Chapter 11
Climate Change Drivers and Soil Microbe-Plant Interactions

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Abstract Climate change is one of the most important global concerns of modern era, with economic, social, scientific, political, moral, and ethical aspects. The soil ecosystem, which encompasses an enormous diversity of microbial life, is critical in this regard because it is a key component of the carbon and nitrogen cycles and is associated in the removal of greenhouse gases in the atmosphere which contribute to climate change. The microbial world is an important component of various biogeochemical cycles, and its role in climate change must be considered. Microbes, on the other hand, are rarely mentioned in climate change discussions. Microbial activity has not been taken into account sufficiently in most climates due to a lack of adequate understanding. Therefore, this book chapter provides an insight into the the intrinsic and extrinsic attributes, direct and indirect mechanism and emerging technologies for understanding of plant–microbe responses to climatic change that confer reason of soil microbial communities to climate extremes.

Introduction

For more than 12,000 years, Earth's climate remained stable which in turn is vital for human kind's very existence [1]. During the past century, the typical global temperature increased close to a 1.5°F, and in next 100 years, it is expected to rise an additional 0.5°F–8.6°F. This is a critical problem since even little changes in the average global temperature can lead to significant changes in the weather and climate [2]. The microbial communiity is extremely significant for this context because it plays a crucial

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role in the nitrogen and carbon cycles and is proportionately involved in the removal and emission of gases that play a partin climate change, such as methane and CO2 [3]. While heterotrophic microorganisms break down organic substances to release greenhouse gases, photosynthetic microbes consume atmospheric carbon dioxide. The net carbon flux is primarily determined by the balance between the two processes, and it varies across different ecosystems based on climatic factors like temperature. As a result, microbial reactions play a critical role in the earth's carbon cycle because they not only lock up large amounts of carbon but also release it, according to [4, 5]. It is important to emphasise that most greenhouse gases, including CO_2, CH_4, and N_2O, are produced by microbes [6]. In this book chapter we have discussed about the various action mechanisms of climate change including the mechanisms affecting the microbial community, alterations in microbial diversity, the physiological alterations, action mechanisms on plants, variations in moisture content, and the various consequences on microorganisms due to change in climate, rising temperatures, altered precipitation, increased CO_2 emissions, drought situations and try to elaborate on emerging technologies and better comprehension of plant and microbe responses to variations in climate and their interactions. Respectively the end of the chapter deals with mitigation strategies like mulching, use of organic residues, fertilisers, crop and landscape administration are also taken into account.

Action Mechanisms of Climate Change

Temperature, precipitation, and changes in length of seasons are all indicators of climate change [7]. Therefore, the major ways in which its mechanism of action is exhibited are changes in temperature and moisture levels.

Mechanisms Affecting the Microbes

Soil microbial populations are affected both directly and indirectly by climate change elements such as increased atmospheric CO_2, changing temperature forms, and overall warming [8]. In addition, as a result of multiple components changing abruptly because of climate change, the terrestrial microbial population undergoes complicated alterations [8]. The microbial population, plants, and soil carbon balance may all be notably impacted by such large-scale changes brought on by climate change [9, 10]. Nonetheless, interactivity between different climate alterationelementsare also possibly discerning towards certain soil microorganisms, which can lead to conversions in factions that may ultimately determine the future condition of ecospheres [8].

Alterations in the Microbial Variety

Negative impact like Abiotic stress brought on by climate change can change the variety and functioning of soil microbes [11]. Because different microbial species prefer different temperature scales for activity and growth, an increase in temperature may have an effect on how the microbial population is formed [6, 12]. Swiftness of processing of microorganisms, yield, as well as activity is prompted with an increase in temperature. Therefore, the microbial community shifts in approval of the species with sped up rates of development and better tolerance for higher temperatures [8]. The effects of climate change on two important cyanobacteria, namely *Microcoleus steenstrupii* and *Microcoleus vaginatus*, present in topsoil of arid region of western USA, exemplifies this impact. As global temperatures rise, the former, which is thermotolerant, has been observed to replace the latter and even outcompeteit, which ispsychrotolerant. These microorganisms are essential for preserving the topsoil's microbial community, whose traits are necessary for preventing soil erosion [13]. For the reason thatmicrobial community differ in terms of sensitivity to temperature, physiology, andgrowth rates,it shows that climate change alters both the relative abundance and activity of soil microbial populations. Therefore, as a result it has a direct impact on how these organisms' particular functions are regulated [9, 10]. Warming-related variations in the population of microbes' organisation may also result in a decrease in the amount of substrate that is readily available [14]. In the same context, it shall be noted that both bacteria and fungi abundance is likely to be impacted by global warming [14]. It is noteworthysincecertain microbes control ecological processes like nitrification, denitrification, nitrogen fixation, and methanogenesis. Therefore, changes in their relative abundance have a direct effect on how quickly these processes occur. Although, because a diversity of organisms manage some activities thattake place at a very coarserate (viz., as mineralization of nitrogen), abiotic factors like moisture and temperature have a greater impact on these processes than microbial community makeup [9, 10].

Conversions in Physiology

Rising temperature increases the upkeep of microbes, which leads to escalation in demand of themaintainence of microbial community (respiration per biomass) [15]. As a result, heat increases soil respiration by accelerating soil microbial activity [16, 17]. Changes occurring in the respiration of soil is started because of alterations in the available carbon comparative abundance [18], composition of the microbial community [19], the quantity and quality of plant litter [17] and the availability of substrate [20, 21], which are all associated with temperature elevation. Therefore, it is believed that due to sensitivity to temperature of microbial metabolism and also the activities they engage in, changes all over the globe changes such as temperature increase can directly impact the rates of respiration of soil bacteria [9, 10]. Temperature and

moisture levels are firmly connected, and high or low moisture levels may restrict soil respiration [22]. Although, until other factors like moisture and substrate become limited or the conformation/formation of a forest stand is reformed or changed, it is unlikely that the microbial community's makeup will change or that adaptations will occur that indicate a rise in soil respiration [14]. Changes in soil temperature and moisture brought on by differences in precipitation can also affect soil respiration [23]. In this context, enzyme activity should also be taken into account. It is important to note that, as temperatures rise, microbes allocate more nutrients for the development of enzymes (to obtain the additional nutrients needed) [24, 25]. In reality, due to direct and indirect effects on microbial production of enzymes and turnover rates, climatic change causes long-term changes in enzyme pools in addition to minisculechanges in activity of enzymes steered by thermodynamics [26, 27]. Due to their impacts on substrate availability, enzyme efficiency, and microbial efficiency, variations in temperature and moisture have an impact on both the comprehensive and relative rates of production of enzymes. If soil temperature rises, increasing the processing of substrate and the existing enzyme pool becomes available, microorganisms may devote less energy to producing enzymes if biomass of micobes stays constant [28]. It should be recognised that C-degrading enzymes are more temperature sensitive than N-degrading enzymes [29–31]. Substrate temperature sensitivity is a related issue that is influenced by a number of variables including oxygen availability, moisture content and accessibility (surface assimilation and accumulation state) [20]. The relationship between temperature and soil respiration can be understood by looking at substrate usage and microbial development [32]. Additionally, the kind of soil influences soil microbial activity, which may be a relevant role in this case. Due to the characteristics of allophone, it ought to be emphasised that microbiological activity is minimal in soil made of volcanic ash [33]. The fact that microbial biomass turnover, respiration and soil organic matter are all higher in tropical soils than in temperate soils serves as an illustration of the importance of temperature with regard to these processes [34].

