for 30 s, 58°C for 45 s, 72°C for 40 s (25 cycles); and 72°C for 10 min, were used for PCR amplification of 16S rRNA gene fragments of archaea. The libraries were analysed using Illumina MiSeq Standard Kit v.3 (Illumina) at the Genomics Core Facility of the Evrogen Join Stock company (Moscow).

2.3. Data preparation and filtering: Bioinformatics analysis

Paired-end sequencing reads were trimmed and filtered by quality using leading and sliding window trimming with the average Phred-value = 25 and window size = 13-15 bases in Trimmomatic version 0.39 (Bolger et al., 2014). The R1 and R2 sequences corresponding to ribosomal RNA amplicons were merged into contigs with the mothur merge.contigs command. The fragments obtained were filtered by size and tested on the contents of respective forward/reverse primers with allowing two mismatch between forward and reverse primer and sequence. Further rRNA sequence processing was performed using mothur v.1.34.4 software (Schloss et al., 2009) according to MiSeq SOP recommendations (Kozich et al., 2013). To compare the microbial diversity among the samples, the bacterial read numbers of each sample were subsampled to those of the sample with the smallest number of reads by random removal of sequencing reads using the sub. sample command of the mothur program. The filtered sequences were aligned, clustered, and identified taxonomically using the SILVA 132 databases (http://www.arb-silva.de). To estimate similarity among bacterial communities, the samples were analysed using non-metric multidimensional scaling and clustered on the basis of the Euclidean distance matrix by the Vegan and Cluster packages in R. For statistical analysis and assessment of the association of individual OTUs with chemical parameters, the concentrations of O_2, POB, SO_4^{2-}, and CH_4 shown in (Zemskaya et al., 2019) were used. The closest homologues of each gene fragment sequence were found with a BLAST search against the NR database (http://blast.ncbi.nlm.nih.gov). The 16S rRNA sequences were deposited in the NCBI's Sequence Read Archive (Accession number: Bioproject PRJNA556789).

3. Results and discussion

The obtained rarefaction curves (data not shown) indicate that the sequencing volume reached in the analysis of the samples is satisfactory for the complete characterisation of diversity of bacterial communities from river samples but insufficient for the reference station. In the latter sample, we obtained the sequences of almost one taxon, cyanobacteria, which differed significantly from the data simultaneously obtained in the pelagic zone of Southern Baikal (Cabello-Yeves et al., 2018). In river microbiomes, the Chao1 and Shannon indices were maximum for 16S rRNA gene libraries of bacteria from the Solzan River (4471.3 and 6.8, respectively) as well as for archaea from the estuarine water area of the Pereyomnaya River (138 and 4.2, respectively, Table 1). The number of archaeal species varied less significantly; the highest values of the Shannon index (4.2) were in the estuarine water area of the Pereyomnaya River, and the lowest ones (3.3) – at the estuary of the Solzan River. Notably, the lower number of the obtained archaeal sequences in comparison with bacterial ones may be due to their low abundance and an insufficient amount of investigated DNA.

Analysis of the 16S rRNA gene libraries of bacteria and archaea in the rivers and estuarine water areas indicated a different taxonomic composition of the communities. OTUs of bacteria and archaea formed two clusters each on dendrograms. The first one included sequences from the estuary and estuarine water area of the Pereyomnaya River, and the second – from the estuaries of the rivers Solzan and Bolshaya Osinovka (Fig. 1A, 1B). Based on the intracluster distances, the diversity of bacterial communities was more similar in the microbiomes from the estuarine water area of the Pereyomnaya River than between microbiomes from the estuary and estuarine water area. According to intercluster distances, the differences in the composition of archaeal communities were more obvious in comparison with bacterial communities.

In the analysed 16S rRNA gene libraries of all rivers, there were sequences of 12 bacterial phyla: *Actinobacteria*, *Bacteroidetes*, *Cyanobacteria*, *Elusimicrobia*, *Epsilonbacteraeota*, *Fibrobacteres*, *Firmicutes*, *Omnitrophicaeota*, *Patescibacteria*, *Planctomycetes*, *Proteobacteria*, and *Verrucomicrobia* (Fig. 2A). The contribution of minor taxa varied: their diversity and percentage of sequences were lower in the microbiome from the water area of the Pereyomnaya River and higher at the estuaries of the rivers Solzan and Bolshaya Osinovka (4.7 and 2.1%) (Fig. 2B). In the microbiome from the estuary of the Pereyomnaya River, the sequences of *Proteobacteria* (46%), *Epsilonbacteraeota* (21%) and *Bacteroidetes* (11.2%) as well as *Cyanobacteria* (7.8%) and *Patescibacteria* (4.1%) had the highest percentage. At a distance of 100 m from the river estuary, the ratio of the dominant taxa in the microbiomes changed, with an increase in the contribution of the members of the phyla *Firmicutes* (8.5%), *Bacteroidetes* (18.2%) and *Cyanobacteria* (18.3%) and decrease in *Proteobacteria* (25.1%). At a distance of 200 m from the river estuary, the ratio of taxa in the microbiomes again changed; the members of *Bacteroidetes* (26.3%), *Cyanobacteria* (25.5%) and *Gammaproteobacteria* (25.3%) had the highest percentage, and the sequences of *Firmicutes* (0.2%) and *Epsilonbacteraeota* (4.1%) were minor. Microorganisms of the *Gammaproteobacteria* (20.0-32.4%) mainly represented Proteobacteria with a large contribution of the sequences of the order *Betaproteobacteriales*. Among them, we identified the sequences of methano- and methylotropic bacteria, in particular, the members of the families *Methylophilaceae* (genus *Methylotenera*) and *Methylomonaceae* (genus *Methylobacter*). The presence of a great number of sequences of these taxa at the estuary of the Pereyomnaya River is likely due to their inflow with the runoff of the river, which flows through wetlands. Moreover, the microbiome of this river (11.7%) had a high percentage of the sequences of the genus *Methylobacterium* (*Alphaproteobacteria*), which also participate in the methane cycle, ensuring the methanol oxidation. In the communities of the estuarine water area of the Pereyomnaya River (2.8 and 4.8%, respectively), the members of this genus were a minor component. The bacterial sequences of the genus *Sphingomonas* (*Alphaproteobacteria*), which closest homologues have proteo- and lipolytic activity and are capable of surviving under low concentrations of nutrients (Yoon et al., 2008), had a large contribution in the microbiomes of all investigated samples.

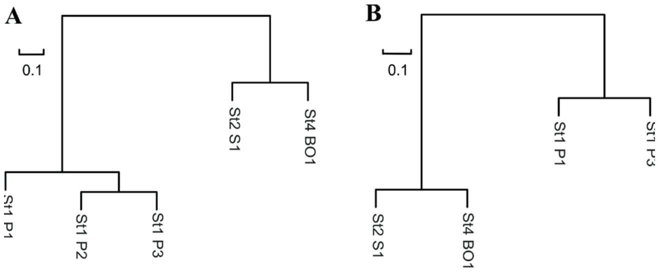

Fig.1. Dendrogram of similarity and difference of bacterial (A) and archaeal (B) communities based on Euclidean distance matrix

Members of the *Deltaproteobacteria* class in the Pereyomnaya River and its water area were not numerous (1.9% or less) and included both aerobic predatory bacteria of the genus *Bdellovibrio* and anaerobic sulphate- (genus *Desulfobulbus*) and metal-reducing microorganisms (genus *Geobacter*). The sequences of the phylum *Bacteroidetes* (11.2-22.5%), which belong to both planktonic (*Flavobacterium, Fluviicola*, *Arcicella,* and *Parasediminibacterium*) and

Table 1. Indices of species richness and diversity (at a cluster distance of 0.03) of bacteria and archaea in the 16 rRNA gene libraries of microbial communities from the rivers Pereyomnaya, Solzan and Bolshaya Osinovka.

Sampling area, sample		Number of reads	Coverage, %	Number of $OTU_{0.03}$	ACE	Chao1	Simpson's Inverse Index	Shannon
Bacteria								
estuary of the Pereyomnaya River	St1 P1	148453	99.6	3821	4110.4	4171.2	15.0	4.67
100 m from the estuary	St1 P2	106195	99.1	3086	3781.9	3701.2	12.4	4.24
200 m from the estuary	St1 P3	100175	99.1	3301	3986.3	3987.0	14.4	4.66
estuary of the Solzan River	St2 S1	162003	99.9	4432	4471.3	4509.7	218.1	6.79
estuary of the Bolshaya Osinovka River	St4 BO1	104767	99.4	4110	4375.9	4442.7	97.6	6.40
reference station	St5 Fon	2941	99.9	8	11.8	9.0	1.0	0.05
Archaea								
estuary of the Pereyomnaya River	St1 P1	1117	99.2	80	83.9	86.0	15.0	3.6
200 m from the estuary	St1 P3	1670	99.4	123	125.6	138.0	37.4	4.2
200 m from the estuary	St2 S1	1278	99.4	66	69.1	70.6	15.2	3.3
estuary of the Bolshaya Osinovka River	St4 BO1	637	98.9	80	81.9	82.3	27.7	3.9

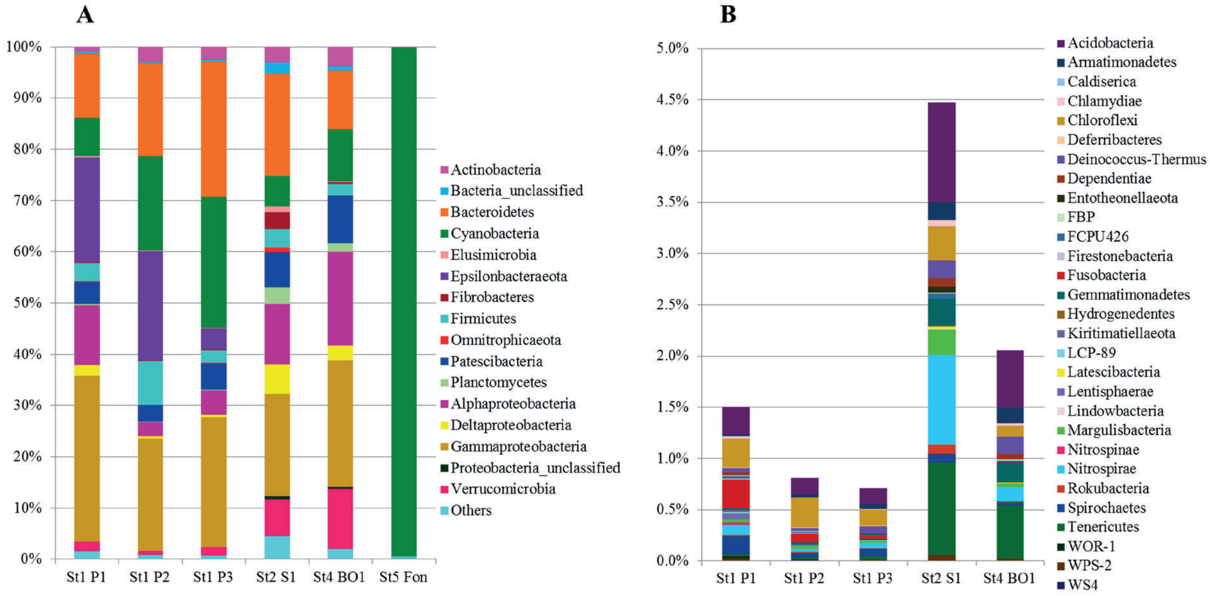

Fig.2. The composition of the bacterial community in the water of the rivers Pereyomnaya, Solzan and Bolshaya Osinovka according to the analysis of sequences of 16S rRNA gene fragments: A – dominant phyla (share of sequences >95.0%); B – minor taxa (share of sequences <5.0%) The composition of the bacterial community in the water of the rivers Pereyomnaya, Solzan and Bolshaya Osinovka according to the analysis of sequences of 16S rRNA gene fragments: A – dominant phyla (share of sequences >95.0%); B – minor taxa (share of sequences <5.0%)

benthic microorganisms (*Paludibacter*), were more diverse and numerous in the microbiomes of this area. The identified bacteria of the genera *Flavobacterium* and *Fluviicola* are capable of decomposing plant polysaccharides, such as starch, cellulose, xylans and pectins, as well as photosynthesizing due to the presence of rhodopsins in the cells (Humphry et al., 2001; Martinez-Garcia et al., 2011; Feng et al., 2015; Park et al., 2017). Additionally, bacteria of the genera *Arcicella* and *Parasediminibacterium* play an important role in protein metabolism (Sheu et al., 2010; Kang et al., 2016), whereas the *Paludibacter* members ferment sugars (Ueki, 2006).

Microbiome in the Solzan River had a wider range of bacterial taxa (Fig. 2A), including dominant *Gammaproteobacteria* (20%), *Alphaproteobacteria* (11.8%) and *Bacteroidetes* (20.1%). In the microbiome of this river, the contribution of *Patescibacteria* (6.8%) and *Verrucomicrobia* (*Opitutaceae* family, 7.2%) increased, and that of *Cyanobacteria* (5.9%) decreased. Like in the microbiomes of the Pereyomnaya River, members of the order *Betaproteobacteriales*, in particular, the sequences of the genera *Paucibacter* and *Rhodoferax*, were numerous among *Gammaproteobacteria*. The strains of the genus *Paucibacter* from lake sediments can cleave cyanobacterial hepatotoxins, microcystins and nodularin (Rapala et al., 2005). In the microbiome of the Solzam River, the share of minor taxa increased (4.5%), among which the intracellular parasites of arthropod from the phylum *Tenerecutes* (*Mycoplasmataceae* family, 0.9%) (Kostanjsek et al., 2007) as well as ammonia- and nitrite-oxidizing bacteria of the phylum *Nitrospirae* (genus *Nitrospira*, 0.9%) (Koch et al., 2015) and *Acidobacteria* (approximately 1%) were the most representative. Furthermore, in the minor component of the microbiome, there were members of the phyla *Planctomycetes*, *Omnitrophicaeota*, *Fibrobacteres*, and *Firmicutes*. A wider range of taxa in the microbiome of this river may be due to the influx of water and microorganisms from sludge and lignin storage pits remaining after the closure of Baikalsk Pulp and Paper Mill.

The structure and diversity of the microbiome from the Bolshaya Osinovka River were similar to those from the Solzan River. *Gammaproteobacteria* (24.7%), *Alphaproteobacteria* (18.3%), *Bacteroidetes* (11.6%), *Verrucomicrobia* (11.6%), and *Patescibacteria* (9.3%) were among the dominant phyla. The contribution of minor taxa did not exceed 2%. Notably, in the microbiomes of the Solzan and Bolshaya Osinovka Rivers, there was a decrease in the contribution of the sequences of sulphur-oxidizing bacteria (genus *Sulfurospirillum*) from the phylum *Epsilonbacteraeota* (0.01%), which had a high percentage in the microbiomes from the Pereyomnaya River (up to 21%).

