International Journal of Agricultural Technology 2021Vol. 17(5):1727-1734
Available online http://www.ijat-aatsea.com
ISSN 2630-0192 (Online)

Phytomicrobiome: A potential resource for agriculture – Short Review

Gopikrishnan, V.[*], Radhakrishnan, M., Joseph, J., Abirami, B. and Manigundan, K.

Centre for Drug Discovery and Development, Dr. Col. Jeppiaar Research Park, Sathyabama Institute of Science and Technology, Chennai, Tamil Nadu - 600 119, India.

Gopikrishnan, V., Radhakrishnan, M., Joseph, J., Abirami, B. and Manigundan, K. (2021). Phytomicrobiome: A potential resource for agriculture – Short Review. International Journal of Agricultural Technology 17(5):1727-1734.

Abstract Plants are living with a plethora of microorganisms playing major roles for plant growth and health. Significant information is currently available on the structure, functional capabilities and dynamics of plant microbiota members. Due to present challenges in crop production and the interesting functional potential of plant microbiota is an urgent need to bring microbial innovations into practice and also for field improvement is required. Microbes like bacteria, fungi, actinobacteria etc. are playing a key role in association with plants. Smart, knowledge-driven selection of microorganisms is needed as well as the use of suitable delivery approaches and formulations. On the other hand, farming practices or the plant genotype can influence plant microbiota and thus functioning and improving the ecology soil ecosystem that indirectly affect the climate changes and stress tolerance. Therefore, various different avenues are improving the plant microbe interactions useful for betterment of plant breading. Still research areas like molecular mechanism of plant microbiome and signaling especially quorum sensing are the valuable for new generation could lead to a better use of the plant microbiome. This paper reviews the importance and functionalities of the plant microbiome.

Keywords: Plant microbiome, Ecosystem, Soil, Bacteria and agriculture

Introduction

Many studies revealed that extremely complex microbial assemblages associated with different plants and specific plant organs (Hurek *et al.,* 2015; Vorholt, 2012; Hardoim *et al.,* 2015). The microbial constituent of the plant holobiont, also termed as plant microbiota (comprising all microorganisms) or the plant microbiome (comprising all microbial genomes) in the rhizosphere, phyllosphere and endosphere has significant in the functions like supporting plant growth and health (Vorholt, 2012; Hardoim *et al.,* 2015; Lemanceau *et al.,* 2017).

---

[*] **Corresponding Author:** Gopikrishnan, V ; **Email:** gopivktk@gmail.com

Research taking place on soil mycobiome (Talbot *et al.*, 2014), phytobiome, or plant microbiome is currently growing along with bigger interest (Azcón *et al.*, 2014). At the same time, generating further information to help navigate towards an ecological and more sustainable agriculture is the focus of academics, non-governmental associations, and farmers (Specht *et al.*, 2015). Changes in greenhouse gas emissions, promotes loss of biodiversity, and increases pollution by applying synthetic fertilizers and pesticides are increasing (DeLonge *et al.*, 2016). Luckily, growing scientific research worldwide points to the preference for the establishment of more ecological sustainable farming systems (Pagano *et al.*, 2016). Accordingly, linking microbial ecological interactions to global nutrient cycling, chemical pollution, green-house gas emissions, carbon (C) and nitrogen (N) management in natural or managed ecosystems within the context of global biodiversity alterations, and microbial diversity loss, is needed (Saleem and Moe, 2014). This review will focus on the role of plant microbiome and its benefits to the plants and its ecosystem.

The plant microbiome

The phytobiome is composed of plants, their environment and diverse interacting microscopic and macroscopic organisms, which together influence plant health and productivity. These organisms form complex networks that are established and regulated through nutrient cycling, competition, antagonism and chemical communication mediated by a diverse array of signaling molecules. Integration of knowledge of signaling mechanisms with that of phytobiome members and their networks will lead to a new understanding of the fate and significance of these signals at the ecosystem level. Such an understanding could lead to new biological, chemical, and breeding strategies to improve crop health and productivity (Leach *et al.*, 2017).

What makes up the phytobiome?