Action Mechanisms on Plants

Plants are significant biotic components that are crucial in this context. By allowing roots to release carbon substrates [35, 36], changing temperature of soilas well asmoisture with the help ofshade and transpiration [37], and changing the quantity of rain that ultimately reaches the soil, they modify rates of soil microbial respiration. Additionally, the type of plant remnants and quality viz., organic matter, that reaches the soil and the respiration of soil, are determined by the constitution of the vegetation. The variation in soil respiration beneath evergreen and deciduous forests serves as one example of this [38]. According to [39], the kind of anthropogenic land use and management and plant cover both affect the nature of organic materials in soils with a comparable geology. This is very significant since the key factors affecting how sensitive soil respiration is to temperature are the availability

of temperature-dependent substrate release and rapidly decomposable carbon [32]. Changes in the sensitivity of temperature of organic matter of soil disintegration can result in significant inaccuracies in models of C-cycle [32].

Undulation in Moisture

Changes in moisture, a major variable that significantly affects the patterns of soil respiration in many terrestrial ecosystems, is another way that climate change has an impact on soil ecosystems [40]. Numerous variables that change with the moisture present and amount of water, such as gas diffusion, water movement, solute diffusion, and the motility and survival of microorganisms, have an impact on microbial activity and, consequently, decomposition [22, 41]. Additionally, moisture could reduce activity of microbes in a variety of settings, including soils and saltwater. Less water availability diminishes intracellular water potential, which in turn lessens enzyme activity and hydration [42]. The release and dynamics of CO_2 can be significantly impacted by soil moisture [40]. All of this is demonstrated by the observation that in grasslands, temperature and soil moisture are the key regulators of respiration in soil, that in turn controls CO_2 response between soil and atmosphere [40].

Consequences of Climate Change on Microbes

Microbes respond dynamically to both abiotic and biotic stimuli [43], therefore the consequences of change in climate on these microorganisms are evident. In general, soil microbes are extremely active and respond promptly to environmental factors [34]. However, the relevance of each environmental component is regulated by temporal and spatial dimensions [44]. At higher latitudes, the consequences of temperature rise on microbial processes are projected to be most severe [20, 45].

Rising Temperature

By 2100, the average global surface temperature is expected to rise by 1.1 to 6.4 °C, which may have an impact on soil carbon sequestration by potentially accelerating heterotrophic microbial activities [46]. Droughts in the [40] area may become more frequent, intense, and long-lasting as temperatures rise [47]. The structure and activities of soil microbial communities are known to be sensitive to variations in both temperature and water accessibility [48]. Temperature increases hasten microbial breakdown, increasing CO_2 released by soil thereby creating a positive feedback loop to climate change [49]. Because of global warming, by 2100, it is anticipated

that 25 percent of permafrost might melt resulting in releasing around 100 Peta-grams (Pg) of carbon for microbial breakdown [20]. The enormous organic carbon stocks (400 Pg, or 4,000 million tonnes) in these soils are susceptible to higher breakdown rates due to higher melting rates and depths in high-latitude permafrost. Flooding of melted permafrost regions generates anaerobic conditions conducive to methanogenesis breakdown. Increased temperature is closely related to increased soil respiration, and a 2 °C increase in world average temperature is anticipated to increase soil carbon release by 10 Pg, owing mostly to increased microbial activity. The ideal scales of temperature for optimum activity and growth are different for different microbial groups. Rising temperatures can influence the composition of the microflora, which can limit the emission of organic carbon of soil in some circum-stances due to the extinction of acclimatised microbiota [50]. Tropical soils emit more CO2 than temperate soils because to higher and longer heat regimes, where the overall rate of disintegration of organic matter is substantially faster due to increased microbial activity. Changes in soil temperature are anticipated to change microbial-operated nitrification and denitrification activities in the environment of soil due to population shifts indenitrifiers and nitrifiers. Changes in the soil microenvironment can induce community changes and changed metabolic reactions in microorganisms engaged in soil nutrient cycle, as well as an increase or decrease in the viability and pathogenicity of soil-mediated pathogenic bacteria such as *Salmonella typhimurium.* As a result of the lower temperature, microbial growth and activities normally reduces in the winter. In general, extremely high temperatures are harmful to many bacteria. Indeed, some organisms may be able to endure such harsh environments by trans-forming into dormant forms that can withstand high temperatures. Although, such typical periodical/seasonal patterns might differ in individual ecosystems of soil. For example, in arctic soil, microbial density is at its peak in late winter when tempera-ture is reduced [51]. The ideal average temperature for microbe life is about around 20 °C, whereas the upper limit is somewhere near 50 °C [52].

Altered Precipitation

The rate of decomposition of soil organic carbon and another significant regulator of terrestrial microbial community structure is soil moisture, which can be influ-enced by the IPCC's (Intergovernmental Panel on Climate Change) projected 20 percent increase or decrease in precipitation. Long dry periods may restrict micro-bial growth and decomposition, having a negative feedback effect on carbon flux in some ecosystems. Carbon dioxide generation is also influenced by the periodic soaking and drying of soil. When dry soils are re wetted, the activities of latent bacteria rises. This adds to increased CO_2 evolution during soil rewetting. Soil mois-ture can have an influence on chemical engineers both directly and indirectly. Soil moisture has a direct impact on bacteria's physiological condition and may impede their ability to breakdown various types of natural substances [53]. The soil mois-ture values required for optimum microbial activity vary according to type of soil

and microbial community diversity [54]. Soil moisture also has an indirect effect on microbial community development, activity, and composition by changing the quality and amount of plant litter formation. These can have an impact on plant–microbe interactions. Since availability of water and temperature are driving forces of N mineralization, denitrification, and microbial activity in dry land soils [55, 56], changing climate will have a significant impact on these processes through its impact on soil water and temperature availability [57, 58].

