The effect of organic fertilizers on the taxonomic composition of microbial communities in agro-soddy-podzolic soils of the middle taiga

Puhalsky Y.V.¹, Loskutov S.I.¹, Lapteva E.M.², Vinogradova Yu.A.², Kovaleva V.A.², Perminova E.M.²

¹"BioEcoTech" LTD, St. Petersburg, Russia; ²IB FRC Komi SC UB RAS, Syktyvkar, Russia

E-mail: puhalskyan@gmail.com

Key message. The taxonomic composition of prokaryotes of agro-soddy podzolic soils of the middle taiga and the patterns of its change with the application of various doses of organic fertilizers were studied.

Keywords: microbiome, microorganisms, soil, organic fertilizers

Maintaining soil fertility in agroecosystems, especially in the bioclimatic conditions of the North, requires the introduction of mineral and organic fertilizers. This can have both positive and negative effects on the soil microbiota complex. The purpose of this work was to identify the response of the prokaryotic complex of arable soils to the introduction of environmentally friendly doses of peat and manure compost (TNC) in agroecosystems of the middle taiga.

The studies were carried out on arable land, where a long-term field experiment is carried out with the introduction of various doses of fertilizer in the feed crop rotation (Republic of Komi, the vicinity of Syktyvkar, the middle taiga subzone). The objects of the study were microbial communities of arable horizons (0-20 cm) of agro-soddy-podzolic soils of three experimental sites - without fertilizing (control), with TNCs in doses of 40 and 80 t/ha. To study the taxonomic composition of prokaryotes, molecular genetics methods were used.

As the studies showed, the soil microbiome complex was formed mainly by representatives of nine phyla: *Acidobacteria*, *Actinobacteria*, *Bacteroidetes*, *Chloroflexi*, *Firmicutes*, *Gemmatimonadetes*, *Planctomycetes*, *Proteobacteria* and *Verrucomicrobia*. Practically in all microbiome dominated a group of the *Proteobacteria*. Considerable share in communities of arable soils constitute as representatives of groups *Actinobacteria*, *Bacteroidetes* and *Acidobacteria*. The latter are typical inhabitants of acidic soils, which include the soils studied by us ($pH_{KCl} \sim 4.2-4.4$). Phyla *Chloroflexi* and *Planctomycetes* accounted for about 1%; the number of prokaryotes from the remaining phyla in communities did not reach 1%.

It was revealed that the introduction of organic fertilizers had a mixed effect on different groups of microorganisms. High doses of TNCs (80 t/ha) contributed to a decrease in the proportion (52%) of *Proteobacteria* relative to the control site (58%) and sites with low doses of TNCs (64%). Close patterns were obtained for the microorganisms of phyla *Bacteroidetes*: in the control - 7%, with the introduction of TNCs at a dose of 40 t/ha - 10%, at a dose of 80 t/ha - 5%. At the same time, organic fertilizers stimulated the growth of microorganisms of the phylum *Actinobacteria*, respectively 22% (control), 23% (40 t/ha), 29% (80 t/ha).

The introduction of TNCs contributed to a change in the taxonomic composition of prokaryotes at the class level. In particular, representatives of *Alphaproteobacteria* (32%), *Betaproteobacteria* (19%), and *Gammaproteobacteria* (4%) dominated in the soil of the control plot in the *Proteobacteria* phyla. The soil with the introduction of TNC at a dose of 40 t/ha in phyla *Proteobacteria* to share *Alphaproteobacteria* has 38%, *Betaproteobacteria* - 21%. When TNCs were introduced at a dose of 80 t/ha, *Alphaproteobacteria* decreased to 27%, and *Betaproteobacteria* - 16%.

The phyla of *Actinobacteria* in all the soils of the foundation comprise microorganisms of the order *Actinomycetales*, in phylum *Bacteroidetes* - representatives of a class and *Flavobacteria*. Some characteristic representatives of the cultivated part of the microbial communities of the soil — the genera *Burkholderia* and *Pseudomonas* — in the studied microbiomes showed a rather high representation in the analysis of the 16S rRNA gene, but others, *Arthrobacter*, *Azotobacter*, *Azospirillum*, and *Variovorax*, mainly have small shares in the community.

Thus, the taxonomic composition of prokaryotes in arable soils of agroecosystems was studied for the first time for the Republic of Komi. It was shown that under bioclimatic conditions of the middle taiga in a six-field fodder crop rotation with various doses of organic fertilizers, the most significant effect on the prokaryotic complex is the introduction of large doses of TNCs (80 t/ha). Low doses of TNCs (40 t/ha) contribute to maintaining (with some variation) the number of individual groups of soil microbial communities at the level of control plots (without fertilizing).

The reported study was funded by RFBR and Republic of Komi, project number 20-44-110009-p_a «Influence of *Heracleum sosnowskyi* invasion on soil fertility and soil microbial communities in postagrogenic ecosystems of the European North-East (on the example of the middle taiga of the Komi Republic)».