



Spatial changes in the prokaryotic community structure across a soil catena

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Mesorelief is a complex biogeochemical factor regulating hydrothermal regimes of the surface soil layer, the type of plant cover, etc., and, therefore, influences on soil microbial community structure. A natural model of soil sequence across the slope is a soil catena. Soils forming on various mesorelief positions significantly differ in physicochemical and biological properties, leading to the changes in spatial distribution of various bacterial and archaeal taxa across the soil catena.

The aim of this study was to determine soil microbial community structure of different ecosystems corresponding to three mesorelief positions within the soil catena.

The catena was located at the right bank of the Oka River (Moscow region, Russian Federation). Soil samples were taken at depths of 0-20 cm, 20-40 cm, and 40-60 cm from three sites within the transect of 960 m with elevation of 80 m, corresponding to the autonomous (AU), transitional (TR) (both Luvisols), and accumulative (AC) (Fluvisol Umbric) positions of the landscape. The dominant vegetation of studied sites were rootstock- and loose bunchgrasses of the fallow ecosystem (AU), a secondary small-leaved forest of the forest ecosystem (TR), and a meadow-bog association of the meadow-bog ecosystem (AC). The distances between the sites were 680 m (AU and TR), and 280 m (TR and AC).

The soil samples were homogenized, and the total community DNA of three replicates was extracted using the FastDNA[®] SPIN kit for Soil. All DNA replicates were combined in a pooled sample and the DNA was used for PCR with specific primers for the 16S V3 and V4 regions. The products were purified and submitted to Illumina MiSeq sequencing. Obtained sequence data were evaluated using the MiSeq Reporter Metagenomics Workflow and QIIME. Quantification of the bacterial and archaeal metabolically active cells was quantified by the FISH-method.

Verrucomicrobia, Proteobacteria, Firmicutes and Actinobacteria were the major phyla in autonomous site; Verrucomicrobia, Proteobacteria and Acidobacteria - in transitional site (both soils with the total dominance of *Chthoniobacter flavus*). In Fluvisol of accumulative landscape position, it was revealed a completely different prokaryotic community with the dominance of *Bacillus*, *Clostridium*, *Desulfovibrio*, *Saccharopolyspora*, and *Gallionella*. *B. longiquaesitum* and *B. nealsonii* were the two most abundant species. In general, prokaryotic community of Fluvisol was characterized by a wide range of microorganisms involved in the biogeochemical cycles of iron (*Gallionella ferruginea*, *Rhodferax ferrireducens*, *Carboxydocella ferrireducens*, *Gallionella capsiferiformans*, etc.) and sulfur (*Desulfomonile iedjei*, *Sulfurospirillum* sp., *Desulfonatronum thiosulfatophilum*, *Thermodesulfovibrio thiophilus*, *Thermodesulfovibrio aggregans*, *Ammonifex thiophilus*, etc.).

Metabolically active archaea of soils across the catena included Thaumarchaeota and Euryarchaeota phyla. In general, 23 species of methanogens were detected in AC position characterized by excessive moisture which explains prevailing of methane emission over consumption. It was also revealed that *Methanolobus taylora*, *Methanococcoides methylutens*, and *Methanosaeta concilii* were the dominant methanogens, while *Methylosinus pucelana* and *Methylosinus acidophilus* were the main methanotrophs in prokaryotic communities of studied soils.

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