The taxonomic composition of archaea was less diverse (Fig. 3) in the investigated areas. We identified members of three phyla (*Thaumarchaeota*, *Euryarchaeota*

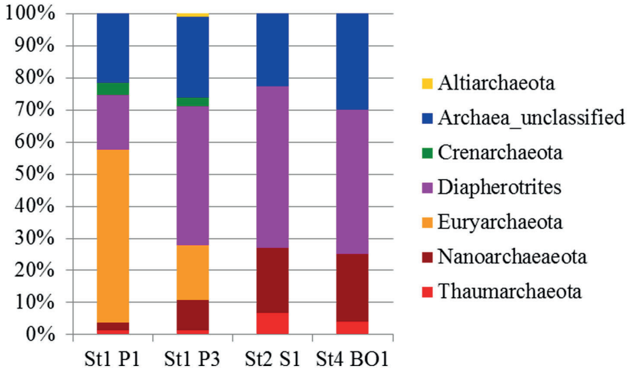

Fig.3. The composition of archaeal community in the water of the rivers Pereyomnaya, Solzan and Bolshaya Osinovka according to the analysis of the sequences of 16S rRNA gene fragments

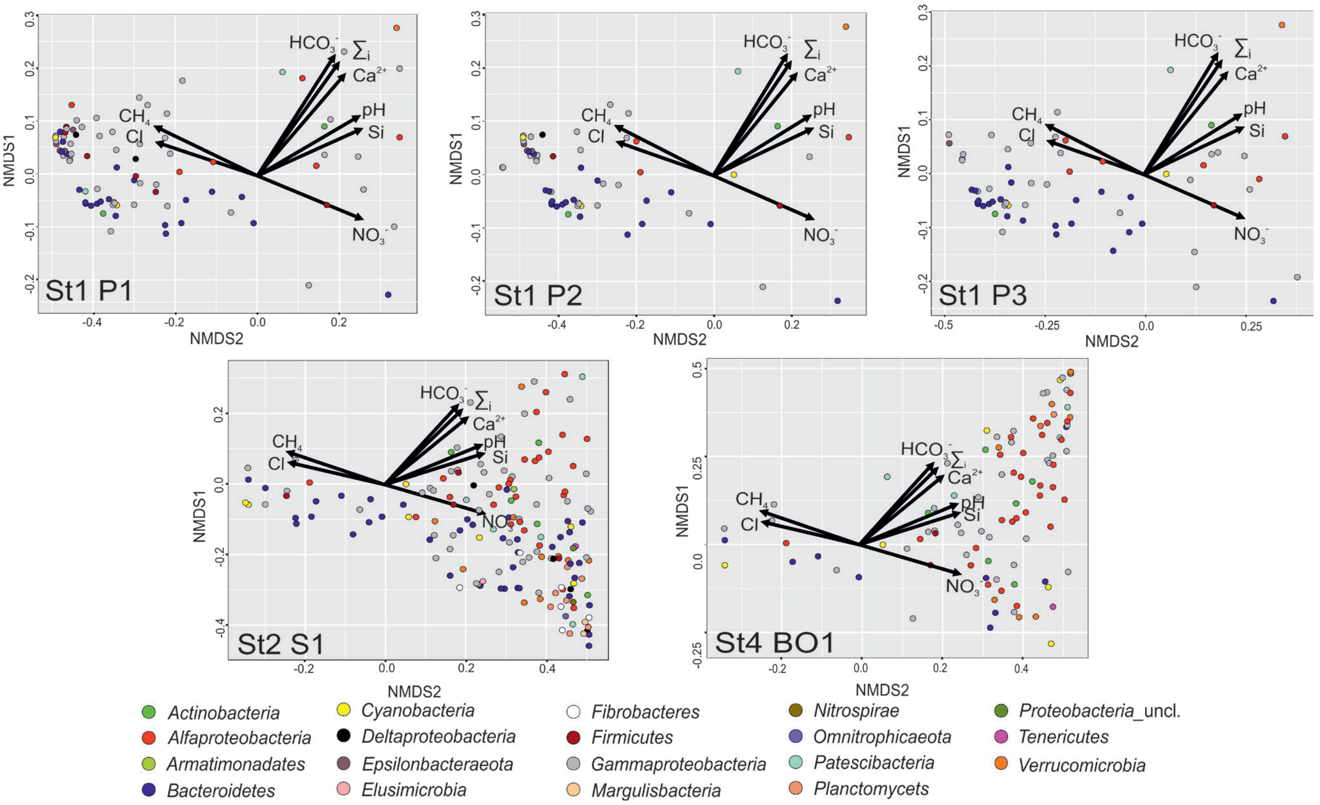

Fig.4. Non-metric multidimensional scaling (NMDS) ordination of bacterial community composition in each sample based on Euclidean distances calculated for abundant OTUs with more than 150 sequences (stress = 1.37). Vectors show correlations of environmental variables ($p < 0.05$)

and *Crenarchaeota*) and one superphylum (DPANN) of archaea. Unlike the archaeal community from the photic layer of the pelagic zone in Southern Baikal, where there were only members of the phylum *Thaumarchaeota* (Cabello-Yeves et al., 2018), microbiomes of the studied rivers had a more diverse taxonomic composition. The contribution of the *Thaumarchaeota* members is insignificant (1.1-6.7%), and the revealed sequences belong to ammonium-oxidizing microorganisms of the families *Nitrosopumilaceae* and *Nitrosotaleaceae* (Park et al., 2012). The microbiome from the water area of the Pereyomnaya River had the greatest number of archaeal taxa, and at the estuary, the bulk of sequences belonged to the methanogenic archaea of the phylum *Euryarchaeota* (53.9%); in the estuarine water area, their contribution was much smaller (16.9%), and they were not detected in the communities from other rivers. The members of *Crenarchaeota* were also found in minor quantities only in the microbiomes from the Pereyomnaya River (3.8-2.6%), and the *Diapherotrites* and *Nanoarchaeota* members of the DPANN superphylum dominated the microbiomes of the rivers Solzan and Bolshaya Osinovka (from 20.3 to 50.4%). Notably, the sequences of the DPANN superphylum were observed only in the near-bottom area of the pelagic zone in Southern Baikal (Cabello-Yeves, personal communication).

The nonmetric multidimensional scaling technic evaluated the association of the individual taxonomic units and chemical indicators in the studied biotopes (Fig. 4, Fig. 5). The analysis included OTUs having more than 150 sequences. To construct dendrograms for data array on bacteria, we used such parameters as decomposable organic matter (DOM), a total number of ions, the concentration of major ions as well as pH. The dendrograms show the data on the association of chemical parameters with the individual OTUs of bacteria (Fig. 4) and archaea (Fig. 5). It is obvious that three clusters of bacterial OTUs form in each water area. In the microbiomes of the Pereyomnaya River and its water area, the OTU group associated with the concentration of Cl^{-} and CH_4 ions is the most evident. This cluster includes members of such taxa as *Bacteroidetes*, *Alpha-* and *Gammaproteobacteria*, among which the most representative are the sequences of the families *Methylophilaceae* (genus *Methylotenera*) and *Methylomonaceae* (genus *Methylobacter*) involved

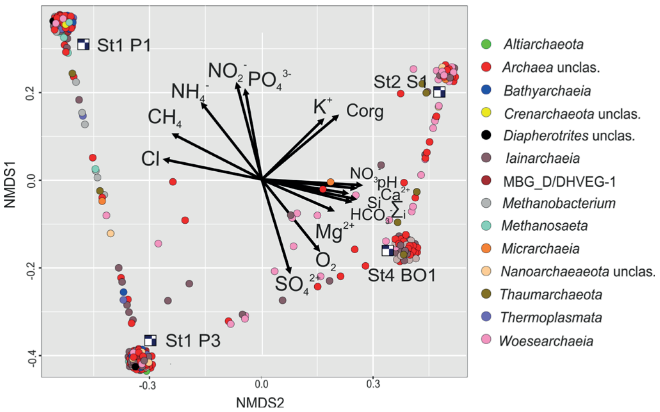

Fig.5. Non-metric multidimensional scaling (NMDS) ordination of archaeal community composition in each sample based on Euclidean distances calculated for abundant OTUs with more than 50 sequences (stress = 1.74). Vectors show correlations of environmental variables

in various stages of methane oxidation. Among *Bacteroidetes*, the members of the genera *Paludibacter*, *Arcicella* and *Flavobacterium* are numerous. In the microbiomes of the rivers Solzan and Bolshaya Osinovka, a large number of OTUs is associated with the total number of ions, the concentration of Ca^{2+}, Si and HCO_3^- ions as well as the pH of the water. In this cluster, the most representative sequences are *Alpha-* (families *Caulobacteraceae*, *Hyphomonadaceae*, *Paracaedibacteraceae*, *Rhodobacteraceae*, and *Rickettsiaceae*), *Gammaproteobacteria* (*Burkholderiaceae, Chitinibacteraceae, Rhodocyclaceae, Cellvibrionaceae,* and *Pseudomonadaceae*) and *Actinobacteria* (*Microbacteriaceae* and *Solirubrobacteraceae*). The third OTU cluster is the most numerous in the microbiomes of the rivers Solzan and Bolshaya Osinovka, and it correlates with the concentration of nitrate ion. This cluster has OTUs of *Gammaproteobacteria* (*Burkholderiaceae*; *Xanthomonadaceae*), *Alphaproteobacteria* (*Hyphomonadaceae*; *Rhodobacteraceae*; *Sphingomonadaceae*), *Tenerecutes*, *Verrucomicrobia* (*Rubritaleaceae*), *Planctomycetes* (*Pirellulaceae*), and *Nitrospiraceae* (*Nitrospira*).

The analysis of data array of the archaeal OTUs indicates their different contribution to the composition of the communities in the studied water areas (Fig. 5) and the lack of reliable associations with most on the analysed parameters. This is most evident for the archaeal community from the water area of the Pereyomnaya River, where we have determined no reliable correlation between dominant OTUs with any of the parameters. The individual OTUs of archaea from the Bolshaya Osinovka River are associated with nitrates, the total number of the Si and HCO_3^- ions as well as the pH of the water (Fig. 5), whereas in the Solzan River – with the concentration of DOM and potassium ions.

4. Conclusions

The studied rivers have different salinity, the pH of the water, the concentration of DOM and individual ions, which affected the diversity of microbial communities. The phylogenetic analysis has shown that their diversity and structure in the rivers are not the same and differ from those simultaneously observed in the pelagic zone (Cabello-Yeves et al., 2018). The level of families and genera mostly shows the taxonomic difference in bacteria, and the level of phyla – in archaea. In the communities of the Pereyomnaya River and its water area, where the waters have the lowest salinity and mildly acidic pH of the environment, the sequences of bacteria involved in various stages of methane oxidation predominated in the microbiomes. This is consistent with higher methane concentrations at the estuary and estuarine water of this river in comparison with other rivers. The taxonomic composition of the communities in the estuarine water area is similar to riverine and pelagic communities. At a distance from the river estuaries, the contribution of the members of *Patescibacteria* and *Epsilonbacteraeota*, as well as minor taxa, decreases. Despite the smaller watershed basin and runoff in comparison with the Pereyomnaya River, the microbiomes of the rivers Solzan and Bolshaya Osinovka have a more diverse phylogenetic composition. This is most likely due to the inflow of wastewater from the sludge and lignin storage pits of Baikalsk Pulp and Paper Mill, which ensure the activity of a wide range of microorganisms. Moreover, the structure of bacterial communities in the rivers differs from the structure of the communities from the photic layer of the pelagic zone in Southern Baikal (5 and 20 m) (Cabello-Yeves et al., 2018). In all microbiomes, the contributions of *Gammaproteobacteria*, *Alphaproteobacteria* and *Bacteroidetes* are comparable, whereas in the microbiomes of rivers, the phyla *Patescibacteria* and *Epsilonbacteraeota* are more representative, and *Actinobacteria* are less representative. Probably, the small representation of the latter ones in the river biotopes during the under-ice period is due to a dense snow cover that does not let in sunlight and, hence, limits the development of photoheterotrophic bacteria. In the pelagic zone of Southern Baikal, where the ice was less covered with snow, actinobacteria with a photoheterotrophic type of metabolism prevailed, whereas, in the river microbiomes, chemoorganotrophic microorganisms capable of using various substrates as well as methane were the most representative. High metabolic activity in the river samples compared to those from the estuarine water area of the Pereyomnaya River implies the lack of a mixing zone typical of large tributaries, which serves as a kind of biofilter that impedes the influx of various compounds in the lake waters.

Acknowledgements

The study was supported by the grant OFI-M No. 17-29-05040 and the LIN SB RAS State Task 0345-2019-0007 (No. AAAA-A16-116122110064-7).

References

Bolger A.M., Lohse M., Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30: 2114–2120. DOI:10.1093/bioinformatics/btu170

Cabello-Yeves P.J., Zemskaya T.I., Rosselli R. et al. 2018. Genomes of Novel Microbial Lineages Assembled from the Sub-Ice Waters of Lake Baikal. Applied and Environmental Microbiology 84: 1–21. DOI: 10.1128/AEM.02132-17

Cloutier D.D., Alm E.W., Mclellan S.L. 2015. Influence of land use, nutrients, and geography on microbial communities and fecal indicator abundance at Lake Michigan beaches. Applied and Environmental Microbiology 81: 4904–4913. DOI: 10.1128/AEM.00233-15

Drucker V.V., Kostornova T.Ya., Molozhavaya O.A. et al. 1993. Water quality assessment of Lake Baikal by sanitary and bacteriological indicators. Geography and natural resources 1: 60–64.

Feng X.-M., Tan X., Jia L. et al. 2015. *Flavobacterium buctense* sp. nov., isolated from freshwater. Archives of Microbiology 197: 1109–1115. DOI:10.1007/s00203-015-1149-5

Halliday E., Mclellan S.L., Amaral-Zettler L.A. et al. 2014. Comparison of bacterial communities in sands and water at beaches with bacterial water quality violations. PLoS One 9. DOI: 10.1371/journal. pone.0090815

Humphry D.R., George, A., Cummings, S.P. et al. 2001. *Flavobacterium frigidarium* sp. nov., an aerobic, psychrophilic, xylanolytic and laminarinolytic bacterium from Antarctica. International Journal of Systematic and Evolutionary Microbiology 51: 1235–1243. DOI:10.1099/00207713-51-4-1235

Kang H., Joung Y., Kim H. et al. 2016. *Parasedimini bacterium paludis* gen. nov., sp. nov., isolated from wetland. International Journal of Systematic and Evolutionary Microbiology 66: 326–331. DOI:10.1099/ijsem.0.000719

Khodzher T.V., Semenov M.Yu., Obolkin V.A. et al. 2002. Monitoring of acid deposition in the Baikal region. Chemistry for Sustainable Development 10: 569–575. (in Russian)

Kim M., Morrison M., Yu Z. 2011. Evaluation of different partial 16S rRNA gene sequence regions for phylogenetic analysis of microbiomes. Journal of Microbiological Methods 84: 81–87. DOI:10.1016/j.mimet.2010.10.020

Koch H., Lücker S., Albertsen M. et al. 2015. Expanded metabolic versatility of ubiquitous nitrite-oxidizing bacteria from the genus *Nitrospira*. Proceedings of the National Academy of Sciences 112: 11371–11376. DOI:10.1073/pnas.1506533112

Kostanjsek R., Strus J., Avgustin G. 2007. "*Candidatus Bacilloplasma,*" a Novel Lineage of *Mollicutes* Associated with the Hindgut Wall of the Terrestrial Isopod Porcellio scaber (Crustacea: Isopoda). Applied and Environmental Microbiology 73: 5566–5573. DOI:10.1128/aem.02468-06

Kozich J.J., Westcott S.L., Baxter N.T. et al. 2013. Development of a dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the MiSeq Illumina sequencing platform. Applied and Environmental Microbiology 79: 5112–5120. DOI: 10.1128/AEM.01043-13

Maksimenko S.Y., Zemskaya T.I., Pavlova O.N. et al. 2008. Microbial community of the water column of the Selenga River-Lake Baikal biogeochemical barrier. Microbiology 77: 587–594. DOI: 10.1134/S0026261708050123

Maksimenko S.Yu., Ivanov V.G., Buryukhaev S.P. et al. 2012. The structure of microbial communities in the confluence zone of the Upper Angara River in Lake Baikal. Gidrobilogichesky zhurnal [Hydrobioogical journal] 48: 55–68. (in Russian)

Maksimov V.V. 1995. Microbiology of large Baikal rivers and their estuarine water areas. Cand. Sc. Dissertation, Irkutsk State University, Irkutsk, Russia. (in Russian)

Martinez-Garcia M., Swan B.K., Poulton N.J. et al. 2011. High-throughput single-cell sequencing identifies photoheterotrophs and chemoautotrophs in freshwater bacterioplankton. The ISME Journal 6: 113–123. DOI:10.1038/ismej.2011.8

Newton R.J., Bootsma M.J., Morrison H.G. et al. 2013. A microbial signature approach to identify fecal pollution in the waters off an urbanized coast of Lake Michigan. Microbial Ecology 65: 1011–1023. DOI: 10.1007/s00248-013-0200-9

Newton R.J., Mclellan S.L., Dila D.K. et al. 2015. Sewage reflects the microbiomes of human populations. mBio 6. DOI: 10.1128/mBio.02574-14

Park S.J., Kim J.G., Jung M.Y. et al. 2012. Draft Genome Sequence of an Ammonia-Oxidizing Archaeon, "*Candidatus Nitrosopumilus koreensis*" AR1, from Marine Sediment. Journal of Bacteriology 194: 6940–6941. DOI:10.1128/jb.01857-12

Park M., Nam G.G., Kim S. et al. 2017. *Flavobacterium chuncheonense* sp. nov. and *Flavobacterium luteum* sp. nov., isolated from a freshwater lake. International Journal of Systematic and Evolutionary Microbiology 67: 4409–4415. DOI:10.1099/ijsem.0.002304

Rapala J., Berg K.A., Lyra C. et al. 2005. *Paucibacter toxinivorans* gen. nov., sp. nov., a bacterium that degrades cyclic cyanobacterial hepatotoxins microcystins and nodularin. International Journal of Systematic and Evolutionary Microbiology 55: 1563–1568. DOI: 10.1099/ijs.0.63599-0

Sambrook J., Fritsch E.F., Maniatis T. 1989. Molecular Cloning: A Laboratory Manual. N.Y.: Cold Spring Harbor Laboratory Press.

