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Article

Phytoplankton as an indicator of the ecosystem state of the Kondopoga Bay of Lake Onego under cage trout farming

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Abstract. Phytoplankton studies in the coastal and pelagic part of the Kondopoga Bay of Lake Onego nearby the cage trout farms (2019, 2021) revealed high quantitative indicators of its development, characterizing the bay as meso-eutrophic. In terms of number, diatoms (up to 79%) were dominant communities, while cyanobacteria and green algae – subdominant (up to 40%). Indicator species of the *β*-mesosaprobic zone prevailed; polysaprobionts were also present. Potentially toxic species *Microcystis aeruginosa* (Kütz.) Kütz., *Aphanizomenon flos-aquae* L. Ralfs., *Coelosphaerium kuetzingianum* Näg., *Oscillatoria limnetica* Lemm. were noted. Analysis of long-term dynamics of phytoplankton showed the increasing development of all groups of phytoplankton (including dominant species) in the pelagic part of the bay. This indicates eutrophication of the previously mesotrophic bay due to nutrients supplied with wastes from trout farms.

Keywords: indicator species, algae, eutrophication, saprobity, cage trout farming, phosphorus load

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Научная статья

Фитопланктон как индикатор состояния экосистемы Кондопожской губы Онежского озера в условиях садкового выращивания форели

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Аннотация. В результате изучения фитопланктона прибрежной и пелагической части Кондопожской губы Онежского озера в районе садковых форелевых хозяйств в 2019 и 2021 гг. выявлены высокие для этого района количественные показатели развития фитопланктона, характеризующие залив как мезо-эвтрофный. Доминантами сообществ по численности являлись диатомеи (до 79%), субдоминантами (до 40%) – цианобактерии и зеленые водоросли. Преобладали индикаторные виды β-мезосапробной зоны, присутствовали полисапробионты. Отмечены потенциально токсичные виды *Microcystis aeruginosa* (Kütz.) Kütz., *Aphanizomenon flos-aquae* L. Ralfs., *Coelosphaerium kuetzingianum* Näg.*, Oscillatoria limnetica* Lemm. Анализ многолетних изменений фитопланктона показал увеличение количественного развития всех групп фитопланктона, в том числе доминантных видов, в пелагической части губы. Это свидетельствует об эвтрофировании ранее мезотрофного залива вследствие поступления биогенных элементов с отходами форелевых ферм.

Ключевые слова: виды-индикаторы, водоросли, эвтрофирование, сапробность, садковое форелеводство, фосфорная нагрузка

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Introduction

The Republic of Karelia, distinguished by its numerous deep cold-water lakes with clean water, is among the priority regions of Russia for commercial trout farming. Data as of 2010, 70% of Russian trout farmed on cage**s** was grown in the Republic of Karelia, and since then its production only increased[1] (Artamonov, 2017; Kuchko and Kuchko, 2010). About 80% of trout of the region is produced in Lake Onego and more than 30% – in its northwestern bays (Sterligova et al., 2011; 2018) that results in a significant load on the ecosystem of the reservoir (Galakhina et al., 2022; Kalinkina et al., 2017; Tekanova et al., 2019).

The main negative consequences for the lake ecosystem caused by wastes from the cage trout farms (CTF) are the increased loads of nutrients, mostly phosphorus and organic matter enriching the water column and forming specific bottom sediments (Kiuru et al., 2012; Timakova et al.., 1992). This leads to eutrophication of the aquatic ecosystem and intensive phytoplankton development, including toxic cyanobacteria. A large amount of oxygen is spent on bacterial oxidation of excess organic matter and anaerobic processes providing an unpleasant water odor. The eutrophication-induced degradation of water quality greatly reduces the drinking, fishery and recreational value of the water body.

In order to avoid the discussed consequences for the aquatic ecosystem, regular environmental assessments of its state in sites of fish farms location should be made (Kuchko and Kuchko, 2010). Such a control seems especially relevant for Lake Onego – the second largest reservoir in Europe, which contains strategic reserves of clean fresh water for the North-Western Region of Russia (Krupneishie..., 2015).

It is well-known that the most informative indicators of any reservoir state are the composition and quantitative indicators of phytoplankton. Being the initial link in the food chain and having a short life cycle, as well as a high reproduction rate, phytoplankton quickly responds to changing environmental factors, i.e. temperature, light, acidification, content of nutrients and toxic substances (Barinova et al., 2006; Reynolds, 2008). In this regard, one of the main tasks in biomonitoring of water bodies is assessing the phytoplankton state and identifying the species and groups of microalgae-indicators of water pollution (Otsenka..., 2012; Petrova, 1990; Rukovodstvo..., 1992).

This work is aimed at studying the current state and probable changes of phytoplankton in sites of CTF location in the central part of the Kondopoga Bay of Lake Onego.

