



Article Soil Bacterial and Archaeal Communities of the Periodic Flooding Zone of Three Main Reservoirs in the South Ural Region (Russia)

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Abstract: Studying the soils in the periodical flood zone of three reservoirs is of promising importance for their subsequent return to economic activities. Research on the bacterial and archaeal communities of soils that are periodically or continuously flooded by reservoirs is still insufficient. To evaluate the chemical status of soils and their microbiota, the study was conducted in the Yumaguzino, Nugush, and Slak reservoir sites in the South Ural area (Russian Federation). The bacterial and archaeal communities of periodically flooded and non-flooded soils were investigated after a comparative investigation of chemical, hydrological, and climatic factors. It was discovered that flooded soils had anoxic conditions during the whole of the year, with brief drying intervals of limited length and low levels of effective temperatures. In terms of chemistry, flooded soils are distinguished by increased acidity, a fall in organic matter, and an increase in alkali-hydrolysable nitrogen. Compared to their counterparts in non-flooded soils, bacterial and archaeal communities in flooded soils are significantly different. Generally speaking, the biodiversity of flooded soils rises with the duration and depth of floods. Significant variations at the phylum level are mostly caused by a decline in the relative presence of Thaumarchaeota and an increase in Proteobacteria and Chloroflexi representation. It was discovered that the Euryarchaeota phylum was either absent or had a significantly decreased relative prevalence at the sites of intermittently flooding soils.

Keywords: water reservoir; flooded soil; soil properties; DNA sequencing; microbial communities

1. Introduction

Building reservoirs, which are artificial (or human-made) lakes in which water is collected and stored in sufficient quantities for usage [1], leads to long-term land disposal. At the same time, the ground cover inside the area covered by the reservoir bed during the building process is not removed and stays under the water seasonally at levels between the normal and dead volume levels or permanently, during the entire operating period,



Citation: Minnegaliev, A.; Abakumov, E.; Suleymanov, R.; Zaitsev, G.; Davydychev, A.; Dorogaya, E.; Zverev, A.; Andronov, E.; Asylbaev, I. Soil Bacterial and Archaeal Communities of the Periodic Flooding Zone of Three Main Reservoirs in the South Ural Region (Russia). *Ecologies* **2024**, *5*, 233–247. https://doi.org/10.3390/ ecologies5020015

Academic Editors: Alan Christian and Hidetoshi Urakawa

Received: 31 January 2024 Revised: 8 April 2024 Accepted: 12 April 2024 Published: 16 April 2024



Copyright: © 2024 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). at levels lower than the dead volume. In flooded water reservoir areas, while retaining the morphological profile of the soil under the reservoir drawdown area [2], silt sediment accumulation [3], and partial or total destruction of the soil profile in the littoral zone (at the development sites of wave extraction activities), specific soil hydromorphic processes are developing.

The soils drowned in water reservoirs are influenced by various processes affecting soil qualitative characteristics. Continuous [2] or seasonal [4] flooding adds to anoxic soil conditions. By accumulating sediments made up of native materials, particularly aquatic creature remnants [5], agricultural soil erosion products [6,7], and soil erosion products from banks and reservoir beds [8], new soil horizons are created. Furthermore, in the littoral zone, the upper horizons of flooded soils are destroyed or partially degraded. Flooded soils cause soil hydromorphic processes to develop or intensify, most notably gleyification and the creation of iron and/or iron-manganese concretions. Changes also occur in the transfer, accumulation, and transformation of major nutrients: nitrogen [9,10], phosphorus [11–13] and organic matter [5]. All these variables might have an impact on soil bacterial and archaeal communities, but the dearth of published research makes it impossible to evaluate these changes for soils in reservoir flood zones. Based on the examination of soils in comparable environments, only a few hypotheses can be made concerning the processes occurring here. Soil from paddy fields [14] and floodplains [15–17], which are well studied in microbiological terms and are also subject to flooding and freshwater drainage processes, is the closest to the flooded soils of water reservoirs.