Schloss P.D., Westcott S.L., Ryabin T. et al. 2009. Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. Applied and Environmental Microbiology 75: 7537–7541. DOI:10.1128/aem.01541-09

Sheu S.Y., Yang C.S., Chen M.H. et al. 2010. *Arcicella aurantiaca* sp. nov., isolated from stream water. International Journal of Systematic and Evolutionary Microbiology 60: 2979–2983. DOI:10.1099/ijs.0.021527-0

Shtykova Yu.R., Suslova M.Yu., Kostornova T.Ya. et al. 2016. Sanitary and microbiological monitoring of the Lake Baikal pelagical zone and Baikal's major triburaries from 2010 to 2015. Izvestiya Irkutskogo Gosudarstvennogo Universiteta. Seriya «Biologiya. Ekologiya» [The bulletin of Irkutsk State University. Series «Biology. Ecology»] 17: 50–61. (in Russian)

Sorokovikova L.M., Sinyukovich V.N., Korovyakova I.V. et al. 2002. The formation of the chemical composition of the water in the tributaries of Southern Baikal under modern conditions. Geografiya i Prirodnye Resursy [Geography and Natural Resources] 4: 52–57. (in Russian)

Sorokovikova L.M., Popovskaya G.I., Belykh O.I. et al. 2012. Plankton composition and water chemistry in the mixing zone of the Selenga River with Lake Baikal. Hydrobiologia 695: 329–341. DOI 10.1007/s10750-012-1200-3

State report on the state and environmental protection of the Irkutsk Region in 2016 / Ministry of Natural Resources and Ecology of Irkutsk Region. 2017. Irkutsk: Megaprint LLC (in Russian)

Tomberg I.V., Sorokovikova L.M., Netsvetaeva O.G. et al. 2016. Chemical composition and trends of oxidation of snow waters and waters of South Baikal tributaries. Optika Atmosfery i Okeana [Atmospheric and Oceanic Optics] 29: 516–520. DOI: 10.15372/AOO20160612 (in Russian)

Ueki A. 2006. *Paludibacter propionicigenes* gen. nov., sp. nov., a novel strictly anaerobic, Gram-negative, propionate-producing bacterium isolated from plant residue in irrigated rice-field soil in Japan. International Journal of Systematic and Evolutionary Microbiology 56: 39–44. DOI:10.1099/ijs.0.63896-0

Whitehead T., Cotta M. 1999. Phylogenetic diversity of methanogenic archaea in swine waste storage pits. FEMS Microbiology Letters 179: 223–226. DOI:10.1111/j.1574-6968.1999.tb08731

Yoon J.H., Kang S.J., Lee S.Y. et al. 2008. *Sphingomonas insulae* sp. nov., isolated from soil. International Journal of Systematic and Evolutionary Microbiology 58: 231–236. DOI:10.1099/ijs.0.65075-0

Zemskaya T.I., Zakharenko A.S., Rusanov I.I. et al. 2019. Ecology of estuarine basins of southern Baikal small rivers according to springtime chemical and microbiological investigation. Microbiology 88: 1–13. DOI: 10.1134/S002636561906020X

Limnology and Freshwater Biology 2019 (4): 266-269 DOI:10.31951/2658-3518-2019-A-4-266

Original Article

ISSN 2658-3518
LIMNOLOGY FRESHWATER BIOLOGY
www.limnolfwbiol.com

Lake Gusinoye (the southern part of East Siberia, Russia): sedimentary history inferred from high-resolution reflection seismic data

Chensky D.A.[1], Grigorev K.A.[2], Chensky A.G.[1], Parkhomchuk E.V.[2], Fedotov A.P.[3]*

[1] *National Research Irkutsk State Technical University, Lermontov st., 83, Irkutsk, Russia*
[2] *Boreskov Institute of Catalysis the Siberian Branch of RAS, Lavrentiev Ave. 5 Novosibirsk, Russia*
[3] *Limnological Institute of the Siberian Branch of the Russian Academy of Sciences, Ulan-Batorskaya 3, 664 033 Irkutsk, Russia*

ABSTRACT. This paper studies the formation of the sediment cover in Lake Gusinoye. For this purpose, we used high-resolution seismic data. Depression of Lake Gusinoye has a tectonic origin; however, there is no evidence of recent tectonic activity. Sediment thickness in Lake Gusinoye is less than 9 m, and its history is short (<35-45 ka). In addition, seismic stratigraphy records contain three contrasting episodes when the lake level dramatically decreased. It is very likely that there were also other shorter episodes of low-level stands. Thus, seismic structures of lakes Gusinoye and Kotokel have a strong resemblance, and it is most likely that their history began at the same time, ca. 40 ka BP.

Keywords: High-resolution seismic data, Lake Gusinoye, East Siberia

1. Introduction

The southern part of East Siberia is characterised by a variety of landscapes, from steppe to mountain zones, and, according to paleorecords from this region, can be very sensitive to climate changes. There are paleorecords from small lakes of this region, however, these records are often until only the Holocene-Bølling-Allerød (e.g. Shichi et al., 2009; Bezrukova et al., 2010; Fedotov et al., 2012; 2013; Solotchina et al., 2014). For example, according to records from Lake Kotokel, intensive warming of the region was during 11.8-9.5 ka BP; regional climate was most likely moderately cold and humid from 9.5 to 7 kyr BP; from 7 to 6 kyr BP there was a trend to drying, the climate pattern at 5.8-1.5 ky BP was very unstable when there were episodes of abrupt cooling by the backdrop of the warm climate (Fedotov et al., 2012)

The climate in this region of East Siberia is continental, which is reflected in the large differences in the mean January (-30 ˚C) and July (15 ˚C) temperatures. Annual precipitation is relatively low, ranging from 220 to 590 mm (NOAA data set ftp://ftp.ncdc.noaa.gov/pub/data). Lake Gusinoye is located in approximately 60 km to the south of Lake Baikal (Fig. 1). The lake is situated at 551 m above sea level. It is approximately 24 km long and 8.4 km wide, with a maximum depth of 26 m. For this reason, this sediment cover may contain long paleorecords.

However, there are probably hiatuses in the paleorecords from Lake Gusinoye due to erosion of sediment cover at the lowest lake levels. Thus, according to historical records, there were two lakes on the place of Lake Gusinoye in 1728, and it is very likely that similar changes also happened before.

In our study, based on the analysis of high-resolution seismic data on the sedimentary infill of Lake Gusinoye, we attempt to reconstruct the evolution of the lake.

2. Methods

Seismic data were collected using a Frequency Modulated (FM) sub-bottom profiler consisted of tree transducers that receive and radiate FM signal (frequency 1-10 kHz). The operation is based on the transducer radiating an acoustic signal directed vertically downwards. An acoustic signal reflects from a bottom, reflecting horizons of sub-bottom sedimentary layer, and proceeds back in a transducer. In the receiving channel of the device, amplification, coordinated filtration and digitization of analogue signals amplification are produced. In data array records, data required for the bottom surface mapping and profiles of sub-bottom, namely, acoustic signals from the transducer and current coordinates are received from GPS receiver. Forty-five kilometers of seismic profiled were obtained in 2018 (Fig. 1). The FM profiler enables to study stratification of sedimentary layers with a resolution of up to 10 cm. For conversion

---

*Corresponding author.
E-mail address: mix@lin.irk.ru (A.P. Fedotov)

of the acoustic travel time into depth, we assumed velocity of 1.45 m/ms in water and 1.6-1.7 m/ms for the uppermost unconsolidated sediments.

In 2019, a sediment core was taken from the northwestern part of Lake Gusinoye N 51°14.720, E 106°25.161 (Fig. 1) using a Uwitec Corer sampler. The water depth was 20 m at the core-sampling site. The core was 80 cm long, but the core sampler cannot penetrate deeper due to a high density of bottom sediments.

Depth-age model based on AMS-technic was performed in Budker Institute of Nuclear Physics (Novosibirsk, Russia). Chemical pre-treatment and graphitization of samples were carried out in Laboratory of Radiocarbon Methods of Analysis at Novosibirsk State University using laboratory installation (Lysikov et al., 2018). Six sediment layers were dated. Calendar date was evaluated from the radiocarbon one by CalPal ver.1.5.

3. Results and Discussion

3.1. Seismic units

Seismic profiles clearly distinguish a two-part subdivision of the stratigraphic section from the sedimentary infill: -a lower part, acoustically un- or poorly stratified; - an upper part, thinly and regularly stratified, with good lateral continuity (longitudinal and transverse). Both can be subdivided with more details as follows.

A lower part – the basement is chaotic unstructured low-amplitude reflections (Fig. 2). Thickness is approximately 2-3 m (deeper, seismic signal damped). It is most likely that reworked fluvial and eolian sediments represent these sediments.

Unit -1 is characterized by sub-parallel, discontinuous coarse high-amplitude reflections. It can indicate that the ratio of sand is high. The lower boundary parallels covered basement. Thickness varied from 1.5 to 3 m. The lithology of this unit is probably coarse-grained sediments, which formed under shallow lacustrine condition. Position of the upper boundary of the unit indicates that the lake can have a depth of approximately 15 m. However, the upper boundary was eroded (erosion level-1).

Unit-2 in the lower part is represented by low-amplitude sub-parallel reflections. High-amplitude of reflectors and a distinct thinning of its rhythmic pattern is increased towards the upper boundary of the unit. Sediment thickness is approximately 1.5-3 m. In general, this reflection pattern can be interpreted as normal lacustrine filling, and its thinning seems to show that the lake depth gradually increased. However, the packets of chaotic low-amplitude reflections embedded into packets of parallel reflections can be associated with a silty sand-rich mudslide, sandslide or river fan (van Rensbergen et al., 1999). The upper boundary also was eroded (erosion level-2) at slope parts of the depression.

Unit -3 is characterized by sub-parallel, distinct coarse high-amplitude reflections with thinning rhythmic pattern. Sediment thickness is ca. 1-2 m. This unit is enriched with lenses or mound-shape geometry bodies with chaotic high-amplitude reflections. These bodies are associated with silty sand-reach sediments. A cross breadth of some bodies is up to 2.5 km (Fig. 3), and it is most likely that these bodies are related to river fan.

A boundary between unit- 3 and 4 is very strong erosion surface (erosion level-3). This erosion denudated distal parts of units 1, 2, and 3 (Fig. 2, Fig. 3). Unit - 4 consists of packages of high-amplitude reflections parallel to discontinuous reflections with packages of seismically semitransparent reflection in the upper part (0-1 m bss). Unit 4 becomes thicker in deep parts of the axial part of the lake, attaining a maximum thickness of approximately 2 m.

3.2 Interpretation

The relief and configuration of the acoustic basement beneath Lake Gusinoye strongly suggest that the lake has a tectonic origin due to the presence of a deep fault. Thus, the morphological structure of the lake is represented by two depressions (southern and northern) restricted by faults (Fig. 3). At the beginning of forming unit-1, the basement of the southern depression was lower than that of the northern depression by ca. 10 m. The southern depression is approximately 9 km long.

Due to this morphological asymmetry, the northern depression was completely dried when erosion levels -1-3 were formed. However, deeps of a paleo-lake in the southern depression were approximately 2-5 m during events of erosion levels-2 and 3. In addition, it is most likely that the southern depression was also completely dried at events of erosion level-1, as the upper boundary of unit-1 was eroded. In general, there are no erosion cuts along erosion levels 2 and 3. For this reason, it is most likely that the duration of low lake levels was not long. To confirm this assumption, the total thickness of sediment covers in the southern and northern depressions are approximately 9 and 7 m, respectively (Fig. 3). Hence, ca. 2 m of total sediment cover in the northern depression can be denudated at a time when the erosion levels were formed.

High content of bodies enriched with sand materials into unit-3 can evidence high activity of tributaries or floods at that time. These bodies are

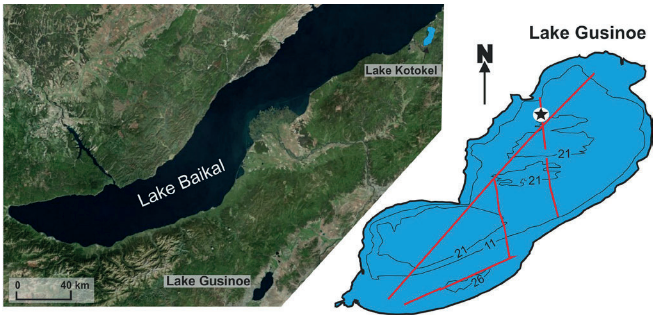

Fig.1. Location of Lake Gusinoye: *red lines* - seismic profiles, *asterisk* – point of the core sampling

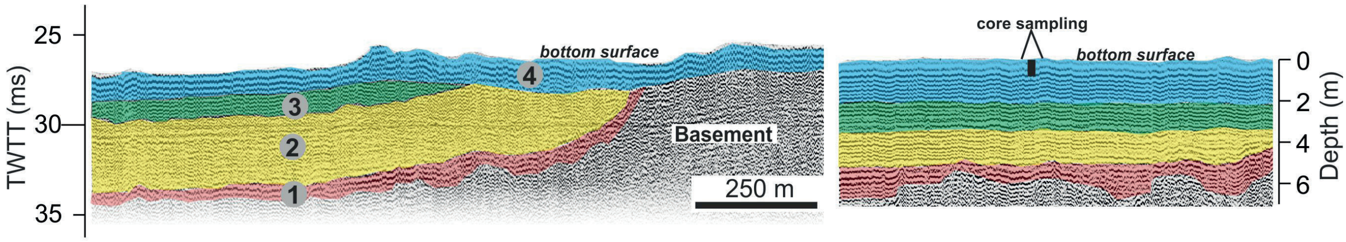

Fig.2. Seismic stratigraphy of Lake Gusinoye, *number* - seismic units

more abundant in the southern depression. At present, all tributaries flow in the lake along the west coastline, and the Khamar-Daban Ridge can be a source for these streams. Hence, it seems that this period had maximum moisture in the region.

The sediment core was composed of fine, light grey and black silty clay in the upper part (0-25 cm bss) as well as olive-green firm silty clay (25-80 cm bss). Interval of 25-80 cm was enriched with shells of ostracods and gastropods. Thus, these sediments formed under lacustrine conditions; however, it was a shallow lake. AMS dating indicates that the layer of 79-80 cm likely deposited ca. 5 cal. ka BP, and a change in sedimentation (approximately 25 cm bss) occurred ca. 1.5-2 cal. ka BP (Fig. 4). According to this age estimation, the mean sediment rate for the upper 0-0.8 m bss was approximately 1 cm/71 yr. If this sediment rate is linearly extrapolated to the layer of the erosion level-3 (approximately 2 m bss), in this case, the unit-4 began to accumulate after 14-15 ka BP. For this reason, it seems that the erosion level-3 can be formed during the Last Glacial Maximum. The results of pollen analysis and pollen-based biome reconstruction from bottom sediments of Lake Kotokel show that steppe and tundra vegetation composed of grasses and various herbs dominated ca. 26.8-19.1 cal. ka BP, and a lake level was low compared to the present (Müller et al., 2014).

The level of Lake Baikal, being by 50 m deeper than the modern lake, as well as a low and irregular discharge of the Selenga River are evidence of high regional aridity in the LGM (Urabe et al., 2004; Osipov and Khlystov, 2010). Hence, the level of Lake Gusinoye most probably was also dramatically low under this LGM-condition.

The seismic pattern indicates that units 2-4 were formed during one limnological cycle, whereas the unit - 1 can be a remnant of other older cycle.

Coarse age estimation for units 2-4 based on the sediment rate for the upper 0-0.8 m shows that these units can deposit approximately 35-45 ka BP. However, this estimation does not take into account the duration of low-levels (erosion levels 2 and 3) and layers of sandslides or turbidities. Nevertheless, it seems that 35-45 ka is most likely the highest possible age for the bottom layer of the unit-2. Moreover, the seismic profiles of Lake Kotokel indicate that the three depositional units were distributed over the entire lake basin (Zhang et al., 2013). Age estimation of these units was the present-15, 15-25 and >32 ka BP (Zhang et al., 2013). The bottom unit in Lake Kotokel is represented by densely-spaced reflections, occurring as chaotic and occasionally hummocky structure, partly alternating with reflections of low contrast. The seismic pattern of this unit is very similar to those of unit 1 and basement from Lake Gusinoye. Thus, seismic structures of Lake Gusinoye and Kotokel have similarity, and it is most likely that their history began at the same time, ca. 40 ka BP.

