



Editorial Advanced Research of Rhizosphere Microbial Activity

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Soils are generally considered a complex and largely unexplored vital "black box" with thousands of microorganism taxa in their networks. The declaration of the "International Decade of Soils" (2015–2024) has drawn attention to the soil as one of the most important natural resources, as well as highlighting uses of soil and the global problem of soil degradation [1]. All soil functions play an important role in everyday human life. The genetic and functional diversity of soil microorganisms is crucial for conserving soil health and functions. Studies on the soil microbial communities of the rhizosphere are essential for developing environmentally friendly practices and agricultural management, soil awareness, sustainability, and security. According to recent publications, the interaction between soil microbes and plants could be much more complex than previously thought. The concept of the rhizosphere originated with Hiltner's work dating back to the beginning of the 20th century [2]. A volume of soil, which was influenced by roots and inhabited by soil microorganisms quite different from the surrounding soil, was conceived and named the rhizosphere. The interface between the roots and the soil is complex, delineated by uncertain boundaries that can change over space and time. The rhizosphere is one of the most significant hotspots in soils and harbors large numbers of microbial species belonging to archaea, bacteria, and fungi [3]. Plants have direct and indirect effects on soil fauna and microorganisms by releasing root exudates and litter deposition serving carbon and energy sources for heterotrophic organisms; meanwhile, they have the selective power to shape microbial communities around the root system and on the root surface, which is called the rhizoplane. Microbial activity in the rhizosphere can be one or two orders of magnitude higher than that of the surrounding bulk soil [4]. Moreover, it is a very dynamic and sensitive system. Microbes in the rhizosphere can aid plant nutrition, water uptake, and plant growth promotion by hormone and siderophore production and protect plants against pathogenic microbes, while in certain conditions some of them become pathogenic too. Climate change, land use change, and different management options are challenges to evaluating soil health in connection with plant-microbe interactions [5].

In this Special Issue, 10 papers were selected and accepted for publication. Most papers focus on rhizosphere microbiome (fungi or bacteria) analysis by DNA amplicon sequencing. Some of these papers used isolation techniques to select and check microbes with plant growth promotion and plant pathogenic defense abilities in order to develop potential biofertilizers. Two papers focused on arbuscular mycorrhizal fungi (AMF), another on nitrifying bacteria and archaea in the rhizosphere, and another on one bacillus strain preselected and thoroughly investigated by genome mining to reveal all functional abilities that may be important for plant-growth-promoting (PGP) properties.

Plants can regulate the composition of the rhizosphere microorganism community. For many hundreds of years, medicinal plants have been used not only for human medicine but also for protection against soil pathogens. The sensitivity of soil fungi to secondary plant metabolites changes with the compound produced by the plant species. When investigating the rhizosphere soils of five medicinal plant species—*Origanum syriacum, Salvia fructicosa, Teucrium capitatum, Myrtus communis,* and *Pistacia lentiscus*—significant differences were found both in the function and in the taxonomical composition of the



Citation: Szili-Kovács, T.; Takács, T. Advanced Research of Rhizosphere Microbial Activity. *Agriculture* 2023, 13, 911. https://doi.org/10.3390/ agriculture13040911

Received: 14 April 2023 Revised: 18 April 2023 Accepted: 19 April 2023 Published: 21 April 2023



Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). fungal communities [6]. The rhizosphere of *M. communis* was rich in saprotrophs, and the rate of symbiotrophs was lower than that in control soils without medicinal shrubs. The abundance of *Alternaria* was significantly lower in the rhizospheres of *M. communis* and *S. fructicosa* than it was in control soils. The abundance of saprotrophs was positively correlated, while the rate of symbiotrophs was negatively correlated with the soil moisture.

Plant-growth-promoting fungi (PGPF) support plant development by increasing the amount of available plant nutrients in soils or enhancing phytohormone production, and PGPF can induce systemic resistance to suppress pathogens. From citrus and olive orchard soils in Egypt, 272 fungal strains of 27 filamentous fungal species were isolated and identified as potential phosphate solubilizers and indole acetic acid (IAA) phytohormone producers [7]. ITS molecular characterization proved that 27 species belong to eight genera of Ascomycota. Most of the fungal isolates were identified as *Aspergillus, Penicillium, Epicoc-cum, Fusarium, Ulocladium, Trichoderma, Cladosporium,* and *Chaetomium* species. The highest species richness was found among Aspergillus with nine species. Strains of *Aspergillus tubingensis* and *A. fumigatus* showed the largest P-solubilizing activity and IAA productivity. Results have highlighted the possibilities of the site- and purpose-specific application of PGPF strains as biofertilizers for reclaimed lands.

In recent decades, the agricultural application of sewage sludge (SS) or sewage sludge composts (SSC) and population explosion has increased the demands for fertilizers and food security. The combined use of SS and PGPR can provide greater nutrition efficiency and reduces human and environmental health hazards related to agricultural practice [8]. The effect of varying doses of SS and *Bacillus subtilis* or *Pseudomonas fluorescence* PGPR was investigated via the germination, biochemical response, heavy metal uptake and the yield of ridge gourd (*Luffa acutangula* L.) during multiple harvests. The combination of 10% SS w/w soil and 10 mL PGPR was found to be the most effective for enhancing plant growth. The bioaccumulation factor (BAF) and health risk index (HIF) of potentially toxic metals such as Cd, Cr, Cu, Fe, Mn, and Zn were detected within the permissible limit values in gourd fruits.