The goal of this research is to comprehend how the bacterial and archaeal communities in soil have changed over time in regions that have experienced recurrent flooding. Furthermore, the goal was to assess the relationship between the chemical properties and the composition of the microbial community in order to ascertain the fluctuations in the periodic flooding process. We believed that the bacterial and archaeal communities in the soil were greatly impacted by recurrent floods, and that the microbial communities in the submerged reservoir bed would differ greatly from those in the surrounding background land plots.

2. Materials and Methods

2.1. Site Description

The study was conducted in the western part of the Republic of Bashkortostan (South Urals region, Russia) (Figure 1). The search focused on three water reservoirs: Yumaguzino, Nugush and Slak.

The Belaya River's Yumaguzino Reservoir (Site 1) is the newest of all the surveys; filling was finished in 2004 [18]. With 456 million cubic meters of reservoir capacity at full capacity, this reservoir is sizable. There are just a few shallow water locations that are suitable for investigation due to the ridges and low ridges topography of the Belaya River's regulated part of the reservoir. The reservoir's river valley is somewhat limited, with the majority of its bottom confined to a remote area that was home to hamlets and tiny settlements prior to inundation. Soil hydromorphism is less evident outside of the trapezoidal valleys, noticeable banks of abrasive type have formed, and destruction and flushing are more common. Because of this, the location with soil hydromorphic conditions that is closest to the Yumaguzino hydroelectric dam—which is located 16 km upstream—is selected. The site, which has an approximate area of 1 km², is situated on the lower left slope of the Belaya River valley. The area is level and slopes up to 10 degrees toward the river from the east to the location next to a stream bed that has been flooded. There, samples 1 and 2 were gathered.



Figure 1. Work areas (**a**,**b**) and location of sample plots (**c**). Site locations: I—The Yumaguzino Reservoir; II—The Nugush Reservoir; III—The Slak Reservoir. 1–6—Sampling point locations: 1, 3, 5—flooded locations; 2, 4, 6—non-flooded locations.

Sample "Yumaguzino Reservoir flooded" was taken from the center of the drained bed outside the outer boundary of the shoreline processing development zone by wind-generated waves. The water table lies at a depth of 30 cm above the surface. The absolute height mark in the area of sample 1 is 249.45 m (Baltic Normal Height System). At the time of sampling (19 November 2020), the lodge was partly drained and occupied by old tree stumps and snags, and no vegetation was present. Sample: dark gray, almost black, crumbling sandy lumpy wet, partially freezing.

Sample "Yumaguzino Reservoir non-flooded" was collected 10 m from the shoreline outside the flood zone. A medium density hardwood forest represents the vegetation with a developing understory and pronounced ground litter. The absolute height in sample 2 is 262.30 m. Sample: dark grey, transitional to black, fine-grained dry, well-structured heavy loam. It contains many plant roots.

The Nugush Reservoir (**Site 2**) was created on the Nugush River in the foothills of the South Urals. The reservoir was filled in 1967 to a total volume of 400 million cubic meters. The shape of the reservoir bed is a kettle, so inside its boundaries, great shoals are formed. The calculated surface area of shoals, based on topographical maps, is 1.1 km², the territory with partial release of water from the reservoir increasing to 5.3 km² or 21% of the total surface area of the reservoir mirror. Within the reservoir bed, three separate large shoals are formed, and the closest shoal to the dam was surveyed by us. The 0.9 km² study area is situated in the lower left of the Nugush River valley. Smooth relief characterizes the site with an overall gradient of approximately 3° towards the Nugush River. A flooded stream runs through the central portion of the site. Here, samples 3 and 4 were collected.

Sample "Nugush Reservoir flooded" was collected from the central part of the drained area outside the shoreline. The water table lies at a depth of 20 cm. The absolute height inside the sampling point is 212.35 m. During sampling (15 November 2020), the reservoir bed at the site was dry, without vegetation. Sample: dark grey, almost black, crumpled heavy loamy, lumpy wet, partially freezing.

Sample "Nugush Reservoir non-flooded" was collected 15 m from the shoreline outside the flood zone. Grassy-type vegetation with overpasture digression is seen. The absolute height of the sampling area is 218.13 m. Sample: dark grey granular dry, well-structured heavy loamy with numerous inclusions of plant roots.

