

S2T4**Water Limitation and Nutrient Excess Influence the Membership and Inheritance of the Seed Microbiome of Common Bean, *Phaseolus vulgaris* L.**

Abby Sulesky-Grieb¹, A. Fina Bintarti¹, Marie Simonin², Matthieu Barret², Ashley Shade¹

¹Michigan State University, East Lansing, MI, USA. ²INRAE, Angers, Pays de la Loire, France

Abstract

Plant microbiome interactions play an important role in plant health, including benefits such as water and nutrient assimilation and plant growth promotion. One particularly interesting compartment of the plant microbiome is the seed endosphere – microorganisms residing inside the seed tissues. These seed microbiome members can have short- and long-term consequences on plant fitness, but they are largely understudied. Our study investigated the microbial taxa inhabiting the seed of common bean, and how these taxa are influenced by environmental factors such as drought and exogenous nutrient addition. We applied water limitation and excess fertilizer to bean plants through a multi-generational plant experiment and conducted 16S rRNA amplicon sequencing to characterize the seed endosphere microbiome. With this design, we determined the impact of the same and opposite consecutive treatments over generations. Using these data, we determined treatment and generational effects on the microbiome, differentially abundant taxa across treatments, and inheritance of taxa for each treatment. Host treatment effects were decreased in gen2 as compared to gen1, suggesting potential influence of the previous generation's exposure. We expect these results to increase understanding of key microbiome members responsive to altered environmental conditions, and their persisting impact on the plant microbiome. Ultimately, this work will provide insights into potential agricultural management techniques to increase plant health and resilience under changing climate conditions.

