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Metagenomic studies of soil chronosequences in various regions of Russia

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Soil is a very special body that is formed due to the interaction between inorganic compounds of the parent material and organic matter of the living organisms. Depending on the intensity and quality of this interaction the certain soil types are formed, carrying the specific horizons in their vertical profile. The majority of the modern metagenomic studies are concentrated on the climax stage of soil evolution and usually only the topsoil layer is analyzed. However, soil is a dynamically developing natural body and thus must be studied in every moment of its ontogenesis. In this context soil chronosequences - the natural sites where we can observe continuous soil formation can serve the perfect and quite informative biological models for metagenomic studies. There are plenty regions on the territory of Russia where one can observe disturbed areas and corresponding chronosequences illustrating the genesis of soils in different climatic zones. Using standard metagenomic methods, such as high-throughput sequencing of 16S rRNA gene of bacteria and archaea, we investigated soil microbiome in chronosequences located in several regions of Russia. Among the chosen sites were: 1) mining sites: the deposits of chromite ores from the north regions with the permafrost soils (Yamal peninsula, Yakutsk); the spoil heaps of phosphorites and sand from the taiga regions of Russia (Leningrad region); the deposits of iron sediments from the forest-steppe region (Kursk Magnetic Anomaly), 2) the washed up walls aging from several hundred to thousands years in the coast of Ladoga Lake and 3) the postpyrogenic sites that were destroyed both with ground and surface fires. In bioinformatic analysis the clear correlation between the composition of microbiome and the corresponding stages of soil formation was revealed. We also found the high levels of biodiversity in lower soil horizons compared to that in the top soil. The upper soil layers were mostly inhabited by bacteria from the phylum Proteobacteria (Comamonadaceae, Pseudomonadaceae), Actinobacteria (Solirubrobacteriaceae) and Bacteroidetes (Pedobacter sp.), while the mineral soil horizons were dominated by archaea from the family Nitrososphaeraceae (up to 4,4% from the total microbiome) and bacteria from the largely undescribed groups like RB41 (Acidobacteria), IS-44 (Proteobacteria), Syntrophobacteraceae and Nitrospiraceae. These results and many other highlights from the big project named “Dynamics of soil biota in chronosequences of post-technogenic landscapes: analysis of soil ecological efficiency of ecosystem restoration processes” will be presented. The study is supported by Russian Science Foundation grant number 17-16-01030.