Microbiome Analysis of Kingisepp area recultivated soils after phosphorite mining

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Land mining has a significant impact on the environment. It results in vast areas of damaged soil cover with altered composition of nutrients, pH and structure, which leads to significant shifts in microbiome. These sites could be a good model for the study of soil formation and ecosystems recovery. One of these sites is the object of the current study – the Kingisepp area of phosphorite mining. It is located to the west of Saint-Petersburg, Russia and occupies around 35 km2. Mining took place in the 1970s and at the end of this period most of the area was subjected to biological reclamation. Part of the area was covered with a mixture of peat and stripping rocks and was planted with spruce. Other part was covered by stripping rocks only and planted with larch and spruce. Monitoring of soil agrochemical properties has been carried out at 3 experimental plots (1 – spruce, 2 – larch, 3 – pine) since 1989. Plots appear to be similar in C, N, P and K composition. Plot 1 has a slightly more acidic pH than the others and less available nitrogen. This study focuses on the microbiome composition of the 3 plots. Samples were taken from the upper organomineral horizon of each plot in four replicates. Assessment of diversity was made by high-throughput sequencing of 16S rRNA gene libraries derived from DNA obtained from soil samples. The majority of sequences was attributed to following soil phyla - Proteobacteria (29,6 – 37%), Actinobacteria (12,8 – 25,2%), Acidobacteria (12,3 – 20,8%), Chloroflexi (4,6 – 11,8%), Planctomycetes (5,7 – 8,2%), Bacteroidetes (4,9 – 9,2%), Verrucomicrobia (3,9 – 5%), Gemmatimonadetes (2,1 – 3,8%); the rest took less than 1%. Prokaryotic community showed low alpha diversity. All plots contained OTUs of genera Agromyces, Rhodoplanes and Delftia, which in many studies are attributed to damaged soils conditions. A lot of detected taxa are plant-associated bacteria, particularly families Bradyrhizobiacea, Rhizobiaceae, Hyphomicrobiaceae, Pseudomonadaceae. The abundances of these taxa didn't differ significantly between three plots. Apparently this stage of succession is pre-climactic, since a significant proportion of the bacteria in the plots belonged to copiotrophic forms.