The first stage toward resolving phytobiome function has been exploration of the composition, distribution, and abundance of organisms within plant-associated communities. Plants associate with billions of organisms in millions of species, from viruses to arthropods, whose gene repertoires far surpass those of plants themselves. Metataxonomic approaches are high-throughput processes used to characterize the entire microbiota and allow comparisons of relationships among microbiome members (Marchesi and Ravel, 2015). Such approaches targeting bacterial and fungal composition have shown that genotype, environment, and plant compartment (i.e., spermosphere, endosphere, rhizosphere, phyllosphere) all influence community composition to varying degrees (Figure 1) (Hartmann *et al*., 2008). The plant aerial surface, or phyllosphere, which experiences fluctuations in nutrient availability and environmental conditions, harbors a more distinct microbiome compared with the more environmentally stable rhizosphere (zone of soil that is directly influenced by the plant root) (Remus-Emsermann *et al*., 2012; Hacquard *et al*., 2015). Whole-metagenome sequencing (WMS) studies, which offer a more comprehensive view of nonbacterial organisms, have determined that bacteria dominate all plant compartments and that bacterial diversity and density are highest in the rhizoplane (external root surface) (Hacquard *et al*., 2015). The finding that plant genotype and plant niche can drive community composition has important implications for crop-improvement programs.

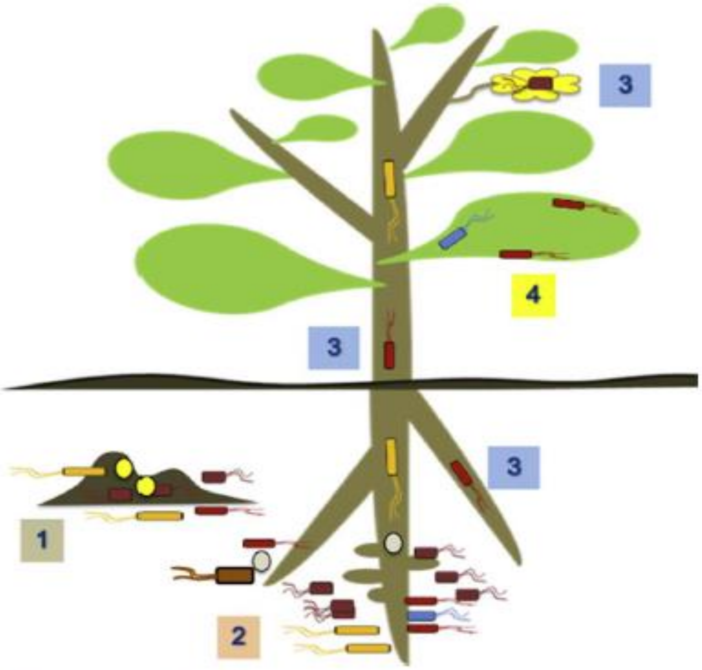

Figure 1. The plant microbiome. (1) Bulk soil: the soil outside the rhizosphere where the root metabolites cannot influence the microbes but where the microbes can nevertheless exert some influence on the plant roots,(2) Rhizosphere: a narrow zone of soil where microbes are found in high concentrations and are influenced by plant exudates,(3) Endosphere: The internal regions of plant tissues inhabited by endophytic microbes,(4) Phylosphere: the surface and apoplast of leaf tissues

Signals for communication within the phytobiome

Communication within and among kingdoms is integral to phytobiome function. While some interactions are mediated by physical cues, such as vibration or blockage of light, most signals are chemical in nature, including lipids, peptides, polysaccharides, and volatile metabolites.

Bacterial Signals

Bacterial quorum sensing (QS) autoinducers, such as N-acyl homoserine lactones (HSLs), lipid-like diffusible signal factors (DSF), and signaling peptides, are among the best-studied communication signals in the phytobiome. Autoinducers mediate plant colonization behaviors, including biofilm development, adhesion and motility, virulence, and production of cell-wall-degrading enzymes. HSLs are produced by a large proportion of rhizosphere strains (Schaefer *et al.,* 2013) and may be conveyed among bacterial cells separated by up to 70 mM (Elasri *et al.*, 2001). QS signals may mediate interspecies competition or cooperativity. In a microbial consortia, bacteria may respond to ‘‘self’’- like autoinducers from other species; the HSL signals required for virulence in the olive knot pathogen *Pseudomonas savastanoi* can be supplied by nonpathogenic species on the plant (Hosni *et al*., 2011). Signals may activate competitive inhibition mechanisms of neighboring bacteria, like antibiotic expression in *P. fluorescens* (Dubuis *et al.,* 2007). Quorum quenching, or autoinducer degradation, among bacteria in the phytobiome can affect the behavior of biocontrol and pathogenic species alike, potentially causing beneficial or detrimental effects to the plant (Teplitski *et al.*, 2011). Bacterial signaling by lipochitooligosaccharide NOD factors and exopolysaccharides, used to establish nodulation symbiosis and confer host specificity, has been reviewed extensively. Less well characterized are the signaling roles of diverse microbial volatile organic compounds (VOC) produced by bacteria. Production of the volatile compound indole can affect biofilm formation, virulence factor production, and stress survival mechanisms in nearby bacteria (Lee *et al.*, 2015). Some volatiles relay a message through alteration of the physical environment: the soil-inhabiting *Streptomyces venezualeae* releases the volatile organic compound trimethylamine, which modifies local pH levels to trigger exploratory activity in physically separated Streptomyces (Jones *et al.,* 2017).

