

Bacterial Community Diversity in Soil under Two Tillage Systems

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Abstract : The soil is a complex ecosystem that is part of our biosphere. The ability of soil to provide ecosystem services is dependent on microbial diversity. Tillage is one of the major factors that affect soil properties. The no-till systems or shallow ploughless tillage are opposite of traditional deep ploughing, no-tillage systems, for instance, increase soil organic matter by reducing mineralization rates and stimulating litter concentrations of the top soil layer, whereas deep ploughing increases the biological activity of arable soil layer and reduces the incidence of weeds. The role of soil organisms is central to soil processes. Although the number of microbial species in soil is still being debated, the metagenomic approach to estimate microbial diversity predicted about 2000 - 18 000 bacterial genomes in 1 g of soil. Despite the key role of bacteria in soil processes, there is still lack of information about the bacterial diversity of soils as affected by tillage practices. This study focused on metagenomic analysis of bacterial diversity in long-term experimental plots of Dystric Epihypogleyic Albeluvisols in western part of Lithuania. The experiment was set up in 2013 and had a split-plot design where the whole-plot treatments were laid out in a randomized design with three replicates. The whole-plot treatments consisted of two tillage methods - deep ploughing (22-25 cm) (DP), ploughless tillage (7-10 cm) (PT). Three subsamples (0-20 cm) were collected on October 22, 2015 for each of the three replicates. Subsamples from the DP and PT systems were pooled together wise to make two composition samples, one representing deep ploughing (DP) and the other ploughless tillage (PT). Genomic DNA from soil sample was extracted from approximately 200 mg field-moist soil by using the D6005 Fungal/Bacterial Miniprep set (Zymo Research®) following the manufacturer's instructions. To determine bacterial diversity and community composition, we employed a culture - independent approach of high-throughput pyrosequencing of the 16S rRNA gene. Metagenomic sequencing was made with Illumina MiSeq platform in Base Clear Company. The microbial component of soil plays a crucial role in cycling of nutrients in biosphere. Our study was a preliminary attempt at observing bacterial diversity in soil under two common but contrasting tillage practices. The number of sequenced reads obtained for PT (161 917) was higher than DP (131 194). The 10 most abundant genus in soil sample were the same (Arthrobacter, Candidatus Saccharibacteria, Actinobacteria, Acidobacterium, Mycobacterium, Bacillus, Alphaproteobacteria, Longilinea, Gemmatimonas, Solirubrobacter), just the percent of community part was different. In DP the Arthrobacter and Acidobacterium consist respectively 8.4 % and 2.5%, meanwhile in PT just 5.8% and 2.1% of all community. The Nocardioideae and Terrabacter were observed just in PT. This work was supported by the project VP1-3.1-ŠMM-01-V-03-001 NKPDOKT and National Science Program: The effect of long-term, different-intensity management of resources on the soils of different genesis and on other components of the agro-ecosystems [grant number SIT-9/2015] funded by the Research Council of Lithuania.

Keywords : deep ploughing, metagenomics, ploughless tillage, soil community analysis

Conference Title : ICEM 2016 : International Conference on Energy Management

Conference Location : Paris, France

Conference Dates : October 24-25, 2016