



# Editorial: Microbe-Mediated Processes in Soils

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## Editorial on the Research Topic

### Microbe-Mediated Processes in Soils

Although only a few chemical elements (H, O, C, N, P and S) are building blocks of microbial cells, microorganisms have evolved over several billion years to use every energy source available on earth. Different microbes require distinct nutrients for their metabolic reactions. However, considering that the vast majority of these organisms live in communities, such huge metabolic diversity allows them to metabolize at least fifty different chemical elements. Given this wide versatility, microorganisms play essential roles in terrestrial ecosystems, including soil fertility, residue decomposition, and nutrient cycling, thus maintaining soil homeostasis (Myers, 1996; Reis Junior et al., 2002). Despite its importance, the soil environment is considered to be one of the less well-studied habitats and only recently we have begun to understand that their biological and functional diversity is a crucial factor for maintaining all ecosystems (Copley, 2000). The study of microbial communities and their relationship with the environment is essential for understanding ecosystem dynamics.

As human activities continue to increase, so too do rates of soil fertility loss, soil erosion, land conversion, and fossil fuel use with drastic consequences for the composition of our atmosphere and therefore climate change. Soil microbial processes are integral to these biogeochemical changes. Anthropogenic activities have raised the concentration of greenhouse gases, pollutants, and particulate matter in the atmosphere to levels that can directly or indirectly alter the development of different components of the biosphere. The increase of about 30 % of the concentration of CO<sub>2</sub> in relation to its concentration at the beginning of the Industrial Revolution is stimulant for the plants' productivity (Saxe et al., 1998), if other factors such as nitrogen concentration, for example, are not limiting. However, the increase in CO<sub>2</sub> concentration has not occurred in isolation. Atmospheric nitrogen (N) deposition has globally increased during the last two centuries (from 34 Tg N year<sup>-1</sup> in 1860 to 100 Tg N year<sup>-1</sup> in 1995) and is expected to continue increasing worldwide (Galloway et al., 2008), as a result of the expansion of grazing areas and N fixing leguminous crop, increased use of nitrogen fertilizer, biomass burning and industrial activities (Vitousek et al., 1997; Goulding et al., 1998). According to the IPCC report (2013) atmospheric nitrogen deposition has increased 3-5 times in the 20th century. An increase in N availability via atmospheric deposition can lead to changes in plant ecophysiology, affecting the dynamics of populations, communities and ecosystem functioning (Bobbink, 1998) since N is one of the main determinants of plant productivity, especially in the ecosystems of tropical and subtropical dystrophic soils (Haridasan, 2001). Similarly, N deposition decreases the soil microbial biomass (Liu and Greaver, 2010; Lu et al., 2011) and also can cause changes to the soil community functional capabilities (Ramirez et al., 2012; Cheng et al., 2017), which in turn affects the soil nutrient cycling and the availability of nutrients to plants. Plants and microbes respond together to these environmental changes and so far, their responses have not been

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fully understood (Yuan and Chen, 2015; Zhang et al., 2018; Adair et al., 2019). There are numerous questions surrounding the role of Bacteria and Archaea in soil and we have a limited understanding of the interplay between microbes and soil processes.

Currently, scientific and technological advances have revolutionized the traditional approaches used to study these biological resources. High throughput sequencing (Roesch et al., 2007; Goodwin et al., 2016) of phylogenetically informative genomic DNA regions such as rRNA 16S gene, or whole-genome sequencing (metagenomics) enables in-depth analyses of the genetic variation of prokaryotic groups, allowing comparative analysis of the diversity, abundance and functional traits of whole microbial communities at far greater depths than ever before. The big challenge here is to understand the microbe-mediated processes in soils, with a view to using soil more rationally and alleviating the impacts of land-use changes.

