

Editorial

Editorial for Special Issue “Environmental Factors Shaping the Soil Microbiome”

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Abstract: Soil is a complex system consisting of various abiotic and biotic factors interacting among themselves in a particular time period. These biotic factors are particularly affected by a large number of disturbances or perturbations occurring in the micro-niches. Soil microbiome is the paramount biotic factor responsible for nutrient cycling that in turn determines soil health and quality. However, there are limitations in studying soil systems as there are a number of unknown boxes that need to be checked before understanding their full-fledged contribution to the environment. The microbial diversity in the soil can be affected by salinity, contaminant, fertilization, nutrient accumulation, and cultivation practices. Additionally, plants can also benefit from these changes in microbial community composition, and novel microbial isolates can be used for enhancing their growth under various stress conditions. Collectively, this Special Issue includes various studies that determine key abiotic and biotic factors that can result in changes in microbial community composition in the soil system. These studies are carried out in specified environmental niches rather than microcosms, which provides a broader context in which to understand microbial dynamics.



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The soil microbiome comprises one of the most important and complex components of all terrestrial ecosystems as it harbors millions of microbes, including bacteria, fungi, archaea, viruses, and protozoa. Together, these microbes and environmental factors contribute to shaping the soil microbiome, both spatially and temporally. This Special Issue covers the nutrient amendments, application of compost, discharge of azo dye effluents, mining, soil salinity, soil acidity, and plant genotypes that affect the soil microbial community structures. Additionally, it provides a glimpse into dominant microbial communities from these environments that may be tapped for biotechnological applications.

Microbial populations in soil are determined by various factors such as soil depth, organic matter, porosity, oxygen and carbon dioxide concentration, soil pH, etc. Factors that influence microorganisms’ roles in nutrient building and cycling in soil and organic matter decomposition are of unique interest. These microbial entities have the potential to be utilized in various biotechnological applications that are necessary to improve soil health and quality. Microorganisms decompose organic matter, and detoxifying toxic substances, fixing nitrogen, and transforming nitrogen, phosphorous, potassium, and other secondary and micronutrients are the major biochemical activities performed by microbes in the soil. They play a major role in supporting life forms in micro-niches by supplying essential nutrients and carrying out bio-transformations that are essential for the survival of living organisms. Soil fertility is considered an important factor for better agricultural production. Microbial community composition and diversity of agricultural soils primarily

depend on management practices. The application of compost to agricultural fields is known to increase soil fertility, which can also help to enhance agricultural productivity. The relative abundance of a few groups of bacteria, such as Firmicutes, Actinobacteria, and Proteobacteria, is significantly higher in compost-amended soil, and several of these bacteria are reported to be beneficial. Thus, a combined application of compost and inorganic fertilizers may be a good way to keep up with agricultural productivity while keeping the environmental balance. The shift in bacterial community composition through compost amendment especially leads to an increase in decomposition-related enzymes, which are a primary factor in enhancing nutrient accumulation, leading to fertile soil that supports better plant growth. Additionally, compost amendment has also been reported to increase the abundance of enzymes that are important during various developmental stages of plants [1].

Soil properties are one of the major factors determining the growth of vegetation. The natural habitat is used in various parts of the world for the cultivation of plants that are important for manufacturing traditional medicines. The soil's properties drive the selection of the dominant bacterial community profiles, which eventually determines the soil quality and fertility, making it conducive to supporting vegetation. The abundance of a preferential bacterial community assists in better productivity of particular types of vegetation [2]. Rhizosphere bacterial diversity is known to affect plant health, and communities with a higher diversity are generally better able to withstand invasion by pathogens and possess higher amounts of plant-growth-promoting bacteria (PGPB). The preferential biodiversity often relates to increasing levels of ecosystem functioning and services. Soil communities are also affected by plant characteristics, primarily through the production of root exudates. Bacterial communities are also known to differ according to plant genotypes and hosts. This was supported by the findings of Vink et al. [3], who concluded that grape cultivars are able to recruit (i.e., attract and select) different, potentially beneficial genera. Further, they summarized that *Desertibacter* and *Rhodothalassium* occurred in relatively high abundance in vine cultivars Calandro and Villaris. Only one genus (*Stenotrophomonas*) was in high abundance in cultivars Felicia and Reberger. However, this effect is by no means ubiquitous, and plant genotypic differences do not always lead to significant differences in microbiomes in the rhizosphere. Even so, this puts forward a novel idea about the preferential plant-microbe interaction based on plant genotypes. These preferential microbial associations can help in identifying key bacterial taxa in the particular environmental niche and determine the particular plant genotype that can be cultivated in that region for better productivity.