QS and volatile signals play important roles in interkingdom communication. Algal zoospores are attracted to bacterial biofilms, their major food source, by perceiving HSLs (Tait *et al.,* 2005). Plant roots may actively take up, perceive, or systemically transport some HSLs, causing measurable hormonal and developmental effects (Hartmann *et al*., 2014). Bacterial VOC can also modulate plant development and defense, with specific volatile blends activating distinct defense and developmental pathways in different plants (Kanchiswamy *et al.*, 2015). Convergent evolution of indole acetic acid biosynthesis in bacteria, microalgae, fungi, and plants suggest that natural selection might have favored indole signaling as a widespread physiological code (Fu *et al.*, 2015). Other phytobiome members can actively enhance or thwart autoinducer signaling through signal degradation, mimicry, inhibition, or induction mechanisms. HSL levels were rapidly diminished when added to the root systems of lotus and clover, but not to those of wheat or corn (Delalande *et al.*, 2005). Some plant secondary metabolites inhibit QS signaling (Vikram *et al.*, 2010), while the metabolites rosmarinic acid and lumichrome are true HSL mimics that bind directly to QS receptors (Corral-Lugo *et al.*, 2016).

Fungal Signals

Fungi employ chemical signals to regulate sexual reproduction, sporulation, and development. Cell-cell recognition signals employed in mating include cyclic AMP or, in the maize pathogen Ustilago maydis, short peptide pheromones (Szabo *et al.*, 2002). Mycorrhizae establish communication with hosts through Myc factors, or chitooligosaccharides that are recognized by receptors in the plant (Smith *et al.*, 2015). Like bacteria and insects, fungi emit species-specific VOC profiles with diverse properties, although only a fraction of these have been studied in detail. Among these, oxygenated lipid pheromones—or oxylipins— are important in regulating development and pathogenesis in fungi (Tsitsigiannis and Keller, 2007). Other fungal VOC may affect the phytobiome through direct antimicrobial activity (Kanchiswamy *et al.*, 2015), but relatively little is known about their roles as intraspecies or interspecies signals.

Fungal signals also are prone to perception or interference by other members of the phytobiome. Plant-produced oxylipins may mimic those of fungi and can regulate fungal development and mycotoxin production during pathogenesis (Gao and Kolomiets, 2009). Similarly, plant mimicry of fungal VOC may serve to attract insect pollinators (Kaiser, 2006). Several fungal VOC affect the motility or exopolysaccharide production of soil bacteria (Schmidt *et al.*, 2016). Insects, microscopic arthropods, nematodes, and earthworms may also perceive and respond to fungal VOC (Werner *et al.*, 2016). Fungal VOC can prime systemic resistance in plants or suppress plant growth, as seen in the induction of lateral root growth by a sesquiterpene from the mycorrhizae

Laccaria bicolor (Li *et al.,* 2016). Some VOC effects on plants appear to be species-specific, but the mechanisms of their perception and function and their overall significance in the phytobiome, are not yet understood.

Conclusions

Research work on plant microbiomes has benefited from holistic ecological studies on one-hand and reductionist mechanistic discoveries on the other. Plant–microbe interactions as well as the molecular mechanisms that facilitate the yield and the ecological processes of plant ecosystem. Increasing the research on the generation of large isolate collections and the study of synthetic microbial communities in combination with plant genetic resources, will allow us to understand the plant–microbe interactions in nature and in agriculture and will contribute extensively to the next green revolution.