Material and methods

Lake Onego (N 61°42' E 35°25') belongs to the Baltic Sea basin. Its water area is 9720 km^2; the average and maximum depth – 30 and 120 m, respectively; the period of conditional water exchange – 15.6 years. Lake waters are meso-humus and slightly alkaline, belonging to the hydrocarbonate class and Ca group (Ozyora Karelii, 2013). The reservoir is characterized as oligotrophic with high water quality, except for the man-disturbed northwestern bays (Krupneishie..., 2015).

The large Kondopoga Bay situated in the northwestern part of Lake Onego (Fig. 1) has the area of 225 km^2 (2.5% of the total lake area), the volume of water masses – 4.3 km^3, the average and maximum depth – 21 and 82 m, respectively. On the coastal apical part of the bay, the Kondopoga Pulp and Paper Mill (PPM) has discharged its wastewater to the bay for 90 years and thereby intensified eutrophication there. Since the 1990s to date, the phosphorus load has decreased significantly, i.e. from 109 to 12 t/year (Litvinova et al., 2021). However, started in 2000 commercial production of cage trout and currently operating 11 trout farms (total capacity of 3870 t/year) in the coastal zone of the central part of the Kondopoga Bay have increased the total anthropogenic load on the bay[1] (Tekanova et al., 2019).

To study phytoplankton, 10 water samples were taken at five stations in the central part of the Kondopoga Bay in August of 2019 and 2021 (Fig. 1). Sampling was made from the surface layer (0.5 m) at stations K50 (depth 36 m) and K_6 (80 m) in the pelagic zone of the central part of the bay, including KF1 (25 m), KF2 (32 m), and KF4 (9 m) located in the coastal zone where trout farming was implemented. The distance between the pelagic stations (K50 and K_6) and KF1, KF2, KF4 was 2.4 km and 6.1 km, 3.2 km and 5.1 km, 3.9 km and 6.3 km, respectively. Water temperature of the surface layer in the studied areas reached on average 12.9 ± 0.36 °C, being within the long-term variations in August (12−17 °C) for Kondopoga Bay (Onezhskoe..., 2010).

[1] Association of Trout Breeders of Karelia. Web page. URL: http://kareliatrout.ru/karta-rybnyh-hozjajstv (accessed: 03.1.2022).

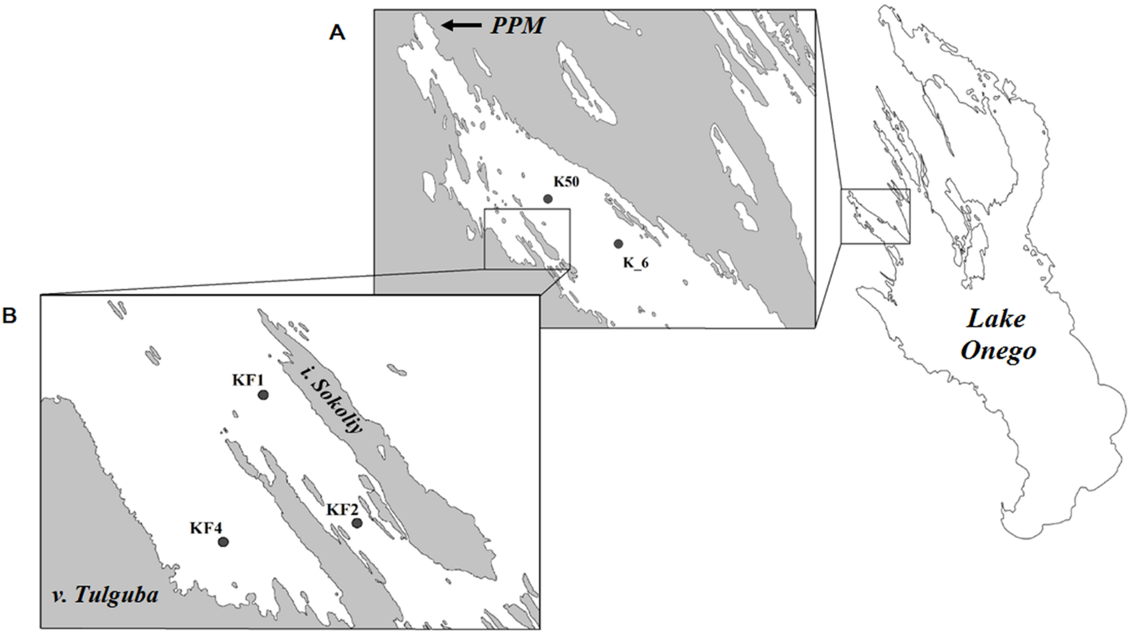

Fig. 1. Schematic map of sampling stations located in the Kondopoga Bay of Lake Onego: **A** – the Kondopoga Bay, **B** –CTF area.

The 500 ml water samples were fixed with 40% formaldehyde and concentrated on membrane filters with a pore diameter of 0.8 μm to a volume of 5 ml. The species composition, number (N_{tot}) and structure of phytoplankton were studied by microscopy at a magnification of ×400 (Fedorov, 1979; Kuzmin, 1975). To identify algae species, we used the Keys "Freshwater algae of North America" (2015) and T. Tikkanen (1986). Phytoplankton biomass (B_{tot}) was determined through the calculation of the individual cells by approximating the cell shape with geometric figures.

