

## Methanotrophic communities in aerobic soils with different stages of natural reforestation

Irina Kravchenko (1), Marina Sukhacheva (2), and Tatyana Kuznetsova (3)

 Winogradsky Institute of Microbiology, Research Center of Biotechnology of the Russian Academy of Sciences, Moscow, Russia, (2) Institute of Bioengineering, Research Center of Biotechnology of the Russian Academy of Sciences, Moscow, Russia, (3) Institute of Physico-chemical and Biological Problems in Soil Science of the Russian Academy of Sciences, Pushchino Moscow Region, Russia

The land use and management has a significant impact on global biogeochemical cycles of biogenic elements and the Earth's climate. Deforestation is known to change the soil from a net sink for CH4 to a net source as a result of alteration in the activity and composition of the methanotrophic communities. At the same time, the recovery of ecosystems after their withdrawal from agricultural use is poorly understood. Currently, in Russia, the former arable lands occupy about 20% of the territory and more than half of them are not used in agriculture since the early 90-s. Here, soil CH4 oxidation rates and associated methanotrophic communities were examined in a chronosequence of gray forest soils, Moscow region, Russia, consisting of cropland soils, soils at the different stages under postagrogenic forest regenerating, and in a mature native forest. CH4 concentrations were measured by GC and several chemical (pH, total C and N, NH4 -N and NO<sub>3</sub> -N) and physical (moisture content, porosity, water-filled pore space and bulk density) soil properties were evaluated.

Methane oxidation rates were significantly influenced by reforestation and the regenerating soils have the potential to reach those of the native forest. In fallow, shrublands and young forest soil CH4-oxidation rates were significantly higher as compared with cropland, but not fully stabilized even after 25 years of reforestation. To examine whether changes in CH4-oxidation rate were linked to a shift in the microbial community, we have analyzed soil methanotrophic communities by cloning and sequencing of particulate methane monooxygenase (pmoA) using the primer pair A189–mb650. Based on the relative proportion of the clones it was shown the dominance Type II related and uncultured methanotrophs in forest soils. Both Type I and Type II methanotrophs were found in arable and postagrogenic soils, and the relative abundance of Type II methanotrophs increased with the age of regeneration and recovered after 15-25 years to that close to finding in the native forest. We suggested that the lower CH4- oxidation rates in soils of older reforestation stages is determined by edaphic factors. Our findings may be useful in future prediction of changes in methane emissions resulting from reforestation.

The study was partially supported by RFBR research project # 16-04-00136\_a.