

Microbiome Mediated Crop Improvement

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Introduction

Microbes are coevolved with crops. Microbes interact with plants both positively and negatively. The rhizosphere, defined as the volume of soil shared by the roots and bacteria and by which the roots have influence is a region with intense microbial activities that play an important role in the acquisition of nutrients for the plants. The kind and number of bacteria in the rhizosphere differ from the bacterial community of the bulk soil. The diversity of microbes in the rhizosphere region is influenced by root exudations. This difference is influenced not only by the root exudates but also by the microbial activities in the roots. The microbial interactions are specific to each crop. The traditional genotypes harbour native microbial flora which are absent in modern cultivars. So, the study of these microbial interactions and root exudations from traditional genotypes and incorporating into modern cultivars will help to improve the growth, yield of the crops and nutritional status of the grain.

Plants co-evolve with their associated microbes, including those that may contribute to crop development. Nowadays, microbiome is realized as plants second genome (Berendsen *et al.*, 2012). Microbes and plants interact with each other in niches of plant and mostly their association is symbiotic. The carbon metabolites secreted by plant roots promote growth and activities of microbes in its rhizosphere. In turn, the rhizosphere microbes benefit plants by supplying nutrients, growth stimulating hormones and protect from biotic and abiotic stress. The root exudates of each plant serve as nutrient source help in specific colonization of microbes in their rhizosphere (Long-Jun *et al.*, 2019).

When art and science of plant breeding started in early 1800s, there were no chemical inputs applied in the soil, the evolved crops were depending upon organic manures for their potential performance, to some extent the crops retained their nutrient acquisition characteristics through microbes. Artificial fertilizers were applied to boost up the yields of



crops and selection of genotypes also done in fertilizers applied which resulted evolution of genotypes with improved translocation of nutrients than increased mobilization and acquisition the network was broken. So losing the root exudation characteristics resulted in commercial varieties which were fertilizer responsive, but having less fitness susceptible to pests, diseases and a biotic stress tolerance.

Yield of major crops are in diminishing trends globally. Maximum yield potentials are obtained where the soil is really fertile implicating the importance of microbes. Bio fertilizers to mobilize, acquire and translocate unavailable nutrients from soil and atmosphere have been routinely used viz., *Rhizobium*, *Bacillus*, *Pseudomonas*, *Azotobacter*, *Azospirillum*, Arbuscular mycorrhizae etc., in major crops, vegetables and perennials. Recent studies reveal that microbes and genotypes of crops have incompatibility issues which lead complete silencing of activity of microbes through inactivation of genes responsible for nutrients mobilization. Root exudation will attract microbes for colonization, but most of the modern high yielding varieties have less efficient root exudation and they were selected for higher fertilizer responsiveness. So evolution of genotypes with improved root exudation can acquire maximum microbes which will in turn improve the yield and fitness.

The Microbial Interactions are Specific to Each Crop:

Rice:

Rice is the staple food crop for more than 50% of world's population, but yield and accumulation of nutrient in the grain is very low. The bacterial community in rice rhizosphere is largely occupied by Proteobacteria, Acidobacteria, Actinobacteria and Chloroflexi phyla (Mendes *et al.*, 2011). The major genera are constituted by *Bacillus* and *Pseudomonas*. Rice has a huge genetic reservoir of local land races, wild cultivars which constitute a high level of native microbial diversity. They can be screened for efficient root exudations, and the traits can be incorporated into modern cultivars.

Legumes:

The legumes are inherently associated with the microbes. The significant genus associated with legume *Rhizobium* has host specificity among the legumes itself. These interactions will enable the legumes to produce protein rich seeds and foliage that are critical to many human and animal diets. The microbe mediated crop improvement in legume needed to be focused for enriched legume seeds.



Figure 1 : Variability of nodulation efficiency in redgram. 1A & 1 B) Nodulation efficient redgram genotypes viz., LRG 41 and BRG1. 2 A & 2 B) Nodulation in efficient genotypes of redgram viz., CO 8 and CO 7

Sugarcane:

It is an important sugar and energy crop that provides 60% of the raw material for the world's sugar and ethanol production. The studies have shown that sugarcane growth is affected by a variety of rhizosphere microorganisms. Actinomycetes and Bacillus are the major organisms which effect the growth of sugarcane. (Liu et al., 2020). The common biofertilizers for sugarcane are *Gluconacetobacter diazotrophicus* and *Azospirillum* which increases the nitrogen content, Phosphobacteria as P solubiliser are applied. The nutrient content of the sugarcane can be increase by incorporating microbial traits in the modern cultivars.

