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Data Article

A dataset on environmental DNA, bacterio-, phyto- and zooplankton from an emerging periglacial lagoon in Svalbard, Arctic

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ABSTRACT

Over the last few decades, climate change in Svalbard (European Arctic) has led to the emergence and growth of periglacial coastal lagoons in the place of retreating glaciers. In these emerging water bodies, new ecosystems are formed, consisting of elements presumably entering the lagoon from the melting glacier, the surrounding tundra water bodies and the coastal ocean. The data presented here were collected from an emerging lagoon in the western region of Spitsbergen, Svalbard, situated between the retreating Eidembreen Glacier and Eidembukta Bay in 2022–2023. The current size of the lagoon area is approximately 6 square kilometers. The sampling was carried out at 26 sites across various sections of the lagoon, spanning from close proximity to the glacier to the furthest point away. The dataset contains the results of bacterioplankton (total cell concentration and carbon biomass), phytoplankton (taxonomic composition, cell size for selected taxa, abundance, biomass and carbon biomass), zooplankton (taxonomic composition, abundance), and environmental DNA (eDNA) metabarcoding. The dataset will be utilized to provide a comprehensive description of the structure of the lagoon ecosystem. It will also facilitate a comparison of its various parts, which vary in terms of their age of

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origin, i.e., release from the glacier. Additionally, the dataset will aid in the understanding of the intricate interactions between the freshwater and marine elements of the ecosystem. It can be used for comparative analysis of biodiversity assessment using eDNA and traditional microscopy methods in the identification of phyto- and zooplankton. Furthermore, these data can be utilized for environmental monitoring, tracing the temporal shifts and conducting comparative analysis of periglacial lagoons that are emerging in various regions of Svalbard as a result of climate change.

Specifications Table

Subject	Marine Biology and Ecology, Biodiversity using microscopy and metabarcoding
Specific subject area	Biodiversity of an emerging Arctic ecosystem after glacier retreat
Type of data	Table (.xlsx format) for bacterio-, phyto- and zooplankton Table (.csv format) for eDNA Analyzed
Data collection	Sampling was carried out in August 2022 and August 2023 at 26 sampling sites distributed across the lagoon at different distance from the glacier. At 5 sites samples were collected above and below halocline. eDNA sampling was performed using the Zodiac type boat, plankton sampling – both from the boat and from the shore. We used a custom plankton sampler with a 5 µm pore size filter for eDNA collection. Bacterioplankton was collected using Ruttner sampler and analyzed with BD Accuri™C6 flow cytometer. For phyto- and zooplankton, Ruttner sampler and limnological Apstein-type net were used, respectively, followed by the methods of light microscopy.
Data source location	Data were collected in a lagoon located in western part of Spitsbergen, Svalbard, European Arctic within these coordinates: • Northernmost point: 78°24′19,1″N / 12°50′33,7″E • Easternmost point: 78°22′10,4″N / 12°55′44,8″E • Southernmost point: 78°21′13,1″N / 12°52′34,4″E • Westernmost point: 78°22′30,8″N / 12°45′26,8″E Data are stored at the Marine Research Institute, Klaipeda University (Klaipeda, Lithuania)
Data accessibility	Repository name: Mendeley data Data identification number for plankton: DOI: 10.17632/824yvn82b5.2 link for plankton data: https://data.mendeley.com/datasets/824yvn82b5/2 Data identification number for eDNA: doi: 10.17632/hnwmh8zkw4.1 link for eDNA data: https://data.mendeley.com/datasets/hnwmh8zkw4/1
Related research article	-

1. Value of the Data

- This dataset provides unique information on the species composition and abundance of phyto- and zooplankton in a newly formed periglacial lagoon in Svalbard, Arctic. The dataset includes also counts of total cell concentration and biomass of bacterioplankton, specifically the fraction of 0.2–1 µm.
- The dataset on plankton taxonomic composition obtained through traditional microscopic identification is complemented by 16S and 18S rRNA data from eDNA samples collected at the same sampling sites in the lagoon.

- The dataset is suitable for providing a thorough description of the biodiversity structure of the emerging lagoon ecosystem. It also allows for a comparison of the different parts of the lagoon, which vary in terms of their age of origin (release from the glacier) and the level of interaction between the freshwater from the melting glacier and the nearby tundra on one side, and the saltwater from the coastal ocean on another.
- The biological dataset can be combined with physical geography data (bathymetry and hydrology) collected in the lagoon at the same time [1] to provide a more complete understanding of the patterns of formation of the new ecosystem and the interactions of its individual parts.
- The data can be used for environmental monitoring and conducting comparative analysis of periglacial lagoons that are emerging in different regions of Svalbard due to climate change.

