

OSMOSE

Project title: impact Of Seed Microbiota On Seedling Emergence

Acronym: **OSMOSE**

Project duration: 24 months - Start date: 01/09/2020 End date: 31/08/2022

Key-words: Plant-microbiome interactions, Plant phenotyping, Seed treatment, Microbiome engineering, Synthetic Ecology

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Total cost of the project : 29 800 €

Financial support from « Objectif Végétal »: 14 800 €

Summary:

Context

All plants harbor a diverse microbiome colonizing aboveground and belowground plant habitats. These microorganisms can play an important role for plant health and yield in an agricultural context. Still, limited knowledge is available on the role of plant microbiota during the early stages of plant life, especially in germination and emergence. Seeds exhibit diverse microbiota but currently the causal relationships between seed microbiota diversity and seedling emergence has not been established. Gaining a better understanding of the role of this microbiota for seed germination and seedling establishment is particularly timely. The seed industry is preparing for a major revolution in seed treatments associated to the reduction of pesticide usage and harnessing the capabilities of the seed microbiota represents one of the most promising solutions.

Goals

This project is part of a research dynamic on the plant microbiome that is aiming to go beyond correlative approaches and starts establishing causality between the plant and its microbiota. In this context, the goals of this project are threefold:

- (i) Determine whether changes in seed microbiota composition can impact the emergence of a crop (common bean)
- (ii) Identify bacterial consortia that impact seedling emergence
- (iii) Validate beneficial consortia on multiple plant genotypes and identify the keystone bacterial taxa driving the effects

Methodology

Synthetic ecology approaches with the reconstruction of synthetic microbial communities (SynCom) will be used to experimentally establish the causal links and truly quantify the influence of microbiota on plant fitness. In this project, we will constitute a bacterial strain pool using high-throughput cultivation approach (i.e. culturomic) on seeds of multiple common bean cultivars and we will select bacterial strains for SynCom reconstruction. Using the phenotypic and genomic information of the selected strains, multiple SynComs will be designed using different hypothesis-driven strategies in order to test biodiversity-functioning theories in the context of plant-microbiome interactions. To assess the influence of seed microbiota composition and diversity on bean seedling emergence, we will then perform high-throughput emergence phenotyping of seeds inoculated or not with contrasting SynComs on one bean genotype. In a second set of experiments, we will assess the reproducibility of the SynCom effects on multiple bean genotypes and will investigate the mechanisms behind the microbiome-associated phenotypes by characterizing the plant metabolic responses and microbial keystone taxa associated to the stimulatory effects. Overall, this project will enable to uncover the role of seed microbiota in emergence success or failure (beneficial or detrimental effects of microbiota) and identify microbial consortia with stimulatory effects for potential phytostimulation or biocontrol applications.

This multi-disciplinary project will stimulate collaborations between three research teams in the IRHS unit by bridging our complementary expertise related to seed microbiota (EmerSys team), seed and seedling physiology (SMS team) and plant phenotyping using high-throughput imaging (ImHorPhen team).