The Slak Reservoir (**Site 3**) is situated on the Kursak River, the second-order left tributary to the Belaya River. The reservoir was commissioned in 1988. The reservoir is of the flat type and situated in the southern part of the Bugulma-Belebey Upland. The reservoir is an average medium-sized type with a total volume of 8.4 million cubic meters. The study area coincides with the Kursak River's left floodplain and the terrace above the floodplain. The shoal being studied covers an area of 0.19 km² and has a generally smooth topography with a 2° gradient towards the Kursak River bed. Samples 5 and 6 were collected from this location.

Sample "Slak Reservoir flooded" was collected from the center of the drained area off the coastline. The absolute height within the sampling site was 167.80 m. At the time of the investigation (10 July 2021), the reservoir bed inside the sampling area was dry. Reed stands (*Phragmites australis*), which provided 80% projective coverage of the sampling area, served as the vegetative representation. Sample: dark grey, almost black, dusty wet, loosely structured loamy with numerous inclusions of plant roots.

Sample "Slak Reservoir non-flooded" was collected outside the flood zone, 20 m from the shoreline. Vegetation within the sampling area is grassland with partial grazing digression. The sampling point's elevation in absolute terms was 169.55 m. Sample: dark grey, granular dry, well-structured heavy loamy with numerous inclusions of plant roots.

2.2. Sample Procedure and Soil Analysis

The topsoil horizon was sampled with samples measuring 1.5 kg apiece (0–20 cm). An additional soil sample was acquired from a neighboring location that had not been flooded. These locations (free of floods) were chosen with the intention of reducing any potential wave effects. All samples were collected in three replicates at each location for basic chemical analyses and in five replications for DNA extraction and further microbiological research.

Chemical analyses were carried out using conventional methods in the fine earth [19–21]. Under laboratory conditions, soil acidity (pHKCl and pH₂O), soil organic carbon (SOC) content, total and mobile phosphorous content, mobile potassium content, nitrogen alkaline hydrolysable content, and iron oxide mobile quantity were determined. The SOC was determined with use of CHN analyzer of the Scientific Park of Saint-Petersburg State University. This method was chosen specially instead of dichromate oxidation method, because the dry combustion approach is more precise for bottom sediments and soil-like bodies [22]. The pH values were determined with the use of pH meter pH-150M with a liquid–soil ratio of 1:2.5. Mobile forms of N, P and Fe content have been evaluated with classical photometry, while the mobile K content was determined by flame photometry. All these elements were determined in the Laboratory of Soil Science at Ufa Institute of Biology.

2.3. Water-Level Data and Meteorological Searches

Water reservoir fill levels were based on daily inspections of water levels at hydropower complexes. The absolute heights of sampling locations were calculated using geodetic data and compared with data from Google Maps. Data from the closest meteorological stations helped identify the climatic conditions of the sampling areas. The calculated effective temperatures were the total effective temperatures above 5 °C that occurred during the time the researched regions were not submerged by the reservoir. A brief stretch of springtime with air temperatures above 5 $^{\circ}$ C was marked; however, this was not considered when calculating the effective temperatures. This is because, during all these periods, the soils studied were covered in snow and were frozen.

Ongoing monitoring of the thermal regime of the water is performed continuously solely within the Nugush reservoir. We considered that the data supplied could be extrapolated for the Yumaguzino and Slak reservoirs given the unavailability of thermal regime information for these reservoirs.

2.4. DNA Analysis

The subsamples for microbiological analysis were stored in double sterile plastic bags, frozen and delivered immediately to the laboratory. The samples were mechanically disaggregated using a Precellys 24 homogenizer (Bertin Technologies, Montigny-le-Bretonneuxc, France). Following the manufacturer's instructions, total DNA was extracted from 0.5 g of soil using the FastDNA Spin Kit (MP Biomedicals, Santa Ana, CA, USA). Electrophoresis in $0.5 \times TAE$ buffer on 1% agarose was used to check the quality and purity of the extracted DNA. Sequencing was performed on the Illumina MiSEQ sequencer (Illumina, San Diego, CA, USA) using the F515 (GTGCCAGCMGCCGCGGCGGTAA) and R806 (GGAC-TACVSGGGTATCTAAT) primers [23], targeting the variable region V4 of bacterial and archaeal 16S rRNA genes. Processing of sequences was performed using R (v3.6.3) and packages dada2 (v1.14.1) and phyloseq (v1.30.0). The main steps were (i) quality filtering and trimming (truncLen 200/180, maxEE 2/5 for forvard/reverse reads respectively, maxN 0, PhiX reads removed); (ii) amplicon sequence variants (ASVs) calling; (iii) bimera removing (using consensus method). Taxonomic annotation was performed using a built-in dada2 realization of a naïve Bayesian classifier [24] with default parameters (k-mer size 8, minimum bootstrap confidence 50 from total 100 bootstrap replicates). The SILVA reference dataset (version 132, November 2020) [25] was used as a training set. All unclassified at Phyla level ASVs were removed.