Increased CO_2

Anthropogenic CO_2 emissions are to blame for the current rise in atmospheric CO_2. Carbon dioxide levels in the atmosphere are rising at a 0.4 percent annual pace and are expected to double by 2100, owing mostly to anthropogenic activities including fossil fuel consumption and land-use changes. An estimated 30–40% of 2o produced by human activities into the atmosphere dissolves in seas, rivers, and reservoirs [59, 60], contributing to ocean acidification. The direct impact of increasing CO_2 on above-ground biomass production has indeed been widely researched [61]. It has been demonstrated that increasing above-ground net plant productivity (ANPP) increases C availability below-ground and boosts soil microbial activity [62]. Plants' average growth rate is accelerated by high $_{CO2}$ concentrations, allowing them to store more CO_2. Plant development was accompanied by a rise in soil respiration as a result of the increased availability of nutrients for breakdown by producing more CO_2 into the atmosphere. Increased CO_2 levels have an impact on the root zone's release of pliable sugars, organic acids, and amino acids, which can promote microbial activity. Long-term, it is thought that increased microbial biomass brought on by improved carbon release from roots may cause soil nitrogen to become immobilised, lowering the amount of nitrogen available to plants and creating a feedback loop that restricts further growth in plant development. The improved soil C:N ratio that follows may favour greater fungus diversity and dominance. Fungal cell walls are mostly made of carbon polymers (chitin and melatin), which are significantly more resistant to being destroyed than those found in bacterial membranes and walls (peptidoglycan and phospholipids). This means that fungi are more efficient at assimilating carbon (they store more carbon than they metabolise) than bacteria. As a result, soil respiration rates are often low in fungi-dominated environments, increasing the potential for carbon storage. A rise in atmospheric CO_2 may be one of the repercussions of climate change, and it can drastically alter the soil environment by changing the distribution of above and below-ground nutrients. Because CO_2 is the basic building block of photosynthesis, a rise in atmospheric CO_2 might result in enhanced plant growth. This may lead to an increase in rate of production of litter and a change in molecular structure of litter, which may result in a change in digestibility. Such changes will subsequently have an impact on the type of organic matter accessible to soil microbes [63]. As a result, altered litter generation may alter total carbon supply and N movement between plants and microbes [64]. Furthermore, rising CO_2 levels

may result in increased root development, which will have a considerable influence on soil structure and serious ramifications for soil biota.

Droughts

As temperatures rise, the intensity and severity of drought episodes in mesic ecosystems are expected to rise as well [65]. Water stress is predicted to have an impact on both microbial and plant populations, by disrupting important nutrient cycles and plant–microbe responses. Drought lowered soil moisture dramatically, generating unfavourable growth circumstances that resulted in a 50–80% fall in microbial population number [66]. Drought stress has been demonstrated to affect both the initiation and functioning of legume Rhizobium symbiosis [67, 68]. According to [69], populations of *Rhizobium leguminosarum* and *Rhizobium japonicum* declined biphasically in drying soils.

New Developments and Improved Knowledge of Plant–Microbe Response to Climate Change

To understand complex community dynamics and function, studies attempting to understand microbial dynamics have traditionally relied on methods like DGGE (denaturing gel gradient electrophoresis), TRFLP (terminal restriction fragment length polymorphism), PLFA (phospholipid fatty acid analysis), or simply measures of biomass. In general, these methods have shown trends in the make-up of microbial communities [70], but they do not show responses from particular taxa and only offer a scant amount of information regarding functional changes. Researchers are now focusing on microbial interactions with hosts that are more functionally significant and at the highest resolution thanks to the development of new sequencing techniques and the -omics revolution. Researchers can identify changes in microbial communities that will enhance their comprehension of which bacteria are present in an environment and what their potential roles are by employing the methods of meta-genomics, transcriptomics, proteomics, and metabolomics [71, 72]. One tool that can be used to focus on the active microbial community, which is involved in a variety of tasks, is stable isotope probing [73]. When these methods are used more frequently, researchers are faced with a number of difficulties, such as determining which methods produce the most accurate results and how to analyse these enormous datasets in the most precise and pertinent ways. Amplicon sequencing of the 16 s rRNA gene has become popular for determining the makeup of the bacterial community in ecosystems [74]. Although this generates a lot of data at a depth where species accumulation curves are starting to saturate, it has very little to no impact on

future functional changes in communities [75]. In order to comprehend the composition of microbial communities as well as their potential for function, some scientists are now using shotgun metagenomics to look at the variety of functional genes that are present in a habitat. The data produced by this method could be used to determine function, but it lacks the depth of amplicon sequencing and might miss rare taxa [76–78]. It is crucial to start sampling microbial communities at a size that is appropriate for the diversity and function of these tiny creatures, especially with the introduction of several new technologies targeted at understanding the dynamics of soil microorganisms.

At such a coarse geographic scale, it could be challenging to detect meaningful diversity patterns about these communities due to the significant variation contained in a soil sample [79]. Microorganisms can interact at the scale of the soil aggregate or at the plant root-soil interface, and there are significant differences between soil aggregates [80]. Future study should take into account the questions regarding diversity and function they are asking and appropriately alter their sampling technique to completely begin understanding how microbes interact with one another and their plant hosts. Beyond the question of what instruments to use to research microbial populations, the problem of how to interpret these significant datasets is a complex one [78]. Today, a variety of software programmes are available to assist with processing and analysis, including qiime [81], mothur [82], and less well-known tools like IMTORNADO [83], which assign taxonomy identity by utilising a variety of different taxonomic databases. The given dataset may produce different results depending on which of these processing approaches is used and which taxonomy is used when accessing the various databases. To enable dataset comparisons between laboratories and research teams, researchers must start contrasting diverse approaches and creating a standard procedure. Researchers must specifically investigate which processing pipeline produces the most pertinent results quickly, which database contains the most up-to-date and accurate taxonomic information for the taxa of interest, and how to standardise analyses across research groups in order to extract the most information from a given dataset. The molecular underpinnings of plant-microbial interactions at the plant root-soil interface, where microorganisms are prevalent and closely interact with plant roots, are also becoming better understood thanks to technological advancements [84]. It is difficult to identify how various soil bacterial subgroups enter the plant root and populate it. We are starting to put together the molecular foundation for these interactions by utilising state-of-the-art sequencing technologies that enable the rapid and affordable sequencing of entire organismal genomes. The genome of the ectomycorrhizal fungus Laccaria exhibits unusual characteristics, such as effector type small-secreted proteins with unknown functions that are only produced in symbiotic tissues, according to studies on the mutualistic relationship between Laccaria and its plant host [85]. Additionally, the plant host Populus has complete D-mannose lectin-like receptor gene deletions, which significantly reduces Laccaria colonisation [86]. By comprehending the molecular underpinnings of these interactions, the microbial population can be controlled to enhance plant and ecosystem level functions. It will also allow researchers to start creating microbial communities that can boost plant

growth, carbon allocation, and carbon storage, as well as beginning to forecast which microbes will live in the plant root endosphere.