4. Conclusions

We have studied sediment cover of Lake Gusinoye based on high-resolution seismic data. Morphology of the lake basement evidences a tectonic origin of this lake. Two depressions (southern and northern) represent the structure of the lake floor. The thickness of lacustrine sediments cover is only 9-6 m, and this cover was divided into four seismic units. Boundaries of these units are three erosion surfaces. The northern

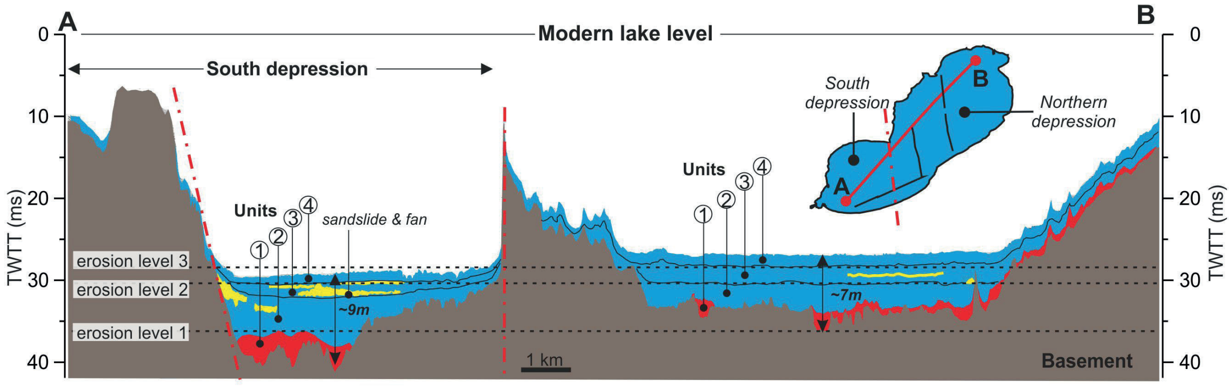

Fig.3. Axial structure of sediment filling of Lake Gusinoye: *dashed redlines* – faults, *yellow lenses* – sediment bodies enriched with sand

depression completely dried in periods when formed erosion levels-2 and 3, and the entire lake was dried at the period of the erosion level-1. According to radiocarbon dating of the short sediment core from the northern depression, approximate age of the erosion level-3 and lacustrine sedimentations are 14 and 35-45 ka BP, respectively. There is also evidence of high fluvial activity towards the southern depression.

Acknowledgements

This study was supported by basic funding No. 0345–2016–0006 (AAAA-A16-116122110063-0), RFBR-17-29-05016 (financial support of laboratory materials and equipment). We thank P.N. Kalinkin and S.A. Rastigeev for AMS dating.

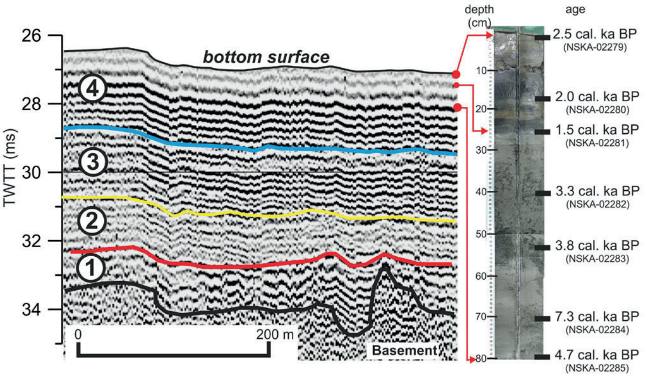

Fig.4. Seismic stratigraphy and the core image, ^{14}C age-dates were converted into calendar ages until present (cal. BP)

References

Bezrukova E.V., Tarasov P.E., Solovieva N. et al. 2010. Last glacialeinterglacial vegetation and environmental dynamics in southern Siberia: chronology, forcing and feedbacks. Palaeogeography, Palaeoclimatology, Palaeoecology 296: 185-198. DOI: 10.1016/j.palaeo.2010.07.020

Fedotov A.P., Phedorin M.A., Enushchenko I.V. et al. 2013. Drastic desalination of small lakes in East Siberia (Russia) in the early twentieth century: inferred from sedimentological, geochemical and palynological composition of small lakes. Environmental Earth Science 68: 1733-1744. DOI: 10.1007/s12665-012-1864-z

Fedotov A.P., Vorobyeva S.S., Vershinin K.E. et al. 2012. Climate changes in East Siberia (Russia) in the Holocene based on diatom, chironomid and pollen records from the sediments of Lake Kotokel. Journal of Paleolimnology 47: 617-630. DOI: 10.1007/s10933-012-9586-5

Lysikov A.I., Kalinkin P.N., Sashkina K.A. et al. 2018. Novel simplified absorption-catalytic method of sample preparation for AMS analysis designed at the laboratory of radiocarbon methods of analysis (LRMA) in Novosibirsk Akademgorodok. International Journal of Mass-Spectrometry 433: 11-18. DOI: 10.1016/j.ijms.2018.08.003

Müller S., Tarasov P.E., Hoelzmann P. et al. 2014. Stable vegetation and environmental conditions during the Last Glacial Maximum: New results from Lake Kotokel (Lake Baikal region, southern Siberia, Russia). Quaternary International 348: 14-24. DOI: 10.1016/j.quaint.2013.12.012

Osipov E.Yu., Khlystov O.M. 2010. Glaciers and meltwater flux to Lake Baikal during the Last Glacial Maximum. Palaeogeography, Palaeoclimatology, Palaeoecology 294: 4-15. DOI: 10.1016/j.palaeo.2010.01.031

Shichi K., Takahara H., Krivonogov S.K. et al. 2009. Late Pleistocene and Holocene vegetation and climate records from Lake Kotokel, central Baikal region. Quaternary International 205: 98-110. DOI: 10.1016/j.quaint.2009.02.005

Solotchina E.P., Sklyarov E.V., Solotchin P.A. et al. 2014. Mineralogy and crystal chemistry of carbonates from the Holocene sediments of Lake Kiran (western Transbaikalia): connection with paleoclimate. Russian Geology and Geophysics 55: 472-482. DOI: 10.1016/j.rgg.2014.03.005

Urabe A., Tateishi M., Inouchi Y. et al. 2004. Lake-level changes during the past 100, 000 years at Lake Baikal, southern Siberia. Quaternary Research 62: 214-222. DOI: 10.1016/j.yqres.2004.06.002Zhang Y., Wünnemann B., Bezrukova E.V. et al. 2013. Basin morphology and seismic stratigraphy of Lake Kotokel, Baikal region, Russia. Quaternary International 290-291: 57-67. DOI: 10.1016/j.quaint.2012.11.029

van Rensbergen P., Morley C.K., Ang D.W. et al. 1999. Structural evolution of shale diapirs from reactive rise to mud volcanism: 3D seismic data from the Baram delta, offshore Brunei Darussalam. Journal of the Geological Society 156: 633-650. DOI: 10.1144/gsjgs.156.3.0633

Limnology and Freshwater Biology 2019 (4): 270-274 DOI:10.31951/2658-3518-2019-A-4-270

Original Article

ISSN 2658-3518
LIMNOLOGY FRESHWATER BIOLOGY
www.limnolfwbiol.com

Zooplankton in two small reservoirs of the Tuva Republic

Kirova N.A.*

Tuvinian Institute for Exploration of Natural Resources of SB RAS, Tuva Republic, Kyzyl, Internacyonalnaya str., 117A, 667007, Russia

ABSTRACT. The article provides information on the species composition and quantitative indicators of zooplankton in two small mountain reservoirs of the Tuva Republic: the Eerbek and Turan. They reflect the first and the third years of the ecosystem existence after seasonal drawdown. Regulation shows a typical pattern in the distribution of zooplankton in the reservoirs: an increase in density in the dam section. In general, the reservoir zooplankton has a floodplain type of formation. The existence periods of reservoirs influences the zooplankton structure and its development: regulation in the first year determines the development of crustacean zooplankton (represented mainly by cladocerans), usually with monodominance; over three years, all main groups of zooplankton develop, but drawdowns interrupt the formation on the normal ecosystem in the reservoir.

Keywords: small reservoirs, zooplankton, Tuva, regulation

1. Introduction

In the Tuva Republic, apart from the well-known large Sayano-Shushenskaya Dam, several small artificial water bodies were created in the 1980s. They were intended for irrigation of fields, watering places and regulation of river flow. Following the aims and tasks, two small reservoirs were also created, whose direct purpose is lost now, and they are mainly popular among the fishing amateurs. Nevertheless, they retain their functioning, being seasonal drawdown reservoirs, which influences the existence features of zooplankton in them. Special scientific research supplemented the construction of such large objects as the Sayano-Shushenskaya Dam, whereas the literature concerning zooplankton in small reservoirs are rather scarce (Kirova, 2014). Our study aims to determine differences in the species composition and quantitative characteristics of the zooplankton in the Eerbek and Turan reservoirs, regarding their different existence periods.

2. Material and methods

The Eerbek and Turan reservoirs were created on the mountain rivers with the same names, the Eerbek (the right tributary of the Ulug-Khem River (the Upper Yenisei)) and the Turan (the left tributary of the Uyuk River, the Biy-Khem basin (Big Yenisei)). The Eerbek reservoir occupies the middle flow of the Eerbek River, in 15 km from its estuary; the Turan reservoir is closer to the upper flow of the Turan River, in 25 km from the estuary (Fig. 1).

According to the classification of Avakyan (Avakyan et al., 1987). both reservoirs are small. They are shallow and river valley reservoirs in origin. The water management passport (Water management..., 1983; 1985) states that both reservoirs have seasonal regulation, but de facto the water drawdown does not occur annually. Based on the data of Tuva Institute for Exploration of Natural Resources of the Siberian Branch of the RAS (TuvIENR SB RAS), waters in both reservoirs are fresh (Table 1); in the Eerbek reservoir, the water is calcium-sodium bicarbonate, soft (1.95 meq/l); in the Turan reservoir – calcium-magnesium bicarbonate, also soft (1.55 meq/l). The coastal zones of the reservoirs warm up well; water temperature in summer reaches 20-23°C.

Zooplankton was sampled and collected by standard methods (Rukovodstvo..., 1992) at the beginning of August 2017. Samples were collected in the centre of upper, middle and dam sections. At the stations with depths of ≤ 1 m, samples were taken by 100-l pouring through a planktonic net with a 100µm-cell size. At other sites, samples were taken totally from the bottom to the surface with the Juday net. A 4% formalin solution was used for fixation. The determination was carried out as possible to the species, Harpacticoida was not identified (Opredelitel'..., 1995). Simultaneously, the water temperature was measured, and the water was sampled for analysis of water chemistry.

---

*Corresponding author.
E-mail address: chink@list.ru (N.A. Kirova)

Table 1. Physical and geographical parameters of the investigated reservoirs

Name	Coordinates	Height, m asl	Area, km²	Depths max, (av), m	T˚C	TDS, g/l	pH
Eerbek	51.726897 94.317023	680	0.51	6 (4)	15-20	0.4*	8.01*
Turan	52.246635 93.908136	934	1.95	8 (5)	14-23	0.125*	7.22*

Note: * TuvIENR SB RAS data

3. Results

The zooplankton from the two reservoirs contains 27 species from 20 genera, 10 families and 2 subfamilies as well as 7 orders of animals. Most taxa (88%) are crustaceans. Among them, the bulk of taxa belongs to cladocerans, 17 species (68% of the total number) and copepods, 5 species (20%); there are also 3 species of rotifers (12%). Families Chydoridae and Daphniidae reach the highest species diversity, eight species each (Table 2). Zoogeographically (according to Rivier et al., 2001), most taxa are cosmopolitan (47%); the share of palearctic ones is 38% and holarctic – 15%, i.e. fauna is represented by widespread species. In terms of biotopes, eurytopic forms (50%) as well as littoral (11%), phytophilic (19%), planktonic (8%), and benthic (4%) species represent the community.

The Eerbek reservoir. In the composition of the Eerbek reservoir, we have found 13 species, of which 9 are Cladocerans, 3 – Copepods and 1 – representative of Rotifers (Table 2). The density of zooplankton is unevenly distributed along the water area; the minimum values (7.2 thou specimens/m³) are in the upper section of the reservoir; in the middle section, the total number increases 8 times and biomass – 15.4 times; in the dam section, the number increases 10.3 times and the biomass – almost 19 times (Fig. 2). Throughout the water area of the reservoir, the species composition is conformed: *D. longispina, D. pulex, B. longirostris*, and *A. denticornis*. In the coastal zone, there are all species of aquatic vegetation from the general list, although in a single number.

In the upper section, Cladocerans *D. longispina* (52%) and *B. longirostris* (31%), as well as Copepod *A. denticornis* (13%), compose the structure-forming core; in the middle and dam sections, *D. longispina* prevails (79-98%). Planktonic and eurytopic species are the main in the number. The value of species diversity index in the upper section (0.94) decrease in the middle and dam sections (0.46 and 0.52), which is due to the dominance of the species *D. longispina.*

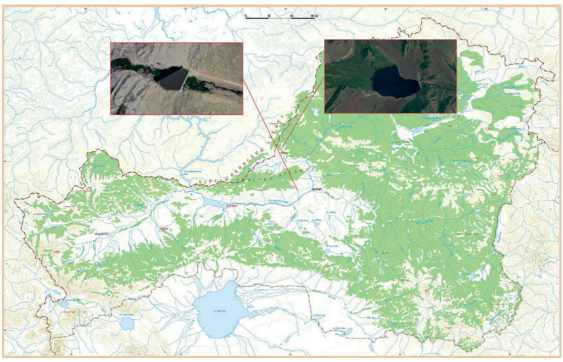

Fig.1. Schematic location map of the Eerbek (below) and Turan (above) reservoirs on the territory of the Tuva Republic

Turan reservoir. There are 16 species in the zooplankton composition, of which 11 are Cladocerans, 4 – Copepods and 3 – Rotifers (Table 2). The number of the species found in the upper section is 13, in the middle and dam sentions – 14 and 8, respectively. Throughout the water area, the composition of the dominant organisms is the same, and it includes nauplii of *Copepoda* (27-48%), *C. pulchella* (20-59%), *H. mira (10-16%), B. longirostris* (6-7%), *M. viridis* (8-13%), *D. brachiurum* (5-6%)*,* and *D. galeata* (6%), i.e. mainly eurytopic and littoral species. The number and biomass increase from the upper section towards the dam (Fig. 3). Low biomass indices against high abundance indices are due to prevailing nauplii of Copepoda (up to 59%) and “lightweight”ceriodaphnia and rotifers.

