2023

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Sociedad Argentina de Microbiología General

XVIII Congreso de la Sociedad Argentina de Microbiología General

Chapadmalal

R.C.T. Club Vacacional & Spa

2 al 5 de octubre

determinants of microbial community composition. Results showed that, despite specifically selecting paired visibly burned vs. visibly not burned sites, fire had no significant effect on overall microbial community composition, with changes limited to a small number of taxa. However, the phylum Actinobacteria with representatives of Thermoleophilia class were identified as significant positive fire responders in the system. The remotely-sensed normalized burn ratio (NBR) ranges from low to moderate in our study, affecting the communities' distribution. Further, there were no significant differences between soil properties. This suggests that soil microbial response to low-moderate severity fires may be primarily mediated by vegetation, rather than a direct death from heat or changes in soil properties. Thus, effects in post-fire microbial communities may need more than one week to emerge. Future investigations are needed to strengthen our understanding of the microbial fire-response framework including direct death from fire exposure, temporal response to fire-induced changes to soil environment, and response to different fire regimes or return intervals.

MS26

MICROFLUIDIC DEVICES FOR HIGH THROUGHPUT MICROBIOLOGY BIOASSAYS IN MICRODROPLETS

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Microfluidics is a promising field for studying and manipulating fluids at the micrometer scale. Microfluidic devices, also known as microchips, offer significant advantages over conventional methods. In particular, microfluidic devices that generate microdroplets can be used for precise cell confinement in small bioreactors. In this way, droplet microfluidics can perform complex experimental protocols such as toxicity bioassays and antibiotic susceptibility testing. This research aims to use microfluidic devices to perform toxicity bioassays in microdroplets. A microfluidic device was designed to inject the oil phase into channel 1 and a suspension of bacterial cells into channel 2. This microchip allows the formation of controlled microdroplets that act as bioreactors for further experiments. The microchips produced microdroplets with an average diameter of 639.41 ± 42.68 µm at a frequency of 0.73 ± 0.06 Hz. *Escherichia coli* cells were successfully incorporated into the microdroplets and incubated under anaerobic conditions for various periods. Bacterial suspensions of $3.03 \pm 0.84 \times 10^6$ CFU/ml were injected into channel 2 of the microchip and in less than 5 minutes 411 microdroplets of 138 ± 27 nl containing 418 ± 82 CFU were generated. After incubation, the microdroplets were collected and the cells were enumerated by the colony method in Petri dishes. The results show comparable growth rates to those obtained using conventional incubation techniques in liquid media. Toxicity bioassays using 3,5-dichlorophenol showed good agreement between microdroplet-based and conventional cultivation methods. These results indicate that 3D-printed microfluidic devices can serve as an economical, automated, and effective platform for microbiological assays. Future research will focus on implementing electrochemical sensors to determine the number of cells within microdroplets and advance in an integrated microfluidic platform. These will open the possibility to perform microbiological bioassays using low-cost and high-throughput technologies.

MS27

IMPACT OF BIOCONTROL YEAST *Clavispora lusitaniae* 146 ON THE LEMON MICROBIOME

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The use of biocontrol agents has been proposed as an effective alternative to reduce citrus decays for promoting sustainable agriculture based on organic fruit production. Among the different microbial biocontrol agents, *Clavispora lusitaniae* 146 stands out as it is able of effectively controlling green mold in lemons. Although there is growing recognition of the role that the microbiome plays in the health and physiology of many plant species, to date, the composition of the lemon microbiome is unknown, nor is the effect of yeast 146 on it. Thus, the aim of this research was to study the impacts of biocontrol yeast *Clavispora lusitaneae* 146 on the composition of the lemon microbiome. Lemons were harvested, and then divided into two treatments: untreated and treated lemons with biocontrol yeast *C. lusitaneae* 146. Fruits were then stored at room temperature for 7 days. DNA was extracted from a pool of 3 pieces of peel per sample, and used for PCR that amplified the bacterial hypervariable V3-V4 region of the 16S rRNA gene. Paired-end sequencing of amplicons was done on an Illumina MiSeq sequencer. To assess the effects of postharvest treatment and storage on the diversity of the lemon microbiome, we used a series of ANOVA and adonis (~PERMANOVA) models with Shannon diversity and community composition as the response variables, respectively. There was no statistically significant difference (Kruskal-Wallies, $p > 0.05$) in bacterial diversity between the treated and untreated fruits. In this sense, the application of *Clavispora lusitaneae* 146 did not produce significant changes on bacterial communities of lemons during storage, including alpha diversity, community composition and structure. The bacterial community was dominated by Proteobacteria, followed by Firmicutes and Actinobacteria. Specific bacterial taxa were only identified for untreated lemons: *Methylobacteriaceae* (*Alphaproteobacteria*) and unclassified bacteria, however in a low abundance. Here, we presented the first lemon microbiome and we showed that the microbial abundance, diversity, and community structures were not significantly different for both treatments, revealing that *Clavispora lusitaniae* 146 didn´t modify the native bacterial population of the fruit microbiome. The present study is part of larger project whose objectives are to define the complete lemon microbiome, assess the effects of the postharvest biocontrol agents on the composition of the lemon microbiome to develop a science-based strategy for manipulating this microbiome to prevent postharvest decay and physiological disorders.

MS28

CO-INOCULATION WITH MICROALGAE IMPROVES PLANT GROWTH PROMOTING BACTERIA PERFORMANCE UNDER DESSICATION

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Plant growth-promoting bacteria (PGPBs) are frequently used to improve extensive and intensive crop performance. *Azospirillum. argentinense*, strain Az39, and *Pseudomonas*