Exploration of plant–microbe interactions for bioenergy crop production are numerous and diverse. In the upcoming, plants and their beneficial symbionts both will be modified to enhance biomass production for a rising population in an altering climate. Major research areas for optimizing beneficial plant–microbe interactions include QS, bacterial motility, biofilm formation and the plant–microbe signalling pathways, particularly those specific to obligate endophytes. In addition, efficient viewing of plants growing in extreme environments are associated with novel microbes harbouring new genes and pathways conferring abiotic stress tolerance, and grow potentially, for optimization and application in energy crops destined for growth on insignificant soils.

Reference

Azcón, R. (2014). Mycorrhizosphere: The role of PGPR. In Root Engineering; Morte, A., Varma, A., Eds.; Springer: Berlin, Germany, pp.107-144.

Corral-Lugo, A., Daddaoua, A., Ortega, A., Espinosa-Urgel, M. and Krell, T. (2016). Rosmarinic acid is a homoserine lactone mimic produced by plants that activates a bacterial quorum-sensing regulator. Science Signaling, 9:1-10.

Delalande, L., Faure, D., Raffoux, A., Uroz, S., D’Angelo-Picard, C., Elasri, M., Carlier, A., Berruyer, R., Petit, A., Williams, P. and Dessaux, Y. (2005). N-hexanoyl-L-homoserine lactone, a mediator of bacterial quorum-sensing regulation, exhibits plant-dependent stability and may be inactivated by germinating Lotus corniculatus seedlings. FEMS Microbiology Ecology. 52:13-20.

DeLonge, M. S., Miles, A. and Car, L. (2016) Investing in the transition to sustainable agriculture. Environmental Science & Policy, 55:266-273.

Dubuis, C., Keel, C. and Haas, D. (2007). Dialogues of root-colonizing biocontrol pseudomonads. European Journal of Plant Pathology, 119:311-328.

Elasri, M., Delorme, S., Lemanceau, P., Stewart, G., Laue, B., Glickmann, E., Oger, P. M. and Dessaux, Y. (2001). Acyl-homoserine lactone production is more common among plant-associated Pseudomonas spp. than among soil borne *Pseudomonas* spp. Applied and Environmental Microbiology, 67:1198-1209.

Fu, S.-F., Wei, J. Y., Chen, H. W., Liu, Y. Y., Lu, H. Y. and Chou, J. Y. (2015). Indole-3-acetic acid: A widespread physiological code in interactions of fungi with other organisms. Plant Signaling & Behavior, 10:1048052.

Gao, X. and Kolomiets, M. V. (2009). Host-derived lipids and oxylipins are crucial signals in modulating mycotoxin production by fungi. Toxin Reviews, 28:79-88.

Hacquard, S., Garrido Oter, R., González, A., Spaepen, S., Ackermann, G., Lebeis, S., et al. (2015). Microbiota and Host Nutrition across Plant and Animal Kingdoms. Cell Host & Microbe, 17(5): 603-613. doi:10.1016/j.chom.2015.04.009.

Hardoim, P. R., Overbeek, L. S., Berg, G., Pirttilä, A. M., Compant, S., Campisano, A., et al. (2015). The hidden world within plants: ecological and evolutionary considerations for defining functioning of microbial endophytes. Microbiology and Molecular Biology Reviews, 79:293-320.

Hartmann, J., Boulet, C. and Robert, D. (2008). Collisional effects on molecular spectra: laboratory experiments and models, consequences for applications, Elsevier Sci., Amsterdam.

Hurek, B., Büinger, W., Burbano, C. S., Sabale, M. and Hurek, T. (2015). Roots shaping their microbiome: global hotspots for microbial activity. Annual Review of Phytopathology, 53:403-24.

Jones, S. E., Ho, L., Rees, C. A., Hill, J. E., Nodwell, J. R. and Elliot, M. A. (2017). Streptomyces exploration is triggered by fungal interactions and volatile signals. eLife, 6:21738.

Kaiser, R. (2006). Flowers and fungi use scents to mimic each other. Science, 311:806-807.

Kanchiswamy, C. N., Malnoy, M. and Maffei, M. E. (2015). Chemical diversity of microbial volatiles and their potential for plant growth and productivity. Frontiers in Plant Science, 6:151.

Leach, J. E., Triplett, L. R., *et al. (*2017). Communication in the Phytobiome. Cell, 169:587-596.

Lee, J. H., Wood, T. K. and Lee, J. (2015). Roles of indole as an interspecies and interkingdom signaling molecule. Trends in Microbiology, 23:707-718.