Climate Change Effects on Plant–Microbe Interactions

Some plant species are adapting to climate change by moving to higher elevations and latitudes, flowering and leafing out earlier in the growing season, and changing the expression of advantageous features [87–92]. On a smaller scale the arctic has become increasingly shrubby as a result of warming, with woody shrubs replacing grasses and forbs in some parts. This change in the ecosystem's features has led to carbon feedbacks in these systems [93–96]. Soil communities, especially those that are strongly connected with plants, have the potential to speed up or slow down changes in plant communities. Studies by [97–99], for instance, found that microbial communities associated with rootscould have a big impact on phenology, plant survival, and the expression of functional characteristics. All of these characteristics are sensitive to climatic variations. There is currently a lack of knowledge regarding how interactions among plants, the microbial population with which they coexist, and climate change impact ecosystem processes [100, 101]. The carbon balance in the soil, changes in the overwhelming majority of the soil microbial community, and plant growth and establishment may all be adversely affected by climate change for a very long time. In reality, interactions between plants and soil ecosystems, such as plant-soil feedbacks, are among the most important yet poorly understood controllers of soil nitrogen and carbon dynamics. The interactions between plants and soil communities will decide how an ecosystem responds if soil microbial populations shift as a result of climate change, which effects the establishment and growth of plant species. Recent studies have shown that the early responses of the local soil ecosystem might shield plants from drought stress [102]. There is mounting evidence that shifts in microbial diversity may affect the selection of functional characteristics in plants [103]. The indirect impacts of climate on plants and the soil communities that support them can differ greatly from the direct effects of temperature on the majority of the soil community. [43] discovered, for instance, that changes in precipitation had an impact on the soil community and its function in an oldfield in TN (USA), but that the impact of precipitation on the composition and function of the soil community varied depending on the plant the soil was obtained from. To evaluate the influence of climate change on communities and functions, soil samples were collected and homogenised from various parts of the site. These results suggest that the reactions of soil ecosystems to climate change may be cancelled out if the mix of plant communities' changes along with climate change. Most research may not adequately capture these community and functional modifications because soils are collected from many plant species and homogenised together [43]. These interactions may progressively build up in the soil system and alter ecosystem function

(like carbon cycling) and trajectory (like plant establishment), given the strong interactions between plants and the soil communities they are linked with;Strong interactions between plants and the soil communities they are linked with may eventually accumulate in the soil system and alter ecosystem function (like carbon cycling) and trajectory (like plant establishment); however, research must be conducted to distinguish these interactions.

Alleviation Schemes

The same methods that boost productivity and resistance to climate change give favourable co-benefits in terms of agricultural GHG reduction. There are three basic techniques for regulating GHGs in agricultural production: (a) lowering emissions, (b) increasing carbon removal from the atmosphere, and (c) minimizing emissions by using bioenergy or agricultural expansion rather than growth [104]. There is a positive relationship amongst soil organic carbon and crop output; methods that improve fertility of the soil productivity also reduce GHG emissions, especially in places wherein soil degradation is a major concern [105]. Reference [106] distinguishes between actions with high and low mitigation potential, as well as those with high and low food security prospects.

Light Soil Sealing/Mulching

The technique of mulching involves covering the soil's surface to prevent erosion and boost fertility. Mulch is frequently laid down at the beginning of the growing season for crops and can be replaced as necessary. By retaining both heat and moisture, it first helps to warm the soil. Mulch can be created from a variety of substances, such as organic waste products (such as hay, bark, and agricultural residue), manures, wastewater sludge, and rubber or plastic covers.

Utilization of Organic Waste (Compost, Manure, and Sludge)

The amount of organic matter in soil is increased by a variety of carbon-rich wastes, including coffee-berry pulp, sludge, grain and legume straw, animal manure, etc. Before being applied to the field for agricultural reasons, organic leftovers should be given time to degrade. For microbes to grow and flourish, they need both carbon and nitrogen, and the addition of carbon-rich substances makes soil nutrients momentarily immobile.

Fertilizers

Microorganisms become more active when nitrogen is made readily available to them by some inorganic nitrogenous fertilisers in large quantities. As a result, low-quality organic inputs and soil's organic content break down more quickly, leaving less soil carbon behind and the organic matter content of the soil continuing to decline. This causes the soil to become less healthy and its ability to hold water to decline.

Crop Administration/Selection of Species of Crop

The sort of habitat that soil fauna can access depends on the agricultural crop that is chosen. Legumes, for instance, can act as organic fertilisers by boosting soil N levels through a symbiotic relationship with rhizobia. Because crop changes affect the populations of biological regulators, crop rotations can also help to reduce the accumulation of diseases and pests. In order to reduce nitrous oxide emissions, it is essential to employ crop management techniques that encourage N usage efficiency and yield.

Landscape Administration/Hedgerows and Grassy Field Margins

The establishment of bushes and trees or grassland strips next to intensively farmed fields offers soil fauna a permanent habitat, food, and a secure environment. Due to their limited mobility, shrubs, as opposed to grassy field boundaries, are much more advantageous to soil critters, especially bio-controls; soil bacteria will have very little spread into the fields. This is important since 10% of the soil-dwelling species found on farms are only found in field edges.

Microbial Communities and Mitigation Strategies

Managing Microbial Communities and Reducing CO_2 Release

Around 2,000 Pg of organic carbon may be found in soils, which is double the quantity in the atmosphere and three times the amount in plants [46, 107]. It has been suggested that land use may be adjusted to sequester an additional 1 Pg of carbon every year in soil since different land types, such as woodlands, pastures, and agricultural land, have varying capacities to store carbon [107, 108].

Using Microbial Community Management to Lower Methane Emissions

Worldwide, methane memissions are perhaps more directly regulated by microbes than carbon dioxide (CO_2) emissions. Microbial methanogenesis, it's a process which is performed by a variety of anaerobic archaea in seas, termite guts, wetlands, etc., accounts for the majority of natural emissions of methane ranging approximately up to 250 million tonnes methane per year. However, emissions from human activity, majorly fossil fuel extraction and landfills, outnumbers the natural sources.

Conclusion

It is admirable that microbes play a role in regulating the amount of greenhouse gases in the atmosphere, but the scientific community still needs to fully comprehend and value this contribution. Given the reported unpredictability, it is obvious that knowing the immediate and long-term impacts of climate change on these bacteria, as well as their associated short- and long-term feedbacks, would aid in our comprehension of the potential contributions of these microbes. If used appropriately, microbes have the potential to be an important natural resource for reducing climate change. It might become a big problem rapidly if not managed carefully. It is imperative that we research this topic thoroughly and comprehend the underlying mechanics and then effectively apply what we learn to the formulation of solutions.

