Chapter 16

Plant-Microbes Interactions and Functions in Changing Climate

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Abstract Climate change is one of the hot topics of the current century because it is not only an issue to our health but also to agriculture, forestry, biodiversity, ecosystem and supply of energy. Climate change is occurring mainly due the emission of greenhouse gases like nitrous oxide (N_2O), methane (CH_4) and *carbon dioxide* (CO_2) and the drastic changes due to these gases are predicted to change the level and various parameters of life in the changing environment. The increase or decrease in the function and composition of terrestrial microbial community is both directly and indirectly affected by climate change. The increasing temperature successively

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causes to increase the structure of microbial community and meanwhile accelerate several processes like methanogenesis, respiration, decomposition and mineralization. When climate change made some changes in the prevailing environmental conditions it will arise changes in plant physiology, root exudation, alteration in signals, C/N ratio, abundance, composition and diversities of soil microbial communities. As a result the environmental changes brought about by climate change also affect the performance of beneficial microbes on plant growth, health and root colonization.

In the current book chapter, we have discussed the impacts of climate change parameters like CO_2, drought, precipitation and temperature on plant microbes interaction. Furthermore, this review also indicate that how microbes in the plant rhizosphere respond to the prevailing climatic conditions in the terrestrial environment.

Keywords Plant-microbes · Climate change · Microbial response · Carbon dioxide · Environmental changes

16.1 Introduction

The crucial concerns of the current century are climate change, sustainable environment, supply of energy and good health. These are considered as the main challenges of the day and especially climate change is one of the hot topics (Abatenh et al. 2018). Since, the predicted patterns of climate change are becoming main challenges in the area of agriculture, forestry, biodiversity and ecosystem (Lepetz et al. 2009). Climate change is occurring mainly due the emission of greenhouse gases like N_2O, CH_4 and CO_2 (IPCC 2007). The drastic changes due to these gases are predicted to change the level and various parameters of life in the changing environment (Houghton et al. 2001). Moreover, the effect of predicted climate change is expected from individual species population to eco-region level (Lepetz et al. 2009). It has also been documented that the levels of atmospheric CO_2 generated naturally or anthropogenically may increase temperature of the global surface between 1.8 and 3.61 °C by the year 2100 (IPCC Climate Change 2017; Fahad et al. 2013, 2014a, b, 2015a, b, 2016a, b, c, d, 2017, 2018, 2019a, b). This increase in temperature is predicted to decrease soil water (Le Hou'erou 1996) in some areas and may induce drought in various areas of the world that will ultimately affect the plant-microbe interaction (Compant et al. 2010) as well as their communities and function in the soil (De vries and Griffiths 2018).

The above and below ground terrestrial ecosystem is affected by climate change, both directly and indirectly. The effects of global change like increasing CO_2, changes in precipitation, temperature and nitrogen will affect the population of plant species above the ground (Tylianakis et al. 2008). While, belowground, the climate change will affect the amount of carbon and architecture of the root zone that will indirectly affect the microbial biomass, composition and community of microbes. Moreover, climate change induced by high level of atmospheric CO_2 will result in increasing intensity of extreme weather events, elevated temperature and change in rainfall patterns (IPCC 2014). All the mentioned climate changes will pose direct and indirect impact on the plant physiological processes as well as soil microbes community and composition (Bardgett et al. 2013).

In the current chapter we are discussing both the direct and indirect impacts of climate change on soil microbes interactions and the consequences which arise and affect their function and community in the wider ecosystem. Climate change effects on plant soil microbe and microbe microbe interaction will definitely intervene in important process like mineralization, plant chemistry, community and other ecological functions (Gilman et al. 2010; Steinauer et al. 2015). The soil microorganisms are the important component of carbon and nitrogen cycles and contribute well in the emission of greenhouse gases like CH_4 and CO_2 which again take part in climate change (Microbiology Online 2015). During organic matter decomposition, the heterotrophs emit greenhouse gases while the Photosynthetic microorganisms consume the CO_2 from the atmosphere and thus this balance between the two processes determine the net carbon flux across ecosystem and mainly depend on temperature. These processes highlight that soil carbon flux is mainly due to microbial responses (Weiman 2015) which not only immobilize but also release a large amount of carbon to the atmosphere (Zimmer 2010) and hence it can also be confirmed that the greenhouse gases including N_2O, CO_2 and CH_4 are released to the atmosphere due to soil microbes (Singh et al. 2010).

When climate change made some changes in the prevailing environmental conditions it will arise changes in plant physiology and root exudation. The increasing CO_2 often increase the carbon allocation of root zone and hence affect the composition of root exudates. Further impacts documented due to climate change include alteration in signal compounds, C/N ratio, nutrients and chemo attractants availability (Kandeler et al. 2006; Haase et al. 2007). Likewise, high temperature and drought affect the activities, abundance, composition and diversities (Drigo et al. 2008) of soil microbial communities. As a result the environmental changes brought about by climate change also affect the performance of beneficial microbes on plant growth, health and root colonization.

