



Succession of Prokaryotic community in Chronosequences of Abandoned Overburden Spoil Heaps of the Kursk Magnetic Anomaly (Kursk, Russia) Using 454 Pyrosequencing

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Introduction

Soil genesis is associated with soil microbiome evolution, as microorganisms play key roles in the cycling of biogenic elements and in soil organic matter formation. Soil microorganisms are able to utilize a wide range of chemical compounds, thereby participating in the bioremediation of disturbed areas. There are very few works describing the soil metagenome during the soil restoration process in technogenic landscapes. Therefore, the objective of this study was evaluation of the taxonomic structure of the soil microbiome in soils formed on the dumps resulting from the iron ore mining in Kursk Magnetic Anomaly (KMA).

Materials and Methods

The objects were embryotic soils formed on the dumps of tertiary Callovian clays (Upper Jurassic), the age were 10, 35, and 50 years. Soil sampling was performed from the upper soil horizon (0-5 cm).

DNA extraction was carried out using a PowerSoil DNA Isolation Kit (Mobio Laboratories, USA); the destruction of soil samples was performed on Precellys 24 homogenizer (Bertin Technologies, France). Pyrosequencing was performed on GS Junior (Roche) according to the manufacturer's recommendations.

Results and Discussion

The comparison of the early and late stages of microbial succession with increasing age of the dump revealed that the abundance and diversity of bacteria from phyla Actinobacteria, Chloroflexi and Acidobacteria increased, whereas the proportions of Proteobacteria, Gemmatimonadetes, and Bacteroides lineages decreased. As the age of the dump increased, the number of archaeal lineages decreased dramatically, which may be due to the replacement of their ecological niches by bacteria in a more developed type of microbial community. Changes in taxonomic composition are associated with the shift from an unstable ecosystem with domination of copiotrophic microorganisms (bacteria from the genus *Pseudomonas* or family Enterobacteriaceae) to a community with a predominance of actinobacteria (*Streptomyces*, *Nocardia*, Gaiellaceae fam. and Solirubrobacterales or.) which presence and diversity indicate effective organic matter transformation. All samples were characterized by the presence of *Delftia tsuruhatensis* – a microorganism commonly associated with disturbed soils and microbiomes of activated sludge. The increase in abundance of these bacteria in the 10-year-old dumps and a maximum in the 35-year-old dumps, as well as the further decreasing, may confirm an active participation of these bacteria in soil-forming processes.

Conclusions

The analysis of microbiological diversity of soil samples investigated allow us to conclude that technogenic dumps formed by clay textured overburden mines in the KMA region were favorable substrate for the development of microorganisms. However, the increase in biodiversity and the transition to a stable (climax) type community were observed only 50 years after the formation of the dumps. This process was characterized by the replacement of copiotrophic microbial forms by oligotrophic ones, among which various types of Actinobacteria played essential roles. This could be considered important in the modulation of soil metabolism, which is essential for the transformation of organic matter and for humification as a holistic process.

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