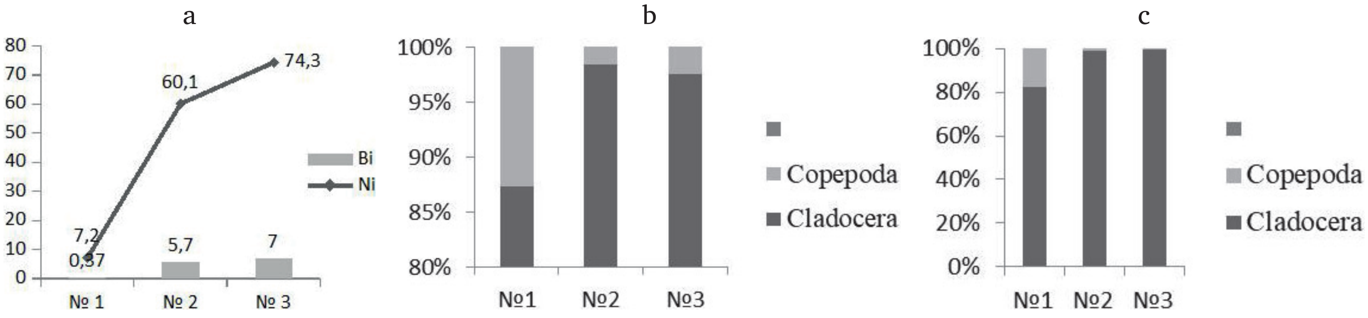

Fig.2. The number (N) (thou specimens/m³) and biomass (B) (g/m³) (a) as well as the share of taxonomic groups by the total number (b) and biomass (c) of zooplankters from the Eerbek reservoir. Sampling stations Nos. 1-3

Table 2. Taxonomic composition of zooplankton from the Eerbek and Turan reservoirs

Taxon	Zoogeography	Biotope	Eerbek	Turan
Type Rotifera **Class Archiorotatoria, Markevich,1990** **Order Bdelloida Hudson,1884**	-	-	+	+
Class Eurotatoria Markevich, 1990 **Order Transversiramida Markevich, 1990** **Family Brachionidae Ehrenberg,** 1838 *Brachionus* sp	-	-	+	-
Kerathella quadrata (Müller, 1786)	C	Eut	+	-
Famiy Mitilinidae *Mitilina mucronata* (Muller,1773)	H	Ph	-	+
Order Protoramida Markewich, 1990 **Family Hexarthridae Bartos, 1958** *Hexarthra mira* (Hudson, 1871)	C	L	-	+
Order Saltiramida **Family Asplanchniidae** *Asplanchna priodonta* Gosse, 1850	C	Eut	-	+
Order Ctenopoda **Family Sididae Baird, 1850** *Diaphanosoma brachyurum* (Liévin, 1848)	P	Eut	-	+
Order Anomopoda Sars, 1865 **Family Bosminiidae Baird,1845** *Bosmina longirostris* (O.F. Müller, 1785)	C	Eut	+	+
Family Daphniidae Straus, 1820 *Daphnia galeata* Sars, 1864*	P	Pl	-	+
D. longispina (O.F. Müller, 1785)	P	Pl	+	-
D. pulex Leydig, 1860	H	Eut	+	
Simocephalus vetulus (O.F. Müller, 1776)	P	L,Ph	-	+
Scapholeberis mucronata (O.F. Müller, 1776)	P	Bt,Ph	-	+
Ceriodaphnia dubia Richard, 1894*	C	Pl, L	+	-
C. pulchella Sars, 1862	P	Eut	-	+
C.quadrangula (O.F. Müller, 1785)	P	Eut	-	+
Family Chydoridae Dybowski et Grachowski, 1894 *Grapholeberis testudinaria* (Fisher, 1851)	C	L	-	+
Coronatella rectangula (Sars, 1862)	P	Eut	+	-
Alona costata Sars, 1862	C	L,Ph	-	+
Alona quadrangularis (Müller, 1785)	C	Ph, L	+	-
Alona guttata Sars, 1862	C	L	+	-
Alona affinis (Leydig, 1860)	C	Ph	+	-
Chydorus sphaericus (O.F. Müller, 1785)	C	Eut	+	+
Pleuroxus truncatus (O.F. Müller,1785)	H	L,Ph	-	+
Family Cyclopinae Burmeister, 1834 *Megacyclops viridis* (Jurine, 1820)	C	Eut	+	+
Mesocyclops leuckarti (Claus,1857)	P	Eut	-	+
Cyclops vicinus Ulyanin,1875	P	Eut	-	+
Cyclops sp.	-	-	+	-
Class Maxillopoda Edwards, 1840 **Subclass Copepoda Edwards, 1840** **Order Cyclopoida Burmeister, 1834** **Subfamily Eucylopinae Kiefer, 1927** *Eucyclops serrulatus* (Fischer, 1851)	C	Eut	+	-
Order Calanoida Sars, 1903 **Family Diaptomidae Baird, 1850** *Acanthodiaptomus denticornis* Wierzejski, 1887	H	L	+	+
Diaptomus sp	-	-	-	+
Harpacrocoida gen. sp.	-	-	+	+

Note: P – palearctic, H – holarctic, C – cosmopolitan (Opredelitel'…, 1995); Eut – eurytopic, Ph – phytophilic, L– littoral, Bt – benthic, Pl– planktonic (Rivier et al., 2001).

4. Discussion

Discussing the reasons for the revealed differences, it is worth noting a high reproductive potential of the members of the genera *Bosmina, Ceriodaphnia* and *Daphnia*, which is almost four times higher than that of copepods (Popkov and Golubykh, 2005). Perhaps this is the reason for the dominance of the members of these genera. The Eerbek reservoir, where the coastal zone is the most warmed up (up to 23°C), having aquatic vegetation, shows the bulk of phytophilic species: *S. mucronata, P. trigonellus, A. costata, G. testudinaria,* and *P. truncatus.* Changes in the species diversity indices are as follows: in the dam section its minimum value (1.6) is accompanied by the dominance of *C. pulchella* (39%) and *D. brachiurum* (5%); in the upper and middle sections of the reservoir, the value is 2.24 and 1.89, respectively. The dominating core of each section included three-four species. In all sections, the share of the Copepoda nauplii is also significant.

An urgent issue is the quality of water in the reservoirs. Zooplankton contains 22 species that indicate the water saprobity. Among them, the quality indicators of 0 and 0-β are 77%. The values of the indicators in the Eerbek reservoir (1.7-1.98) correspond to moderately polluted waters. The water from the upper section of the Turan reservoir is characterized as pure (1.4); in the middle and dam sections – moderately polluted (1.59 and 1.51) (Makrushin, 1974; Sladecek, 1983). Since reservoirs are located at a distance from settlements and do not experience anthropogenic impact, the natural processes, which occur during the flooding of the surrounding areas, influence water quality.

There are four common species in the two reservoirs: *B. longirostris, C. sphaericus, M. viridis*, and *A. denticornis*. The Sorensen-Chekanovsky similarity index is 0.27, i.e. species composition is very specific for each reservoir. It is largely determined by the plankton fauna from the upstream water bodies, and the mountain rivers Eerbek and Turan play a transit role. High current velocities (0.5-0.7 m/s) and straight channels do not allow the development of zooplanktonic species, which are typical of stagnant water bodies.

Among three types of zooplankton formation in reservoirs (lake, floodplain and river) (Luferova, 1964), the floodplain type is typical of the Eerbek and Turan reservoirs. In the upstream floodplain water bodies of the Eerbek River, we have found *A. denticornis, C. spahericus, A. affinis, C. rectangula, E. serrulatus, M. viridis, D. pulex,* and *D. longispina.* In the upstream channel of the Eerbek River, there are single specimens of *C. rectangula, C. Sphaericus* and *E. serrulatus*, the members of the orders Harpacticoida and Bdelloida. In the channel of the Turan River, we have found *S. vetulus, M. viridis*, *C. quadrangula, B. longirostris*, and *D. Longispina*, immature stages of Cyclopes. There is a similar composition of the plankton fauna in several upstream water bodies.

The processes that take place during the development and formation of biota in reservoirs are long-term and take years. There are three stages in the development of reservoirs: formation, depression and relative stabilization (Sharonov, 1966; Kudersky, 1992; Krylov, 2014). Biota of the investigated reservoirs is at the first stage, including a change in the composition and the quantitative development of limnophilic components as well as a change in the proportion of certain groups, but the seasonal drawdown interrupts this process. The 2017 study at the Eerbek reservoir was conducted after the water drawdown in autumn 2016. In fact, we observed the state of zooplankton in the first year after the regulation. In this case, an increased role of crustacean zooplankton is a natural phenomenon (Vorobyova et al., 1981; Dzyuban and Dzyuban, 1976). Based on the 2012 data, which were obtained in the second year of the reservoir existence (there was no drawdown in the preceding year), we revealed that against the mass development of cladocerans (up to 90%) and dominance of *B. longirostris, D. longispina* and *C. shaericus*, the share of copepods and rotifers, despite the small number, was 5% each (Kirova, 2014). At the time of our investigations, the Turan reservoir had no drawdown during two preceding years; therefore, in 2017, we observed the third year of its existence. We indicate that the different existence periods without drawdowns explain the superiority of the Turan reservoir over the Eerbek reservoir in the number of species and dominants as well as the development of rotifers and copepods.

5. Conclusion

The duration of the reservoir existence infuences the structure of the zooplankton community: regulation in the first year determines the development of the crustacean zooplankton with prevailing cladocerans

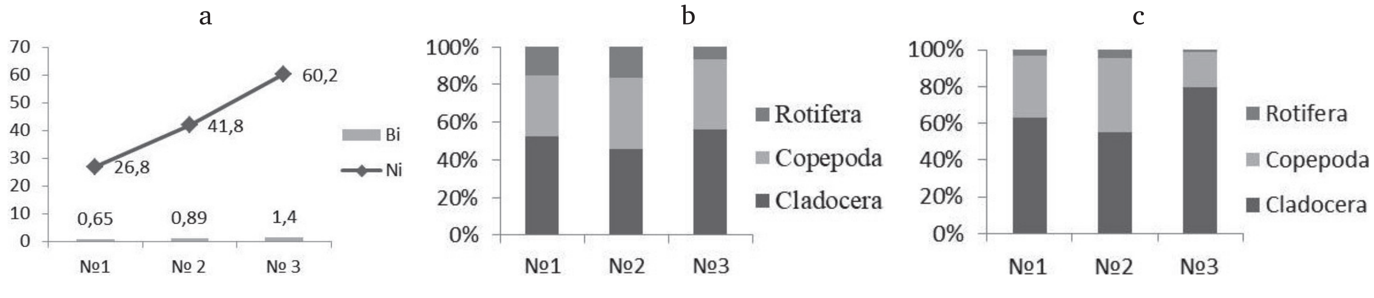

Fig.3. Number (N) (thou specimens/m^3) and biomass (B) (g/m^3) (a) as well as the share of taxonomic groups by the total number (b) and biomass (c) of zooplankters from the Turan reservoir. Sampling stations Nos. 1-3

and dominance of one species throughout the water area; over three years of the existence, the species diversity of plankton increases; the members of other groups, rotifers and copepods, develop. At the same time, the reservoir drawdown returns its community to the initial stage as in the first year of regulation.

References

Avakyan A.B., Saltankin V.P., Sharapov V.A. 1987. Vodokhranilishcha. Moscow: Mysl. (in Russian)

Dzyuban N.A., Dzyuban M.N. 1976. Biologicheskiye produktsionnyye protsessy v basseyne Volgi. Leningrad: Nauka. (in Russian)

Kirova N.A. 2014. The first information about the zooplankton of the Eerbek reservoir (Central Tuva). Sostoyaniye i Osvoyeniye Prirodnykh Resursov Tuvy i Sopredel'nykh Regionov Tsentral'noy Azii. Ekologo-Ekonomicheskiye Problemy Prirodopol'zovaniya [State and Development of Natural Resources of Tuva and the Central Asia Related Regions. Ecological and Economic Problems of Nature use] 13: 118-120. (in Russian)

Krylov A.V. 2014. Zooplankton of the Durgun and Taishir reservoirs (Western Mongolia) at the end of the filling period. Aridnyye Ekosistemy [Arid Ecosystems] 20: 48-55 (in Russian)

Kudersky L.A. 1992. Ecological basis of the formation and use of fish resources of reservoirs. Dr. Sc. Dissertation, State Scientific Research Institute of Fisheries, Moscow, Russia. (in Russian)

Luferova L.A. 1964. The formation of zooplankton in the Gorky reservoir. Cand. Sc. Dissertation, Moscow State University, Moscow, Russia. (in Russian)

Makrushin A.V. 1974. Biologicheskiy analiz kachestva vod. Leningrad: USSR Academy of Sciences. (in Russian)

Opredelitel' presnovodnykh bespozvonochnykh Rossii i sopredel'nykh territoriy. Rakoobraznyye.1995. In: Tsalolikhin S.Ya. (Ed.). St. Petersburg: Nauka. (in Russian)

Popkov V.K., Golubykh O.S. 2005. Changes in the ecological state of Lake Chagytai and its fish population. In: Proceedings of the 7th International Conference "Natural conditions, history and culture of Western Mongolia and adjacent regions", pp. 244-247. (in Russian)

Rivier I.K., Lazareva V.I., Gusakov V.A. et al. 2001. Mezofauna verkhnevolzhskikh vodokhranilishch (1953 – 2001). In: Kopylov A.I. (Ed.), Ekologicheskiye problemy Verkhney Volgi. Yaroslavl', pp. 409-412. (in Russian)

Rukovodstvo po gidrobiologicheskomu monitoringu presnovodnykh ekosistem. 1992. In: Abakumov V.A. (Ed.). St. Petersburg: Gidrometeoizdat. (in Russian)

Sharonov I.V. 1966. Formirovaniye ikhtiofauny vodokhranilishch. In: Ekologiya vodnykh organizmov. Moscow, pp. 103-110. (in Russian)

Sladecek V. 1983. Rotifers as indicators of water quality. Hydrobiologia 100: 169-201.

Vorobyova S.S., Zemskaya T.I., Skryabin A.G. et al. 1981. Plankton Bratskogo vodokhranilishcha. Novosibirsk: Nauka. (in Russian)

Water management passport of a seasonal regulation reservoir on the Turan River of the Piy-Khem District of the Tuva Autonomous Soviet Socialist Republic. 1983. Chita: Chita Branch of Rosgiprovodkhoz. (in Russian)

Water management passport of a seasonal regulation reservoir on the Eerbek River of the Erbek farm in the Piy-Khem District of the Tuva Autonomous Soviet Socialist Republic. 1985. Chita: Chita Branch of Rosgiprovodkhoz. (in Russian)

Limnology and Freshwater Biology 2019 (4): 275-280 DOI:10.31951/2658-3518-2019-A-4-275

Original Article

ISSN 2658-3518

LIMNOLOGY FRESHWATER BIOLOGY
www.limnolfwbiol.com

Transformation of the chemical composition of waters from the Barguzin River in the Barguzin Bay (Lake Baikal)

Tomberg I.V.*, Sinyukovich V.N., Ivanov V.G., Sorokovikova L.M.

Limnological Institute of the Siberian Branch of the Russian Academy of Sciences, Ulan-Batorskaya 3, 664 033 Irkutsk, Russia.

ABSTRACT. We have studied the changes in the chemical composition of the Bargizin River waters that inflow to Lake Baikal under the different water level. We have shown that river and lake waters that involved in the mixing differ in the ion composition and temperature. Despite this, the mixing in the Barguzin Bay under the influence of circulation currents and thermal barrier occurs in a comparatively narrow coastline, which is usually less than four kilometres. Mixed waters distribute north- and northwestward and reach the southern end of the Svyatoy Nos Peninsula. In summer, the distribution scale of river waters in the bay becomes greater but is mainly limited to the surface layer. In the central part of the bay, within one-two kilometres from the river estuary, a lens of lake waters can form. Not only the change in the chemical composition and temperature of the water but also its colour indicate the influx of these waters. The change in the concentrations of individual ions at a distance from the estuary of the Barguzin River occurs linearly, which indicates ordinary dynamic mixing of river and lake water masses.

Keywords: Barguzin Bay, chemical composition of waters, river runoff, thermal bar, dynamic mixing

1. Introduction

The Barguzin Bay is the largest on Lake Baikal. Its area is 725 km^2, average depth is approximately 200 m, and the maximum depth reaches 1284 m. The Barguzin River (the third largest Baikal tributary), as well as several small watercourses, flow into the bay. The bay warms up well under the influence of the Barguzin River and owing to the extended coastal shallow water. The hydrochemical regime of the bay results from the mixing of river and lake waters and shows high variability in time and space. The active economic development of the Barguzin River basin between the 1950s and 1980s (logging, ploughing, increasing the area of an irrigated land, influx of drainage water enriched with various chemical components to the channel network, etc.) accompanied by a decrease in quality of river water and, consequently, an increase in the emissions of chemical components to the bay (Obozhin et al., 1984; Bogdanov, 1986; Drucker et al., 1997; Urbazaeva et al., 2016).

We aimed to study the transformation of the chemical composition of the Barguzin River water that inflows to Lake Baikal, seasonal and spatial dynamics of concentrations of major ions in the Barguzin Bay as well as their variability in long-term aspect.

2. Materials and methods

We analysed the results of hydrochemical investigations that were conducted in 2004, 2007, 2011, and 2016 at the estuary of the Barguzin River and in the water area of the Barguzin Bay. Sampling was carried out in different seasons, considering the shift of the main inflow of the Barguzin water along the constant northeast coast of the bay (Verbolov, 1996). Water was sampled from three transects: southern, central and northern (Fig. 1). From each transect, the samples were taken with a Niskin bathometer at four-eight stations from depths of 0, 5, 10, and 25 m as well as at the bottom. Temperature and electroconductivity were measured with an SBE 19 plus CTD-probe (Sea-Bird Electronics).

The cations were determined by atomic absorption and flame emission methods; anions – by HPLC (Baram et al., 1999; Guidelines…, 2009). The reliability of the obtained results was controlled by ion balance error and through comparison of the calculated and measured specific electroconductivity (Technical Documents …, 2000).