Future Perspectives

According to projections on the World Meteorological Organization Website, the average global surface air temperature could rise from 1.4 °C and 5.8 °C by the year 2100, and predictions state that a 2 °C rise in global temperature would result in an increase in the release of soil carbon of 106 kg (i.e., 10 petagrams) of CO2 and some other greenhouse gases [62, 109, 110]. This could set off a chain reaction that would cause the temperature to rise even more and the surroundings to alter. Climate change is predicted to result in more precipitation throughout the winter months in northern medium and high latitudes as well as Antarctica. Instead of being spread out over multiple mild occurrences, larger amounts of rainwateris more probable to be discharged withiin a few extremely large outbreaks (World Meteorological Organization Website). As a result, various ecological factors in terrestrial and aquatic environments are anticipated to alter, which will have a significant effect on microbes. There are several models that forecast how such environmental changes may affect bacteria [111, 112]. Recent modelling methods and research, however, have shown that soil warming over a long period of timedepicts a larger greater than

initially believed positive feedback between atmospheric soil organic matter release and climate warming [113]. Terrestrial ecosystems in the region of arctic are predicted to be especially hard hit by the issue. Consequently, the Arctic has been emphasised as a crucial area for identifying climate change [114]. But there are few mechanically determined models that forecast how soils will respond to climate change [115]. Separate ecosystems are probably going to react to the problem in different ways. For instance, it has been predicted that in reaction to climate change, European forest soils will behave as CO_2 sinks, on the other handsoils in the agricultural areacould lose organic matter and subsequently release CO_2 [116, 117].

References

1. NASA (2015) http://climate.nasa.gov/solutions/adaptation-mitigation/. Accessed 15 Dec 2015
2. US EPA (2015) Climate change: basic information. http://www3.epa.gov/climatechange/basics/. Accessed 15 Dec 2015
3. Microbiology online (2015) Microbes and climate change. http://www.microbiologyonline.org.uk/aboutmicrobiology/microbesandclimatechange. Accessed 15 Dec 2015
4. Weiman S (2015) Microbes help to drive global carbon cycling and climate change. Microb Mag 10(6):233–238. https://doi.org/10.1128/microbe.10.233.1
5. Zimmer C (2010) The microbe factor and its role in our climate future. http://e360.yale.edu/feature/the_microbe_factor_and_its_role_in_our_climate_future/2279/
6. Singh BK, Bardgett RD, Smith P, Reay DS (2010) Microorganisms and climate change: terrestrial feedbacks and mitigation options. Nat Rev Microbiol 8(11):779–790. https://doi.org/10.1038/nrmicro2439,PMID20948551
7. Smith P, Fang C, Dawson JJC, Moncrieff JB (2008) Impact of global warming on soil organic carbon. Adv Agron 97:1–43. https://doi.org/10.1016/S0065-2113(07)00001-6
8. Castro HF, Classen AT, Austin EE, Norby RJ, Schadt CW (2010) Soil microbial community responses to multiple experimental climate change drivers. Appl Environ Microbiol 76(4):999–1007. https://doi.org/10.1128/AEM.02874-09,PMID20023089
9. Classen AT, Sundqvist MK, Henning JA, Newman GS, Moore JAM, Cregger MA et al (2015) Direct and indirect effects of climate change on soil microbial and soil microbial plant interactions: what lies ahead? Ecosphere 6(8):1–21. https://doi.org/10.1890/ES15-00217.1
10. Classen AT, Sundqvist MK, Henning JA, Newman GS, Moore JAM, Cregger MA et al (2015) Direct and indirect effects of climate change on soil microbial and soil microbial-plant interactions: what lies ahead? Ecosphere 6(8):130. https://doi.org/10.1890/ES15-00217.1
11. Shade A, Peter H, Allison SD, Baho DL, Berga M, Bürgmann H et al (2012) Fundamentals of microbial community resistance and resilience. Front Microbiol 3:417. https://doi.org/10.3389/fmicb.2012.00417,PMID23267351
12. Fierer N, Schimel JPA (2003) A Proposed mechanism for the pulse in carbon dioxide production commonly observed following the rapid rewetting of a dry soil. Soil Sci Soc Am J 67(3):798–805. https://doi.org/10.2136/sssaj2003.7980
13. DiGregorio BE (2015) Climate change affecting microbes in North America soils. American society for microbiology. https://www.microbemagazine.org/index.php?option=com_contentandview=articleandid=6497:climatechangeaffectingmicrobesinnorthamericasoils. Accessed 15 Dec 2015

14. Schindlbacher A, Rodler A, Kuffner M, Kitzler B, Sessitsch A, Zechmeister-Boltenstern S (2011) Experimental warming effects on the microbial community of a temperate mountain forest soil. Soil Biol Biochem 43(7):1417–1425. https://doi.org/10.1016/j.soilbio.2011.03.005,PMID21760644

15. Anderson JPE, Domsch KH (2010) A physiological method for the quantitative measurement of microbial biomass in soil. Soil Biol Biochem 2010:215–21

16. Wu Z, Dijkstra P, Koch GW, Peñuelas J, Hungate BA (2011) Responses of terrestrial ecosystems to temperature and precipitation change: a meta-analysis of experimental manipulation. Glob Change Biol 17(2):927–942. https://doi.org/10.1111/j.1365-2486.2010.02302.x

17. Rustad L, Campbell J, Marion G, Norby R, Mitchell M, Hartley A et al (2001) A meta-analysis of the response of soil respiration, net nitrogen mineralization, and aboveground plant growth to experimental ecosystem warming. Oecologia 126(4):543–62. https://doi.org/10.1007/s004420000544, PMID 28547240

18. Fierer N, Craine JM, McLauchlan K, Schimel JP (2005) Litter quality and the temperature sensitivity of decomposition. Ecology 86(2):320–326. https://doi.org/10.1890/04-1254

19. Balser TC, McMahon KD, Bart D, Bronson D, Coyle DR, Craig N et al (2006) Bridging the gap between micro- and macro-scale perspectives on the role of microbial communities in global change ecology. Plant Soil 289(1–2):59–70. https://doi.org/10.1007/s11104-006-9104-5

20. Davidson EA, Janssens IA, Luo Y (2006) On the variability of respiration in terrestrial ecosystems: moving beyond Q(10). Glob Change Biol 12(2):154–164. https://doi.org/10.1111/j.1365-2486.2005.01065.x

21. Eliasson PE, McMurtrie RE, Pepper DA, Stromgren M, Linder S, Agren GI (2005) The response of heterotrophic CO_2 flux to soil warming. Glob Change Biol 11(1):167–181. https://doi.org/10.1111/j.1365-2486.2004.00878.x