Microbiological diversity was investigated through several diversity indices. Alphadiversity was estimated using taxa richness (Observed ASVs index: reveals the number of procaryotic ASVs) and evenness (Simpson's index: reveals the probability that two randomly selected reads belong to the same ASV). Indices were calculated using phyloseq package, formulas are available in a review [26]. Beta-diversity was investigated using PCoA ordination of Bray–Curtiss dissimilarity (reveals distance between samples through the differences in abundances of every ASV). Calculation and ordination were performed in phyloseq package, the diversity index is described in the original source [27].

3. Results

The chemical characteristics of the sites being studied are shown in Table 1. The soils of the study locations have a medium availability of organic carbon. The organic carbon content of the soil in the non-flooded areas of the Nugush and Slak reservoirs is slightly greater than that of the flooded soils. In contrast, the Yumaguzino Reservoir's non-flooded parts have an organic carbon concentration that is less than half that of the flooded areas. With the exception of the Yumaguzino Reservoir's non-flooded locations, which have highly acidic soil, the examined sites' soils have an acidity that is comparable to that of the neutral. All reservoir flooded soils have more iron (III) oxide (Fe_2O_3) than their non-flooded counterparts. For hydrologically disturbed soils, a rise in iron oxide concentration is typical [28–30].

For all reservoirs, the total phosphorous content was greater at the non-flooded locations compared to the flooded ones. Mobile phosphorus levels vary considerably for the non-flooded soils of reservoirs. The quantity of mobile phosphorus in non-flooded parts of the Nugush and Slak reservoirs is characterized to have very low availability and is lower than that in the sites being flooded. Areas of the Yumaguzino Reservoir that are not flooded are characterized by an average availability of mobile phosphorus, and its contents are superior to those of flooded areas.

	Sites							
Indicator	Yumaguzino Reservoir		Nugush Reservoir		Slak Reservoir			
	Non-Flooded	Flooded	Non-Flooded	Flooded	Non-Flooded	Flooded		
Total phosphorous, mg/kg	135 ± 7.0	152 ± 9.0	123 ± 7.0	135 ± 6.0	175 ± 8.0	210 ± 9.0		
Mobile phosphorous, mg/100 g of soils	1.35 ± 0.04	2.23 ± 0.04	1.33 ± 0.03	0.43 ± 0.02	1.58 ± 0.04	0.97 ± 0.03		
Nitrogen alkaline hydrolysable, mg/kg	210 ± 18.0	392 ± 27.0	266 ± 21.0	280 ± 24.0	262 ± 23.0	270 ± 21.0		
Soil organic carbon, %	2.66 ± 0.4	5.59 ± 0.5	5.55 ± 0.6	5.05 ± 0.4	5.58 ± 0.6	5.34 ± 0.4		
pH (KCl)	4.5 ± 0.2	5.6 ± 0.2	5.3 ± 0.1	5.6 ± 0.2	6.1 ± 0.3	6.3 ± 0.2		
рН (H ₂ O)	5.9 ± 0.2	6.4 ± 0.3	6.1 ± 0.3	6.4 ± 0.3	6.8 ± 0.3	6.9 ± 0.3		
Mobile potassium, mg/kg	116 ± 6.1	195 ± 6.9	106 ± 5.2	92 ± 5.3	154 ± 5.8	138 ± 4.9		
Fe ₂ O ₃ , %	0.72 ± 0.08	0.68 ± 0.09	1.15 ± 0.07	0.91 ± 0.09	3.11 ± 0.08	2.85 ± 0.08		

Table 1. Chemical characteristics of soils in flooded and non-flooded areas of the Yumaguzino, Nugush, and Slak reservoirs (South Urals region, Russia) (Means \pm SEM (n = 3)).