The degree of transformation of river water masses into lake ones was estimated (Sinyukovich et al., 2008) through the share of lake water (K_{lake}) at a certain

---

*Corresponding author.
E-mail address: kaktus@lin.irk.ru (I.V. Tomberg)

site of the bay, depending on the measured concentration (C_{bay}) of the indicator substance as well as its initial value in river (C_{river}) and lake (C_{lake}) water:

$$K_{lake} = (C_{river} - C_{bay})/(C_{river} - C_{lake})*100\ \%.$$

The concentrations of major ions (Na^+, K^+, Ca^{2+}, Mg^{2+}, SO_4^{2-}, Cl^-, and HCO_3^-) and their total concentration (Σi) were used as indicators of lake and river waters.

3. Results and discussion

Analysis of concentrations dynamics of components in the river runoff to the Barguzin Bay reveals their substantial spatial and vertical heterogeneity, which is due to a complex of hydrometeorological factors, in particular, the volume of the river runoff and the temperature of the mixed waters (Sorokovikova et al., 2010). A substantial variability throughout the year as well as in long-term aspect distinguishes the influence of each factor, which determines a complex nature in the formation of the mixing zone of river and lake waters and their transformation in the water area of the bay. The waters of the Barguzin River enter the bay in a single flow and, being carried away with a stream of the Baikal current, distribute along the northeast and north coasts of the bay, reaching Nizhneye Izgolovye Cape (Verbolov, 1996), and inflow to Lake Baikal (Ivanov, Sherstyankin, 2015).

In the closed Barguzin Bay, the mixing of river and lake waters is much lower than at open near-delta sites, such as the Selenga shallow waters (Tomberg, 2008). There is also a lower influence of the wind mixing since 75 % are southeast- and eastward winds, which, in the absence of a thermal bar, can extend the mixing zone but do not detach it from the northeast coast of the bay.

Seasonal changes in water temperature and hydrophysical conditions also predetermine the distribution and transformation features of river waters in the water area of the bay (Fig. 1, Fig. 2).

In spring, after the river ice breakup, the temperature of river waters rapidly increases, and in mid-May and early June, it reaches 13-15 °C. At this time, the temperature in Baikal is approximately 3-5 °C. The different temperature of the Barguzin and Baikal waters leads to the formation on a thermal bar in the water area of the bay at a distance of one-three kilometres from the site of the river inflow (see Fig. 1b). The front of the thermal bar serves as a natural barrier that prevents a free entry of river waters to the lake, and they mainly distribute from the river estuary along the coast of the bay. Consequently, the chemical composition

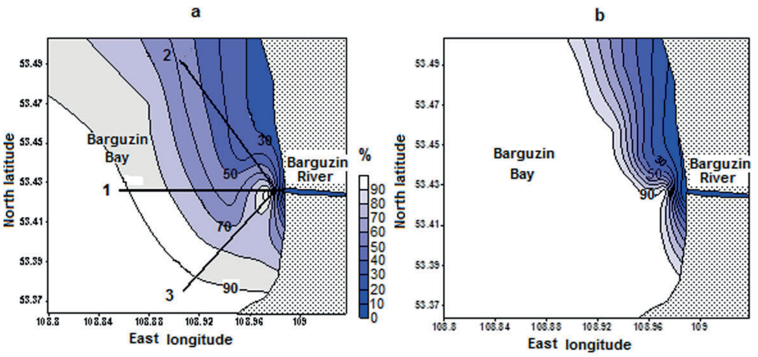

Fig.1. Distribution of mixed (%) river and lake waters in the water area of the Barguzin Bay in July 2004 (a) and June 2007 (b). Straight lines (a) are transects: 1 – central, 2 – northern and 3 – southern

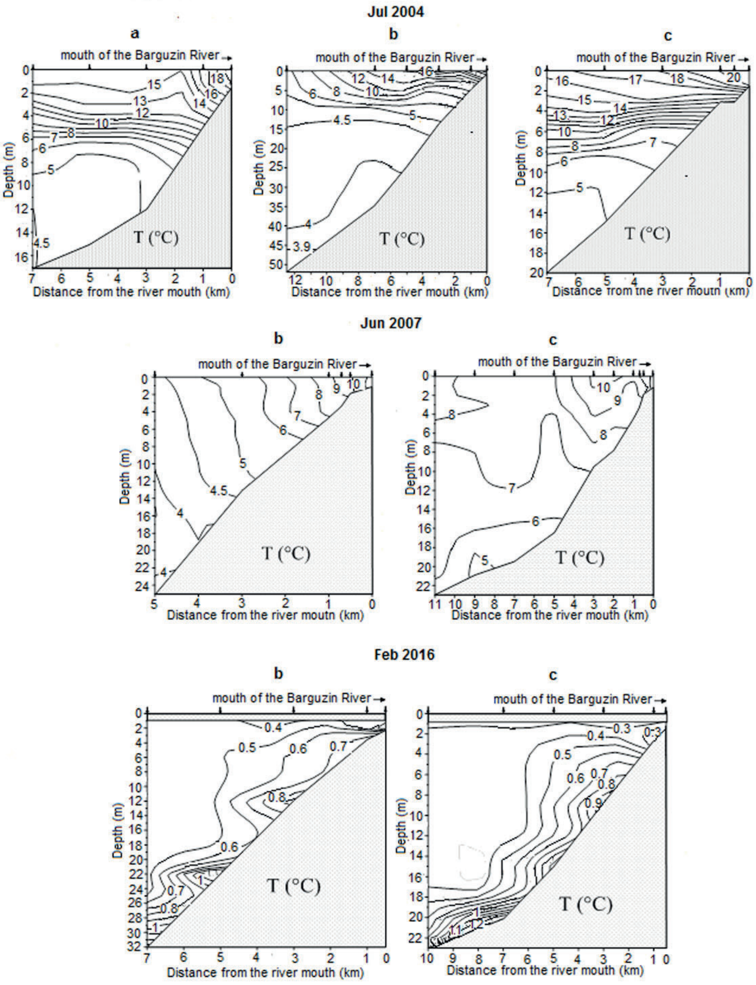

Fig.2. Water temperature distribution in the Barguzin Bay in different periods along the southern (a), central (b) and northern (c) transects

throughout the entire water column from the water edge to the thermal bar remains typical of the river waters, and beyond the thermal bar, it corresponds to the Baikal water.

Subsequently, when the water temperature in the bay rises higher than 4 ˚C, convection ceases, and a direct temperature stratification sets in with the maximum warm-up of the river and coastal waters of up to 18-20 ˚C, as it was on 1st July 2004 (Fig. 2). At the same time, the near-bottom temperature in the bay does not exceed 5.5 ˚C.

In summer, there is a seasonal increase in the Baikal water level, and a significant volume of lake water enters the Barguzin Bay, which additionally impedes the distribution of river water masses deep into the water area of the bay. In June-August, an increase in water level averages 0.5-0.7, which corresponds to the influx of the Baikal waters to the bay in the amount of up to 0.5 km^3. Under these conditions, the warmer Barguzin waters distribute in the surface layer of 5-10 m (Fig. 1, Fig. 2). At a distance of 1.5-3 km, water masses actively transform, and at the station of 4 km from the estuary, the concentration of major ions is mainly close to the composition in waters of open Baikal. In summer, warm river waters can distribute in the water area of the bay for a considerable distance, but their share in the surface layer does not exceed 3-5% (Fig. 1).

Considering insignificant amount of the river waters influx in comparison with the total amount of water in the bay (approximately 150 km^3), there may be a local influence of the Barguzin River on the chemical composition of water in the bay, i.e. limited mixing zone, which is confined to the northeastern coast of the bay.

As mentioned above, the features of the currents in the Barguzin Bay cause the transfer of the Barguzin River waters from the estuary mainly along the northeast and north coasts, explaining the heterogeneity in the distribution of mixed waters and differences in the chemical composition of water in the bay. Thus, along the central and southern transects, we recorded the total number of ions typical of the Baikal water at a closer distance from the river estuary than along the northern transect (Fig. 3). Moreover, along the central transect, in one-two kilometres from the river estuary, the influx and formation of a lens of lake waters can influence the chemical composition of water (see Fig. 1a). Not only the change in the chemical composition but also water temperature (see Fig. 2) and the colour of water indicate this. Further deep into the lake, during all seasons, there is a gradual decrease in the concentration of the components that were brought by river waters (see Fig. 3).

There is a special situation in the mixing zone during floods when the river runoff forms mainly due to low-mineralized snow waters, and low-mineralized waters enter the bay. In 2007, along with the influx of river waters to the bay and their mixing with the Baikal waters, the concentration of most components in the salt composition and their total number increased (Fig. 4). Sulfates and chlorids, whose concentrations were higher in river water than in lake water, were the exception.

In winter, the main changes in the water mineralization were at a distance of 3 km, and deeper into the bay, they gradually faded. Other researchers also showed a similar distribution pattern of hydrochemical indicators in the bay in winter (Vorobyevskaya et al., 2016).

The obtained results have shown that despite the different hydrological conditions in the bay during our investigations, the nature of changes in the water composition in the estuarine area remains rather close. Indeed, thermal conditions in the bay significantly differed (2004: straight thermal stratification; 2007: thermal bar; 2016: inverse thermal stratification), and the river runoff was in different phases of water regime (2004: summer low water; 2007: flood; 2016: winter low water). All this was accompanied by significant differences in concentrations of major ions and their total number both in the river and the bay. Nevertheless, the maximum gradients of the total number of ions along the central and southern transects, regardless of the water-level conditions and temperature, were at a distance of up to one kilometre from the river estuary (Fig. 5). The gradient values and their vertical arrangement remained sufficiently similar.

Along the northern transect, the maximum changes in ion concentrations were also within the first kilometre from the estuary. However, in the surface layer, they were much lower than in the near-bottom area, and their significant values were at a

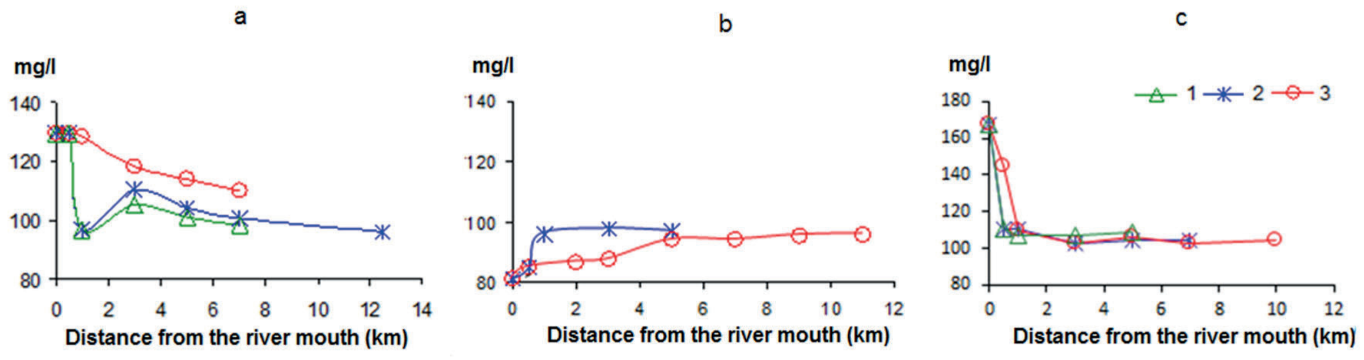

Fig.3. Distribution of the total number of ions in the surface water layer of the Barguzin Bay: a – July 2004; b – June 2007; c – March 2016. Transects: 1 – southern; 2 – central; 3 –northern

great distance, which indicates a lesser dilution of river waters and their more active distribution over the water area of the bay.

Analysis of the obtained results has shown that with the increased share of the Baikal water in samples from the estuarine area of the Barguzin Bay, the concentrations of some ions in the salt composition change linearly (Fig. 6). Linearity remains regardless of the greater or smaller concentration of the element in the water and its increased or decreased content in the mixing zone. This enables to conclude that during the mixing of river waters with lake waters, the change in the ion concentrations of the salt composition in the zone where river and lake waters interact results from ordinary dynamic mixing. This conservative behaviour is typical of both individual ions and their total number, and this does not change within the year.

Long-term investigations of the hydrochemical regime in the Barguzin Bay reveal the chemical composition features of its waters over the past 60 years. In 1950-60s, the chemical composition of water in the bay formed under the influence of natural factors, and the Baikal waters as well as those of the rivers that inflow to the bay, mainly the Barguzin River, determined seasonal and interannual changes in the concentrations of components (Votintsev, 1961). During the regulation of Baikal and rise of its water level, lake waters flowed to the bay, increasing the

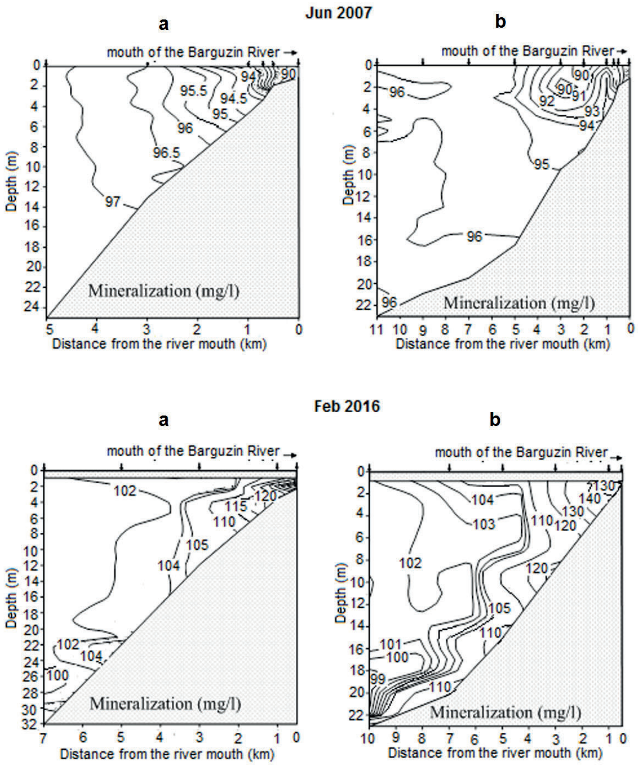

Fig.4. Change in the water mineralization in the Barguzine Bay in spring and winter along the central (a) and northern (b) transects

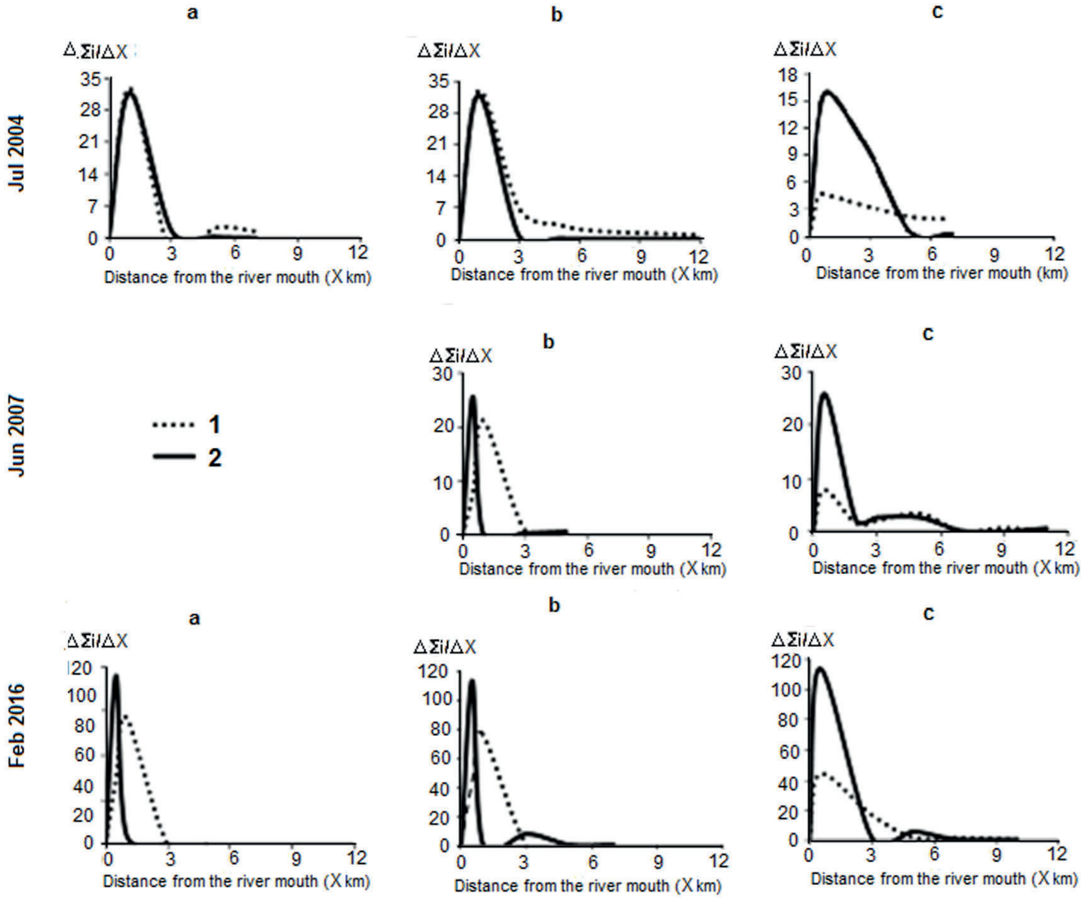

Fig.5. Horizontal gradients of the total number of ions in the salt composition ($\Delta\Sigma i$) of the surface layer (1) and near the bottom (2) along the three transects from the estuary of the Barguzin River. Transects: a – southern; b – central; c –northern

concentrations and the total number of ions (Table) there. At the same time, the water composition did not change and still corresponded to bicarbonate class and calcium group (Mescheryakova and Verbolova, 1977).

