

Phyllospheric microbiomes for agricultural sustainability

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EDITORIAL

Plants phyllosphere, or aerial surface, is the largest and peculiar microbial habitat throughout the world, supporting rich and varied species of bacteria, fungi, viruses, cyanobacteria, actinobacteria, nematodes, and protozoans. The physiology of the host and the functioning of the ecosystem are influenced by these diversified microbial communities, which are linked to the host's unique functional characteristics. The last few years have seen remarkable progress in elucidating a number of phyllosphere microbiology-related issues, including diversity and the composition, dynamics, and functional relationships of microbial communities. This highlights the influence of both ecological and evolutionary considerations, resulting in the classification of microbial species and the identification of keystone species or microbial hubs, which are facilitated by networking and communication between kingdoms. Characteristics that support growth and survival in the hostile environment of the phyllosphere are the production of hormones, pigments, volatiles, extracellular polysaccharides, cross-kingdom signaling, and quorum sensing. Recent scientific and technological developments have made it easier to use phyllosphere microbiota; in particular, developments in genomic and metagenomics methodologies provide new opportunities to comprehend the role of phyllosphere microbiota on plant growth promotion (PGP).

A plant serves as a variety of habitats for different endophytic and epiphytic microbial lineages to colonize interior tissues and plant surfaces both above and below ground. The aerial portions of plants, recognized as the phyllosphere, offer an immensely dynamic and ecologically significant environment for the development of microbial colonization [1]. The phyllosphere is regarded as one of the most active and expanding biological surfaces, offering an ideal habitat for nematodes, bacteria, fungi, algae, protozoa, and archaea. The phyllosphere is thought to contribute over 60% of the biomass of all taxonomic plants on Earth, making it an appropriate candidate for microbial colonization [2]. The word "phyllosphere" was initially used by plant pathologist F.T. Last to describe a microhabitat on the leaf surface where peculiar microorganisms are similar to the rhizosphere in plant roots. With a total leaf surface area of about 1,017,260,200 km² and an estimated 10²⁶ bacterial cells, the phyllosphere represents

promising opportunities for integrative research on microbial communities associated with the phyllosphere and their function in environmental sustainability [3].

The phyllosphere can be categorized into different groups based on a variety of plant surfaces, including the carposphere (fruit surface), caulosphere (stem surface), anthosphere (flower surface), and phylloplane (leaf surface) [4]. Recent advances in our knowledge of phyllosphere microbiology suggest that the phyllosphere interface can be divided into two areas that overlap and are closely related: the phylloelma, which represents the leaf surface waterscape, and the phylloplane, which represents the leaf surface landscape [5]. Each of these areas has a distinct dimensional niche that allows a wide variety of microbial communities to colonize it. The majority of a plant's phyllosphere is composed of its leaves, which are home to several microbial communities [4]. Among the various plant surfaces that are home to microorganisms, the phyllosphere represents poor nutrients but is generally a dynamic environment. Only a small portion of the microbial communities can be grown in a lab setting; the majority are not isolated due to the high influx of abiotic factors and frequent exposure to various environmental cues [6]. There are still knowledge gaps that need to be filled despite the phyllosphere microbiome having been the subject of much research in recent years.

Plant performance is significantly impacted by the phyllosphere microbiome, which in turn offers a unique habitat for a variety of microorganisms. Plant-associated microbiome interactions are essential for host function and environmental stress tolerance [7]. Due to the varied microenvironments (habitats) of phyllosphere, it contains a heterogeneous collection of microbial associations at the micrometer scale area. The phyllospheric microorganisms have adapted to the harsh environmental circumstances. In particular, microbial epiphytes are more exposed to light, UV rays, temperature, water, and nutrition availability in the atmosphere. These outside variables have an impact on the diversity and make-up of phyllospheric microbial communities [2]. A wide variety of actinomycetes, bacteria, fungi, and viruses make up the phyllosphere's microbiome. The physiochemistry, habitat, and host plant immunity have an effect on the diversity, dispersal, and development of microbial communities on the leaf surface. A colonization process is an important process in which the host plant and the microorganism have both benefited [8].