22. Luo Y, Zhou X (2006) Soil respiration and the environment. Academic Press, London

23. Aanderud ZT, Jones SE, Schoolmaster DR Jr, Fierer L (2013) Sensitivity of soil respiration and microbial communities to altered snowfall. Soil Biol Biochem 57:217–227

24. Wang G, Post WM, Mayes MA (2013) Development of microbialenzyme-mediated decomposition model parameters through steady-state and dynamic analyses. Ecol Appl 23(1):255–272. https://doi.org/10.1890/12-0681.1, PMID 23495650

25. Wang G, Post WM (2012) A theoretical reassessment of microbial maintenance and implications for microbial ecology modeling. FEMS Microbiol Ecol 81(3):610-617. https://doi.org/10.1111/j.1574-6941.2012.01389.x, PMID 22500928

26. Trasar-Cepeda C, Gil-Sotres F, Leirós MC (2007) Thermodynamic parameters of enzymes in grassland soils from Galicia, NW Spain. Soil Biol Biochem 39(1):311–319. https://doi.org/10.1016/j.soilbio.2006.08.002

27. Schimel J, Balser TC, Wallenstein M (2007) Microbial stressresponse physiology and its implications for ecosystem function. Ecology 88(6):1386–1394. https://doi.org/10.1890/06-0219,PMID17601131

28. Allison SD, Vitousek PM (2005) Responses of extracellular enzymes to simple and complex nutrient inputs. Soil BiolBiochem 37:937–944

29. Stone MM, Weiss MS, Goodale CL, Adams MB, Fernandez IJ, German DP et al (2012) Temperature sensitivity of soil enzyme kinetic sunder N-fertilization in two temperate forests. Glob Change Biol 18(3):1173–1184. https://doi.org/10.1111/j.1365-2486.2011.02545.x

30. Wallenstein MD, McMahon SK, Schimel JP (2009) Seasonal variation in enzyme activities and temperature sensitivities in Arctic tundra soils. Glob Change Biol 15(7):1631–1639. https://doi.org/10.1111/j.1365-2486.2008.01819.x

31. Wallenstein MD, Haddix ML, Lee DD, Conant RT, Paul EA (2012) A litter-slurry technique elucidates the key role of enzyme production and microbial dynamics in temperature sensitivity of organic matter decomposition. Soil Biol Biochem 47:18–26. https://doi.org/10.1016/j.soilbio.2011.12.009

32. Larionova AA, Yevdokimov IV, Bykhovets SS (2007) Temperature response of soil respiration is dependent on concentration of readily decomposable C. Biogeosciences 4(6):1073–1081. https://doi.org/10.5194/bg-4-1073-2007

33. Joa J, Moon K, Chun S, Kyung-San C, Hae-Nam HH (2010) Effect of temperature on soil microbial biomass, enzyme activities and PLFA content during incubation period of soil treated with organic materials. In: Proceedings of the 19th world congress of soil science, soil solutions for a changing world, Brisbane, Australia. Published on DVD

34. Joergensen RG (2010) Organic matter and micro-organisms in tropical soils. In: Dion P (ed) Soil biology and agriculture in the tropics. Springer, Berlin pp 17–44

35. Cardon ZG, Gage DJ (2006) Resource exchange in the rhizosphere: molecular tools and the microbial perspective. Annu Rev Ecol Evol Syst 37(1):459–488. https://doi.org/10.1146/annurev.ecolsys.37.091305.110207

36. Scott-Denton LE, Rosenstiel TN, Monson RK (2006) Differential controls by climate and substrate over the heterotrophic and rhizospheric components of soil respiration. Glob Change Biol 12(2):205–216. https://doi.org/10.1111/j.1365-2486.2005.01064.x

37. Lauenroth WK, Bradford JB (2006) Ecohydrology and the partitioning AET between transpiration and evaporation in a semiarid steppe. Ecosystems 9(5):756–767. https://doi.org/10.1007/s10021-006-0063-8

38. Rey A, Jarvis P (2006) Modelling the effect of temperature on carbon mineralization rates across a network of European forest sites (FORCAST). Glob Change Biol 12(10):1894–1908. https://doi.org/10.1111/j.1365-2486.2006.01230.x

39. Guntiñas ME, Gil-Sotres F, Leirós MC, Trasar-Cepeda C (2013) Sensitivity of soil respiration to moisture and temperature. J Soil Sci Plant Nutr 13(2):445–461

40. Aanderud ZT, Schoolmaster DR Jr, Lennon (2011) Plants mediate the sensitivity of soil respiration to rainfall variability. Ecosystems 14:156

41. Rodrigo A, Recous S, Neel C, Mary B (1997) Modelling temperature and moisture effects on C-N transformations in soils: comparison of nine models. Ecol Modell 102(2–3):325–339. https://doi.org/10.1016/S0304-3800(97)00067-7

42. Stark JM, Firestone MK (1995) Mechanisms for soil moisture effects on activity of nitrifying bacteria. Appl Environ Microbiol 61(1):218–221

43. Kardol P, Cregger MA, Company CE, Classen AT (2010) Soil ecosystem functioning under climate change: plant species and community effects. Ecology 91(3):767–781. https://doi.org/10.1890/09-0135.1, PMID 20426335

44. Savage K, Davidson EA, Richardson AD, Hollinger DY (2009) Three scales of temporal resolutionfrom automated soil respiration measurements. Agric For Meteorol 149(11):2012–2021. https://doi.org/10.1016/j.agrformet.2009.07.008

45. The Core Writing Team (2007) Climate change 2007: synthesis report contribution of working groups I, II and III to the fourth assessment. Report of the intergovernmental panel on climate change. IPCC, Geneva, Sweden

46. IPCC (2007) The physical science basis. Clim change.

47. Global climate change impacts in the United States (GCCI) (2009). In: Karl TR, Melillo JM, Peterson TC (eds) Cambridge University Press, New York

48. Hartel PG (2005) Soil abiotic environmental factors. Sylvia, 2nd edn. Principles and applications of soil microbiology, pp 41–51

49. Allison SD, Wallenstein MD, Bradford MA (2010) Soil carbon response to warming dependent on microbial physiology. Nat Geosci 3:336–340

50. Li WKW, Dickie PM (1987) Temperature characteristics of photosynthetic and heterotrophic activities: seasonal variation in temperate microbial plankton. Appl Environ Microbiol 53(10):2282–2295. https://doi.org/10.1128/aem.53.10.2282-2295.1987, PMID 16347449

51. Schadt CW, Martin AP, Lipson DA, Schmidt SK (2003) Seasonal dynamics of previously unknown fungal lineages in tundra soils. Science 301(5638):1359–1361. https://doi.org/10.1126/science.1086940, PMID 12958355

