

Microbiome and Plant Health

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Recent researches have shown that plants are associated with plethora of microorganisms also called plant microbiome. Plant microbiome interactions primarily affect plant growth, development, plant -fitness and productivity. Depending upon the specific habitat of plant, microbial communities are mainly predominant in three different regions namely rhizosphere, phyllosphere and endosphere. The full range of microbes and their association with plants and hence maintenance of crop productivity has recently begun to be explored. In this article, we primarily focus on the interaction of plants and root associated bacteria enhancing plant mineral nutrition, summarizing the current knowledge in several research fields that can converge to improve our understanding of the molecular mechanisms underpinning this phenomenon.

Keywords: Inoculum, Microbiome, Plant health, Rhizosphere, Seed, Phyllosphere

Introduction

The plant microbiome also known as phytomicrobiome has recently become a very important aspect of research with plant scientist. This is mainly due to the strong evidences that have emerged that plant microbiome plays a very important role in maintaining plant health and crop production (Witton *et al.*, 2018). A better understanding of the plant microbe interactions and plant microbiome is expected to contribute significantly to the crop productivity in future. This article gives a glimpse of the recent developments in this area to indicate that this area is extremely important to explore in order to increase crop productivity in future.

The Plant Microbiome

The plant microbiome comprises of huge amounts of beneficial, commensal and pathogenic microorganisms that play critical essential roles in plant growth and maintaining plant health. (Naylor *et al.*, 2022). Recent studies have revealed that soil microorganism in association with plant microbiome especially in the rhizosphere are the facilitators of several plant processes. This they do by secreting hormones like auxins that help

in root growth changes. Some microbes take up iron from the soil and they solubilise phosphorus and make this nutrient available to the plants (Nelson, 2018). Plant microbiome provides protection against pathogens to the plants by indirectly activating the immune responses. The conversion of atmospheric nitrogen to ammonia is also taken by nitrogen fixers.

The plant microbiomes are very specific and their role to complex interconnected microbial networks that are important in plant health and ecosystem functioning has recently been explored (Babalola *et al.*, 2020). It will not be out of place to mention here that the plant microbiome is also specific to the genotype of plant, plant species, edaphic and other environmental factors, but the roles of this makeup are difficult to separate from each other in natural environments (Compant *et al.*, 2019). These microbial inhabitants in soil and around the plants are also responsible for production of antibiotics and fungal cell wall degrading enzymes. It has also been reported that by changing the genetic makeup of keystone microbial community, the overall performance of the plant can be enhanced. There are

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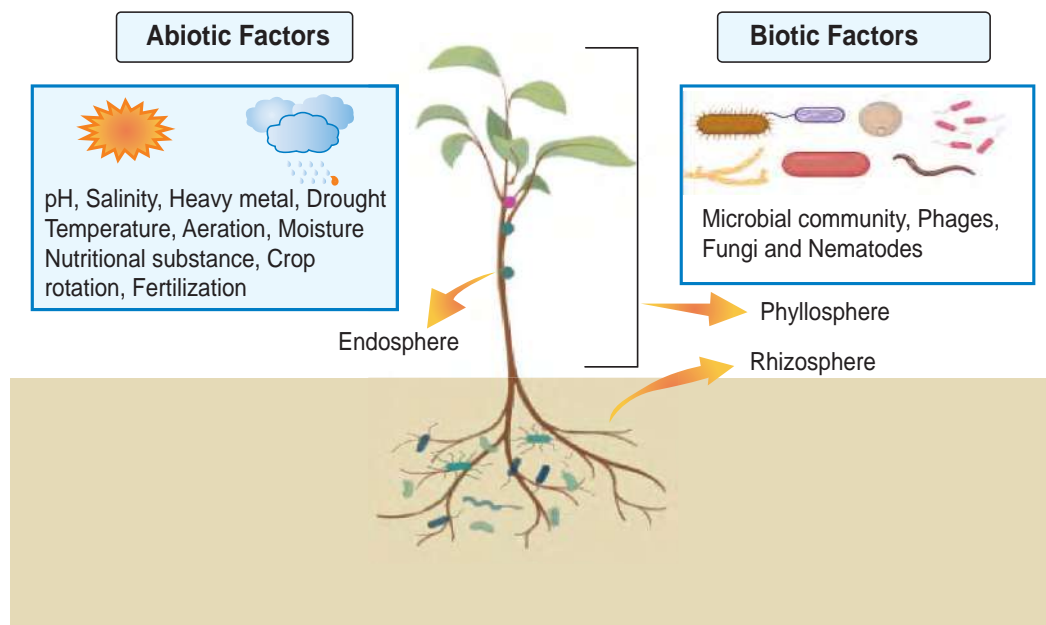


Fig. 1. Biotic and abiotic factors affecting the plant-microbe interaction

various biotic and abiotic factors that affect the soil microbiome interaction (Fig. 1).

