**The Metagenomics Analysis of Two Waste Mine Ponds from Turkey.**

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**Highlights**

* High boron concentrations
* Microbial diversity
* Metagenomics approach
* Bioinformatic analysis
* Environmental biotechnology potential

**1. Introduction**

Boron can be directly and indirectly involved in different functions and mechanisms in many different organisms. There is some information about this area in literature [1, 2, 3, 4]. Moreover, boron may be toxic to living cell at high concentration [5]. However, some special microorganisms can easily survive in regions with high boron concentrations and these microbes have potential at environmental biotechnology field [6, 7, 8]. Researchers are interested in microorganisms living in high boron content because of their metabolic characteristics. Classical microbiological cultural techniques are not always useful to determinate of microbial species in extreme conditions due to their extreme characteristics and there is no study about specifying microbial diversity by molecular techniques. Therefore, in this study, metagenomics approach as next generation sequencing was used to present of microbial community in area with high concentration boron.

**2. Methods**

Two different environmental water samples were taken from two places with boron contaminated field in Balıkesir-Bigadiç and Eskişehir-Kırka Works. Metal contents of these samples were determined. The experimental studies were started with the total DNA extraction and metagenomics analysis method was performed. 16S amplicon sequencing in Illumina Miseq Platform was practiced to keep all of microorganisms survive in sampling areas. Metadata of microorganisms was analyzed bioinformatically by QIIME 1.

**3. Results and discussion**

According to chemical analysis; B, Li, Na, S and Sr contents in Kırka samples were found higher than water samples of Bigadiç. Metagenomics data is shown in Table 1.

**Table 1.** Dominant genera in sampling areas

|  |  |
| --- | --- |
| **Sampling area** | **Dominant genera** |
| K1 (Kırka boron mine drainage, station 1) | *Rhodobaca, Gloeobacter, Luteolibacter, Fluviicola, Verrumicrobium, Bacteriovorax* |
| K2 (Kırka boron mine drainage, station 2) | *Rhodobaca, Gloeobacter, Luteolibacter, Verrumicrobium* |
| B1 (Bigadiç boron mine drainage, station 1) | *Pseudanabaena, Gloeobacter, Hyphomonas, Algoriphagus, Rhodobacter, Anaerospora* |
| B2 (Bigadiç boron mine drainage, station 2) | *Rhodobacter, Hydrogenophaga, Roseococcus, Anaerospora* |

**4. Conclusions**

This study will provide information about inhabiting microorganisms which are able to tolerate high boron. In future studies, these organisms can be used for environmental biotechnology field.

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