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# Diversity, Interaction, and Bioprospecting of Plant-Associated Microbiomes

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Received: 10 October 2020; Accepted: 11 October 2020; Published: 13 October 2020

**Abstract:** Plant-associated microbiomes have been suggested as pivotal for the growth and health of natural vegetation and agronomic plants. In this sense, plant-associated microbiomes harbor a huge diversity of microorganisms (such as bacteria and fungi) which can modulate the plant host response against pathogens and changing environmental conditions through a complex network of genetic, biochemical, physical, and metabolomics interactions. Advances on next-generation omic technologies have opened the possibility to unravel this complex microbial diversity and their interactive networks as never described before. In parallel, the develop of novel culture-dependent methods are also crucial to the study of the biology of members of plant-associated microbiomes and their bioprospecting as sources of bioactive compounds, or as tools to improve the productivity of agriculture. This Special Issue aims to motivate and collect recent studies which are focused on exploring the diversity and ecology of plant-associated microbiomes and their genetic and metabolic interactions with other microorganisms or their plant hosts, as well as their potential biotechnological applications in diverse fields, such as inoculants for agriculture.

**Keywords:** bioprospecting; inoculants; plant growth-promoting bacteria; plant microbiome; plant–microbe interactions

## Introduction

Currently, the study of plant-associated microbiomes in natural and agroecosystems is a research area of huge interest for microbiologists, ecologists, biotechnologists, and agriculturists, because microorganisms play a crucial role in the growth, health, and productivity of their plant hosts. In this sense, plants are complex organisms containing diverse external (e.g., phyllosphere, rhizoplane, and phylloplane) and internal (e.g., endosphere, endorhiza, and spermosphere) compartments, where the plant host provides a habitat and nutrients to the microorganisms (mainly bacteria and fungi), inducing their colonization, proliferation, interaction, and association. In contrast, microorganisms can provide to the host plant nutrients (e.g., atmospheric nitrogen fixation and soil phosphorus solubilization), growth inducers (e.g., auxins and cytokinin), and protection against pathogens by releasing of bioactive compounds (e.g., antimicrobial and siderophores), among others. Thus, current evidence shows the growth, tolerance, and health of many plants can be modulated by members of their associated microbiomes; however, our knowledge on the diversity, interactions, and biotechnological potential is still very limited, and further discoveries need to occur to improve the productivity of agricultural crops, as well as to protect natural vegetation against the changing environmental conditions.

The ecological interactions are probably one of the most important and complex aspects in the study of microbial communities that comprise the plant-associated microbiomes. In recent years, next-generation omic technologies, such as high-throughput sequencing (HTS), have significantly expanded our knowledge on the abundance and composition of microbial communities present in plants and their surrounding environments [1]. However, the analysis of microbial communities is difficult, due to the complex intracommunity relationships shared between their microbial components. In this sense, co-occurrence analyses have unraveled that microbes do not prosper as individual units, but rather as complex connected and interactive networks [2]. Such analyses hold special importance to understand how microbe–microbe associations modulate the plant responses to the changing environmental factors [3–5]. Omic studies have suggested that certain keystone taxa or key phylotypes govern the networking interactions between community members, expanding our knowledge about how microbes adapt to the plant's environmental pressures [6]. The occurrence of those microbial indicators or key taxa has been reported in a wide range of samples of planted soil [7] and plant compartments (rhizosphere, endosphere, and phyllosphere) [8], as well as in plants grown in agricultural soils or extreme environments [9,10]. However, the molecular mechanisms that modulate these plant–microbe selections and interactions are still poorly understood at the community level; thus, deeper studies are highly required.

On the other hand, plant-associated microbiomes comprise members that can be beneficial, neutral, or pathogenic to their hosts. In this context, beneficial microorganisms, also named as plant growth-promoting microorganisms (PGPM), have been widely studied and proposed as inoculants (e.g., biofertilizer, biostimulators, and biopesticides), mainly due to their capacity to produce or regulate the concentrations of growth factors, control of pathogens, and increase the availability of essential nutrients for plants [11]. In addition, the plant benefits can be improved when members of different taxa can exert a combined effect, such as fungi and bacteria, where fungi transport water, soil metabolites, and nutrients to the plant and parallelly act as 'highways' for PGPM dispersion within the plant–soil continuum [12]. Thus, the positive effect of inoculants formulated with fungal strains, bacterial strains, or their combination has been reported in many crops, categorizing them as effective microbial probiotics for agroecosystems [13,14]. However, the use of traditional culture-based methods has resulted in a limited diversity of isolated microbial taxa for their bioprospecting [15], where it is estimated that 1% (or less) of the environmental bacteria can be cultured, compared with the diversity revealed by HTS [16].

During the last few years, novel culture-dependent methods have been developed to unravel the diversity, activity, and biotechnological potential of previously "unculturable" microbial taxa present in plant compartments. Some novel techniques have focused on mimicking of the natural environment (e.g., nutrient availability, pH, osmotic potential, temperature, and others) [17], whilst other techniques have considered the use of additional chemical factors (e.g., siderophores or hormones) that are essential for microbial growth [18]. Similarly, certain organisms may not grow if other members of their communities are absent, hence, co-cultures have also been proposed as a strategy for isolation of those taxa considered as uncultured under laboratory conditions [19]. Considering the aforementioned, the bioprospecting of "rare", or unculturable, microorganisms appears as an exciting field with a huge biotechnological potential for the discovery of new bioactive compounds and efficient novel inoculants more adapted to the *in planta* conditions.

In this Special Issue of Diversity, we expect to collect manuscripts that explore the diversity of plant-associated microbiomes and their microbial interactions that modulate the plant's response to the changing environment, as well as the bioprospecting of plant-associated microorganisms as a source of novel bioactive compounds and inoculants for agriculture. We also hope this Special Issue provides scientifically valid, technically sound, and innovative manuscripts of broad interest, improving our understanding of the complex diversity, composition, interactions, and ecological role of microbiomes in natural vegetation and agronomic plants.

**Acknowledgments:** We thank the Editorial staff of Diversity for their collaboration in this Special Issue (more information and submission guidelines can be found at https://www.mdpi.com/journal/diversity/special_issues/plant_microbiomes). The authors also thank the support given by The National Fund for Scientific and Technological Development (FONDECYT) project no. 1201386, and by Science and Technology Research Partnership for Sustainable Development (SATREPS JICA/JST) project code JPMJSA1705.

**Conflicts of Interest:** The authors declare no conflict of interest.

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