Species diversity was assessed using the Shannon–Weaver index (H), while the uniformity of their distribution in the community – by the Pielou index (E). We applied the Sørensen coefficient for calculation of similarity of the species composition of plankton algae at different stations (Korosov, 2007), the methods of S.S. Barinova et al. (2006), S.P. Vasser et al. (1989), and A.V. Makrushin (1974) – for establishment of indicator significance of phytoplankton species, the Pantle–Buck method modified by Sladecek – for calculation of the water saprobity index (Sladecek, 1973), the ecological classification of O.P. Oksiyuk et al. (1993) – for determination of a saprobity zone.

To analyze long-term dynamics of phytoplankton from the Kondopoga Bay, a registered database "Plankton of the pelagic zone of Lake Onego" (1993–2010) was employed (Syarki et al., 2015). Statistical analysis of the material was performed using nonparametric methods in the Statictica Advanced 10 package for Windows (median and its error, the Mann–Whitney test).

Results and discussion

State of phytoplankton in the Kondopoga Bay before commercial trout production

The sixty-year studies of the Kondopoga Bay ecosystem revealed gradual phytoplankton changes caused by PPM wastewater pollution (Chekryzheva, 2008; Timakova et al., 2014; Vislyanskaya, 1986, 1990, 1999). In the 1960−1970s, phytoplankton was mainly represented by a diatom complex, characteristic of oligotrophic waters. The average number and biomass of algae in the bay made up 30 thous. cells/l and 0.03 mg/l, respectively. In the 1980s, the increased PPM-related phosphorus loads caused eutrophication of the bay. Abundance of cyanobacteria and green algae, which often became subdominants, increased significantly. The average number of phytoplankton in the Kondopoga Bay reached 1400 thous. cells/l and biomass – 2.4 mg/l. A drop in phosphorus loads in the 1990s, reduced quantitative indicators of phytoplankton on average to 880 thous. cells/l and 0.9 mg/l, respectively. A proportion of species recorded in the 1960−1970s (oligotrophic period), i.e. *Aulacoseira islandica* (O. Mull.) Sim., *A. subarctica* (O. Mull.) Howort., *Asterionella formosa* Hass., *Tabellaria fenestrata* (Lyngb.) Kutz., *Fragilaria crotonensis* Kitt., *Diatoma tenuis* Ag. was increasing. Note that this trend was observed in the 2000s as well (Chekryzheva, 2008).

In the 2000s, phytoplankton of the Kondopoga Bay of Lake Onego consisted of 228 taxa with a predominance of Bacillariophyta, Chlorophyta, Chrysophyta and Cyanobacteria. The dominant species of the spring-autumn complex included *Aulacoseira islandica*, *A. subarctica, A. italica* (Ehr.) Sim. var. *tenuissima* (Grun.) Sim., the summer one – *Asterionella formosa* and *Tabellaria fenestrata* (Chekryzheva, 2008). The waters of the bay may be generally characterized as mesotrophic (Chekryzheva, 2008) and attributed to the *β*-mesosaprobic type (Chekryzheva, 2008, 2015).

Current state of phytoplankton at trout farms in the coastal zone of the central part of the Kondopoga Bay

According to chemical indicators, some signs of biogenic and organic water pollution were noted in the coastal central part of the Kondopoga Bay in sites of CTF location in the period preceding our research (summer 2018). For instance, peak concentrations of total phosphorus (36–130 µg/l), as well as low oxygen saturation (61%) and high concentrations of carbon dioxide (9.7 mg/l) were present in the bottom layer suggesting of intensive decomposition of organic matter (Tekanova et al., 2019).

In August of 2019 and 2021, in sites of CTF location at stations KF1, KF2 and KF4, N_{tot} and B_{tot} of phytoplankton were extremely high: 1742−9150 thous. cells/l and 1.890−5.402 mg/l, respectively (Table 1). According to the S.P. Kitaev classification (2007), the values of phytoplankton biomass pointed to the meso-eutrophic state of the ecosystem. It was confirmed by summer concentrations of total phosphorus (23−46 µg/l) (Tekanova et al., 2019; Zobkov et al., 2022). Such a development of phytoplankton was much higher ($p < 0.05$) than in the apical part of the bay polluted by PPM wastewaters with N_{tot} reached 240−8480 thous. cells/l (1787 ± 384, n = 23), B_{tot} – 0.2−17.687 mg/l (1.72 ± 1.14, n = 23) in summer of the 1990−2000s (Syarki et al., 2015).

