resistant and susceptible lines could lead to a better understanding of the potential role of foliar microbiomes in causing or resisting P. maydis infection.

maize, microbial diversity, microbiome, phyllosphere, tar spot, Phyllachora maydis

RAKSHA.SINGH@USDA.GOV

1 Crop Production and Pest Control Research Unit, U.S. Department of Agriculture-Agricultural Research Service (USDA-ARS), West Lafayette, IN 47907-2054, U.S.A. 2 Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN 47907-2054, U.S.A.

Session 6: Microbiome-mediated effects on plant physiology and stress tolerance

116. Unearthing the Secrets of the Rhizosphere: Unlocking the Potential of Microbial Functional Genes for Drought-Resistant Agriculture

Ana Vitória R. da Silva, Izadora C. M. Cunha, Thierry A. Pellegrinetti, Eduardo M. Boleta, Teresa M. L. Mafra, Francisco D. Andreote, Rodrigo Mendes, Siu M. Tsai, Lucas W. Mendes.

Water stress poses a significant challenge to global agricultural productivity, impacting major agricultural regions worldwide through drought conditions and adversely affecting economies and societies. Recognizing the importance of enhancing crop resilience to drought, recent attention has been directed towards genetic improvements for drought tolerance. Emerging research highlights the role of soil microorganisms in influencing the plant's ability to withstand drought stress. This study aimed to investigate the rhizosphere microbiome of the common bean, aiming to identify microbial functions that contribute to the plant's resilience to water stress. To achieve this goal, we cultivated both drought-tolerant (BAT-477 and SEA-5) and susceptible (IAC Milenio and IAC-Carioca 80-SH) common bean cultivars in a greenhouse experiment under drought conditions for 96 hours. Measures including plant height, biomass, gas exchange, and nutritional content, alongside molecular analysis of rhizosphere soil through metagenomics sequencing, were used to evaluate the functional profile of the microbiome. Our initial findings reveal that tolerant cultivars showed an increase in microbial functions associated with biofilm formation and long-term survival in the dormant state. Conversely, susceptible cultivars displayed an enhanced abundance of membrane-associated proteins, signaling, and cellular processes, including DNA replication/repair and microbial metabolism in extreme environments under drought stress. Notably, co-occurrence network analysis revealed that, under stress conditions, the tolerant (SEA-5) and susceptible (80-SH) cultivars experienced increased modularity and a greater number of communities linked to the functional profile. Species diversity was particularly marked in one tolerant (BAT-477) and one susceptible cultivar (80-SH), pointing to complex interactions between plant types and their rhizosphere microbiomes. These insights significantly advance our understanding of plant-microbe interactions, highlighting microbial functions that could be harnessed for biotechnological solutions to enhance drought resilience. Moreover, this research underscores the critical need for further microbial ecology studies to innovate sustainable agricultural practices.

Rhizosphere, microbiome, drought, functional genes, metagenomics.

anareina@usp.br