The plant microbiome is primarily divided into: Rhizosphere, phyllosphere, endosphere and seed microbiome.

Rhizosphere Microbiome

Rhizosphere microbiome is very important for maintaining plant health. For instance, rhizosphere microbiome interactions have been proved to be beneficial in increasing stress tolerance and providing pathogenic resistance to plants. (Qu *et al.*, 2020) It was observed that in soyabean rhizosphere, the presence of limonene, naphthalene and pinene resulted in increased detoxification, reduced carbon metabolism pathways such as starch, mannose pathways and the available compounds were used as a carbon source. Rhizosphere bacteria like *Pseudomonas fluorescens* have utilised pinene as the source of carbon while the naphthalene was metabolized by several other bacterial genera including *Ralstonia*, *Pseudomonas*, *Streptomyces*, *Mycobacterium* etc (Lui *et al.* 2019). In other study, it was observed that the disease resistance in Cassava against *Xanthomonas axonopodis* pv. *manihotis* (Xam) was conferred by the *Lactococcus* sp., which produces nisin, a lantibiotic. It was also observed that the amylose content of cassava can be attributed to *Enterobacter cloacae* while the starch content and viscosity was provided by *Pseudomonas* and *Stenotrophomonas* sp (Zhang *et al.*,

2021). Genera like *Lysobacter* and *Aeromicrobium* which are prevalent in high pH agricultural soils produces some secondary metabolites. These metabolites are responsible for antimicrobial activities against many soil-borne pathogens in common bean (*Phaseolus vulgaris*) plant (Pérez-Jaramillo *et al.*, 2019). Recent-rhizospheric microbiome analysis of maize plant revealed that the most recent germplasm has evolved mechanisms for reduced nitrogen conversion and enhanced amino-acid synthesis when compared to the decade old microbiome (Van *et al.*, 2018). It suggested that the maize plant has a microbiome full of copiotrophs which resulted in decreased yields in modern agro-systems. Such results demand for inter-breeding processes to enhance the microbiome and can lead to differential soil-management practices. Rhizospheric microbiome can also act as a good indicator of soil-pollution and hence plant health (Wang *et al.*, 2019). Bamboo soil contaminated with heavy-metals like chromium has shown lesser concentrations of phylum Proteobacteria. Some species of phylum Acidobacteria (*Bryobacter* and *Granulicella*) and Actinobacteria (*Lamia* and *Arthrobacter*) have the ability to reduce the heavy metals like chromium in soil (Zhang *et al.*, 2020). Phylum Chloroflexi is known to perform anoxygenic photosynthesis using several inorganic elements as the electron donors. Drought-stress tolerance can also be brought about by engineering the rhizospheric microbiome of plants. Microbiota of phylum Betaproteobacteria and Actinobacteria

produces extracellular polysaccharides which resulted in better plant growth, enhanced water retention and high respiration rate in wheat seedlings (Jochum *et al.*, 2019).

Phyllosphere Microbiome

The plant leaf surface or phyllosphere represents a distinctive and diverse microbiome even though it is exposed to various abiotic stresses such as nutrient stress, ultraviolet radiations and desiccation. Bacteria, fungi, viruses, and cyanobacteria are the predominant colonizers of phyllosphere. Studies reveal that amongst bacteria, Proteobacteria (alpha-, beta-, and gammaproteobacteria), Bacteroidetes, Actinobacteria, and Firmicutes are the dominant phyla with *Bacillus* and *Pseudomonas* representing the most abundant genera. The other common species found are *Pantoea*, *Erwinia*, *Sphingomonas*, *Acinetobacter*, *Xanthomonas*, and *Gluconobacter*. (Thapa *et al.*, 2018). Yeast like fungus *Aureobasidium pullulans* is dominant in the phyllosphere as well on the surface of fruits. Common fungal genera occurring in the leaves are *Cladosporium*, *Alternaria*, *Penicillium*, *Acremonium*, *Mucor*, and *Aspergillus*, whereas commonly occurring yeasts are *Cryptococcus*, *Sporobolomyces*, and *Rhodotorula* (Thapa *et al.*, 2018). The diversity of Cyanobacteria is determined by the species of plant it inhabits and also on ecosystem. The dominant orders are Nostocales and Oscillatoriales (Stone *et al.*, 2018). These microbes interact with the host plant in several ways and promote plant growth directly by modulating phytohormones, improved nutrient acquisition by increasing their bioavailability and indirectly by pathogen suppression (Bashir *et al.*, 2022). The analysis of phyllosphere microbiome and community plays a vital role in framing policy related to sustainable agriculture and design of consortia for their use as inoculants for rhizoremediation, phytostimulation, and biocontrol and overall plant growth enhancement. Recent evidence suggests that neighboring plants also modulate the host phyllosphere microbiota via aerial dispersal and genetic factors (Shakir *et al.*, 2021; Meyer *et al.*, 2022).