The increase or decrease in the function and composition of terrestrial microbial community is both directly and indirectly affected by climate change. The increasing temperature successively causes to increase the structure of microbial community and meanwhile accelerate several processes like methanogenesis and respiration. The climate change can accelerate the different phenomenon like heat waves, extreme heat, flood rises, poor air, natural disaster, intense storms and heat waves that will ultimately cause injury, illness and death to both biotic and abiotic components. Due to climate change different microbes like fungus, bacteria, algae and archae will trigger global warming through organic matter decomposition and amount of CO_2 released in the atmosphere (Swati et al. 2014; Weiman 2015).

Both the microbial biomass and their enzymes in the soil environment can efficiently take part in stimulating of warming and it is because during decomposition organic matter release carbon based toxic materials to the wider environment but at the same time it has also been observed that it can prevent climate change. Similarly, temperature can affect microbial physiological property and their enzymes activity directly and therefore the microbes using carbon can efficiently determine the response of carbon to climate change (Bardgett et al. 2008; Allison et al. 2010).

It is essential for the toughness of microbial communities that there should be some dispersal mechanisms and connectivity amongst them and it is because when the regional dispersal become successful it affects the maintenance of local and confined diversity (Matthiessen et al. 2010; Lindstrom and Langenheder 2012). It has also been shown that proper connectivity and the group population is important for the proper function and survival of microbial communities (Altermatt et al. 2011; Carrara et al. 2012; Wahid et al. 2019; 2016a, b) but for soil such information is not yet proved well. Due to heterogenous nature (Ritz et al. 2004) the dispersal mechanism can play a crucial role in the recovery of soil microbial communities and also the spatially dispersed soil microbial population can be hinder because of low moisture content (Treves et al. 2003).

On the other hand, some microbes in the soil can also disperse through above ground mechanisms. For example fungi that depend on active dispersal mechanisms (Roper et al. 2010) can show more resistance than bacteria lacking active dispersal mechanisms (Kasel et al. 2008). Furthermore, due to large population bacteria and small body position, phytoplankton cells and archaea are suggested to disperse passively (Finlay and Clarke 1999).

The microbes like fungi and bacteria has been found to play important role in ecosystem functions like cycling of mineral nutrients (Baseer et al. 2019), decomposition of biological materials as well as pathogen of animals and plants. Recently, scientists are paying much attention to the direct effect of climate change on microorganisms and especially their direct contact with sunlight if they are present in litter or foliage surfaces. The effects of climate change on the microbes biodiversity and species composition change have been well documented and most of these changes have been found to be related to the tolerance of different species and strains of fungi and bacteria (Johnson et al. 2002; Djanaguiraman et al. 2010; Fritioff et al. 2005). The arbuscular mycorrhizal fungi form symbiosis with other plants and help in absorption of nutrients is thought to be indirectly affected by UV-B by the time its host plants shoot is exposed (Braga et al. 2001). With regards to climate change both beneficial microbes and plant pathogens have gained more attention than animals pathogens because some bacteria and fungi can be pathogenic for plants and animals (Zaller et al. 2002; Jacobs and Sundin 2001). Several environmental factors can reduce or increase the plant growth and productivity as well as disease incidence. When the severity of disease is high then it is thought to be involved in plant tissue modifications on the other hand when the severity is decreased then it may cause the direct damage to host plant or create some changes in the host plant (Van de Staaij et al. 2001). The aim of the current review is to discuss the impacts of climate change parameters like CO_2, drought, precipitation and temperature on plant microbes interaction. Furthermore, this review also indicate that how microbes in the plant rhizosphere respond to the prevailing climatic conditions in the terrestrial environment.

16.2 Impacts of Elevated CO_2

Elevated CO_2 has stimulatory impacts on various physiological parameters of the plant including the growth, reproduction, photosynthesis and yield (Ainsworth and Rogers 2007). Though, the rising level of CO_2 will also enhance the incidence of extreme weather events like drought and heatwaves, which are harmful to crop expansion and yield (Wang et al. 2013; Gray and Brady 2016). Similarly, rising CO_2 concentrations will also stimulus the consequence of plant-pathogen interactions (Eastburn et al. 2011) with rhizosphere inhabiting microorganisms (Gschwendtner et al. 2016) thus disturbing plant growth, development and plant yield. In additions, rising atmospheric CO_2 can enhance photosynthetic activity and plant production (Ainsworth and Long 2007). The elevated rise in carbon dioxide can stimulate various processes in plants including photosynthesis, respiration and plant production (Ainsworth and Long 2007; Khan et al. 2019). The enhanced carbon sequestration and its assimilation in the plants may balance the enhanced CO_2 emissions. Improve carbon sequestration under enhanced levels of CO_2, can only occur if (i) carbon input in the soil are sustainable (ii) the rate of carbon loss will be less over to carbon inputs.