In terms of number, Bacillariophyta (68−79%), represented by large diatoms *Aulacoseira islandica*, *A. subarctica, Fragilaria crotonensis, Melosira varians* Ag., dominated in the algae community during both years of our research. They formed 90−94% of phytoplankton biomass. In 2019, Chlorophyta amounted 8–12%, Cyanobacteria – 11–14% of the total number of algae. In 2021, small-sized green algae developed in even greater quantities, reaching 5–23% of $N_{tot.}$ The contribution of Cyanobacteria to N_{tot} made up 9–19%. Among Cyanobacteria, *Coelosphaerium kuetzingianum* Näg., able to release cyanotoxins hazardous to human and animal health, were dominant (Davydov, 2021; Kasperovičienė, 2007). Another dangerous cyanobacteria species identified in sites of trout farms location included *Oscillatoria limnetica* Lemm. (Mohamed, 2016), *Microcystis aeruginosa* (Kütz.) Kütz., *Aphanizomenon flos-aquae* L. Ralfs (Cameán and Jos, 2020), including the ones from the genera *Dolichospermum* sp., *Phormidium* sp., *Merismopedia* sp. (Toxic cyanobacteria..., 2021). According to WHO classification, the average number of cells (3138 cells/ml) of potentially dangerous cyanobacteria did not threaten health and life of humans and animals (Guidelines..., 2003).

In sites of CTF location, a total of 88 taxa of algae were identified to species and 6 taxa – to genus (note: taxa were referred to 7 divisions). By species number, Bacillariophyta – 31 (33%), Chlorophyta – 29 (30.8%), Cyanobacteria – 14 (14.9%), Chrysophyta – 12 (12.8%) prevailed. Euglenophyta – 3 (3.2%), Cryptophyta – 3 (3.2%), Dinophyta – 2 (2.1%) were the least common. The main representatives of these divisions are given in Table 2.

Table 1. Average quantitative indicators of phytoplankton in sites of CTF location in the Kondopoga Bay of Lake Onego in 2019, 2021. N_{tot} – number, B_{tot} –biomass of phytoplankton.

Phytoplankton indicators	KF1		KF2		KF4	
	2019	2021	2019	2021	2019	2021
N_{tot}, thous. cells/l	3516	5638	1742	9150	2369	8213
B_{tot}, mg/l	3.528	2.036	1.890	3.562	2.006	5.402

The index H (averaged as 3.58 ± 0.16 for number and 3.19 ± 0.13 for biomass of phytoplankton) indicated high species diversity, while E (2.27 ± 0.09 and 2.02 ± 0.07) demonstrated a relatively uniform distribution of species in the community.

The saprobiological analysis suggests that in contrast to *β*-*α*-mesosaprobionts (4.5%) and *α*-mesosaprobionts (2.3%), *β*-mesosaprobionts (33%), oligo-*β*-mesosaprobionts (26%), and oligosaprobionts (17%) were the most abundant in the community (Table 3). We also detected *α*-polysaprobionts *Chlorella vulgaris* and *Astasia dangeardii* (2.3%), including *p*-polysaprobiont *Chlamydomonas incerta* Pasch. (1.5%). In 2019 and 2021, the saprobity index averaged 2.35 and 2.10, respectively, thus corresponding to a *β*-mesosaprobic type of water.

Current state and long-term dynamics of phytoplankton in the pelagic zone of the central part of the Kondopoga Bay

Because of manifest signs of coastal water eutrophication in sites of trout farms location, it seems important to find out whether the influence of CTF extends to the adjacent deep-water pelagic zone of the Kondopoga Bay, where the formed cyclonic currents able to transport pollutants into the open reach of Lake Onego.

As compared to the previous study period, values of N_{tot} and B_{tot} of phytoplankton in the pelagic zone of the central part of Kondopoga Bay (stations K50 and K_6) were extremely high in August of 2019 and 2021. In contrast to the data for the previous years, a statistically significant increase in the total phosphorus content was also recorded (Galakhina et al., 2022). In summer of 2019 and 2021, this indicator in the surface water layer varied within 17−37 µg/l (Tekanova et al., 2019; Zobkov et al., 2022).

During our study, N_{tot} made up 1366−6063 thous. cells/l, B_{tot} – 1.128−2.289 mg/l (Table 4). The level of phytoplankton biomass corresponded to the mesotrophic state (Kitaev, 2007).

Diatoms prevailed in number (56−75%) and biomass (80−95%). Large forms of diatoms constituted the basis of phytoplankton. Chlorophyta also made a significant contribution to N_{tot} (14−31%). In 2021, cyanobacteria developed intensively, reaching 17−26% of N_{tot}.

Like in CTF sites, potentially dangerous species of cyanobacteria *Microcystis aeruginosa* and *Aphanizomenon flos-aquae*, *Coelosphaerium kuetzingianum*, as well as species from the genera *Dolichospermum*, *Phormidium*, *Limnothrix*, *Oscillatoria*, *Merismopedia*, *Synechococcus* were iden-

Table 2. The most common (except for dominant) species of phytoplankton in sites of CTF location. * – subdominants species (more than 5% of the total number).