Endosphere Microbiome

Complex microbial communities and microorganisms colonize internal parts of the plants (endosphere) and play significant role in plant's growth and health by, for example, making the plants resistant to many diseases or by other mutualistic interactions (Hassani *et al.*, 2018).

Studying endosphere microbiome, thus, constitutes an important aspect to understand and modulate plant traits, physiology and ecosystem functioning.

The structure of endosphere microbiome was found to be continuously varying during growth and wilting processes in plants (Liu *et al.*, 2019). For instance bacterial and fungal diversity increased with the development of banana plantlets with bacterial groups belonging to Enterobacteriaceae family found to be present with different relative abundance in all the samples (Dong *et al.*, 2019). The endosphere microbiome was engineered to improve *Fusarium* wilt resistance in banana plant (Liu *et al.*, 2019). Inoculation with engineered *Enterobacter* sp. and *Kosakonia* sp. for expression 1-Amino Cyclopropane-1-Carboxylate (ACC) deaminase on their cell walls increased resistance to *Fusarium* wilt disease as compared to controls without inoculations (Liu *et al.*, 2019). Similarly, *Pseudomonas* strain (LTGT-11-2Z) was found to be widespread in root endosphere microbiome of a desert plant *Alhagis parsifolia*. LTGT-11-2Z was found to promote drought resistance in wheat plant which pointed towards its potential to be a biotechnological agent that can make crop plants more resistant to drought conditions which would be very useful for agriculture (Zhang *et al.*, 2020).

To ascertain the influence of soil on the diversity of endosphere microbiome of roots and leaves (Pangesti *et al.*, 2020) mixed sterilize soil with 10% grass-grown soil and planted *Chrysanthemum* plants in the mixed soils. Control plants were raised in sterilized soils only. All the plants were exposed to thrips and then roots and leaves were collected from both the *Chrysanthemum* and control plants. Analysis of endosphere microbiome revealed increase in bacterial diversity post-inoculation only in the roots and not in the leaf tissues. Endosphere of both roots and leaves showed dominance of the Pseudomonadaceae family. In case of leaves Pseudomonadaceae was higher in abundance in inoculated plants than in control ones. Whereas in case of roots, abundance is higher in control plants. Rare bacterial families were mostly found in leaves, showing that bacterial communities in roots and leaves differed substantially and thus had differential impacts on their growth (Pangesti *et al.*, 2020).

Recently (Goodwin, 2022), endosphere microbiome study of Ginseng (*Panax* sp.) has shown that large number and types of fungal, bacterial, archeal and viral endophytes are present in its endosphere. Bacterial and

fungal endophytes are abundantly present in its roots and some of these endophytes are specific to tissues present above and below the ground. Many endophytes are found to metabolize ginsenosides which are major active pharmacological component of Ginseng. The ability of endosphere microbes to produce/metabolize ginsenosides shows that they acquire certain specific or altered genes which help them to grow in Ginseng apoplast.

It is thus very clear that endosphere microbiome studies, provide information for better understanding of the endophytes and plants interactions, adaptations and evolution. This can contribute towards designing and developing strategies for more sustainable microbe-based agriculture.

Seed Microbiome

Microbiome in plants has been extensively studied as microbes associated with both root (rhizosphere) and shoot (phyllosphere). To date, very less emphasis is given to the role of the microbiota that exists as part of the seed. Recent studies have shown that microbiomes affect the germination, health, and productivity of the plants in both agricultural and natural ecosystems (Nelson, 2018)

As all plant tissues have been reported to have endophytic and epiphytic microbial associations, seeds have also been reported to have both types of microbial associations reported as Endospermosphere and Spermosphere (Nelson, 2018). Seeds of different plants are associated with diverse microbial communities that depend on the genotype of the plant, its environment, and to some extent anthropogenic interventions. Bacterial and fungal populations are reported to be the abundant inhabitants of the seed microbiome, however, in the seeds of native alpine plants, Archaea has also been reported as newly discovered seed endophytes (Wassermann et al., 2019).

Deciphering the healthy microbiome can be essential for improving crop yield, and improved plant tolerance to biotic and abiotic stress. It can be targeted by harnessing seed microbiomes of wild crop cultivars and re-introduce missing beneficial seed microbes (Berg and Raaijmakers, 2018). The role of soil has also been shown to be pertinent as the transmission of microbiota to seed is majorly from the soil (Rocheffort et al. 2021). Recently, it has been shown that the endophytic seed microbiome can be altered by abiotic treatment and also by climatic stress (Bintarti et al., 2022)

Seeds being the carrier of the next generation of the plants and act as a primary inoculant for microbiota, future 'omic' studies targeted on seeds and will surely play a significant role in microbiome and plant.

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