While it is uncertain that how the higher CO_2 will effect the soil carbon additions and degradation in long terms. Specifically, the relationship between soil carbon inputs and breakdown is not quite linear, subsequently, the processes are inter-reliant; for example, soil carbon inputs impact degradation and degradation impacts soil nutrient uptake, which is the feedback response of the plant growth to the rising level of CO_2. So far, various studies has contrasting outcomes with respect to the effects of rising CO_2 on nutrient turnover and plant growth, including both positive and negative feedbacks in the carbon and nitrogen (N) turnovers.

Enhanced soil carbon inputs increased the nitrogen mineralization in some researches, however, hindered it in others. Such as the results of one study revealed that enhanced C additions under rising CO_2 enhanced the population of soil microbes, thus total rates of nitrogen mineralization (Freeman et al. 2009). In addition, Diaz et al. (1993) also revealed that enhanced C inputs in the rising level of CO_2 enhanced the antagonism among the soil microbial growth and plants for soil nitrogen, leading to a reduction in nitrogen uptake. Similarly, nitrogen fertilization may counter balance the reduction in nitrogen availability in the rising level of CO_2 (Norby 2007).

Therefore, it remains unclear how initial increases in soil C input under elevated CO_2 feedback to microbial regulation of N availability. In addition, it is uncertain how the increase or decline in N availability ultimately feeds back to soil C sequestration. If sufficient N is available, enhanced plant growth and soil C input under elevated CO_2 are likely to be sustained, resulting in net soil C sequestration (Luo et al. 2004). However, it has also been contended that abundant soil N uptake might consecutively increase the soil C breakdown (Norby 2007). Therefore, the enhanced CO_2 emission rates might offset a probable rise in soil C assimilation. The uncertainty adjacent to the link of soil C addition to soil microbial N-transformations, and the role of N uptake for the potential of soil C-sequestration, makes it challenging to envisage whether the soil can act as a C sink to mitigate rising atmospheric CO_2.

Impact of elevated CO_2 can accurately be predicted in the long-term field studies and have a key role in the soil carbon turnover, nitrogen cycling, and plant production. For example, Free Air Carbon dioxide Enrichment (FACE) trials are the most suitable field experiments for such research endeavors. The application of FACE approached has permitted for long term CO_2 fumigation experiments under actual growing environments (Ruhil et al. 2015). However, due to the procedural complications, the key constituents of ecological unit responses to rising CO_2 often exist in out of prospect in such field experiments; the belowground structure of soil, roots, soil and linked microorganisms. Subsequently, the living root system is vital for the link of soil nutrient turnover to plant production, laboratory experiments particularly setup to mechanically linkage with the soil-root system, soil C and N turnover would be joined with field experiments.

The source of various ecological units' responses to rising CO_2 is most likely the plant since rising CO_2 secondarily affects soil carbon and nitrogen cycling by directly influencing plant growth. Consequently, much of the uncertainty adjacent soil C sequestration may be detached if we begin to recognize the causes behind wavering plant responses to rising CO_2. Up to now, results of some studies showed slightly consistent that C4 plants respond to a minor level to rising CO_2 over to C3 plants, which can be attributed to the various philological processes including photosynthetic pathways. Though, distinct response to rising CO_2 of plant species among these functional groups (C3 vs. C4) generally varies (Nowak et al. 2004). In attempts to predict plant species-specific responses to elevated CO_2, plants have been classified within broad groups, relying on a broad suite of related plant traits that can generalize how species respond to environmental changes (Eviner and Chapin 2003). For example, various experiments have been piloted using slow and fast-growing plant species with different life forms, for example, woody species over to herbaceous (García Palacios et al. 2015). Though, these taxonomies have not succeeded at finding a collective plant trait that can describe the variable responses of plants to rising CO_2.