Exogenous nutritional inputs are an inevitable process in crop production and can change the structures of soil bacterial communities. Among the several nutrients, nitrogen and phosphorous are the most limiting nutrients in agricultural productivity. This Special Issue cautions that higher deposition or accumulation of N in the urban green space deeply affects the patterns of bacterial diversity and community structure. Nitrogen addition has a negative impact on bacterial richness and diversity in urban green space. The decrease in biodiversity induced by N deposition may pose a serious threat to the stability of urban soil ecosystems, which emphasizes the necessity of thorough and concerted studies to prompt adequate policies to counteract these globally increasing threats [4]. Phosphorus removal from phosphorus-enriched soils (PES), such as agricultural lands, grasslands, and phosphate mining regions, is a major cause of eutrophication in aquatic environments and an increasing environmental problem worldwide. Phytoremediation with *Erianthus rufipilus*, *Coriaria nepalensis*, and *Pinus yunnanensis* is one of the most promising technologies for the removal of excess P in agricultural systems. In a study, rhizospheric microbial communities are shaped not by the plant species but by soil water content, soil organic matter, and total nitrogen contents of the P-contaminated sites [5]. This eventually reveals the complex interaction between different niches and ecosystems in determining the soil microbial diversity.

Discharge of untreated wastewater is one of the major problems in various countries. The use of azo dyes in textile industries is one of the key xenobiotic compounds that affect

both soil and water ecosystems and result in a drastic effect on the microbial communities. Orathupalayam dam, which is constructed over the Noyyal river in Tamil Nadu, India, has become a sink of wastewater from the nearby textile industries, and this polluted site especially supports the abundance of *Saccharibacteria*; hence, enrichment isolation of this bacterium could be used to degrade the azo dyes and remediation of textile effluent degrading sites [6]. The agricultural soils that use the dam water for irrigation purposes have also shown a minor shift in bacterial diversity that implies potential contamination due to azo dye compounds. However, determining the key bacterial taxa from these contaminated soils can assist in designing potential bioremediation techniques that are sustainable and environmentally friendly. Further studies designing potential biotechnological technologies will not be possible if the microbiomes of the particular environment are not scrutinized beforehand. Hence, studying these particular sites is of utmost importance for putting forward industrially important products.

Mine heaps and mine wastes created by the mining industry are some of the extreme habitats made by anthropogenic activity. Interestingly, mine heaps create an environment with specific ecological conditions for plant adaptation. They are characterized by the lack of soil, nutrients, and moisture, as well as an absence of a humus layer. Orchids represent a unique group of plants that are well adapted to these extreme conditions. In this Special Issue, Böhmer et al. [7] addressed the microbial diversity of orchids in polluted sites. They found that the pH of the initial soils does not significantly affect the presence of fungi and bacteria. Similarly, toxic elements (e.g., As, Pb, Cr, Ni, Co, Cu, Fe) do not affect the occurrence of fungi, bacteria, or orchids. Moreover, microbial communities also provide a huge benefit for orchids to be able to grow in these polluted areas. Additionally, it can be concluded that some of these microbial communities possess huge biotechnological potential in bioremediation of heavy-metal-contaminated areas. This addresses another key feature of microbial community composition in remediating toxic compounds that are a result of anthropogenic activity. Heavy metals have been a matter of concern in various mining-rich locations that possesses a high threat to human health. The chemical remediation of heavy metals is expensive, and exploring an unorthodox pathway can prove to be a sustainable approach.

Soil salinity is a severe agronomical, ecological, and socioeconomic concern in most arid and semi-arid regions of the world. It is estimated that salinization will threaten more than 50% of arable land worldwide by 2050. Hence, this silent hazard will continue to threaten agricultural sustainability, food security, ecosystem stability, human health, and income generation. The use of plant-growth-promoting bacteria for salt stress alleviation is practiced widely. Since it has no harmful impact on the environment, this method has huge benefits and is widely applied. Arbuscular Mycorrhizal Fungi (*Glomus mosseae*) inoculation, alone or in combination with plant-growth-promoting bacteria (*Bacillus amyloliquefaciens*), increased biomass accumulation, morphological characteristics, photosynthetic capacity, and rhizospheric soil enzyme activities in saline soils [8]. Acidic soils occupy around 40% of the total agricultural lands worldwide, representing one of the most important limiting factors of agriculture production. Both liming and plant residue incorporation are widely used practices for the amelioration of acidic soils—however, the difference in their effects is still not fully understood, especially regarding the microbial community. In this Special Issue, Li et al. [9] demonstrated that liming was effective in elevating soil pH, while plant residue incorporation exerted a comprehensive influence not only on soil pH but also on soil enzyme activity and microbial community. Nannipieri [10] critically reviewed the soil as a biological system. Still knowledge gaps can be found. This Special Issue shows that technology-driven and hypothesis-driven research should be combined in order to fill the remaining gaps. Particularly imaginative research should address the simulation of the soil microenvironment so as to understand which factors regulate microbial activities in micro-niches.

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