



Microbiome of Yermic Regosol in southern Kazakhstan

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Biological activity is of utmost importance for the genesis of extremely arid desert soils. The soil surface in arid regions is often covered by biofilms representing a complex biocenosis of algae, bacteria, micromycetes, and, sometimes, mosses or lichens.

Biofilms of extremely arid soils form a significant part of the living matter in the desert ecosystems and play the central role in their dynamics.

Study of the genetic material recovered directly from the soil samples is the main approach in soil metagenomics. Modern sequencing methods were used to describe the diversity of the microorganisms in soil samples. For the first time, such data were obtained for the extremely arid desert soil (Yermic Regosol) in southern Kazakhstan (flat alluvial plain; 43° 42'53.2" N; 79°25'29.1" E; 615 m asl).

Taxonomic identification of nucleotide sequences and comparative analysis of microbial communities were performed using VAMPS. The classification of the sequences was performed using RDP.

As the primers used were based on the sequences of 16S-rRNA gene of bacteria and archaea, we could analyze the prokaryotic community. Along with bacteria and archaea with established systematic position, all soil samples contained unidentified sequences (5.2-5.3%).

Bacteria predominated at the domain level (65.9-74.9%), although their portion was much lower in comparison with that in less arid soils, where it reached 94–100%. Archaea were present as minor components (0.3-0.5%).

Dominant groups of bacteria were represented by Proteobacteria (43.9-50.8%), Actinobacteria (9.5-10%), Firmicutes (0.8-2.4%), Verrucomicrobia (1.1-3%), Acidobacteria (1.1-2%), Bacteroidetes (1.2-1.4%). The portion of other phyla was less than 1%.

Thus, bacterial phyla Proteobacteria, Actinobacteria and Acidobacteria constitute the core component of the microbiome. Archaea are represented by phylum Crenarchaeota.

A key feature of the extremely arid soils is the presence of large numbers (24.7–33.6%) of cyanobacteria in the composition of DNA of the microbial community. Cyanobacteria play the major role in immobilization of carbon in the course of their photosynthetic activity.

The biogenome of the studied soil consists of 27 families including dominant: Cyanobacteria (24.7-33.6%), Enterobacteriaceae from the class Gammaproteobacteria (13.0-15.6%), Pseudomonadaceae (1.6-11.7%), order Myxococcales (0.9-13.2%), which is found only in desert soils, and Moraxellaceae (0.7-8.1%) and Acetobacteraceae (2.9-3.2%) (also endemic organisms).

Unclassified (at family level) bacteria from the order Burkholderiales were found in the soil samples (36 and 54 sequences, or 1.2-2.1%). We suppose that these are DNA of iron bacteria *Leptothrix*, whose presence in the soils was identified using the method of fouling glasses.

The data on the biodiversity and genomic characterization of extremely arid desert soils in Kazakhstan reflect the actual species diversity of soil microorganisms.

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