The rising level of CO_2 elevated temperature and seasonal drought can affect soil microorganisms directly and indirectly (Williams et al. 2018). The variation in soil moisture with rising temperature can also have direct effects on belowground microorganisms. Thus, heating frequently has beneficial impacts some microbes including the nematode abundance (Blankinship et al. 2011) and impacts on the composition of other microbes (Allison et al. 2008). The limited rainfall has been found to reduce the abundance of various microbes such as; collembolan, enchytraeids and fungi (Blankinship et al. 2011). The CO_2 impacts on soil microbes are frequently unintended via plant responses such as the enhanced distribution of resources below the ground (Drigo et al. 2013). The rising CO_2 usually enhanced the total biomass of the microbes (Blankinship et al. 2011) and the richness of mycorrhizal-fungi due to increased plant-mutualism (Treseder 2004). In addition, the rising CO_2 had direct beneficial impacts on the soil moisture content, shoot biomass, microbial population and soil micro-arthropod taxa abundance (Eisenhauer et al. 2012). In another study, greenhouse experiment of grassland soil, the author found that CO_2 had a greater impact on increasing the population of trophic groups of nematodes including herbivores (30%) and bacterivores, and predators (110%); possibly for the reason that advanced trophic levels were controlled by resource constraint, although subordinate levels persisted inadequate by predation (Yeates et al. 1997). The meta-analysis of soil biota response to global change revealed that the rising CO_2 usually effects in an enhanced the population of microbes and their activity at the lowest of the food web, for example, protozoa and nematodes including bacteria, fungi, and micro-fauna (Blankinship et al. 2011).

Now a days, rising CO_2 will not happen unaccompanied but in combination with other climatic variations such as higher temperature and varied rainfall pattern. Subsequently, the responses of microbes to global variations are distinctive for every global variation element (Blankinship et al. 2011) and relations among various global variation element might generate responses not projected by single factor studies (Dam 2014), multi-factor studies are required. One of the little footage of multi global variation elements that effect soil microbe found important impacts including the rising CO_2, nitrogen deposition and seasonal drought (Eisenhauer et al. 2012). Now, the CO_2 was the global variation element disturbing most soil microbial groups, with enhancing richness at micro, meso and macro-fauna level. Additionally, CO_2 turned out to be the only global variation element playing a part when constructing a model of global variation impacts on the soil food web (Eisenhauer et al. 2012). The probable justification as previously given by Osler and Sommerkorn (2007) is that environmental change affecting the magnitude and quality of photosynthetic-C additions to the soil affects the soil microbiology that controls the soil C-cycle.

16.3 Impacts of Drought Stress

Under drought stress, the shoot and root growth is reduced due to the fact that plant homeostasis is regulated by ethylene endogenously (Glick et al. 2007). On the other hand, the bacteria that exist on the surface of roots contain ACC deaminase that helps the plant to modify the normal growth under drought by degrading the ethylene precursor ACC deaminase (Glick et al. 2007). The *Achromobacter piechaudi* has been shown to provide tolerance to tomato and pepper due to the activity of ACC deaminase under water deficit condition. Likewise, compared to non-inoculated plants, the ethylene production was decreased in inoculated plants showing improved recovery from low water condition (Mayak et al. 2004). Research on the effect of drought stress on the balance of plant hormone indicate an increase in abscisic acid (ABA) in leaves, showing decrease in endogenous cytokinin levels amplify ABA content, making stomata unsecure (Figueiredo et al. 2008; Cowan et al. 1999). The antagonism between cytokinin and ABA might be due to metabolitic interactions because they are showing a similar biosynthetic origin (Cowan et al. 1999). To know about the rhizobia nodulation or the plants ABA signaling, it would be more likely to find out the cytokinin produced by P. polymyxa (Timmusk and Wagner 1999; Figueiredo et al. 2008). When rhizobia face low water content during drought stress, it decrease the amount of nitrogen fixation. Similarly, when Rhizobium tropici was co-inoculated with two strains of P. polymyxa it enhanced plant height, dry shoot biomass and nodule formation (Figueiredo et al. 2008).

During water stress, the plants increased the cells osmotic potential as well as the osmolytes synthesis (Farooq et al. 2009) exudated by bacteria in the root zone. The drought tolerance is increased when the osmo tolerant bacteria synergistically produced Glycine betaine with plants in response to stress. Similarly, under severe stress condition, the inoculation effects of osmolyte producing bacteria on rice dry shoot and root biomass and number of tillers were more significant than the un-inoculated controls (Yuwono et al. 2005). Consistent with this, the osmo tolerant bacteria have the ability to produce IAA because under drought stressed rice this hormone has improved root proliferation (Yuwono et al. 2005).

Under drought stress, inoculation of maize seedlings with *Azospirillum brasilense* showed better absolute and relative water contents as compared to that of uninoculated treatments. Similarly, bacterial inoculation has been found in improving total aerial biomass, root growth, foliar area as well as accumulation of proline in leaves and root during low water condition. Compared to 50% reduction, these effects on growth parameters were higher at 75% reduction (Casanovas et al. 2002). Under deficit water, higher mineral contents (Mg, K and Ca) and reduction in grain yield losses of wheat were observed after inoculation with *Azospirillum* (Creus et al. 2004). Likewise, the relative water content, water potential, increases in water content as well as apoplastic water were also measured. Consequently, elastic adjustment and a better water status is thought to be important in increasing drought tolerance (Creus et al. 2004). Improving plant tolerance to drought and bringing about changes in its root morphology is widely thought to be due to inoculation of *Azospirillum.* Although the exact changes in root morphology in the presence of bacterium inoculation is not well known but it is believed that this process is enhanced by the bacterium producing hormone like substances that help in activating the levels of endogenous hormones (Cassan et al. 2001). Furthermore, recently it has been documented that during the adventitious root improvement the *A. brasilense* produces a considerable quantity of nitric oxide that take action as a signalling molecule in stimulating IAA pathway (Molina-Favero et al. 2008).