With a maximum of 392 mg/kg of soil, the potential nitrogen availability of soil (nitrogen alkaline hydrolysable content) for all plots under study is described as high. In every case, the non-flooded plots also had higher nitrogen contents. This might be because of the high mobility of nitrogenous compounds, which make them simple to remove from the soil layer, as well as the suppression of nitrification in an anoxic environment.

Except for the locations of the Nugush Reservoir, where a low potassium concentration was discovered, the soils are characterized by medium availability based on the con-tent of mobile potassium. Mobile potassium levels in non-flooded sites compared to flooded areas were higher only within the Yumaguzino Reservoir.

Our data are very different from those obtained for the largest artificial lake Poyang, located in China, where natural cycles of mineral nutrients have been completely replaced by anthropogenic ones. This is due to the colossal chemical pressure of the surrounding ecosystems and the long history of the lake's development. The reservoirs in our study are much less chemically pressurized and younger [31].

With the exception of the organic matter content, which was lower than the regional average for soils at all of the research locations, the chemical characteristics of both flooded and non-flooded soils were generally similar to those of the study region [32].

The examined reservoirs' flooded soils are mostly in a dry state (i.e., under oxic conditions) in the fall and winter. This is a result of the features of reservoir drawdown in the examined reservoirs, which are filled in the spring, typically in late March to early June, and are used until March of the following year. The process of lowering reservoir levels through water uptake for water management purposes is accelerated by evaporation from the water surface but is partially mitigated during summer and autumn rainfall. The maximum fill level of the reservoir affects how quickly the sites dry out (the lower the level, the quicker the sites are cleared of water), which results in the soil. The maximum flood level for the areas studied inside the Yumaguzino Reservoir is 10.55 m, the Nugush Reservoir is 4.65 m, and the Slak Reservoir is 0.20 m. The Slak Reservoir is therefore found to have the most favorable conditions (by the sum of effective temperatures) at the time when soils are in the dry state (not flooded) (Table 2).

Alpha diversity analysis showed a more reliable variety of flooded soils across all sites considered (Figure 2). Both indices under consideration have a similar relationship (Simpson and Observed ASVs).

Table 2. Sum of effective air temperatures (above 5 °C) throughout the drying time and the length of the drying period up to the temperature transition date of 5 °C (2009–2020) for the Yumaguzino, Nugush, and Slak reservoirs (South Urals region, Russia).

Sites	Sum of Effective Air Temperatures, $^{\circ}C$			Length of the Drying Period, Days		
	Min	Mean	Max	Min	Mean	Max
Yumaguzino Reservoir	0 (100%)	-	-	-	0 (100%)	-
Nugush Reservoir	0 (37.5%)	54.0	309.5	0 (37.5%)	6.4	33
Slak Reservoir	67.8	623.6	1598.6	6.0	51.8	100



Alpha-diversity Indices

Figure 2. Observed ASVs and Simpson alpha diversity indices for microbial communities in flooded and non-flooded areas of the Yumaguzino, Nugush, and Slak reservoirs (South Urals region, Russia).

Beta diversity distinguishes Slack samples within a distinct cluster: the bacterial and archaeal communities of flooded and non-flooded soils is very similar here and at the same time is isolated from soil samples from Yumaguzino and Nugush (Figure 3). The difference between flooded and non-flooded areas in the phylum is determined by the various proportions of *Thaumarchaeota* (higher share in non-flooded soils), *Proteobacteria* and *Chloroflexi* (higher share in flooded soils).