52. Vannier G (1994) The thermo biological limits of some freezing intolerant insects -the super cooling and thermo stupor points. Acta Oecol 15:31–42

53. Harris RF (1980) Effect of water potential on microbial growth and activity. In: Water potential relat soil microbiol water potential, pp 23–95. https://doi.org/10.2136/sssaspecpub9.c2

54. Prado AGS, Airoldi C (1999) The influence of moisture on microbial activity of soils. Thermochim Acta 332(1):71–74. https://doi.org/10.1016/S0040-6031(99)00062-3

55. Gallardo A, Merino J (1998) Soil nitrogen dynamics in response to carbon increase in a Mediterranean shrubland of SW Spain. Soil Biol Biochem 30(10–11):1349–1358. https://doi.org/10.1016/S0038-0717(97)00265-4

56. Gallardo A, Schlesinger WH (1992) Carbon and nitrogen limitations of soil microbial biomass in desert ecosystems. Biogeochemistry 18(1):1–17. https://doi.org/10.1007/BF00000423

57. Schlesinger WH, Bernhardt ES (2013) Biogeochemistry: an analysis of global change. Academic Press, San Diego

58. Robertson GP, Groffman P (2007) Soil microbiology, biochemistry, ecology. Springer, New York

59. Feely RA, Sabine CL, Lee K, Berelson W, Kleypas J, Fabry VJ et al (2004) Impact of anthropogenic CO_2 on the $CaCO_3$ system in the Oceans. Science 305(5682):362–366. https://doi.org/10.1126/science.1097329,PMID15256664

60. Millero FJ (1995) Thermodynamics of the carbon dioxide system in the oceans. Geochimicaet Cosmochim Acta 59(4):661–677. https://doi.org/10.1016/0016-7037(94)00354-O

61. Pan Y, Melillo JM, McGuire AD, Kicklighter DW, Pitelka LF, Hibbard K et al (1998) Modeled responses of terrestrial ecosystems to elevated atmospheric CO_2: a comparison of simulations by the biogeochemistry models of the vegetation/ecosystem modeling and analysis project (VEMAP). Oecologia114(3):389–404. https://doi.org/10.1007/s004420050462, PMID 28307783

62. Pendall E, Bridgham S, Hanson PJ, Hungate B, Kicklighter DW, Johnson DW et al (2004) Below-ground process responses to elevated CO_2 and temperature: a discussion of observations, measurement methods and models. New Phytol 162(2):311–322. https://doi.org/10.1111/j.1469-8137.2004.01053.x

63. Zak DR, Pregitzer KS, Curtis PS, Holmes WE (2000) Atmospheric CO_2 and the composition and function of soil microbial communities. Ecol Appl

64. Berntson GM, Bazzaz FA (1997) Nitrogen cycling in microcosms of yellow birch exposed to elevated CO_2: simultaneous positive and negative below-ground feedbacks. Glob Change Biol 3(3):247–258. https://doi.org/10.1046/j.1365-2486.1997.00070.x

65. Knapp AK, Beier C, Briske DD, Classen AT, Luo Y, Reichstein M, Smith MD, Smith SD, Bell JE, Fay PA, Heisler JL (2008) Consequences of more extreme precipitation regimes for terrestrial ecosystems. Bioscience 58(9):811–821

66. Sheik CS, Beasley WH, Elshahed MS, Zhou X, Luo Y, Krumholz LR (2011) Effect of warming and drought on grassland microbial communities. Int Soc Microgr Ecol 5(10):1692–1700. https://doi.org/10.1038/ismej.2011.32,PMID21451582

67. Sprent JI (1971) Effects of water stress on nitrogen fixation in root nodules. Plant Soil (Special Volume):225–228

68. Kirda C, Danso SKA, Zapata F (1989) Temporal water stress effects on nodulation, nitrogen accumulation and growth of soybean. Plant Soil 120(1):49–55. https://doi.org/10.1007/BF02370289

69. Pena-Cabriales JJ, Alexander M (1979) Survival of Rhizobium in soils undergoing drying. Soil Sci Soc Am J 43(5):962–966. https://doi.org/10.2136/sssaj1979.03615995004300050030x

70. Gray SB, Classen AT, Kardol P, Yermakov Z, Mille RM (2011) Multiple climate change factors interact to alter soil microbial community structure in an old-field ecosystem. Soil Sci Soc Am J 75(6):2217–2226. https://doi.org/10.2136/sssaj2011.0135

71. Castro HF, Classen AT, Austin EE, Crawford KM, Schadt CW (2012) Development and validation of a citrate synthase directed quantitative PCR marker for soil bacterial communities. Appl Soil Ecol 61:69–75. https://doi.org/10.1016/j.apsoil.2012.05.007

72. Muller EE, Glaab E, May P, Vlassis N, Wilmes P (2013) Condensing the omics fog of microbial communities. Trends Microbiol 21(7):325–333. https://doi.org/10.1016/j.tim.2013.04.009,PMID23764387

73. Mau RL, Liu CM, Aziz M, Schwartz E, Dijkstra P, Marks JC et al (2015) Linking soil bacterial biodiversity and soil carbon stability. ISME J9(6):1477–1480. https://doi.org/10.1038/ismej.2014.205,PMID25350158

74. Sanschagrin S, Yergeau E (2014) Next-generation sequencing of 16S ribosomal RNA gene amplicons. J Vis Exp 90(90):e51709–e51709. https://doi.org/10.3791/51709,PMID25226019

75. Fierer N, Leff JW, Adams BJ, Nielsen UN, Bates ST, Lauber CL et al (2012) Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. Proc Natl Acad Sci USA 109(52):21390–21395. https://doi.org/10.1073/pnas.1215210110,PMID23236140

76. Shade A, Jones SE, Caporaso JG, Handelsman J, Knight R, Fierer N et al (2014) Conditionally rare taxa disproportionately contribute to temporal changes in microbial diversity. MBio5(4):e01371-14. https://doi.org/10.1128/mBio.01371-14, PMID 25028427

77. Lynch MD, Neufeld JD (2015) Ecology and exploration of the rare biosphere. Nat Rev Microbiol 13(4):217–229. https://doi.org/10.1038/nrmicro3400,PMID25730701

78. Zhou J, He Z, Yang Y, Deng Y, Tringe SG, Alvarez-Cohen L (2015) High-throughput metagenomic technologies for complex microbial community analysis: open and closed formats. MBio6(1):e02288–02214. https://doi.org/10.1128/mBio.02288-14, PMID 25626903

