Abstract

We formulated consortia of soybean-associated beneficial bacteria for seed treatment, which showed growth-promoting effects on soybean plants. In this study, we characterized the microbial communities of soybean plants in the endosphere and rhizosphere compartments influenced by two sets of soybean-associated bacterial consortia, Set2 and Setm4. These consortia are composed of multiple beneficial bacteria predominantly belonging to genera of Bacillus, Pseudomonas, Strepotomycetes, Enterobacter, Achromobacter and Enaffer. The microbial community patterns were not significantly different among different seed treatments in the level of species richness and diversity (alpha-diversity), although Setm4 showed the highest alpha diversity among the treatments in both compartments, followed by Set2 and the untreated control. However, the microbiome structure (beta diversity) in the rhizosphere compartment was significantly different among the treatments (49-31% of variation, P<0.01). The microbiome analysis indicated that four and seven SABB strains of the bacterial consortia had highest percentage similarity in the microorganisms of the root endosphere and rhizosphere samples, respectively. The network analysis indicated that the seed-treated SABB strains influenced the diversity and complexity of the microbe in the rhizosphere. The result of this study contributes to the development of innovative seed treatment using beneficial microorganisms for more sustainable soybean culture.

Introduction

- In cognizant with the adverse effect of climate change, declining crop production and increasing tolerance of pest and diseases to synthetic chemicals. An alternative but effective disease management is sought for sustainable soybean production. Soybean (Glycine max) is one of the most valuable crops in the world as oil seed crop, biofuel, feeds for livestock and aquaculture, and as a good source of protein in human diet.
- Soybean production decline is attributed to abiotic and biotic stresses. The most common soilborne disease caused by *Rhizoctonia solani* can significantly reduced stand, nodulation and yield. Hence, a sound disease management is vital to upkeek the production of soybean.
- Seed inoculation with beneficial bacteria as a seed treatment is an ideal tool to deliver high densities of viable microorganisms to the soil.
- However, there is still a limited understanding on the effect of seed treatment with beneficial bacteria to the microbial communities within and surrounding the plant roots.

Objectives

1. To identify new soybean-associated beneficial bacteria (SABBs) & formulation of SABB consortia
2. To determine the effect of the SABBs on the growth and defense of soybean plants and associated microbial community
3. To assess the effect of the SABB seed treatment strains on the microbial network structure through co-occurrence network analysis

Methodology

- Isolation of SABBs
- Screening in the laboratory
- Characterization of microbiome
- Testing in the GH and field conditions

Results and Discussion

![Image](https://example.com/image1.png)

**Figure 1**: UPGMA phylogenetic tree (A) and SABB consortia composition of Set2 (B) and Setm4 (C).

**Figure 2**: Inoculation and greenhouse experiment for the three initial consortia (A) and with the minimal subsets (B).

**Figure 3**: Alpha-diversity measure using Observed and Shannon index at the genus level represented as barplot. Each barplot represents the diversity distribution of a group present within Treatment class: (A) Endosphere compartment; Statistical significance: Observed index p-value: 0.4438, Shannon index p-value: 0.4579), and (B) Rhizosphere compartment; Statistical significance: Observed index p-value: 0.84405, Shannon index p-value: 0.3040).

**Figure 4**: PCA plot using Bray Curtis distance, unweighted UniFrac, and weighted UniFrac and the explained variance shown in the X and Y axis in the (A) endosphere and (B) rhizosphere compartments.

**Figure 5**: Microbial network structure of the root endosphere (A) and the rhizosphere compartment (B) Network topological characteristics of microbial communities with corresponding statistics calculated based on co-occurrence network comprising all significant microbe-microbe interactions at α < 0.01

Conclusion

The positive effects of multiple SABBs (Set2 and Setm4) showed significantly positive effects on soybean growth and defense through seed treatment. The microbial community patterns were not significantly different among seed treatments in the level of species richness and diversity (alpha-diversity). However, there was a significant difference in the community structure (beta diversity) in the rhizosphere compartment. Effects of Set2 and Setm4 on the microbiome structure in the root endosphere were not significantly different from the no treatment control. Nevertheless, the relative abundance of Bradyrhizobium was higher with the SABB mixtures treated. While, in the rhizosphere, more complex microbial network structure was observed with the treatment of Set2 or Setm4 compared to the no treatment control.

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