The agricultural productivity is mostly affected by the widely extended drought that is considered as one of the important effective natural calamity (Gornall et al. 2010; Lesk et al. 2016) and due the wide and global climate change the increasing events and intensity of drought can be predicted for the future from the current established environmental models (Lesk et al. 2016). Generally, during drought stress and arid soils having precipitation gradient (Bachar et al. 2010) a reduction in the total bacterial biomass has been observed (Alster et al. 2013) due to shortage of resources (Khan et al. 2016). It is also observed that due to the continuous exposure of bacteria to low water content (Hueso et al. 2011) or changing its functional potential (Bouskill et al. 2016), the biomass of bacteria under drought raminas stable (Hartmann et al. 2017) or shoot up (Fuchslueger et al. 2014). A proper explanation for the increasing or decreasing trend in soil bacterial biomass is still not well explained, meanwhile to study the soil microbiome community diversity is of another phenomenon where we can easily explain that the huge diversity of these microbes is beneficial for the overall soils and it is because the presence of high number of rich species predict more metabolic activities and greater decomposition of organic matter and efficient nutrients availability in the soils (Nautiyal and Dion 2008). The overall impacts of drought on bacterial phylogenetic diversity within the soil community is less (Armstrong et al. 2016; Tóth et al. 2017) and therefore this trend might be dependent on the drought pattern because in one of the studies 40% reduction in phylogenetic alpha-diversity was observed when the plots were exposed to drought in comparison to some pre exposed plots (Bouskill et al. 2013). Generally, with drought pattern the difficult factor that take part in inconsistency is the requirement of proper consistency for the drought treatment. The drought stress to soil have been imposed in a variety of ways including rain for different time periods (Yuste et al. 2014; Tóth et al. 2017) observing samples in a precipitation gradient (Bachar et al. 2010) as well as analyzing samples within drought and non drought time periods (Acosta-Martínez et al. 2014).

Apart from microbial diversity, serious impacts of drought stress have also been reported for community composition. The observed change in soil microbial community due to drought may be the change in relative abundance instead of complete abolition and therefore it give proper detail for any transformation in alpha diversity. Under drought stress, a broadly noticed events is the increased community and ratio of Gram negative than Gram-positive bacteria (Fuchslueger et al. 2014, 2016; Chodak et al. 2015). The change in relative abundance of some bacteria have been observed under low moisture containing soils. For example, under drought a reduction in the Gram-negative includes Verrucomicrobia, Bacteroidetes and Proteobacteria (Barnard et al. 2013; Acosta-Martínez et al. 2014; Yuste et al. 2014) while an enhancement in Gram positive include Actinobacteria and Firmicutes (Bouskill et al. 2013; Hartmann et al. 2017).

Often these changes in relative abundance are driven by one or a few members of a phylum, as seen in Barnard et al. (2013); while relatively few groups had a large magnitude of change, most bacterial groups only had small shifts in response to drought. An experimental reduction of precipitation in German forest ecosystems provoked an increase of 300% for the family Micromonosporaceae, which was far more than its parent phylum Actinobacteria (Felsmann et al. 2015); another study found increases in Actinobacteria that were mainly attributable to members of order Actinomycetales (Bouskill et al. 2013).

16.4 Impacts of Temperature Stress

Soil is the naturally occurring physical covering of the earth's surface that represents the interface of three material states: solids (geological and dead biological materials), liquids (water) and gases (air in soil pores). Soil is the foundation of all terrestrial ecosystems and is home to a vast diversity of microorganisms like bacteria, archaea, fungi, insects, annelids, and other invertebrates as well as plants and algae.

Soil microbes including bacteria, archaea and fungi play diverse and often critical roles in the ecosystem services. The vast metabolic diversity of soil microbes means their activities drive or contribute to the cycling of all major elements (C, N, P) and this cycling affects the structure and the functions of soil ecosystems as well as the ability of soils to provide services to the people. Microorganism are biochemically involved in the turnover of elements through two main processes like immobilization and mineralization (Torsvik et al. 2002; Crawford et al. 2005). Plant growth is largely dependent on the availability of inorganic nutrients provided by biomineralization, so understanding nutrient cycling in soils under a variety of conditions is of major importance.