2. Background

It is crucial to establish characteristics that describe the current state of coastal ecosystems in the Arctic, particularly in areas where glaciers are melting and retreating. This understanding is essential for comprehending the processes occurring in the region due to global warming. As of now, there is a lack of available data on periglacial lagoons, despite the fact that there are already over one hundred of these lagoons on Svalbard [1]. Our investigations were performed in a lagoon next to Eidembukta Bay in West Spitsbergen, simultaneously with bathymetric and hydrological surveys [2]. This is a complex coastal water body that has formed in the place of the retreating glacier, Eidembreen. It is connected to the glacier and separated from the coastal ocean by a narrow gravel spit on the other side. The emerging ecosystem is a result of freshwater and coastal ocean interaction, characterized by presence of both limnic and marine elements. The data collected will provide a basis for future in-depth studies on the structure and functioning of coastal ecosystems, particularly those developing in the context of climate change.

3. Data Description

The dataset consists of five .xlsx files (Table 1).

4. Experimental Design, Materials and Methods

4.1. Environmental DNA sampling

A total of 14 samples (with 3 replication each) were collected at 8 sites in 2022. We used a custom plankton sampler for rapid in-water concentration of e-DNA on a 5 µm pore size nylon filter designed and manufactured by Sequench Ltd, Nelson, New Zealand. The sampler was made by adjusting in-water capture modified cod-end device, by attaching metal clamps to the inlet side for their fixing to a towing line [3]. This allowed the collection of waterborne e-DNA while towing the sampling device at three different water layers: surface, around halocline and near bottom in deep parts of the lagoon. The selection of a 5 µm pore size membrane was based on results reported by experimental study [4], which demonstrated effective capture of different fractions of eDNA material on coarser membranes, while allowing processing larger volumes of water and thus maximizing the efficiency of the rare taxa discovery. At the sampling stations, eDNA samplers were deployed simultaneously at different depths and towed horizontally for 5 min at 5 knots within an area of ca. 300 m^2. In shallow lagoon parts, e-DNA samples were collected by towing of the sampling device at the surface. Following each tow, filters were transferred into 2 mL vials containing RNA-Shield (Zymo, CA, USA) isolation buffer. All samples were

Table 1
Description of data files.

Name of the file	Content of the file	Comments/Abbreviations
Table_1_Sampling sites.xlsx	Sampling site, date of sampling, coordinates, labels for collected zooplankton, phytoplankton, bacterioplankton, and eDNA samples	• dec –decimal degrees of latitude and longitude; • Rep. – replicates
Table_2_Zooplankton.xlsx	1st sheet: List of taxa and their salinity range	
	2nd sheet: List of taxa, abundances of organisms in the samples for each taxon, for main groups (rotifers, crustaceans), and for zooplankton in total	• ind m^{-3} – individuals per cubic m
Table_3_Phytoplankton.xlsx	1st sheet: List of taxa and their salinity range	
	2nd sheet: List of taxa, abundances in the samples for each taxon, for main groups, and for phytoplankton in total;	• 10^3 units L^{-1} – one thousand of units per liter
	3rd sheet: List of taxa, biomass in the samples for each taxon respecting the cell size, for main groups, and for phytoplankton in total;	• mm^3 L^{-1} – cubic millimeters per liter
	4th sheet: List of taxa, carbon biomass in the samples for each taxon respecting the cell size, for main groups, and for phytoplankton in total	• mkg L^{-1} – micrograms per liter
Table_4_Bacterioplankton.xlsx	Bacteria concentration and bacteria carbon biomass in the samples for each observation (replica), and average values for each site with standard deviation	• cells · mL^{-1} – number of cells per milliliter • mkg · L^{-1} – micrograms per liter • SD – standard deviation
eDNA_sample_data.csv	Information about samples: amplicon Id, sample name, marker, sample depth, water layer, geographical coordinates	
eDNA_metabarcoding_data	eDNA sequencing reeds: each sample has two fastaq files, indicating forward (R1) and reverse (R2) reads.	

stored at −20 °C until further analyses. Between sampling stations, the samplers were decontaminated by soaking in 2 % bleach solution for 10 min and rinsing with coastal ocean water from the sampling site. For metabarcoding analysis of bacterial (16S rRNA) and eukaryotic (18S rRNA) markers, DNA from the filter samples was extracted, PCR amplified and sequenced on the Illumina's MiSeq platform, following the established protocols [3–5].