Similar patterns were found in the soils of the Yumaguzino and Nugush reservoirs. Communities of non-flooded soil form a separate cluster, whereas communities of flooded soil form another cluster in these areas. Both clusters had a comparable taxonomic composition at the phylum level (Figure 4). These reservoirs' non-flooded soils are distinguished by a significant portion of *Thaumarchaeota*, *Proteobacteria*, and *Actinobacteria*, but the flooded soils are characterized by an increasing portion of *Firmicutes* and *Chloroflexi*. Similar variations at a taxonomic level as high as phylum are probably caused by the prevalence of spore-forming bacteria (*Firmcutes*) and phototrophs (*Chloroflexi*) in flooded soils.







Figure 4. Phylum-level (n = 14 plus ">0.02 abundance") taxonomic structure of samples in flooded and non-flooded areas of the Yumaguzino, Nugush, and Slak reservoirs (South Urals region, Russia).

Based on a correlation analysis, the link between the chemical properties of the soil and the taxonomic structure of the bacterial and archaeal communities has been evaluated (Figure 5). According to the findings of the analysis, there is a strong, multidirectional relationship between each phylum and the soil's characteristics. The strongest correlation was discovered for pH, where *Bacteriodetes* and *Patescibacteria* showed a high negative correlation while *Actinobacteria* showed a positive correlation. The SOC content, on the other hand, is characterized by lower correlation values; for the *Patescibacteria* phylum, there is a strong negative connection with SOC, while for the *Bacteriodetes* and *Nitrospirae*, there is an average negative correlation. Alkaline-hydrolyzed nitrogen has a negative correlation with *Cloroflexi* and *Firmicutes* and a high correlation with the proportional prevalence of *Rokubacteria, Thaumarchaeota,* and *Verrucomicrobia*. Furthermore, there are significant positive correlations between the prevalence of the phylums *Actinobacteria, Euryachaeota,* and *Gemmatimonadetes* and the Fe₂O₃ level. There is less of a correlation between relative phylum representations, mobile potassium, and mobile phosphorus.



Figure 5. Correlation matrix between the relative representations of the bacterial and archaeal populations (n = 14 plus ">0.02 abundance", top 1000 most abundant taxa were used) and the primary chemical properties of the soil. Furthermore, a connection is provided for each sampling point's relative phylum representations and the length of drying period. TP—total phosphorus, MP—mobile phosphorus, NAH—nitrogen alkaline hydrolysable, MPT—mobile potassium, LDP—length of drying period.

Furthermore, the correlation between the taxonomic structure and the length of drying period (LDP) was evaluated. Despite the fact that LDP is not a direct indicator of nutritional content, there are significant positive correlations between it and the relative abundance of *Proteobacteria, Gemmatimataeota,* and *Euryachaeota.* Regarding the relative representation of *Planctomycetes,* a substantial negative LDP association has been found.

4. Discussion

Flooded soils have different chemical properties than their non-flooded counterparts. The chemical features of the zone soils in the area are similar to those of the non-flooded areas' soils, which have a neutral reaction, a high availability of alkaline hydrolysable nitrogen, and an average level of organic carbon. Soils at flood sites are characterized by nutrient accumulation and increased acidity.

The assumption of a major effect of site flooding on bacterial and archaeal communities is validated, as evidenced by a comparison of the diversity indices of the analyzed sites. All periodically flooded locations have greater levels of alpha diversity in their communities, and the difference becomes more noticeable the longer the time of flooding. The Yumaguzino Reservoir exhibits the largest variances since it is not drained during the warm season because of its morphometric features and the relief's mountainous nature. The Slak Reservoir's flooded sites, which have an average long-term drying time of 51 days, are the ones closest to the non-flooded area, according to the alpha diversity index.

Because of the limited investigation of the microbial communities of the examined items, soil from paddy fields, wetlands, and river floodplains were used as analogues. Through comparison with these locations, we discovered several other variables that can influence the bacterial populations in flooded soils, such as the risk of contamination from heavy metals and petroleum products.

Pollution can affect bacterial and archaeal populations by interacting with flooded soils and melting surface waters. Studies have demonstrated that frequent floods can lead to significant soil pollution [33] and negatively impact plant populations [34]. Nonetheless, the research sites are situated in regions with low background concentrations of heavy metals and minimal anthropogenic load. The basins of the Yumaguzino and Nugush reservoirs are located inside a poorly reclaimed mountain-forest zone. The Slak Reservoir's water collecting region is located in the steppe zone, which has a human effect on the territory due to agriculture. Major sources of pollution (industrial plants, urban agglomerations, etc.) are not present in any of the three reservoirs. Therefore, while evaluating the variations in microbial communities, the pollution effect was disregarded.