Subsequent investigations, which were conducted in 2000, indicated an increase in the concentration of major ions and their total number in the water of the bay compared to the 1970s (Table). This can be due to an increase in the flow of ions with the waters of the Barguzin River, resulting from the economic activity in its watershed and influx of sewage and drainage waters to the river channel and then the bay (Drucker et al., 1997). Furthermore, during the past two decades, there was a low water level in the Baikal basin, including the basin of the Barguzin River (Sutyrina, 2019), which could also contribute to the increase in the water mineralization in the bay.

Despite the change in absolute concentrations ions, their relative concentration remains unchangeable, and the water in the bay still corresponds to bicarbonate class and calcium group.

4. Conclusions

The conducted hydrophysical and hydrochemical investigations of the Barguzin Bay have shown that formation of the chemical composition and its waters, water-level conditions on the Barguzin River as well as water temperature differences determine seasonal changes in the concentration of major ions and their spatial distribution. Moreover, the system of currents in the bay predetermines the main transfer of the Barguzin River waters from the estuary along the northeast coast of the bay, which explains the heterogeneity in the distribution of the component concentrations of the ion composition in the water area of the bay. Along the central and southern transects, the concentrations of major ions and their total number, which are typical of the Baikal water, are recorded at a closer distance from the estuary than those along the northern transect. At the same time, the nature of changes in the chemical composition of water, which take place in the mixing zone of river and lake waters, is rather similar along all transects. The maximum gradients of the total number of ions are located at a distance of less than

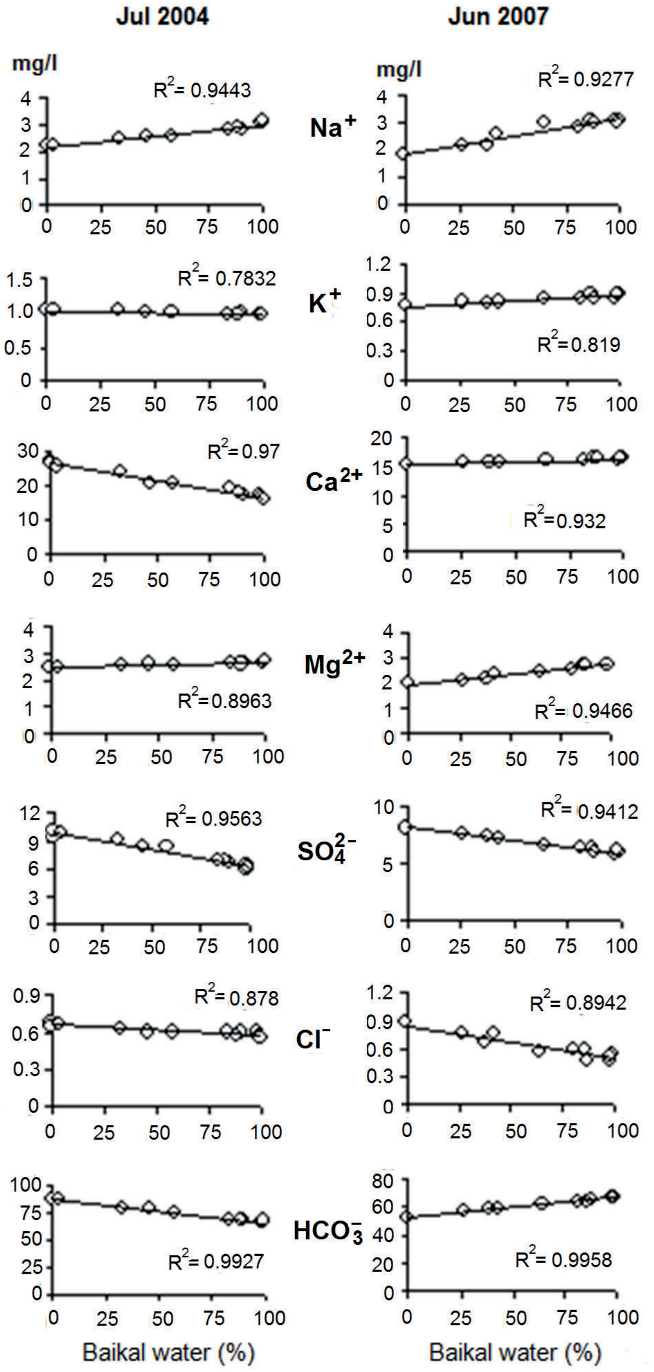

Fig.6. Change in the concentrations of major ions in the mixing zone "the Barguzin River – Lake Baikal"

Table. Concentrations of major ions at the central station of the Barguzin Bay in different periods, mg/l

Year/month	HCO_3^-	SO_4^{2-}	Cl^-	Ca^{2+}	Mg^{2+}	$\Sigma Na^+ + K^+$	Σi
1955*	66.8	5.3	0.56	17.1	3.1	3.4	96.4
1974**	56.7	5.5	0.17	15.5	3.0	3.4	87.9
2004/July	67.1	6.5	0.61	19.8	2.8	2.8 + 1.0	100.5
2007/June	66.4	6.5	0.8	16.3	2.8	3.1 + 0.8	96.7
2011/February	70.8	6.8	0.46	16.1	3.3	3.5 + 1.1	102.0
2016/March	71.4	6.8	0.51	17.4	3.4	3.8 + 1.1	104.4
2016/August	62.4	6.4	0.49	16.1	3.1	3.5 + 1.0	93.4

*Votintsev, 1961; ** Mescheryakova and Verbolova, 1977 one kilometre from the river estuary.

In spring, the thermal bar influences the distribution of river waters in the bay. The front of the thermal bar serves as a natural barrier that prevents the free entry of the Barguzin waters into the lake. Consequently, the chemical composition throughout the water column from the water edge to the thermal bar corresponds to river waters, and beyond thermal bar – lake waters. In different phases of the water regime, when water mineralization in the river can be both higher and lower than in the bay, the change in the ion concentrations of the salt composition in the mixing zone results from ordinary dynamic mixing of river and lake waters.

In the long-term aspect, the chemical composition of the water from the Barguzin Bay remains stable, corresponding to bicarbonate class and calcium group. The increase in the Baikal water level led to an insignificant decrease in the concentrations of major ions under the influence of lake waters. However, there is currently an increase in the concentrations of major ions under the influence of the economic activity in the watershed of the Barguzin River and, probably, a decrease in the runoff of the Barguzin River in conditions of the continuous low-water level.

Acknowledgements

The study was carried out within the framework of the LIN SB RAS State Task (topic no. 0345-2019-0008).

References

Baram G.I., Vereshchagin A.L., Golobokova L.P. 1999. The use of microcolumn high-performance liquid chromatography with UV detection to determine anions in environmental objects. Zhurnal Analiticheskoy Khimii [Journal of Analytical Chemistry] 54: 962-965. (in Russian)

Bogdanov V.T. 1986. The chemical composition of the Barguzin River and the lakes of its basin. In: Ozera Barguzinskoy doliny. Novosibirsk, pp. 53-63. (in Russian)

Drucker V.V., Sorokovikova L.M., Sinyukovich V.N. et al. 1997. Water quality of the Barguzin River in modern conditions. Geographiya I Prirodnyie Resursy [Geography and Natural Resources] 4: 72-78. (in Russian)

Guidelines for the chemical analysis of land surface water. Part 1. 2009. In: Boeva L.V. (Ed.). Rostov-on-Don: NOC. (in Russian)

Ivanov V.G., Sherstyankin P.P. 2015. The thermal bar in the Barguzin Bay. In: The VI-th International Vereshchagin Baikal Conference, pp. 108-109. (in Russian)

Mescheryakova T.I., Verbolova N.V. 1977. Hydrochemical characteristics of some isolated areas of Lake Baikal. In: Limnologiya pribrezhno-sorovoy zony Baykala. Novosibirsk, pp. 107-123. (in Russian)

Obozhin V.N., Bogdanov V.T., Klikunova O.F. 1984. Geokhimiya rek i ozer Buryatii. Novosibirsk: Nauka. (in Russian)

Sinyukovich V.N., Tomberg I.V., Sorokovikova L.M. 2008. Indication of river and lake waters in the mixing zones of the main tributaries of Lake Baikal. In: International Scientific Conference “Environmental Problems of Large River Basins”, p. 154. (in Russian)

Sorokovikova L.M., Zemskaya T.I., Popovskaya G.I. et al. 2005. Processes of the transformation of the Barguzin waters into lake waters and their determining factors. In: The IV-th International Vereshchagin Baikal Conference, pp. 173-174. (in Russian)

Sorokovikova L.M., Tomberg I.V., Sinyukovich V.N. et al. 2010. Formation features of a mixing zone of river and lake waters in the Barguzin Bay of Baikal. In: The V-th International Vereshchagin Baikal Conference, pp. 256-258. (in Russian)

Sutyrina E.N. 2019. Current trends in climatic conditions within the watershed of Lake Baikal. Vestnik Zabaikalskogo Gosudarstvennogo Universiteta [Bulletin of Transbaikal State University] 25: 49-55. DOI:10.21209/2227-9245-2019-25-5-27-49-55 (in Russian)

Technical documents for wet deposition monitoring in East Asia. March 2000. URL: http://www.eanet.asia/product/manual/prev/techwet.pdf

Tomberg I.V. 2008. Transformation of the chemical composition of river waters in the mixing zone with lake waters (on the example of the main tributaries of Lake Baikal). Cand. Sc. Dissertation, Institute of Geography SB RAS, Irkutsk, Russia. (in Russian)

Urbazaeva S.D., Pavlov I.A., Bazarsadueva S.V. et al. 2016. The content of heavy metals in water and bottom sediments of the Barguzin River in modern conditions. Nauchnoye Obozrenie [Scientific Review] 5: 114-120. (in Russian)

Verbolov V.I. 1996. Currents and water exchange in Baikal. Vodnyie resursy [Water resources] 23: 413-423. (in Russin)

Vorobyevskaya E.L., Gorshkova O.M., Dyunin O.P. et al. 2016. Hydrochemical indicators of water quality in the Barguzin Bay on the territory of the Trans-Baikal National Park in the winter of 2016. Almanakh mirovoy nauki [Almanac of world science] 3-3: 133-137. (in Russian)

Votintsev K.K. 1961. Hydrochemistry of Lake Baikal. Trudy Baikalskoi limnologicheskoi stantsii AN SSSR [Proceedings of the Baikal Limnological Station of the Academy of Sciences of the USSR] 20: 1-311. (in Russian)

Limnology and Freshwater Biology 2019 (4): 281-285 DOI:10.31951/2658-3518-2019-A-4-281

Original Article

ISSN 2658-3518
LIMNOLOGY
FRESHWATER
BIOLOGY
www.limnolfwbiol.com

Influence of solar radiation on chlorophyll *a* concentration assessment using fluorescence measured by the submersible sensor in Lake Baikal

Moiseeva N.A.[1,*], Efimova T.V.[1], Churilova T.Ya.[1], Makarov M.M.[2], Gnatovsky R.Yu.[2]

[1] *Kovalevski Institute of Biology of the Southern Seas, Russian Academy of Sciences, 2 Nakhimov Ave, Sevastopol, 299011, Russia*
[2] *Limnological Institute of the Siberian Branch of the Russian Academy of Sciences, Ulan-Batorskaya 3, 664 033 Irkutsk, Russia*

ABSTRACT. Assessment of chlorophyll *a* concentration based on fluorescence intensity is actively used at present. In natural waters, profile fluorescence is measured using submersible sensors. These sensors are equipped with no special chamber for phytoplankton dark adaptation before measurement. Effect of irradiance in the upper layer leads to a decrease in chlorophyll *a* fluorescence due to closing some reaction centers of photosystem 2. The conducted research on Lake Baikal has revealed the relationship between the share of open reaction center in photosystem 2 and photosynthetically available radiation in the lake. The relationship between these parameters was described by an exponential function with a high determination coefficient ($r^2 = 0.97$). Based on the obtained relationship, an algorithm was developed to compensate for the decrease in chlorophyll *a* fluorescence intensity due to the light influence *in situ*. The algorithm enables to retrieve the "real" fluorescence profile, which is necessary for the correct retrieval of the vertical distribution of the chlorophyll *a* content.

Keywords: chlorophyll *a*, fluorescence, submersible sensor, photochemical and non-photochemical quenching, open and closed reaction centers

1. Introduction

Content of chlorophyll *a* (C_a), which is the main photosynthetically active pigment, is widely used as water trophic status and productivity indicator. At present, values of the chlorophyll *a* fluorescence measured in situ by submersible sensors are used for the analysis of temporal and spatial C_a variability as well as for validation of remote sensing data (C_a) (Odermatt et al., 2012; Xing et al., 2012; Wojtasiewicz et al., 2018).

In situ fluorescence intensity (F) depends on a number of variables: the photosynthetically available radiation (PAR, μmol/m^2/s); the C_a values (in mg/m^3) and phytoplankton functional characteristics, in particular, the chlorophyll *a* specific light absorption coefficient of phytoplankton ($a^*_{ph}(\lambda)$ m^2/mg), the quantum yield of fluorescence (φ_F, mol emitted quantum (mol absorbed quantum)$^{-1}$) and fluorescence intracellular reabsorption factor (Q^*_a, dimensionless) (Babin, 2008).

Submersible fluorescence sensors that measure in situ the chlorophyll *a* fluorescence intensity (F_{CTD}) are not equipped with a special chamber for adapting phytoplankton to the dark (so-called "dark chamber"). Due to this technical peculiarity, the sensors can measure the fluorescence of phytoplankton adapted to the environmental conditions, in particular, light intensity. In this case, some of the reaction centers (RC) of photosystem 2 are in an inactive state. These inactive RC are closed for acceptance of the electron, pathing the electron transport chain (Govindjee et al., 1990). It results in decreased F values (Pogosyan and Matorin, 2005) due to the effect of light only but not C_a (Falkowski and Raven, 2007).

Correct assessment of chlorophyll *a* concentration via fluorescence requires additional processing of the fluorescence signal to compensate the decreasing effect of PAR on the fluorescence intensity, which is especially obvious in the upper part of the euphotic layer, i.e. in the upper mixed layer (UML).

Quasi-synchronous in situ measurements of temperature, fluorescence and PAR profiles as well as pulse amplitude modulation (PAM) fluorescence parameters were carried out during the scientific cruise on Lake Baikal in September 2019. The obtained results represent the required scientific basis, allowing an attempt for a correction of the PAR influence on the fluorescence intensity measured by the submersible sensor.

---

*Corresponding author.
E-mail address: nataliya-moiseeva@yandex.ru (N.A. Moiseeva)

Therefore the aim of this research is to investigate in situ the effect of PAR on the fluorescence intensity and PAM fluorescence parameters; to develop a general algorithm for restoring the fluorescence affected by PAR and test the algorithm for Lake Baikal.

2. Methods

The research was carried out in different areas of Lake Baikal (Fig. 1) during the scientific cruise onboard the RV "Titov" on September 3-11, 2019. The measurements were fulfilled at 21 stations during daylight time (from 7:00 AM to 7:00 PM).

The vertical profiles of temperature, salinity, density, fluorescence (chlorophyll *a* concentration), and photosynthetically available radiation (PAR) were measured by a JFE Rinko AAQ-177 water quality probe (Japan) (Table 1).