4.2. Bacterioplankton sampling

Sampling was carried out in 2023, both from the surface (0–5 m) and from different depth horizons. Water for analysis of heterotrophic bacteria was collected in sterile 1.5 mL cryotubes using Ruttner-type 2.0 L sampler. 14 sites were sampled, total number of samples was 42 (each site included three replicas). Glutaraldehyde was added to each sample with micropipette bringing its final concentration to 0.25 %. Samples were frozen at −80 °C [6] for later counts using a BD Accuri™C6 flow cytometer (BD Biosciences). The frozen samples were quickly thawed in a 30 °C water bath and pre-filtered through a 50 µm mesh. Heterotrophic bacteria samples were diluted with Milli-Q water, stained with SYBR Green I (Invitrogen) to a final concentration of 1: 10,000 [6] and kept in the dark at room temperature for 15 min. 1µm microspheres (Fluoresbrite

plain YG, Polysciences) were added to each sample as internal standard, and analyses were run at a medium flow rate of 35 µl min^{-1} with an acquisition time of 2 min. A factor of 20 fg C per cell was used to convert bacteria counts to carbon biomass [7].

4.3. Phytoplankton sampling

A total of 26 samples were collected at 22 sites (12 and 14 in 2022 and 2023, respectively), mostly from the surface (0–1 m), with few samples from deeper horizons. For each sample approximately 300 mL of water was collected in 0.5-l plastic containers using Ruttner-type 2.0 L single water sampler. Phytoplankton samples were fixed with acetic Lugol's solution (0.5 mL solution per 100 mL sample), species identification and abundance counting were carried out using an inverted microscope (OLYMPUS IX51, magnification 100× and 400×) following the standards [8–11]. During the counting process, the species (cells or counting units) were categorized into size classes for further determination of cell volume according to the scheme of [12] and its updated appendix [13]. Biovolume of phytoplankton cells was determined using formulas for geometric figures specific to each species [10,12], and cell carbon content was calculated according to [14].

4.4. Zooplankton sampling

In total, 33 zooplankton samples were collected at 25 sites, 13 in 2022, and 20 in 2023. Sampling was carried out at the surface of the lagoon in shallow areas, while in deeper parts (> 20 m depth) samples were collected separately in different water layers, including the freshwater surface layer and the saline water below the halocline, using a limnological Apstein-type plankton net (55 µm of mesh size). For layered sampling, a simple mechanism was used that closed the net at a given depth horizon, thereby preventing water filtration and the entry of organisms from the upper layers when the net was raised. All samples were fixed with 4 % formalin and stored in ambient and then room temperature. The samples were processed using binocular microscope Olympus SZ61 with magnification x6.7–45 for identification of main groups and counting. Selected animals were isolated and placed on slides for taxonomic identification under magnification x200–400 using light inverted microscope Nikon Eclipse Ts2R. In parallel, we used microphotography (Nikon DS-Ri2 digital camera and NIS Elements BR analysis 5.10.00 software) for measuring the sizes of the organisms and their body parts.

Limitations

Sampling was performed in summer months, July 2022 and August 2023, representing only one season in the lagoon.

Ethics Statement

The authors have read and follow the ethical requirements for publication in Data in Brief and confirming that the current work does not involve human subjects, animal experiments, or any data collected from social media platforms.

Credit Author Statement

Sergej Olenin: Supervision, Conceptualization, Resources, Assistance in the field studies, Writing – original draft, review & editing. **Dzmitry Lukashanets:** Methodology, Surveys in the la-

goon, Data curation, Writing – review & editing. **Anastasija Zaiko:** Conceptualization, Resources, Processing eDNA samples, Bioinformatics, Data curation, Writing – review & editing. **Aurelija Samuilovienė:** Resources, Processing eDNA samples, Data curation, Writing – review & editing. **Irina Olenina:** Resources, Processing phytoplankton samples, Writing – review & editing. **Evelina Grinienė:** Resources, Processing bacterioplankton samples, Writing – review & editing. **Tobia Politi:** Resources, Surveys in the lagoon, Writing – review & editing. **Aleksej Šaškov:** Surveys in the lagoon, Writing – review & editing. **Greta Kilmonaitė:** Surveys in the lagoon, Data curation, Writing – review & editing. **Andrius Šiaulys:** Conceptualization, Surveys in the lagoon, Data curation, Writing – review & editing.

Data Availability

A dataset on bacterio-, phyto- and zooplankton from an emerging periglacial lagoon in Svalbard, Arctic (Original data) (Mendeley Data).
A dataset on environmental DNA from an emerging periglacial lagoon in Svalbard, Arctic (Original data) (Mendeley Data).

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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