Division	Species
Bacillariophyta*	*Aulacoseira italica, Tabellaria fenestrata, Cyclotella ocellata* Pant., *Surirella elegans* Ehr., *Discostella stelligera* (Cleve et Grunow) Houk et Klee
Chlorophyta*	*Eudorina elegans* Ehr., *Chlorella vulgaris* Beijer., *Botryococcus braunii* Kütz., *Coenococcus planctonicus* Korschik.
Cyanobacteria*	*Oscillatoria limnetica*, *Coelosphaerium kuetzingianum*, *Dactylococcopsis irregularis* G.M. Smith., *Microcystis aeruginosa*, *Aphanocapsa elachista* W. et G.S. West., *Gloeocapsa minuta* (Kiss.) Hollerb., *Merismopedia punctata* Meyen.
Chrysophyta	*Dinobryon divergens* Imhof., *Dinobryon sociale* (Ehr.) Ehr. var. *stipitatum (Stein)* Lemm., *Chrysococcus rufescens* Klebs., *Mallomonas tonsurata* Teil., *Mallomonas crassisquama* (Asmund.) Fott., *Mallomonas caudata* Iwan. Sensu Krieger, *Chrysopyxis ulna* Kütz.
Dinophyta	*Peridinium cinctum* (Müll.) Ehrb., *Glenodinium oculatum* Stein.
Cryptophyta	*Cryptomonas ovata* Ehr., *Rhodomonas lacustris* Pascher et Ruttner.
Euglenophyta	*Trachelomonas volvocina* Ehr., *Astasia dangeardii* Lemm.

Table 3. Number (thous. cells/l) of *β*-mesosaprobiont species in the central part of the Kondopoga Bay of Lake Onego. "–" – no data, "0" – species not found, * – according to Chekryzheva (2008), ** – according to Chekryzheva (2018).

Indicator species	CTF area		Pelagic area		
	2019	2021	1999	2019	2021
Aulacoseira islandica	463	288	143*	275	40
A. italica var. *tenuissima*	0	125	–	0	106
Melosira varians	246	188	–	0	63
Dinobryon divergens	6	50	10**	0	20
Mallomonas tonsurata	33	13	–	6	0
Aphanizomenon flos-aquae	46	25	15**	41	100
Microcystis aeruginosa	54	0	–	0	100
Chlamydomonas monadina Ehr.	25	13	32*	19	38
Planctococcus sphaerocystiformis Kors.	0	0	18*	0	0
Coenococcus planctonicus	21	63	–	194	0
Monoraphidium contortum (Thur.) Komárk.-Legn.	83	100	–	0	63
Trachelomonas volvocina	13	13	–	0	25
Cryptomonas spp.	4	13	15*	0	20

tified in the central part of the bay (Toxic cyanobacteria..., 2021). The average number of their cells amounted 1665 cells/ml that according to WHO classification did not pose a threat to life and health of humans or animals (Guidelines..., 2003). Representatives of other phytoplankton groups were found in small numbers**.**

In 2019 and 2021, a sharp rise in N_{tot} and B_{tot} occurred in the pelagic zone of the central part of the Kondopoga Bay along with a synchronous increase in biomass and number of golden algae and, especially, diatoms(Fig. 2**A**, **B**, **E**). The number and biomass of diatoms increased 8 times as compared to 1993–2017. In comparison with 1993–2017, a 4-fold rise in indicators of golden algae development was registered in 2019–2021 (Table 4).

An analysis of long-term dynamics of cyanobacteria and green algae showed the periodic "outbreaks" in their number after the year 2000, when trout farms appeared in the coastal zone (Fig. 2**C**, **D**). The gradual increase in number of algae of these groups was statistically significant. The Spearman's rank correlation coefficient between a green algae number and a year of research (1993−2021) made up 0.80 ($p < 0.05$, $n = 14$), whereas for cyanobacteria it was 0.79 ($p < 0.05$, $n = 14$). However, a small size and scale of such 'outbreaks' did not affect N_{tot} and B_{tot} of phytoplankton (Fig. 2**A**).

In total, 87 algae taxa identified to species and 4 taxa – to genus and belonging to 7 systematic divisions were found in the pelagic zone of the central part of the Kondopoga Bay: Bacillariophyta – 33 (36.3% of the total number of species), Chlorophyta – 28 (30.8%), Chrysophyta – 13 (14.3%), Cyanobacteria – 11 (12%), Euglenophyta – 2 (2.2%), Dinophyta – 2 (2.2%), Cryptophyta – 2 (2.2%). In terms of abundance, the dominant species during the study period were *Fragilaria crotonensis*, *Aulacoseira islandica*, *A. subarctica*, *Tabellaria fenestrata*, *Coenococcus planctonicus,* and by biomass – *Cyclotella meneghiniana* Kütz., *Aulacoseira islandica*, *Tabellaria fenestrata*, *Fragilaria crotonensis*. The main representatives of phytoplankton are shown in Table 5.