Millets:

The millet rhizosphere is composed of microbial communities with multifunctional traits which remained mostly unexplored (Prabha et al., 2019). The water and osmotic stress tolerance of these subtropic crops are attributed to the colonization and physiological activities of microflora by their systemic presence and niche oriented colonization. The major phyla in the mille rhizosphere are Actinobacteria and Proteobacteria. The exploration of microbial communities in millets is required for crop improvement.

Oilseeds:

The oil seeds need balanced uptake and utilization of micronutrients for accumulation of oil and increasing the seeds yield. Most of the times oil seeds show typical micronutrients

deficiency symptoms viz., groundnut with sulphur, iron and zinc deficiency, sunflower with zinc deficiency. Application of micronutrients and foliar application are effective to some extent for preventing yield losses, but every season, application is a must. Even then the nutrient use efficiency of micronutrients was not optimized. Their uptake is mainly depending upon solubilisation through secretion of low molecular weight organic acids secreted both by microbes and roots. It is important to identify oil seeds with enhanced rhizosphere activity for secretion of organic acids.

Traits to be Bred for Association with Microbiome:

1. Low input responses
2. Root exudation traits
3. Induced systemic acquired resistance against soil, seed borne plant pathogens and nematodes
4. Higher volatile releasing genotypes: to attract natural enemies for ecological engineering aspects of integrated pest management

Characterization of Donors of Plant genetic Resources for Microbiome Association:

1. Local land races/farmers varieties/traditional varieties grown by farmers with low input response practices viz., brown rice varieties, minor millets, minor pulses.
2. Crops grown in higher altitude regions with high levels of fertility and no input responses
3. Wild relatives: wild species will serve as important sources for exploitation of microbiome as they have no input responses and weedy growth habit.

Scope for Development of Microbiome Enhanced Varieties of Crops

1. maximum yields with low input applications viz., disease management and nutrients application
2. Improved soil fertility over a period of time by following systematic crop rotation with microbiome mediated genotypes which will increase the diversity and activity of beneficial microbes in the soil
3. Pre and probiotic quality enhancement of foods as associated microbes carried over from soil to grains.

The microbiome and root exudation is differed genotypically in crops. Root exudation will attract microbes for colonization. The modern high yielding cultivars have less efficient

root exudation and microbial diversity. So, these traits can be incorporated into modern cultivars from traditional cultivars and landraces for sustainable crop growth and nutrient enrichment of product.

References:

- Berendsen, R.L., Pieterse, C.M and Bakker, P.A. 2012. The rhizosphere microbiome and plant health. *Trends Plant Sci.* 2012 Aug;17(8):478-86. doi: 10.1016/j.tplants.2012.04.001.
- Liu, Y., Yang, H., Liu, Q., Zhao, X., Xie, S., Wang, Z. 2020. Effect of two different sugarcane cultivars on rhizosphere bacterial communities of sugarcane and soybean upon intercropping. *Frontiers in Microbiology.* 11:596472.
- Long-Jun Ding, Hui-Ling Cui, San-An Nie, Xi-En Long, Gui-Lan Duan, Yong-Guan Zhu, 2019. Microbiomes inhabiting rice roots and rhizosphere, *FEMS Microbiology Ecology.* 95:5. <https://doi.org/10.1093/femsec/fiz040>
- Mendes, R., Kruijt, M., De Bruijn, I., Dekkers, E., van der Voort, M., Schneider, J. H. & Raaijmakers, J. M. 2011. Deciphering the rhizosphere microbiome for disease-suppressive bacteria. *Science*, 332(6033): 1097-1100.
- Prabha R, Singh DP, Gupta S, Gupta VK, El-Enshasy HA, Verma MK. 2019. Rhizosphere Metagenomics of *Paspalum scrobiculatum* L. (Kodo Millet) Reveals Rhizobiome Multifunctionalities. *Microorganisms.* 7:608. <https://doi.org/10.3390/microorganisms7120608>