Arbuscular mycorrhizas are the most ancient and widespread types of mycorrhiza, infecting more than 80% of terrestrial plants. This multifunctional symbiotic (mutual) relationship improves host vitality, fitness, and nutrition, especially phosphorus uptake. The glomalin production of AM fungi even significantly contributes to soil aggregates stability and water holding capacity. The diversity of indigenous AM fungi communities and their functionality significantly influence plant vegetation and ecosystem stability. Unfortunately, intensive fertilization and tillage damage AMF diversity, infectiveness, and effectiveness. The developmental strategy of AMF symbiosis can be represented on a map by converting the colonization types of plots to colors [9]. It was demonstrated by investigating the effect of long-term organic and mineral fertilization on AMF root colonization parameters and the colonization pattern of Agrostis capillaris estimated by MycoPatt tool was translated into colors. The intensity of mycorrhizal colonization and the arbuscularity of roots decreased with the intensity of the mineral fertilization, while organic fertilization promoted the infectivity of the soil indigenous AMF. Multi-point analysis of AMF colonization combined with developmental state characterization-AMF proliferation, resistance conditions, transfer, and storage strategies—provides a good tool both for status description, for the estimation of functional aspects of AMF colonization, and for exploring host–plant interactions in depth.

In an integrated nutrient and plant health management system—especially in lowfertility soils—it is essential to rely on plant-growth-promoting microbes to enhance the efficiency of nutrient utilization of crops. Effects of inoculation with a single AMF and with a mixture of four AMF species on citrus fruit quality and root physiological activity were examined in the second year after AMF treatments [10]. The size parameters, weight, and quality of fruits increased under AMF treatments. In AMF management, a higher AMF diversity can provide a higher chance for compatible partnerships. The functional processes and mutual benefits of the wild plant *Moringa oleifera* and its rhizosphere microbiome were studied using metagenomic whole-genome shotgun sequencing (mWGS) in comparison with a bulk soil microbiome [11]. The KEGG (Kyoto Encyclopedia of Genes and Genomes) databases were applied to the data of shotgun metagenome sequencing to analyze the main functional genes and their abundances across rhizosphere and bulk soil sample microbiomes. This study can provide more insight into the knowledge of plant–rhizosphere relationships considering biochemical signaling and metabolic relationships, especially on phytopathogen protection and plant growth promotions. Most of the metabolic genes in the rhizosphere microbiome occurred in enhanced abundance and were related to amino acid metabolisms.

Nitrification is an important process in soil N cycling, providing nitrate as a nutrient for plants. Nitrification also contributes to soil acidification, formation, and the loss of N in the form of NO and N₂O from soils, providing nitrate leaching as an adverse environmental impact. Due to the central role of nitrification the contributor of nitrifying bacteria and archaea are extensively studied. Ayiti et al. (2022) investigated maize rhizosphere microbiome for the abundance and diversity of nitrifying bacteria and archaea using 16 S rRNA gene sequencing at different growth stages of the plant. The results of their study reveal nine genera of nitrifying bacteria and one archaeon genus [12]. It is known from other studies that the richness, diversity, and structure of microbial communities can be affected by soil parameters, especially soil organic carbon, pH, nitrate, and other nutrients. In this study, the correlation between different soil properties and abundances of different genera of nitrifying bacteria and archaea provided information that could aid the future use of biotechnology in various soil environments.

The degradation of grasslands due to direct human impacts (such as overgrazing, habitat fragmentation and road construction) and indirect impacts (such as global warming and invasive plant species) is a worldwide problem. Alpine meadow degradation causes a notable decrease in palatable grasses and an increase in forbs and toxic plants, especially *Stellera chamaejasme* weed, which is distributed in the Qinghai–Tibetan Plateau. Aside from vegetation patterns and soil properties, land management and climate condition are considered to be the main factors influencing the distribution of soil microbial communities. The spatial patterns and determinants of these communities are still limited because few studies investigated the effect of geographical location on the soil and rhizosphere microbiome. In a pioneering study, Liu et al. (2022) combined DNA amplicon sequencing of soil fungi from soil extracts with geostatistics and interpolation mapping, where soil, vegetation, and soil fungal data were evaluated in an alpine meadow [13]. In their study, they were able to determine the spatial distribution of soil fungal diversity and taxonomic composition in a typical degraded alpine meadow invaded by *S. chamaejasme*.

The potential of plant growth promotion and biocontrol were investigated in a *Bacillus subtilis* Strain RS10 using a genome mining technique [14]. The strain RS10 was isolated from a soil sample collected from the *Cynodon dactylon* rhizosphere and tested for antimicrobial activity and plant growth promotion. Further genome analysis reveals that *B. subtilis* RS10 can solubilize inorganic phosphate, producing siderophore and phytohormones. Next, the genome mining of RS10 also confirms its ability, encodes genes for chemotaxis and adhesion to plant root surfaces, and contains genes for colonization and metabolic versatility to use root exudate.

Immature soils have limited ability for crop production without amendments. The increased demand for food production requires added organic matter to improve soil properties, and the addition of plant-growth-promoting (PGP) microorganisms may have a positive impact. Li et al. (2021) focused their research on immature soil fungal microbiomes [15]. Fungal isolates from different abandoned wastelands, including P solubilization, siderophore production, and indole acetic acid production, were checked for their plant growth promotion abilities. One fungal strain of *Penicillium oxalicum* showed a good ability to promote the plant growth of eggplant and can be a potential biofertilizer in immature soils.

In summary, this set of papers provides an opportunity to examine some of the most recent advances made in rhizosphere research. These papers will be interesting for many readers, especially those working in the field of soil science and interested in land management, with the anticipation of opportunities for practical applications.

Author Contributions: Conceptualization, original draft preparation, review and editing; T.S.-K. and T.T. All authors have read and agreed to the published version of the manuscript.

Funding: This research was financed by Eötvös Loránd Research Network (ELKH—SA-26/2021).

Acknowledgments: The authors would like to thank all manuscript authors and peer reviewers of this Special Issue.

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

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