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COMPOSITION AND MOLECULAR STRUCTURE OF MICROORGANISMS IN BIOLOGICAL SOIL CRUSTS FROM A DRY, HIGH-ALTITUDE GLACIER FORELAND IN THE EASTERN PAMIR (TAJIKISTAN)

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Biological soil crusts (BSC) constitute an extremely important group of organisms, especially in environments where the conditions for higher plants are unfavorable, such as mountains and deserts. BSCs are formed by cyanobacteria, fungi, lichens, bryophytes, and algae in various proportions. This complex community is responsible for soil formation and nutrient sequestration and constitute a step in a succession of organisms. Especially important role play cyanobacteria which as autotrophs enrich soil with organic carbon and thanks to N₂ fixation are, together with some other bacteria, responsible for nitrogen sequestration. Thanks to secretion of the extracellular polymeric substances, they also play a structuring role in this environment, stabilizing the soil, increasing its porosity and water retention capacity. Still the knowledge on composition and structure of bacterial components in BSC and on relations between them especially in extreme environments is limited.

We studied (10 study plots) biological BSC in the Koksoy River Valley in Eastern Pamir Mountains in July 2018 and in July 2019. This valley was recently characterized as exceptionally poor in terms of organic carbon and with its harsh weather conditions can be considered an extreme environment. In the present study we used amplicons sequence variants (ASV) approach recovered from a high-throughput analysis of hypervariable region V3-V4 of 16S rRNA gene.

The results showed that among bacteria dominated Actinobacteria (18% of ASVs), Proteobacteria (14%), Bacteroidota and Chloroflexi (13% each) and the next phylum was Cyanobacteria with 9% contribution to the bacteria community. However, the most numerous single genus was a cyanobacterium - *Microcoleus vaginatus*. *Microcoleus* is known to have a structure-forming role for BSC and to form “cyanosphere” which attracts bacteria, among which are N₂ fixing taxa. In this way presence and domination of *Microcoleus* influences the nitrogen cycle in the BSC.

A filamentous, green non-sulfur bacteria “AKIW781” from the Chloroflexia class was another dominant taxon followed by Abditibacterium, an oligotroph, adapted to occur in an environment with a very low concentration of nutrients. Also in each sample, though in lower abundance we noticed genus Sphingomonas, a diazotrophic photoheterotroph. Another diazotrophic bacteria belonged to Cyanobacteria: Nostocales and Chroococcidiopsidales present in more developed BSC, in 15 out of 24 samples. Thus, the study confirmed that the BSCs were functionally diverse communities with complex interactions between its components and with cyanobacteria playing a crucial role in its functioning.

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