Many studies have been conducted on the effects of vegetation on microbe and archaea communities in analogue settings, particularly flooded agricultural fields situated in flood plains. Even brief flooding may result in dramatic changes in the bacterial biota of the rhizosphere [35]. Moreover, vegetation does not reduce soil communities' sensitivity to flooding [36]. Possible contributing factors include the vegetation at the Slak Reservoir site. In sites with a high diversity of plant functional groups, there is a drop in microbial biomass because of increasing oxygen restriction, which has more substantial effects on soil processes [37]. Sites 1 and 2's flooded regions include high aquatic vegetation and a rare juvenile willow, which are representative of the shallow area flora. However, there was no vegetation at the sample locations at sites 1 and 2. Therefore, for sites 1 and 2, there is no evidence of the rhizosphere effect on the soil microbiome, whereas additional research is needed for site 3.

We do not have direct measurement of microbial taxonomy of waters in our plots. Thus, we can only compare these data with those of other research. It has been shown that pH does not seriously affect the microbial composition of Baikal waters and adjacent rivers, while the dissolved organic carbon demonstrated more pronounced effect on the alpha diversity of the microbial community [38]. This research also demonstrates the dominance Proteobacteria, Actinobacteria, Bacteroidetes, Cyanobacteria, and *Verrucomicrobia* predominated in the estuaries and estuarine waters of the rivers. It seems that the number of OTUs and alpha diversity of micro-organisms is more changeable in water flows and reservoirs than in bottom sediment, as it was shown for Mongolia [39]. The data obtained by us can be useful for organizing monitoring of changes in microbiome composition under the influence of external pollution, as it was performed by colleagues in Baikal [40]. It seems that comparison of water and bottom soils hardly makes sense, since, as microbiological studies of Baikal waters have shown, the microbiome of different layers of the water column

and in different periods of time is extremely variable [41]. Moreover, the composition of the water microbiome can vary significantly between day and night as has been shown in a meromictic soda lake [42]. Due to this dynamic nature of the water microbiome, the design of our experiment based on comparing more stable mineral soils with each other is reasonable.

We observed that the relative abundance of the *Euryarchaeota* phylum was significantly reduced in the flooded soils of the Nugush and Yumaguzino reservoirs. This group of *Archaea* contains numerous methanogens and nitrificators, including anaerobes [43,44]. The change in the relative representation of this group is related to the flooding of sampling points, which may be caused by both changes in soil aeration during flooding and the quantity of ammonium available during seasonal changes in the hydrological regime. On the flooded soils of the Slak Reservoir, there are just a few *Euryarchaeota* species, according to an analysis of phylum relative abundance. Samples from this site were collected during the summer flood season, when the water cover was approximately 20 to 30 cm thick above ground level. Since *Euryarchaeota* representatives are a sign of flooding and the average no-flooding time for the Slack Reservoir site is the longest of all those analyzed, we assume that drainage has a negative impact on their population. Following floods, their population recovers by moving from the locations of the remaining submerged and deep-lying soil strata.

The high transformation or humification rate in the areas of the Nugush and Yumaguzino reservoirs explains the existence of the *Rokubacteria* phylum, which inhabits peat swamp environments [45]. Swampy meadows or wet deciduous woods with debris layers are typical examples of the coastal vegetation found at these locations. These locations have also been identified to have the phylum *Patescibacteria*. *Patescibacteria* are small, slow-moving micro-organisms that thrive in low oxygen environments and the absence of sunlight, such as aquifers, lake waters, and sediments [46,47]. The brief period and shallow depth of the flooding can be directly attributed to the total absence of *Patescibacteria* in samples from the Slack Reservoir sites.

All identified archaeal ammonia oxidizers and species whose metabolism has not been thoroughly explored are members of the *Thaumarchaeota* phylum [48]. *Thaumarchaeota* has a reverse correlation with soil organic matter that inhibits ammonia oxidation [49]. The relative contribution of *Thaumarchaeota* in our situation is dictated by the nitrogen concentration and acidity of the soil because both non-flooded and flooded soils have significant levels of organic material.