Lemanceau, P., Blouin, M., Muller, D. and Loccoz, Y. (2017). Let the core microbiota be functional. Trends in Plant Science, 22:583-95.

Li, N., Alfiky, A., Vaughan, M. M. and Kang, S. (2016). Stop and smell the fungi: Fungal volatile metabolites are overlooked signals involved in fungal interaction with plants. Fungal Biology Reviews, 30:134-144.

Marchesi, J. R. and Ravel, J. (2015). The vocabulary of microbiome research: a proposal. Marchesi and Ravel Microbiome , 3:31.

Pagano, M. C., Dantas, B. D., Weber, O. B., Correa, E. A., Tancredi, F. D. Duarte, N. F., Bago, A. and Cabello, M. N. (2016). Mycorrhizas in Agroecosystems. In Recent Advances on Mycorrhizal Fungi; Pagano, M.C., Ed.; Springer: Basel, Switzerland, 91-100.

Remus-Emsermann, M. N. P., Tecon, R., Kowalchuk, G. A. and Leveau, J. H. J. (2012). Variation in local carrying capacity and the individual fate of bacterial colonizers in the phyllosphere. ISME J., 6:756-765.

Saleem, M. and Moe, L. A. (2014).Multitrophic microbial interactions for eco- and agro-biotechnological processes: Theory and practice, Trends in Biotechnology, 32:529-537.

Schaefer, A. L., Lappala, C .R., Morlen, R. P., Pelletier, D. A., Lu, T. Y., Lankford, P. K., Harwood, C. S. and Greenberg, E. P. (2013). LuxR- and luxI-type quorum-sensing circuits are prevalent in members of the Populus deltoids microbiome. Applied and Environmental Microbiology, 79:5745-5752.

Schmidt, R., Etalo, D. W., de Jager, V., Gerards, S., Zweers, H., de Boer, W. and Garbeva, P. (2016). Microbial small talk: Volatiles in fungal–bacterial interactions. Frontiers in Microbiology, 6:1495.

Smith, D. L., Praslickova, D. and Ilangumaran, G. (2015). Inter-organismal signaling and management of the phytomicrobiome. Frontiers in Plant Science, 6:722.

Specht, A., Guru, S., Houghton, L., Keniger, L., Driver, P., Ritchie, E. G., Lai, K. and Treloar, A. (2015). Data management challenges in analysis and synthesis in the ecosystem sciences. Science of the Total Environment, 534:144-158.

Szabo, Z., Tonnis, M., Kessler, H. and Feldbru ̈gge, M. (2002). Structure-function analysis of lipopeptide pheromones from the plant pathogen Ustilago maydis. Molecular Genetics and Genomics, 268:362-370.

Tait, K., Joint, I., Daykin, M., Milton, D. L., Williams, P. and Ca ́mara, M. (2005). Disruption of quorum sensing in seawater abolishes attraction of zoospores of the green alga Ulva to bacterial biofilms. Environmental Microbiology, 7:229-240.

Talbot, J. M., Bruns, T. D., Taylor, J. W., Smith, D. P, Branco, S., Glassman, S. I., Erlandson, S. z, Vilgalys, R., Liao, H. L., Smith, M. E. *et al.* (2014). Endemism and functional convergence across the North American soil mycobiome. Proceedings of the National Academy of Sciences, 111:6341-6346.

Teplitski, M., Mathesius, U. and Rumbaugh, K. P. (2011). Perception and degradation of N-acyl homoserine lactone quorum sensing signals by mammalian and plant cells. Chemistry Review, 111:100-116.

Tsitsigiannis, D. I. and Keller, N. P. (2007). Oxylipins as developmental and host-fungal communication signals. Trends in Microbiology, 15:109-118.

Vikram, A., Jayaprakasha, G. K., Jesudhasan, P. R., Pillai, S. D. and Patil, B. S. (2010). Suppression of bacterial cell-cell signalling, biofilm formation and type III secretion system by citrus flavonoids. Journal of Applied Microbiology, 109:515-527.

Vorholt, J. A. (2012). Microbial life in the phyllosphere. Nature Reviews Microbiology, 10:828-40.

Werner, S., Polle, A. and Brinkmann, N. (2016). Belowground communication: impacts of volatile organic compounds (VOCs) from soil fungi on other soil-inhabiting organisms. Applied Microbiology and Biotechnology, 100:8651-8665.

(Received: 18 June 2021, accepted: 30 August 2021)