



Conference Abstract

# Spatial Variations of the Bacterial Diversity in an Alkaline Lake

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## Abstract

Lake Iznik is one of the largest lake of Turkey covering 308 km<sup>2</sup> surface area with 65 m max. depth. The lake has alkaline characteristics (Akcaalan et al. 2014). It is a mesotrophic lake that becomes stratified between June-September and well mixed between October-April. Although there are almost 200 lakes in Turkey, there is very little published research focused on the bacterial diversity structures (Ozbayram et al. 2020.) The specific objective of this study was to evaluate the bacterial community profile in the surface water and sediment of the alkaline lake during the winter turnover. For this purpose, the samples were collected from 6 stations (5 on the shore and 1 in the middle of the lake) in February 2020 when the lake was completely mixed. In addition to the surface water and sediment samples, a sample was also collected from the depth of 40 m from the station located in the mid-lake. The water samples were filtered from a 0.22 µm filter and the sediment samples were taken into sterile plastic containers. The total DNAs were extracted using the NucleoSpin® Soil Kit (Macherey-Nagel, Germany) following the manufacturer's instructions. Bacterial community profiles of the samples were analyzed by 16S rRNA gene-targeted sequencing using Illumina® MiSeq™. Physicochemical parameters were measured as explained by Ozbayram et al. 2020.

The pH was between 8.29-8.67 and the Electrical Conductivity (EC) was in the range of 734-996 µS/cm (Suppl. material 1 -Table S1). Whereas the Dissolved Oxygen (DO) levels were measured as 10.12-11.65 mg/L in the surface waters, it was 9.72 mg/L in the 40 m. Among all samples, the highest value of the Shannon and Pielou's evenness indices were

calculated for the surface water sample collected from station 2 indicated a more evenly distributed and diverse bacterial community (Suppl. material 1-Table S2). Bacterial diversity patterns of the samples were presented at the phylum level in Figure 1. In compliance with the literature on freshwaters (Zhang et al. 2014), the community was dominated by Proteobacteria species, and higher abundances were determined in the sediment samples (ranged 40.4-50.0 %). Especially, Gammaproteobacteria, Deltaproteobacteria were the major classes of this phylum in the sediment. On the other hand, the composition of bacterial communities in water samples showed a difference in which Actinobacteria and Bacteroidetes (in particular, the order: Flavobacteriales) were also predominated the communities. However, the community profile slightly differed with depth (station 6). At the genus level, most of the reads were not assigned any genera. *Ilumatobacter*, *Fluviicola*, and *Flavobacterium* were represented 3.4-7.1% of the bacterial community of water samples. Fig. 1

	Water Samples							Sediment Samples					
	Station_1	Station_2	Station_3	Station_4	Station_5	Station_6	Station_6 4ftm	Station_1	Station_2	Station_3	Station_4	Station_5	Station_6
Acidobacteria	3.4	3.61	3.33	3.72	5.31	4.52	3.31	6.23	4.91	6.99	5.66	4.32	7.61
Actinobacteria	16.97	11.25	17.73	15.72	21.03	22.11	20.33	8.34	7.53	11.09	7.7	8.52	7.63
Bacteroidetes	15.74	15.15	17.01	11.97	9.46	11.21	12.99	5.49	6.85	7.01	5.69	7.72	3.92
Chloroflexi	3	3.63	2.74	3.37	3.22	3.12	3.1	6.52	6.07	5.68	6.19	6.02	6.81
Cyanobacteria Chloroplast	9.25	7.12	6.75	5.57	2.65	2.51	3.96	3	2.64	2.5	6.11	3.12	4.52
Firmicutes	0.71	3.03	0.87	5.08	2.29	2.59	1.16	2.42	2.41	0.91	1.55	1.75	1.03
Gemmatimonadetes	0.22	0.27	0.15	0.28	0.83	0.75	0.62	0.2	0.11	0.52	0.57	0.14	0.26
Ignavibacteriae	0.42	0.52	0.32	0.5	0.39	0.26	0.23	0.73	1.08	1.27	0.84	0.72	1.09
Planctomycetes	1.47	1.12	1.14	1.16	1.27	1.56	0.95	0.52	0.71	0.84	0.49	0.53	0.85
Proteobacteria	30.92	38.33	33.21	35.53	34.71	34.73	35.74	44.64	50.3	40.43	46.1	45.74	48.05
Verrucomicrobia	3.54	3.81	2.97	3.6	2.45	2.65	2.87	2.49	2.64	9.05	2.85	2.51	3.14

Figure 1. [doi](#)

**Figure 1.** The relative abundance of bacterial phyla with a proportion of at least 0.5% in at least one sample.

Overall, due to the complete mixing conditions in the lake, there was a homogenization of the bacterial communities and the diversity patterns were quite similar in the water samples. In further studies, samples will be collected during the stratification and the community structures will be compared.

## Keywords

Bacterial Diversity, 16S Amplicon Sequencing, Freshwater, Sediment, Surface water

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## Conflicts of interest

The authors declare no conflict of interest.

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## Supplementary material

### Suppl. material 1: Spatial Variations of the Bacterial Diversity in an Alkaline Lake [doi](#)

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**Data type:** Physicochemical, alphadiversity

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