Indices H and E showed high species diversity and uniform distribution of species in number (3.94 ± 0.14 and 2.42 ± 0.08) and biomass (3.35 ± 0.33 and 2.04 ± 0.13, respectively). The taxonomic composition of phytoplankton in the pelagic zone of the Kondopoga Bay remained unchanged, as compared to the 2000s. (Chekryzheva, 2008).

Table 4. Statistical characteristics of phytoplankton divisions responsible for the increased number and biomass of the pelagic algocenosis of the Kondopoga Bay in 2019–2021. Me ± m – median and standard error; min and max – minimum and maximum indicators, N_{tot} and B_{tot} – total number (thous. cells/l) and biomass (mg/l) of phytoplankton, N and B – number and biomass of algae divisions. Calculated according to M.T. Syarki et al. (2015).

Algal division	Indicator	1993–2017		2019–2021	
		Me ± m	min/max	Me ± m	min/max
Total community	N_{tot}	592 ± 128.6	48/1360	3295 ± 1188	1366/6063
	B_{tot}	0.374 ± 0.04	0.026/0.926	1.993 ± 0.25	1.128/2.289
Bacillariophyta	N	254.5 ± 112.71	14/945	1991 ± 701.21	788/3813
	B	0.228 ± 0.09	0.012/0.522	1.772 ± 0.2	0.991/1.838
Chrysophyta	N	19 ± 4.34	3/44	75 ± 38.91	9/170
	B	0.011 ± 0.006	0.003/0.042	0.047 ± 0.033	0.009/0.151

β-Mesosaprobionts (42% of the total number of species), oligo-β-mesosaprobionts (20%), oligosaprobionts (16%) were the most numerous species, while β-α-mesosaprobionts (4.6%) and α-mesosaprobionts (2.3%) were rare.. In addition, in the pelagic zone of the central part of the bay and in sites of trout farms location we detected *α*-polysaprobionts *Chlorella vulgaris* and *Astasia dangeardii* (2.3%), *p*-polysaprobiont *Chlamydomonas incerta* (1.5%) – the indicator species of waters heavily polluted with organic matter. The average values of the saprobity index in August of 2019 (1.40) and 2021 (2.05) corresponded to the oligo-*β*-mesosaprobic zone.

To identify phytoplankton similarities or differences in sites of CTF location and in the pelagic part of the bay, we applied the Mann–Whitney test. The statistical analysis revealed no significant (p = 0.29) differences in phytoplankton number for these study areas. By structure, algae communities also was similar, as evidenced by the Sørensen similarity index (0.62). In the area of CTF, PPM and in the pelagic zone of the central part of the Kondopoga Bay, the dominant communities were represented by summer and spring-autumn diatom complexes, which accounted for 75 and 79% of the total number, respectively. In both study areas, a similar high proportion of cyanobacteria number (in sites of CTF and in the pelagic zone: 19% and 23%, respectively) and green algae (23% and 31%) was observed. In the phytoplankton community, the predominance of indicator species of the *β*-mesosaprobic zone was obvious; *Chlorella vulgaris*, *Astasia dangeardii*, *Chlamydomonas incerta* – indicators of waters heavily polluted with organic matter were present. The homogeneity of communities in these areas of the bay indicated similar conditions of their functioning, i.e. the significant influence of CTF.

The scale of the detected eutrophication in the Kondopoga Bay can be imagined if we take into account the huge water volume in the central part of the bay with depths up to 80 m (water volume – 4.3 km^3). The trophy level of this area is increasing, despite the supply of a large amount of clean water from the open reach of the lake (Lozovik et al., 2019). This is quite obvious since the current phosphorus load (wastewaters from PPM, CTF and river runoff) on the Kondopoga Bay is 2 times higher than maximum permissible load (Lozovik, 2015).

An increase in quantitative development of diatom plankton, which is a natural dominant of the community, was a clear sign of eutrophication in the pelagic zone of the central part of the Kondopoga Bay (Fig. 2**B**) (Lund, 1969; Trifonova, 1990; Trifonova and Afanasyeva, 2008). In summer of 2019 and 2021, there was a sharp increase in quantitative indicators both of summer (*Asterionella formosa*, *Tabellaria fenestrata*, *Fragilaria crotonensis*) and spring-autumn (*Aulacoseira islandica*, *A. subarctica*) dominant