The measured parameters (downcast data) were displayed in real time on the screen of a laptop.

The submersible F sensor provided the fluorescence measurements of the sample (phytoplankton) adapted to the environment, i.e. the light intensity at the sampling depth (z) - PAR(z).

For the laboratory measurements, water samples were collected from different depths within the UML using Niskin bottles. PAM fluorescence parameters were measured with laboratory fluorometer "Smart", which was developed in Moscow State University, Biophysical Department (Konyukhov et al., 2017). The fluorescence intensity due to colored dissolved organic matter (F_{CDOM}) was used as a background fluorescence, which was subtracted from each sample measurement (Moiseeva et al., 2018). For measurement of F_{CDOM}, the sample was filtered through a membrane filter (Sartorius), which was prerinsed with 50 ml of deionized water. Before measurements, the samples were adapted to the dark for 15-30 minutes (Gaevsky and Morgun, 1993). The laboratory fluorometer "Smart" provided the measurements of maximum (F_m) and minimum (F_0) fluorescence intensity of the sample: the F measured at 0 μmol/m²/s (dark measurement) corresponds to the parameter F_0, when all RC are open; the F measured at saturating light flash – F_m, when all RC are closed (Schreiber et al., 1994; Matorin et al., 2012). Using laboratory fluorometer, we measured the dependence of the fluorescence parameters (F_0, F_t, F_m and $F`_m$) on the light intensity, varying from 0 to 1000 μmol/m²/s (90 s light adaptation to each light intensity before measurements). The F value measured at light intensity PAR(z) (the sampling depth) was denoted as F_t (steady-state fluorescence). The difference between the maximum F value measured after continuous illumination ($F`_m$) and $F_t$ is proportional to the number of open RC (Schreiber et al., 1994; Matorin et al., 2012). The relative amount of open RC in phytoplankton that exists at a depth –z with radiance – PAR(z) can be assessed based on parameters $F_0$, $F_t$, $F_m$ and $F`_m$ according to (Falkowski and Kiefer, 1985):

$$d_{open} = \frac{F'_m - F_t}{F_m - F_0} \qquad (1)$$

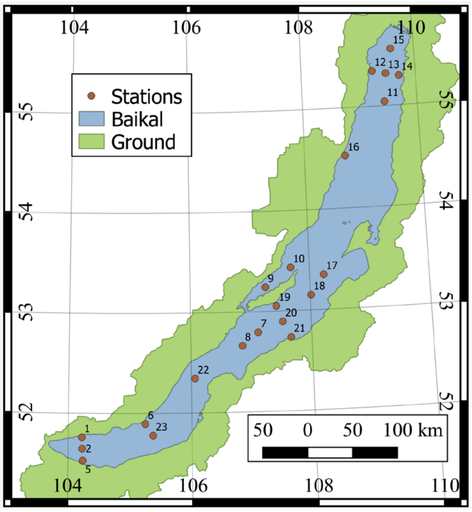

Fig.1. Map of the stations (●) that were investigated during the scientific cruise onboard the RV "Titov" on Lake Baikal on September 3-11, 2019

3. Results and discussion

Due to different cloudiness and different daytime of sampling, the solar radiance incidence on the lake surface varied from ~200 to 1950 μmol/m²/s (Table 2). The UML depth changed from 3 m to 19 m between almost all stations, except for three stations with more shallow UML (< 3 m) and one station with deepest UML (21m) (Table 2).

Table 1. Characteristics of the JFE Rinko AAQ-177 water quality probe (Japan) and sensors equipped

Measured parameter	Measurement range	Resolution	Accuracy	Response time
Depth	0 - 100 m	0.002 m	±0.3% of full scale	0.2 s
Water temperature	-3 - 45 °C	0.001 °C	±0.01 °C (0 - 35 °C)	0.2 s
Fluorometer	0 to 400 ppb (Uranin reference)	0.01 ppb	±1% of full scale	0.2 s
Photosynthetically available radiation in water	0 – 5000 μmol/m²/s	0.1 μmol/m²/s	±4%	0.2 s

For the UML, we have revealed a relationship between the d_{open} and the intensity PAR_Z (Fig. 2) and described it by the exponential function:

$$d_{open} = A \cdot e^{-0.0025 \times PAR}, \; n = 42, \; r^2 = 0.97 \quad (2)$$

where the coefficient A = 1 since all RC are open (d_{open} = 1) in the dark (PAR = 0).

The fraction of closed RC, which do not contribute to the fluorescence intensity recorded by the CTD probe, can be calculated using equation 6:

$$d_{closed} = 1 - d_{open} \qquad (3)$$

Consequently, the F value of closed RC (potential fluorescence, F_{closed}), which is not detected by a submersible sensor (without a dark chamber), can be calculated as follows:

$$F_{closed}(z) = F_{CTD}(z) \times d_{closed} \qquad (4)$$

To compensate for the decreasing effect of PAR and restore the fluorescence profile, it is necessary to take into account the value of F_{closed} (z):

$$F_{real} = F_{CTD} + F_{closed}, \qquad (5)$$

where F_{real} is the fluorescence intensity provided that all RC are in the open state.

Based on equations 4 and 5, we get equation 6:

$$F_{real}(z) = F_{CTD}(z) + \left(F_{CTD}(z) \times (1 - e^{-0.0025 \times PAR_Z})\right) \qquad (6)$$

which is transformed into equation 7:

$$F_{real}(z) = F_{CTD}(z) \times (2 - e^{-0.0025 \times PAR_Z}) \quad (7)$$

The fluorescence profiles were restored at all stations based on the obtained relationship (equation 7). Figure 3 shows the restored F profiles, which were measured in different day-time. We have revealed that F_{real} exceeds F_{CTD} within the UML at all stations. The relative differences between F_{real} and F_{CTD} (ΔF) reflect a decrease in chlorophyll *a* fluorescence intensity in the upper layer due to light effect. We have correlated the ΔF values with the PAR_0 (Table 2).

Early in the morning, when PAR_0 was 11 μmol/m²/s, there was almost no effect of light on F. At noon, under a cloudless sky, PAR_0 reached 1950 μmol/m²/s. In this case, the F values in the surface layer decreased ~ 2 times (Table 2).

Correct assessment of C_a based on the fluorescence measured by the submersible sensor requires the compensation of the PAR effects of on the chlorophyll *a* fluorescence. This problem remains relevant to date (Barbieux et al., 2019). To solve this problem, it was proposed to use chlorophyll *a* fluorescence profiles measured at night only when there is no PAR effect (Wojtasiewicz et al., 2018). However, this approach significantly reduces the data set for analyzing the spatial and temporal variability of C_a and limits the use of this data (nightly) for validation of satellite data (daily). In this study, the observed two-fold decrease in F under the influence of solar insolation evokes one doubt about the validation of satellite data, according to BioArgo floats, without this correction of the light effect on fluorescence (Kubryakov et al., 2017).

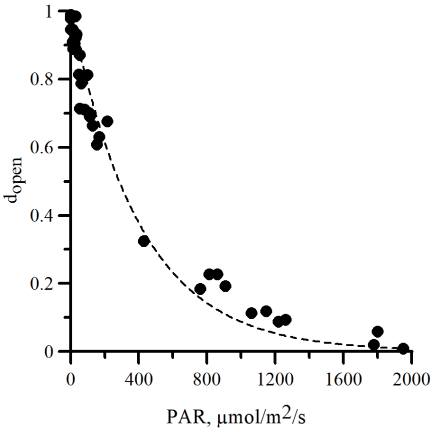

Fig.2. Dependence of the fraction open reaction centers (dopen) on light intensity (PAR) in the UML layer of Lake Baikal on September 3-11, 2019

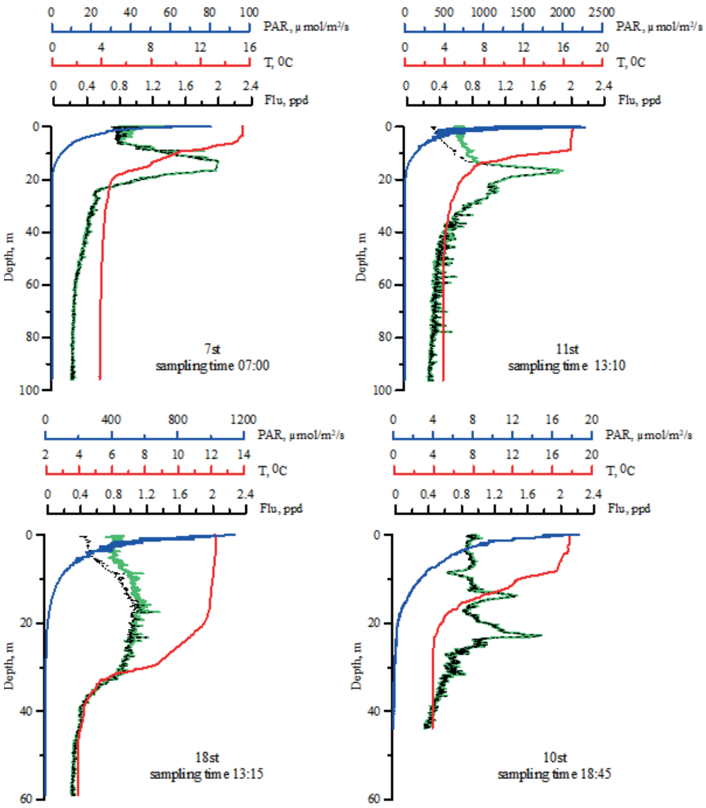

Fig.3. Vertical profiles: photosynthetically available radiation (PAR, blue line), temperature (T, red line), fluorescence intensities (F) measured by the submersible sensor (black line) and F, which was reconstructed, taking into account the light intensity (green line) in Lake Baikal on September 3-11, 2019

Table 2. The effect of the developed algorithm for compensation of chlorophyll *a* fluorescence intensity (F) decreased under the surface photosynthetically available radiation (PAR_0): increased F in the surface layer ($\Delta F = (F_{real} - F_{CTD})/F_{CTD}$) and averaged within the upper mixed layer (UML) (ΔF_{UML}) at the stations on Lake Baikal in September 2019.

Station no.	date	sampling time	UML, m	PAR_0, μmol/m²/s	$\Delta F = (F_{real} - F_{CTD})/F_{CTD}$, %	ΔF_{UML}, %
1	03.09.2019	16:45	-	1260	72	-
2	04.09.2019	07:05	3	30	7	5
5	04.09.2019	10:35	5	810	83	74
6	04.09.2019	18:35	-	110	18	-
7	05.09.2019	07:00	3	80	14	12
8	05.09.2019	09:35	5	910	75	69
9	05.09.2019	15:30	-	1780	82	-
10	05.09.2019	18:45	4	20	4	3
11	06.09.2019	13:10	8	1800	96	78
12	06.09.2019	16:10	4	1060	65	61
13	06.09.2019	17:40	4	170	23	17
14	07.09.2019	08:05	19	760	69	20
15	07.09.2019	13:35	8	170	30	19
16	08.09.2019	15:40	6	860	72	56
17	09.09.2019	11:05	6	430	55	49
18	09.09.2019	13:15	18	1150	87	33
19	09.09.2019	16:15	10	1220	87	44
20	09.09.2019	18:10	2	60	10	9
21	10.09.2019	07:00	28	110	15	3
22	11.09.2019	07:00	12	10	2	1
23	11.09.2019	12:10	16	1950	74	45

Conclusions

In this study, we have developed an algorithm that compensates a decrease in fluorescence intensity due to the light influence in situ. The algorithm enables to retrieve the “real” fluorescence profile, which is required for the correct retrieval of the vertical distribution of the chlorophyll *a* content as the main photosynthetically active pigment. The upper layer of water, being most illuminated, makes the main contribution to the primary productivity of the water column. Consequently, the correction of the C_a estimation affects the accuracy of the primary productivity assessment.

Acknowledgements

The research was funded by the Russian Academy of Science within the topic “Comprehensive investigation of the current state of the ecosystem in the Atlantic sector of the Antarctic” and within the topics No. AAAA-A19-119061190081-9 and No. AAAA-A17-117041250054-8.

References

Babin M. 2008. Phytoplankton fluorescence: theory, current literature and in situ measurement. In: Babin M., Roesler C., Cullen J. (Eds.), Real-time coastal observing systems for marine ecosystem dynamics and harmful algal blooms. Paris: UNESCO Publishing, pp. 237-281.

Barbieux M., Uitz J., Gentili B. et al. 2019. Bio-optical characterization of subsurface chlorophyll maxima in the Mediterranean Sea from a Biogeochemical-Argo float database. Biogeosciences 16: 1321-1342. DOI: 10.5194/bg-16-1321-2019

Falkowski P., Kiefer D.A. 1985. Chlorophyll *a* fluorescence in phytoplankton: relationship to photosynthesis and biomass. Journal of Plankton Research 7: 715-731. DOI: 10.1093/plankt/7.5.715

Falkowski P.G., Raven J.A. 2007. Aquatic photosynthesis. Princeton and Oxford: Princeton University Press.

Gaevsky N.A., Morgun V.N. 1993. Using variable and slow chlorophyll fluorescence to study plant photosynthesis. Fiziologija Rastenij [Plant physiology] 40: 119-127. (in Russian)

Govindjee M., Van de Ven C., Preston C. et al. 1990. Chlorophyll *a* fluorescence lifetime distributions in open and closed photosystem II reaction center preparations.

Biochimica et Biophysica Acta 1015: 173-179. DOI: 10.1016/0005-2728(90)90017-X

Kirk J.T.O. 2011. Light and photosynthesis in aquatic ecosystems. Third edition. Cambridge: Cambridge University Press.

Konyukhov I.V., Vorobyova O.V., Pogosyan S.I. et al. 2017. Fluorometer with pulse modulation of exciting light for estimating the functional state of natural phytoplankton by chlorophyll fluorescence parameters. In: II Vserossijskaja nauchnaya konferenciya molodyh uchenyh “Kompleksnye Issledovanija Mirovogo Okeana”, pp. 345-347. (in Russian)

Kubryakov A.A., Stanichny S.V., Kubryakova E.A. 2017. Variability of the bio-optical characteristics of the Black Sea from measurements of Bio-Argo buoys and satellite data. In: II Vserossijskaja nauchnaya konferenciya molodyh uchenyh “Kompleksnye Issledovanija Mirovogo Okeana”, pp. 130-131. (in Russian)

Matorin D.N., Osipov V.A., Rubin A.B. 2012. Metodika izmereniy obiliya i indikatsii izmeneniya sostoyaniya fitoplanktona v prirodnykh vodakh fluorestsentnym metodom. Teoreticheskiye i prakticheskiye aspekty. Moskow: Al’teks. (in Russian)

Moiseeva N., Churilova T., Efimova T. et al. 2018. Dependence of fluorescence intensity on chlorophyll *a* concentration and light absorption coefficients by phytoplankton in the Black Sea (October 2017). Proceedings of the SPIE 10833. DOI: 10.1117/12.2505415

Odermatt D., Pomati F., Pitarch J. et al. 2012. MERIS observations of phytoplankton blooms in a stratified eutrophic lake. Remote Sensing of Environment 126: 232-239. DOI: 10.1016/j.rse.2012.08.031

Pogosyan S.I., Matorin D.N. 2005. Variability in the condition of the photosynthetic system of the Black Sea phytoplankton. Oceanology 45: 139-148.

Schreiber U., Bilger W., Neubauer C. 1995. Chlorophyll fluorescence as a nonintrusive indicator for rapid assessment of in vivo photosynthesis. In: Schulze E.D., Caldwell M.M. (Eds.), Ecophysiology of photosynthesis. Berlin, Heidelberg, pp. 49-70. DOI: 10.1007/978-3-642-79354-7_3

Suggett D.J., Borowitzka M.A., Prášil O. 2010. Chlorophyll *a* fluorescence in aquatic sciences: Methods and applications. Dordrecht: Springer. DOI: 10.1007/978-90-481-9268-7

Wojtasiewicz B., Hardman-Mountford N.J., Antoine D. et al. 2018. Use of bio-optical profiling float data in validation of ocean colour satellite products in a remote ocean region. Remote Sensing of Environment 209: 275-290. DOI: 10.1016/j.rse.2018.02.057

Xing X., Morel A., Claustre H. et al. 2012. Combined processing and mutual interpretation of radiometry and fluorometry from autonomous profiling Bio-Argo floats: 2. Colored dissolved organic matter absorption retrieval. Journal of Geophysical Research: Oceans 117. DOI: 10.1029/2011jc007632