Current climate changes are leading to an increase of high temperature events (Stocker et al. 2013) and misuse of soil capabilities and poor management of vegetation can lead towards desertification and formation of arid or semi-arid soils. Soils with poor or highly reduced plant cover are exposed to intense solar radiation which leads to increasing temperatures at the upper soil layers. Altogether, these factors lead to soil temperature values well above the optimum for commonly studied mesophilic soil bacteria; values above 40 °C are frequently observed with measurements reaching 75 °C (Portillo et al. 2012a, b; Gonzalez et al. 2015) and some investigators have reported temperatures higher than 90 °C in deserts (McCalley and Sparks 2009). As a consequence, microbial activity at upper soil layers (the outermost layer of soil, usually the top 5 cm in our study) has been suggested to be highly reduced during such extreme temperature events, similar to animals and plants inhabiting these soil zones (Townsend et al. 1992; Conant et al. 2011).

Like other organisms, microorganisms are very sensitive to temperature changes and in other forms, temperature is a key limiting factor. It must be kept in mind that each species and often each strain has its own minimum, optimum and maximum temperature and the interactions with other factors occur in the field, which may induce alteration of the response curve to temperature. Moreover, when symbiotic systems are dealt with, one should take into account the effect of temperature on each of the partners and on the association itself. In his recent review, Gibson (1977) draws the attention to the possibility of compensation by the symbiotic legume system for adverse effects of moderately low or high temperatures. For example, under moderately to high temperatures nodule numbers and/or nodule weight may be higher than under optimum temperature conditions. The greater volume of bacteroid tissue formed under these conditions is interpreted as resulting from the ability of the system to compensate for unfavorable temperature conditions.

Some cases of potential activity by mesophilic bacteria have been reported at temperatures above 40 °C (Gonzalez et al. 2015) or after exposure to these temperatures as a result of metabolic stimulation (Ho and Frenzel 2012) or germination of resting cells (Whittenbury et al. 1970). In general, mesophilic bacteria undergo a decline in activity and survival period under high temperature events although other microorganisms, adapted to these high temperatures, may succeed in finding suitable temporal conditions to develop. Recent reports have highlighted the occurrence of peaks of enzymatic activity at high soil temperatures (in the 55–75 °C range) (Gonzalez et al. 2015) and the ubiquitous presence in all tested soils of thermophilic bacteria, specifically species belonging to Geobacillus and related genera (Marchant et al. 2002, 2008; Portillo et al. 2012a, b; Santana et al. 2013). These thermophiles exhibit optimal growth between 50 and 70 °C under laboratory conditions. In addition, these thermophilic bacteria are mostly present in temperate soils as vegetative viable cells (Marchant et al. 2008; Portillo et al. 2012a, b) which strongly suggest that they can be potential participants of soil biogeochemical reactions (Gonzalez et al. 2015). Therefore, the study of these soil thermophilic bacteria and their role in soil ecosystems is an aspect deserving further consideration.

Temperature is one of the most important factors influencing soil organic matter decomposition and microbial communities. For example, temperature significantly affects the soil microbial phospholipid fatty acid composition associated with straw decomposition at the early stage (Zhou et al. 2016). Bacterial abundance increases in conditions of elevated temperature and CO_2 concentration (Castro et al. 2010). The complex responses of bacterial composition and diversity of bamboo soils across altitudinal gradients have been suggested to result from interactions with multiple factors, including temperature (Lin et al. 2015).

Soil bacterial communities include different phylotypes that likely represent different functional groups, and their relative abundances are affected by carbon (C) availability. For example, some members of Proteobacteria are considered copiotrophs, and their relative abundances appear to be higher in C-rich environments. In contrast, oligotrophs (e.g., Acidobacteria) can live in stressful environmental conditions (Fierer et al. 2007). However, little is known about how these two groups respond to the environmental temperature changes. Here, we hypothesized that the temperature changes would alter the structure and diversity of soil bacterial communities at different elevations, and that bacterial taxa, including copiotrophic and oligotrophic groups, would have distinct responses to altered nutrient availability caused by temperature changes.

The microbial decomposition process of soil organic matter is highly sensitive to such change in surrounding environmental condition (temperature increase) which has the potential to modify the enzyme kinetics and associated nutrient availability in the soil system through alteration in resource allocation strategy and community composition of the soil biota (Stone et al. 2012; Steinweg et al. 2012). The modified dynamics of soil microbial activity in warmer environment may determine the effective direction and net magnitude of C flux among the source-sink components of global carbon cycle as well as the status of soil C pools, available nutrient status and the soil C stock that ultimately affect the crop production (Majumder et al. 2008; Wall et al. 2013). In courtesy, Mganga et al. (2016) observed that the traditional agroforestry systems promoted soil fertility with enhanced soil microbial biomass C and associated enzyme activities, than the monocropping with agricultural crops (maize) for the soils of natural to slightly acidic soils of tropical Africa. The beneficial role of minimum disturbance in different land use systems enhanced soil enzyme activities involved in C, N, P, S cycling Acosta-Martínez et al. (2007) that resulted the increase net nutrient availability for acid soils in different land use systems (orchards, grasslands and agricultural crops) of subtropical China Liu et al. (2010).