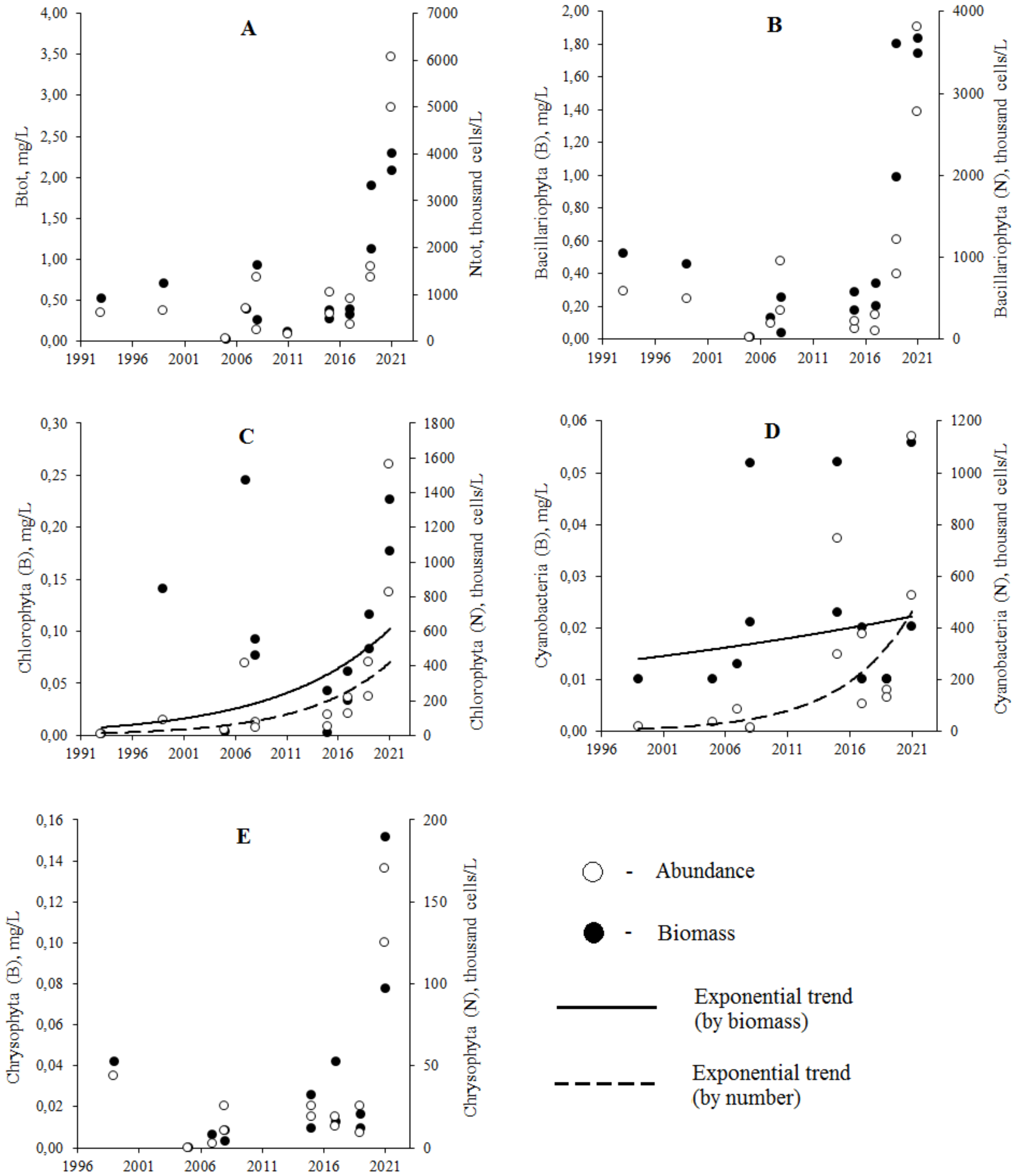

Fig. 2. Long-term dynamics in terms of number and biomass of phytoplankton in the pelagic zone of the central part of the Kondopoga Bay: **A** – the whole community, **B** – Bacillariophyta, **C** – Chlorophyta, **D** – Cyanobacteria, **E** – Chrysophyta. Data for 1993−2010 are presented from Syarki et al. (2015).

Table 5. The most common species of phytoplankton (except for dominant) in the pelagic zone of the central part of the Kondopoga Bay. * – subdominant species (more than 5% of the total number).

Division	Species
Bacillariophyta*	*Aulacoseira granulata* (Ehr.) Sim., *Melosira varians*, *Puncticulata bodanica* (Grun.) Håk.
Chlorophyta*	*Eudorina elegans*, *Chlorella vulgaris*, *Monoraphidium contortum*, *Dictyosphaerium ehrenbergianum* Näg., *Pediastrum boryanum* (Turp.) Menegh.
Cyanobacteria*	*Coelosphaerium kuetzingianum*, *Aphanocapsa elachista*, *Synechocystis aquatilis* Sauv., *Dolichospermum flos-aquae* (Bréb. ex Born. et Flah.) Wack., Hoffm. et Kom., *Aphanizomenon flos-aquae*, *Microcystis aeruginosa*, *Oscillatoria limnetica*
Chrysophyta	*Dinobryon divergens*, *D. suecicum* Lemm., *Chrysococcus rufescens*, *Mallomonas crassisquama*, *M. acaroides* Perty emend Fott.
Dinophyta	*Ceratium hirundinella* (O.F. Müll.) Schrank., *Glenodinium oculatum*
Cryptophyta	*Cryptomonas ovata*, *Rhodomonas lacustris*
Euglenophyta	*Trachelomonas volvocina*, *Astasia dangeardii*

complexes. This phenomenon is typical for large northern oligotrophic lakes with increasing phosphorus concentrations (Petrova, 1990). “Outbreaks” in number of dominant species reflect a disturbed stability of the community at initial stages of eutrophication (Fedorov, 1970).