A notable increase in the relative proportion of *Firmicutes* is a defining trait of the microbiome of all analyzed flood locations. *Firmicutes* are characterized by the formation of endospores, which remain viable for an extended period [50]. The growth of this phylum that we discovered conforms to the findings of earlier research [51], which demonstrated that *Firmicutes* had a greater relative presence in paddy soils.

The nature of the effect of floods on the soil ecosystems of bacteria and archaea cannot be conclusively determined by analyzing published research. Individual investigations have revealed that flooding causes notable changes in microbial activity [17] and the structure of the soil bacterial community [52], including modelling of flooded soils and river water. Nonetheless, there is evidence that the following flooding, microbial community numbers revert to their initial condition in both flood and biosolids application trials [53]. Bacterial communities are also quite stable and recovering from brief floods, according to model tests conducted on organic soil [54]. Research conducted on paddy soils subjected to prolonged recurrent flooding revealed notable alterations in the composition of microbial communities [55]. Our findings also reveal a statistically significant change in the organization of soil bacteria and archaea communities at reservoir locations following recurrent flood and drainage operations.

5. Conclusions

Flooded soils were quite different from non-flooded soils in terms of key chemical indexes. Comparing the diversity indices revealed that flooding had a considerable effect on bacterial and archaeal communities, with low-depth areas draining more rapidly and having microbial communities that were more comparable to those of non-flooded soils. All flooded areas have higher alpha biodiversity of bacterial and archaeal communities than their non-flooded counterparts. The Yumaguzino Reservoir, which is not emptied during the warm season because of its morphometric characteristics and the relief's mountainous nature, exhibits the largest variances. Based on the alpha biodiversity index, the non-flooded soil is most comparable to the flooded soils of the Slak Reservoir, which has an average drainage period of 51 days. Thus, hydromorphic regime changes essentially not only basic soil properties, but, also the microbiological state of soils.

The relative representation at the phylum level has undergone major alterations, which highlights the differences between flood and drainage areas. The microbiome of lake sediments and soils of periodically flooded zone, when compared, show more similarity with the analyzed areas, according to an analysis of related publications. We believe that this is caused by the recurrent floods and the movement of the microbial mass from the area next to the examined locations. The absence of specific phyla from flooded locations (*Euryarchaeota, Thaumarchaeota*) is determined by restrictions caused by lower ammonia and pH changes in flooded soils, not the existence of oxic and anoxic periods.

Metagenomic techniques may be used to locate areas that experience frequent floods and the development of anoxic conditions because the microbial communities of the analyzed soils differ significantly from one another in terms of structure.

Author Contributions: Conceptualization, E.A. (Evgeny Abakumov) and R.S.; data curation, A.M. and E.A. (Evgeny Abakumov); formal analysis, A.D. and E.A. (Evgeny Andronov); funding acquisition, E.A. (Evgeny Abakumov), R.S. and G.Z.; investigation, A.M., E.A. (Evgeny Abakumov), R.S., G.Z., A.D., E.D., A.Z., E.A. (Evgeny Andronov) and I.A.; methodology, A.M. and E.A. (Evgeny Abakumov); project administration, E.A. (Evgeny Abakumov), R.S. and G.Z.; supervision, R.S.; Validation, R.S. and G.Z.; visualization, E.D. and I.A.; writing—original draft, A.M., E.A. (Evgeny Abakumov) and R.S.; writing—review and editing, A.M., E.A. (Evgeny Abakumov), R.S. and G.Z. All authors have read and agreed to the published version of the manuscript.

Funding: The work was supported by the Russian Science Foundation, project No. 23-16-20003, dated 20 April 2023, and the Saint Petersburg Scientific Foundation, agreement No. 23-16-20003, dated 5 May 2023.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Acknowledgments: The authors thank Scientific Park of Saint-Petersburg State University for their help in determination of carbon (Chemical Analysis and Material Research Center) and assistance in microbiological research (Biobank research center).

Conflicts of Interest: The authors declare no conflicts of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript; or in the decision to publish the results.

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