However, many of the studies on temperature sensitivity do not take into account the effects of the natural soil micro-environment and microbial community, which are often severely disturbed in artificial field and laboratory experimental warming experiments (Bradford et al. 2010; Thomson et al. 2010). Respiration/soil C was highest for soils from high native temperatures. Increased nitrogen (N) mineralization and microbial enzyme activity in soils from high native temperatures shown here have the potential to mitigate soil C losses by increasing allocation of C into plant and microbial biomass. However, this effect may not be sufficient to offset the larger potential losses of C in soils from low native temperature sites. This suggests that soils from low native temperatures have a greater potential to release C over time, since C stocks in these soils are not depleted as quickly as are carbon stocks in soils with high native temperature sites. Increased temperature-induced respiration combined with large soil carbon stocks and low N mineralization rates may make soils from low native temperatures regimes more likely to further increase atmospheric carbon dioxide levels.

Forests ecosystems account for approximately half of the Earth's terrestrial surface and their responses to increased temperature are of great concern (Dixon et al. 1994). The amount of carbon dioxide (CO_2) respired from all soils is over 11 times larger than the CO_2 pumped into the atmosphere via anthropogenic processes (Bader and Korner 2010) and forests account for approximately 40% of global soil C (Dixon et al. 1994). Increasing global temperatures can induce greater soil respiration (Bond Lamberty and Thomson 2010), and the potential for a positive feedback between soil carbon (C) release and temperature remains unclear (Campbell et al. 2009; Bader and Korner 2010). The fate of soil C is therefore of paramount importance for projected climate change scenarios. The distribution of this C stored in soils will also affect potential mineralization of soil C since climate change is variable at regional scales (CCSP 2007; Christensen et al. 2007).

A greater respiration/soil C indicates that more of the available substrate was being used for microbial metabolism when cores were incubated at higher temperatures in the laboratory. In general, we observed an increase in dehydrogenase, fluorescein diacetate hydrolase and β-glucosidase activities with increase in incubation temperature. Dehydrogenase and fluorescein diacetate hydrolase represent microbial activities in general, while β-glucosidase is a carbon degrading enzyme involved in carbon depolymerization. The probable reason of increase of these enzyme activities may be due to increase in the substrate (e.g. microbial biomass) availability at elevated temperature (Joergensen et al. 1990). On the contrary, the decrease in acid phosphomonoesterase and aryl sulphatase activities may be due to their denaturation at higher temperature.

16.5 Impacts of Soil Moisture Stress

Soil moisture is a crucial variable that has a significant role in managing the patterns of soil respiration and hence decomposition of soil organic matter in ecosystems (Aanderud et al. 2011). In soil several process like water movement, gas, and solute diffusion as well as survival and motility of microorganisms are controlled by soil moisture (Rodrigo et al. 1997; Luo and Zhou 2006). Moisture can also overwhelm microbial activity in several environments such as salt water and soils. Moisture stress reduces intracellular water potential and thus decreases enzymatic activity and hydration (Stark and Firestone 1995). Aanderud et al. (2011) also documented that, soil moisture have intense effects on the dynamics and emission of CO_2. According to Aanderud et al. (2011) in grasslands, soil moisture and temperature mainly control soil respiration, correspondingly, determines carbon dioxide (CO_2) flux between soils and air.

Very often, temperature changes are combine with fluctuations in soil moisture, which may explain some unpredictable results from experiments exploring how microbial communities respond to climatic change. Such as, rates of microbial activity decrease at warmer temperatures by diffusion and microbial contact with available substrate (Zak et al. 1999). Whereas bacterial communities may react quickly to moisture changes and the slower-growing fungal community may respond slowly (Bell et al. 2008; Cregger et al. 2012, 2014). Additionally, drought intensifies the differential temperature sensitivity of fungal and bacterial groups (Briones et al. 2014). Even as mall changes in soil moisture may shift fungal communities from one dominant member to another but may not affect bacterial communities. Though, it is still uncertain that (1) how temperature, moisture and their interaction, affect specific microbial functional groups, such as methanogens, within a community; (2) what is the effect of changes in microbial community decomposition of fresh and old soil organic matter; and (3) which mechanisms drive the net ecosystem response of microbial activities to climate change.

Climate models have projected un even pattern of rain fall for many regions of the world (Jentsch et al. 2007; IPCC 2013) which is expected to increase abiotic and biotic stress on plants (Jentsch et al. 2007; IPCC 2013). Furthermore, indirect impact of climate change like nutrient availability and soil microbial community composition may also occur, both of which affect plant growth (van der Heijden et al. 1998; Bardgett and Wardle 2010).