The papers brought together in this Research Topic have a focus on important issues pertaining to different microbe-mediated processes in soils. Three articles investigate N cycle processes. de Chaves et al. explores the carbon degradation potential mediated by Acidobacteria subgroups in tropical soil under sugarcane, with the addition of nitrogen fertilizers and vinasse (a byproduct of the ethanol industry generally composed by 93% water and 7% organic and mineral compounds). Such an amendment negatively affects the C metabolism mediated by Acidobacteria in the soil. The availability of Ca, Mg, K, Al, B, and Zn increase and the abundance of Acidobacteria subgroups and gene families associated with carbon degradation decrease. Also studying tropical soils, Nishisaka et al. shows differences in N<sub>2</sub>O fluxes and the abundance of denitrification genes in response to land-use changes (conversion of forest to agricultural soils). They report higher N<sub>2</sub>O fluxes from natural forest soils than from the adjacent agricultural soils cultivated with citrus and eucalyptus, using both field- and incubation-based analyses. Based on these findings, both predicted outcomes were rejected: (1) that citrus- and eucalyptus-cultivated soils emit higher amounts of N<sub>2</sub>O to the atmosphere than their adjacent natural forest soil counterparts and (2) that the abundance of denitrification genes would increase in agricultural soils. They suggest that the differences observed in the N<sub>2</sub>O fluxes, and in some cases the *nirK*, *nirS*, and *nosZ* gene copy numbers, are related to seasonal environmental variables and soil and plant residue characteristics. Their results highlight the role that environmental drivers (e.g., moisture dynamics) play in mediating soil microbe-mediated processes, increasing our understanding of N cycling processes in tropical soils.

Potential applications of microbe-mediated processes in soils and the effect of amendments on soil microbial communities were also explored within this Research Topic. Peng and Bruns, evaluated the growth of a soil surface consortium comprising both cyanobacteria and non-photosynthetic bacteria on agricultural soil surfaces and its potential contribution to modulating soil mineral N in agroecosystems. This consortium was able to fix N<sub>2</sub> over a range of soil mineral nitrogen concentrations and retained 50–70% more soil N after rainfall

compared to non-inoculated treatments. The work from Peng and Bruns highlighted the potential of naturally occurring or intentionally inoculated soil surface consortia as a renewable source of biologically fixed N and means for soil stabilization and N retention in diverse agricultural systems. Vollú et al. evaluated the impact of applying mineral (triple superphosphate) or organomineral [triple superphosphate with poultry litter, and reactive Bayovar phosphate with poultry litter] fertilizers on the abundance and composition of the soil bacteria associated with the maize rhizosphere, based on a 16S rRNA gene survey (metataxonomics). Maize is very important as a food source worldwide, being subjected to several industrial processes in order to be used in the food industry. Poultry litter is a phosphorus-rich animal waste, but usually contains antibiotic residues, particularly fluoroquinolones, which may influence soil microbial community assemblage and its resistome. They reported that the amount of fertilizer and the plant growth stage may shift the maize rhizosphere bacteria community, but no effect was observed in response to the type of fertilizer applied. The abundance of phosphate-mineralizing bacteria was also positively correlated to sampling time (plant growth stage) and to the rhizosphere effect. Also, they stated that the use of poultry litter mixed with inorganic fertilizers does not increase the concentration of fluoroquinolones in soil and the copy number of genes related to quinolone-resistant bacteria. Their results support the use of poultry litter in agricultural fields as a source of nutrients, e.g., phosphorus, to improve maize production.

Different soil compartments select different microorganisms. The rhizosphere is the interface between plant roots and the soil, it is rich in carbon (mainly exuded from plant roots) and densely populated by soil microorganisms. Generally, anaerobic respiration in soils is most discussed for aqueous environment and paddy soils, but Lecomte et al. have pointed out in a review, that anaerobic respiration also occurs in the plant rhizosphere, where anaerobic respiration flexibility contributes to the rhizosphere competence of microbes. They explore the current research concerning the different types of anaerobic respiration that occur in the rhizosphere, including denitrification, anammox, Fe (III) and Mn (IV) respiration, among others. Also, the authors have suggested that anaerobic respiration using different terminal electron acceptors may confer competitive advantage for plants' root colonization, thus highlighting the ecological and environmental importance of anaerobic respiration in the rhizosphere. Finally, they state that the understanding of how bacterial anaerobic respiration modulate root colonization and its environmental adaptation and persistence is a creative research field.

Finally, this Research Topic provides a useful assessment of the value of qPCR versus microfluidic PCR, valuable tools for monitoring shifts in soil functional community abundances. Crane et al. explore microfluidic qPCR as an alternative for the quantification of functional genes like those involved in nitrogen-cycling and hydrocarbon degradation. The authors intensively evaluated the applicability of commonly used PCR assays, and propose criteria for primer selection for successful

micorfluidic PCR applications. Within this paper readers will obtain explanations about the constraints and the utility of using micorfluidic PCR for studying the functional capacity of soil bacterial communities.

The collection of these original works provides important advances and perspectives of microbe-mediated processes in soils including basic and applied studies related to this field. The main subjects included the nitrogen cycle processes, the potential applications of microbe-mediated processes, the different types of anaerobic respiration that occur in the rhizosphere, and a high-throughput alternative for functional gene quantification.

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