Agricultural and native plant phyllosphere is dominated by members of the phyla Proteobacteria, Firmicutes, and Actinobacteria, while the relative abundance of each taxa can vary based on phenotype, season, location, plant species, and human activity [9]. In a report,

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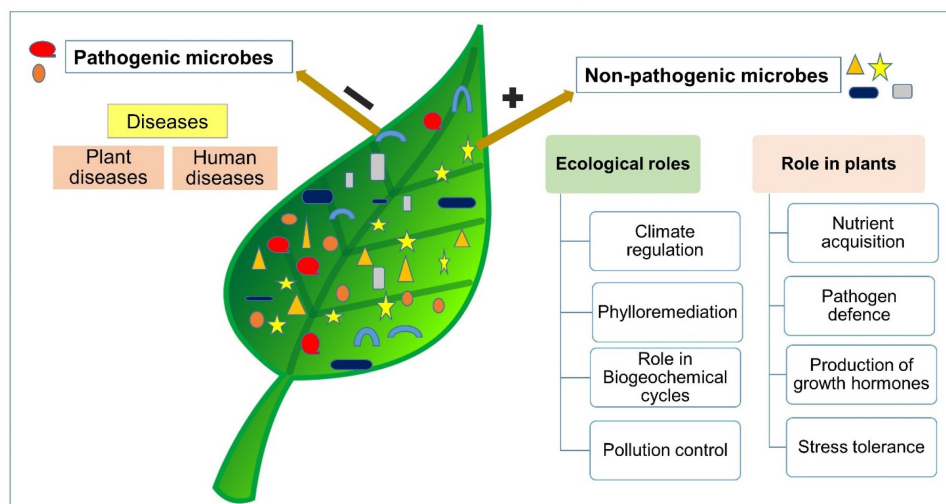


Figure 1. Important roles of phyllosphere microbiome. Adapted with permission from Bashir [1].

Ogata-Gutiérrez *et al.* [10] revealed the isolation and characterization of phyllobacteria from *Coffea arabica*. In another report, *Ancylobacter crimeensis* sp. nov., a new species of aerobic methylotrophic bacteria was isolated from the phyllospheric region of the oak plant [11]. In an investigation, Liu *et al.* [12] reported the isolation of *Bacillus velezensis* from tobacco leaves in Luzhou. In another investigation, Abadi *et al.* [13] studied the diversity of culturable N_2 -fixing bacteria in the phyllospheric region of the maize plant.

The phyllospheric microbiomes have an impact on the host plants' function and health (Fig. 1). They can function as antagonistic pathogens, commensals that use the leaf habitat for their own growth and reproduction, or mutualists that encourage plant growth and tolerance to environmental stressors [8]. Phyllospheric microbes have been shown to have a positive impact on plant growth through a variety of mechanisms, such as increased nutrient availability through nitrogen (N_2) fixation, solubilization of phosphorous (P), potassium (K), and zinc (Zn), and the generation of growth-promoting hormones and siderophores. The indirect mechanism of PGP includes pathogen inhibition by antagonistic phyllospheric microorganisms, 1-aminocyclopropane-1-carboxylate (ACC) deaminase enzyme production, secretion of exopolysaccharides, and mitigation of abiotic stresses [14]. The most prevalent PGP bacteria found in the phyllosphere were those belonging to the genera *Bacillus*, *Enterobacter*, *Microbacterium*, *Methylobacterium*, *Stenotrophomonas*, *Pseudomonas*, *Pseudarthrobacter*, and *Kocuria* [15].