The beginning of algocenosis restructuring in the pelagic zone of the central part of the Kondopoga Bay is manifested in the increased share of cyanobacteria and green algae (up to 23 and 31% of the total number, respectively). Because of a small size of cells, abundant (since the 2000s) small cyanobacteria (Fig. 2**D**) and green algae (Fig. 2**C)** did not affect the total biomass of phytoplankton. In summer of 2019 and 2021, cyanobacteria were represented mainly by *Aphanocapsa elachista*, *Coelosphaerium kuetzingianum*, *Synechocystis aquatilis*, *Aphanizomenon flos-aquae*, *Dolichospermum flos-aquae*, *Microcystis aeruginosa* with cells less than 70 μm^3. Green algae included mainly *Coenococcus planctonicus*, *Chlorella vulgaris*, *Eudorina elegans*, *Monoraphidium contortum*, *Pediastrum boryanum*, *Dictyosphaerium ehrenbergianum* with cells less than 150 μm^3. Meanwhile, an increase in the proportion of more efficiently assimilating phosphorus and more productive small-celled forms of algae contribute to boosting productivity of the entire community (Gutelmacher, 1986).

The increased number of large golden algae (*Mallomonas caudata, M. acaroides, M. crassisquama, M. tonsurata, Dinobryon divergens, D. sociale var. stipitatum*) with cell size up to 3000 μm^3 inevitably brings to increased biomass (Fig. 2**E**, Table 4). However, large golden algae can hardly serve as indicators of eutrophication. The matter is that some researchers are of opinion that these species are indicators of oligotrophy (Chekryzheva and Sharov, 2006). Other authors, on the contrary, believe that their increased number (especially the species of the genera *Mallomonas* and *Dinobryon)* is an indicator of water body eutrophication (Kristiansen, 1986; Nicholls, 1995).

By and large, rapid eutrophication in the central part of the Kondopoga Bay in recent years may be associated with a secondary phosphorus-related pollution. This is confirmed by extremely high concentrations of total phosphorus found in the bottom water layers (36–130 μg/l) as compared to the water column (26–43 μg/l) in sites of CTF location (Tekanova et al., 2019; Zobkov et. al., 2022).

Although the saprobity index in the deep-water pelagic zone of the Kondopoga Bay remained within the oligo-*β*-mesosaprobic zone (Chekryzheva, 2008), abundance of *β*-mesosaprobiont species (*Aulacoseira islandica*, *Melosira varians*, *Dinobryon divergens*, *Aphanizomenon flos-aquae*, *Monoraphidium contortum*, *Chlamydomonas monadina*) in the years 2019 and 2021 was higher than in the late 1900s (Table 3). This could evidence of water quality degradation. Moreover, high number and biomass of phytoplankton indicate the eutrophic status of the reservoir in the central part of the bay. It is worth noting that earlier studies always characterized the Kondopoga Bay ecosystem as mesotrophic (Chekryzheva, 2008).

Conclusion

In 2019 and 2021, phytoplankton-based bioindication allowed to detect the eutrophication zone in the coastal central part of the Kondopoga Bay of Lake Onego, the formation of which was associated with trout farms located here about 20 years. Here, phytoplankton development corresponded to meso-eutrophic type of water. At the predominance of diatom plankton, small-sized cyanobacteria and green algae were subdominant in number that is atypical for a cold-water deep northern lake. Potentially dangerous cyanobacteria *Microcystis aeruginosa*, *Aphanizomenon flos-aquae*, *Coelosphaerium kuetzingianum*, *Oscillatoria limnetica* were also discovered. In general, abundance of cyanobacteria did not threaten to humans and animals.

The eutrophication process has developed in the pelagic zone of the central part of the Kondopoga Bay as well. The analysis of the long-term data showed that in summer of 2019, 2021 there was a sharp increase in the development of the dominant diatom complex, being a sign of the initial stage of eutrophication. In addition, we noted an increase in number and biomass of cyanobacteria and green algae, which became subdominants in the community. In the pelagic zone of the Kondopoga Bay, the number of *β*-mesosaprobe species increased. The trophic level in the area of trout farms location became eutrophic. The rapid development of eutrophication processes in both areas under study was associated with exceeding maximum permissible phosphorus load on the bay.

Thus, the intensive development of algae in 2019 and 2021, as well as long-term changes of quantitative and qualitative indicators of phytoplankton in the central part of the Kondopoga Bay are evidenced of eutrophication caused by a significant supply of nutrients from CTF wastes. To prevent degradation of the Kondopoga Bay ecosystem, it is necessary to reduce anthropogenic loads from the trout farms.

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