These indirect effects can result in the establishment of “soil moisture legacy effects” where plants are impacted by conditions prior to plant establishment (Meisnera et al. 2013). Plants have evolved many strategies and traits for optimizing nutrient acquisition (Lynch 2007), including the formation of arbuscular mycorrhizas (AM) (Lambers et al. 2008; Smith and Read 2008). In poor soils the formation of AM can improve plant fitness and competitiveness, which has significant contribution in ecosystem productivity and biodiversity (van der Heijden et al. 1998; Facelli et al. 1999; Cavagnaro et al. 2004). The adverse effect of soil moisture legacy effects may be a poor root colonization by AMF. Furthermore, if soil moisture legacy effects induce nutrient deficiency (e.g. via stimulation of denitrification under wet conditions leading to gaseous soil N loss), the relative benefit of forming AM may be higher. In contrast, if soil moisture legacy effects nutrient availability (e.g. via stimulation of mineralization N and P), the role of AM may be diminished. Interactively, adverse effects of soil moisture legacy on AM may be a change in the balance between the costs and benefits of forming AM, with shift from negative, neutral or positive mycorrhizal responses resulting (Johnson et al. 1997). Since most plants form AM, and these associations can have a vital role in improving growth and nutrition of plant. Soil moisture legacy significantly effect on the formation and functioning of AM. Here, are presented a result which shows the response of AM, to changing soil moisture. The experiment involved growing a mycorrhiza defective tomato mutant, and its mycorrhizal wild type progenitor (Barker et al. 1998) in soils with (experimentally established) different soil moisture legacies. This genotypic approach for controlling the formation of AM was selected as it allows for the comparison of mycorrhizal and non-mycorrhizal plants with the wider soil biota intact (Rillig 2004; Watts- Williams and Cavagnaro 2015), and because the two genotypes exhibit very similar growth patterns when grown in the absence of AMF (Watts-Williams and Cavagnaro 2014).

Climate change rainfall pattern throughout the world (IPCC 2014). Globally, a deviation of rainfall patterns is documented in mid latitudes (having dry regions), subtropics having low rainfall and higher latitudes receiving abundant rainfall Due to these changes, severe rainfall events are expected to happen in the current century in the nearer future specially in Asia and Eastern Africa, North America, Northern and Central Europe (IPCC 2012, 2014). In different regions of the world including South Africa, Mediterranean, Central America, the Amazon and North East Brazil more longer and dry spells have been documented In several terrestrial ecosystems, the changes brought about by precipitation and temperature that affect evaporation will definitely bring changes in soil moisture and consequently will bring extended water logged conditions after severe flooding and rainfall. These changing events will affect the plant microbe interaction, plant growth, water patterns, the soil flora, fauna and microbial activities as well as the fungal hyphal growth directly and indirectly it may affect the plant microbe interaction by altering the plant chemistry. But on the other hand, the dry conditions will lead to stomata closure, which consequently affect the carbon assimilation and as a result the plant growth is reduced. Due to plant growth under stress conditions the abundant carbon is stopped and may cause increase in the chemical compounds (carbon based) like phenols and tannins that become a threat to herbivores and several decomposers (Herms and Mattson 1992).

In waterlogged condition, oxygen is depleted from soil pores which bring about changes in different physico-chemical properties of soil and ultimately lead to plant damage. The toxic ions and fermented materials become poisonous to plant fine roots that restrict the carbohydrates and energy for proper plant growth and metabolism and therefore the whole plant is affected finally (Colmer and Voesenek 2009).

The metabolic and growth changes not only damage the symbiotic relationship between organisms and plant roots but also affect the presence and quality of food supply to decomposers, pollinators and herbivores. Moreover, the change in populated species of the plant community may have more intensive effects on close partner because the species disrupted in stress condition can also affect the particular plant partners as well the overall chemical composition of plants is also affected due to community shifts. The Autecological species are also changed due to different moisture regimes, and these changes may be in plant biomass (Ciais et al. 2005; Jentsch et al. 2011), species distributions or migration (Harschand et al. 2016) that have been properly managed in the last decades, with an intention on a strong edge on the cause of drier soil moisture conditions. Still there is a lack of research studies plant microbe and microbe microbe interaction in in reaction to change in soil moisture conditions (Tylianakis et al. 2008). It has also been reported that the interactions of species may reverse or even override the autecological responses (Angert et al. 2013; Trzcinski et al. 2016) and that the species interactions with each other strongly affect the stability and diversity of ecosystem (Bascompte et al. 2005). Tylianakis et al. (2008) reported that most of the symbiotic interactions specially with plants will be affected by global change, but not only CO_2 enrichment and concluding all other climatic phenomenon, not suitable for a detailed opinion about the effects of changed soil moisture.

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