

56 - Metagenomic study of the plant selective pressure to shape root-associated microbiome in apple orchard

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Replant disease is a well-known problem in the areas with intensive apple tree cultivation, including Nova Scotia, Canada. The old trees in the well-established orchards are adapted to the soil environment and are resistant to soil pathogens. The big part of this adaptation is the presence of root-associated microbial population that works as antagonist to the pathogens. This could have overall beneficial effect on the host-plant by promoting its growth, development, and fitness. Plant Growth Promoting Bacteria can facilitate plant growth and development by growth stimulation or prevention of disease. This study employs next-generation sequencing to understand the microbiomes associated with Nova Scotia apple orchards and to evaluate the plant selective pressure to shape root-associated microbiome. DNA of samples from orchard soil, tree roots and un-cultivated soil were extracted. 16S rRNA/ITS2/18S RNA and 16S rRNA/ITS2 amplicon sequencing was used to study soil and plant associated microbiomes, respectively. Different pattern of diversity was observed in the root and soil microbiomes. Analysis of variance using distance matrices statistical method was used to determine a statistical significance of sample grouping such as the sampling locations and sample types (root, soil, and un-cultivated soil). Several microbial taxa were identified as differential represented between environments. Through this study comparison between mature plant and soil microbiomes will help to identify plant preference to specific microorganisms and which might contribute to development of new strategy to the replant disease management. Future direction will be the comparison of abundance of microbial taxa in mature tree root and young tree root microbiome.