In an investigation, Abadi *et al.* [16] reported that *Microbacterium arborescens* and *Stenotrophomonas maltophilia* with the ability to secrete indole-3-acetic acid (IAA) had a positive influence on the dry weight of the maize shoot. *Enterobacter hormaechei* was the most successful treatment in increasing the absorption of the majority of nutrients, exhibiting notable nitrogenase activity, P solubilization, and IAA generation. Five potential strains from the phyllosphere of the cotton plant, *Pseudomonas stutzeri*, *Acinetobacter* sp., *Bacillus mojavensis*, *Pseudomonas chlororaphis*, and *Enterobacter asburiae*, were found to have PGP potentials such as siderophore and IAA production, P, Zn, and K solubilization Sharath *et al.* [17]. In a report, Herpell *et al.* [18] studied that *Paraburkholderia dioscoreae*, a yam phyllosphere symbiont, colonizes the tomato phyllosphere and promotes plant growth by action of its ACC deaminase activity. In another report, Geat *et al.* [19] demonstrated the efficacy of phyllospheric growth-promoting and antagonistic bacteria including

B. velezensis, *Bacillus amyloliquefaciens*, *Pseudomonas fluorescens*, and *Stenotrophomonas rhizophila* for management of black rot disease of cauliflower incited by *Xanthomonas campestris* pv. *Campestris*.

The phyllosphere is a comprehensive regulatory network comprising various plant-associated characteristics that affect the physiological and metabolic processes of host plants directly or indirectly, controlling plant growth, development, reproduction, and systemic resistance mechanisms [20]. The phyllospheric microbiota protects the host plant from phytopathogenic microorganisms, maintains the plant's developmental dynamics by increasing the production of phytohormones, maintains biogeochemical balances, maintains absorption of nutrients and acquisition, and improves agronomic sustainability, ecosystem functioning, and productivity [21]. Agro-ecosystem sustainability and agricultural productivity are enhanced by the widely recognized function of phyllospheric microbial communities as potential biofertilizers, biological pesticides, and phytostimulators, which demonstrate their significance in sustaining plant development and systemic immunity [6]. By synthesizing bioactive metabolites such as alkaloids, terpenes, their derivatives, steroids, and antioxidant enzymes, they give host plants resistance against phytopathogenic invasion [22]. Since the beginning of time, plants and plant-based microbiota have been intrinsically linked and have a distinctive impact on one another's physiological and metabolic processes. The phyllospheric associated microbial communities also significantly increased the metabolic profile and physiological pattern, which improved the host plants' capacity to absorb resources, acquire nutrients, and withstand stress from a wider variety of environmental factors and phytopathogens [1].

The phyllosphere is a peculiar microbial environment that is extensively populated by numerous microbial communities that play a variety of roles in the ecology and growth of plants. Despite the fact that the mechanisms influencing microbial dynamics are now well established, our knowledge is limited to specific groups of microorganisms, and we still do not fully understand how the major groups of microbiota interact and perform. In addition, we still do not fully understand the phyllosphere microbiota, their roles, and the factors that influence ecosystems. Additionally, in the realm of biological invasion, while the phyllosphere microbial diversity of certain invasive plants has been described, their contribution to the spread of introduced species remains unclear, necessitating more ecological research on the microbial interactions influencing the unusual behavior of these plant

species. Gaining a thorough understanding of phyllosphere habitat is extremely difficult, and current research is only partially sufficient. Thus, further research is required to comprehend the molecular interactions between diverse microbial populations and the host phyllosphere in various environments, since this could lead to a number of novel insights in biological and ecological systems. The identified gaps need to be filled by future research, which should primarily focus on identifying the: phyllosphere microbiome and its organization rules in the leaf core; plant characteristics that contribute to the immigration of selective beneficial microbial populations; biological diversity of leaf exudates and how they affect the integration of leaf microbial; microbial-specific genes and their characteristics that enhance plant and ecosystem functioning; implications of current environmental factors on phyllosphere microbiota and their resilience mechanisms; and profitable microbial consortia that could be used commercially in the agricultural, pharmaceutical, and other domains.

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CONFLICTS OF INTEREST

The authors report no financial or any other conflicts of interest in this work.

USE OF ARTIFICIAL INTELLIGENCE (AI)-ASSISTED TECHNOLOGY

The authors declare that they have not used artificial intelligence (AI)-tools for writing and editing of the manuscript, and no images were manipulated using AI.

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