

production from native microbiota of lower himalayan region of Pakistan

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Depletion of oil reserves at a high rate and global climate change are the greatest challenges for society in the 21st century. Fuel deficiency is increasing day by day and to overcome this issue, different techniques have been invented for conversion of lignocellulosic waste into glucose for biofuel production, as an alternative way for energy production. Researchers are emphasizing on environmental and financial benefits of biofuel by using microbes to further improve lignocellulosic ethanol processes by making this process cost effective. In this context lower himalayan region has continuous addition of lignocellulosic waste residue thus indicating highest potential of unexplored native microbiota that produces enzymes for degradation of lignocellulosic wastes. The present work aimed at isolating, identifying and characterizing effective microbes that efficiently degrade lignocellulosic waste and produce high production of biofuel in a cost effective manner. To do so, microbes having high cellulase index and efficient enzymatic activities were isolated, characterized and identified and later may be used in industries for biofuel production. The study achieved the generation of microbes having efficient enzyme activities and cellulase index thereby enhancing the use of such microbes in bio fuel industries for efficient biofuel production. These effective microbes are useful in enzyme engineering or biotechnology for future biofuel production in industries.

510A - Insights into apple and pear bark microbiota: characterizing composition and population dynamics of beneficial and pathogenic microorganisms

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Plants host a large variety of microbial communities whose composition is shaped by host traits, environmental factors and agronomic practices. Despite the importance of bark as a potential reservoir of pathogenic and beneficial microorganisms, little is known about the associated microbiota. In this study, we evaluated the composition and dynamics of fungal and bacterial communities associated with apple bark through a metabarcoding approach. The influence of plant species, plant variety and bark age on the composition of bark-associated microbiota was assessed. Bark samples were collected from three-four years-old branches and one year-old shoots of pear (Abate and Williams cultivars) and apple (Golden and Gala cultivars) at the dormancy stage. A protocol for sample processing, DNA extraction and PCR amplification of fungal and bacterial sequences was optimized and followed by high-throughput sequencing. Results showed that bark age and plant species shape the composition of microbial communities. Bark communities are dominated by genera with ubiquitous attitude,

such as *Aureobasidium* and *Hymenobacter*, indicating that bark partially shares its microbial communities with the surrounding environment. Moreover, the abundance of fungal (*Aureobasidium*, *Rhodotorula*, *Sporobolomyces*) and bacterial (*Bacillus*, *Methylobacterium*, *Sphingomonas*) genera with potential biocontrol and/or plant-growth promotion functions, as well as that of potential plant pathogens (*Alternaria*, *Rosellinia*, *Curtobacterium* and *Pseudomonas*) changed according to bark age and host genotype. This metabarcoding approach was then applied to assess dynamics and composition of microbial communities associated with apple bark in two locations and two consecutive growing seasons. The influence of environment and agronomical practices will be further discussed.

511A - Repeated exposures of low-dose antimicrobials can cause dysbiosis in plant-endophyte interplay

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Recent studies on the plant-bacteria partnership have revealed the importance of bacterial endophytes for plant fitness. This partnership is particularly important in constructed wetlands treating wastewater. Here we asked whether antimicrobials commonly found in wastewater may disturb the plant-microbe interplay. To this end, we exposed wetland model systems planted with the common wetland plant, *Juncus effusus*, with sulfamethoxazole (SMX) and trimethoprim (TMP) at low aqueous concentrations. Plant fitness was evaluated based on evapotranspiration rates and by visual inspection. Changes of endophytic communities in roots and shoots of exposed and unexposed plants were tracked via culture-dependent (CFU, isolation of strains) and culture-independent (qPCR, 16S amplicon sequencing, FISH) approaches. The plant defence response was determined via recording reactive oxygen species (ROS) generation. We found that evapotranspiration decreased during exposure to SMX and TMP. After several exposures, plants became infested with insects and plant tissues turned necrotic. Total and phylum specific abundances of endophytes increased significantly in exposed roots but not in shoots. Culture-dependent and independent approaches revealed substantial changes in community composition, which were particularly pronounced in the roots. FISH analysis showed microbial colonization in the vascular bundles of the exposed plant roots. Invasion of pervasive bacteria was indicated by intense ROS production. In conclusion, a lasting dysbiosis of the bacterial endophytic community was observed in plant roots. The observation is analogous to the animal gut where microbes play key roles in disease, health, growth and host development. In the end, wetland's performance may be affected by disturbance of the plant-endophyte interplay.

512A - Composition of the rhizobacterial community and putative plant growth-promoting rhizobacteria from Atacama's Flowering Desert phenomenon