79. Ranjard L, Lejon DPH, Mougel C, Schehrer L, Merdinoglu D, Chaussod R (2003) Sampling strategy in molecular microbial ecology: influence of soil sample size on DNA fingerprinting analysis of fungal and bacterial communities. Environ Microbiol 5(11):1111–1120. https://doi.org/10.1046/j.1462-2920.2003.00521.x,PMID14641591

80. Lombard N, Prestat E, van Elsas JD, Simonet P (2011) Soil-specific limitations for access and analysis of soil microbial communities by metagenomics. FEMS Microbiol Ecol 78(1):31–49. https://doi.org/10.1111/j.1574-6941.2011.01140.x,PMID21631545

81. Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK et al (2010) QIIME allows analysis of high-throughput community sequencing data. Nat Methods 7(5):335–336. https://doi.org/10.1038/nmeth.f.303,PMID20383131

82. Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB et al (2009) Introducing Mothur: opensource, platform-independent, community-supported software for describing and comparing microbial communities. Appl Environ Microbiol 75(23):7537–7541. https://doi.org/10.1128/AEM.01541-09,PMID19801464

83. Jeraldo P, Kalari K, Chen XF, Bhavsar J, Mangalam A, White B et al (2014) IM-Tornado: a tool for comparison of 16S reads from paired-end libraries. PLoS ONE 9(12):e114804. https://doi.org/10.1371/journal.pone.0114804,PMID25506826

84. Hol WHG, Bezemer TM, Biere A (2013) Getting the ecology into interactions between plants and the plant growth-promoting bacterium *Pseudomonas fluorescens*. Front Plant Sci 4:81. https://doi.org/10.3389/fpls.2013.00081,PMID23596447

85. Martin F, Aerts A, Ahrén D, Brun A, Danchin EG, Duchaussoy F et al (2008) The genome of Laccaria bicolor provides insights into mycorrhizal symbiosis. Nature 452(7183):88–92. https://doi.org/10.1038/nature06556,PMID18322534

86. Labbé J, Jorge V, Kohler A, Vion P, Marçais B, Bastien C et al (2011) Identification of quantitative trait loci affecting ectomycorrhizal symbiosis in an interspecific F1 poplar cross and differential expression of genes in ectomycorrhizas of the two parents: populus deltoides and Populus trichocarpa. Tree Genet Genomes 7(3):617–627. https://doi.org/10.1007/s11295-010-0361-3

87. Grabherr G, Gottfried M, Paull H (1994) Climate effects on mountain plants. Nature 369(6480):448. https://doi.org/10.1038/369448a0, PMID 23320303

88. Walther GR, Post E, Convey P, Menzel A, Parmesan C, Beebee TJC et al (2002) Ecological responses to recent climate change. Nature 416(6879):389–395. https://doi.org/10.1038/416389a,PMID11919621

89. Parmesan C, Yohe G (2003) A globally coherent fingerprint of climate change impacts across natural systems. Nature 421(6918):37–42. https://doi.org/10.1038/nature01286, PMID 12511946.

90. Verheijen L, Aerts R, Brovkin V, Cavender-Bares J, Cornelissen J, Kattge J et al (2015) Inclusion of ecologically based trait variation in plant functional types reduces the projected land carbon sink in an earth system model. Glob Change Biol. https://doi.org/10.1111/gcb.12871

91. Hudson JMG, Henry GHR, Cornwell WK (2011) Taller and larger: shifts in Arctic tundra leaf traits after 16 years of experimental warming. Glob Change Biol 17(2):1013–1021. https://doi.org/10.1111/j.1365-2486.2010.02294.x

92. Walker MD, Wahren CH, Hollister RD, Henry GH, Ahlquist LE, Alatalo JM et al (2006) Plant community responses to experimental warming across the tundra biome. Proc Natl Acad Sci USA 103(5):1342–1346. https://doi.org/10.1073/pnas.0503198103,PMID16428292

93. Sturm M, Racine C, Tape K (2001) Climate change—increasing shrub abundance in the Arctic. Nature 411(6837):546–547. https://doi.org/10.1038/35079180,PMID11385559

94. Hinzman LD, Bettez ND, Bolton WR, Chapin FS, Dyurgerov MB, Fastie CL et al (2005) Evidence and implications of recent climate change in northern Alaska and other arctic regions. Clim Change 72(3):251–298. https://doi.org/10.1007/s10584-005-5352-2

95. Lawrence DM, Swenson SC (2011) Permafrost response to increasing Arctic shrub abundance depends on the relative influence of shrubs on local soil cooling versus large-scale climate warming. Environ Res Lett 6(4):8. https://doi.org/10.1088/1748-9326/6/4/045504

96. Pearson RG, Phillips SJ, Loranty MM, Beck PSA, Damoulas T, Knight SJ et al (2013) Shifts in Arctic vegetation and associated feedbacks under climate change. Nat Clim Change 3(7):673–677. https://doi.org/10.1038/nclimate1858

97. van der Heijden MGA, Klironomos JN, Ursic M, Moutoglis P, Streitwolf-Engel R, Boller T et al (1998) Mycorrhizal fungal diversity determines plant biodiversity, ecosystem variability and productivity. Nature 396(6706):69–72. https://doi.org/10.1038/23932

98. Friesen ML, Porter SS, Stark SC, von Wettberg EJ, Sachs JL, Martinez-Romero E (2011) Microbially mediated plant functional traits. Annu Rev Ecol Evol Syst 42(1):23–46. https://doi.org/10.1146/annurev-ecolsys-102710-145039

99. Wagner MR, Lundberg DS, Coleman-Derr D, Tringe SG, Dangl JL, Mitchell-Olds T (2014) Natural soil microbes alter flowering phenology and the intensity of selection on flowering time in a wild Arabidopsis relative. Ecol Lett 17(6):717–726. https://doi.org/10.1111/ele.12276,PMID24698177

100. Fischer DG, Chapman SK, Classen AT, Gehring CA, Grady KC, Schweitzer JA et al (2014) Marschner review: plant genetic effects on soils under climate change. Plant Soil 37:91–19

101. Mohan JE, Cowden CC, Baas P, Dawadi A, Frankson PT, Helmick K et al (2014) Mycorrhizal fungi mediation of terrestrial ecosystem responses to global change: mini-review. Fungal Ecol 10:3–19. https://doi.org/10.1016/j.funeco.2014.01.005

102. Lau JA, Lennon JT (2012) Rapid responses of soil microorganisms improve plant fitness in novel environments. Proc Natl Acad Sci USA 109(35):14058–14062. https://doi.org/10.1073/pnas.1202319109,PMID22891306

103. Lau JA, Lennon JT (2011) Evolutionary ecology of plant-microbe interactions: soil microbial structure alters selection on plant traits. New Phytol 192(1):215–224. https://doi.org/10.1111/j.1469-8137.2011.03790.x,PMID21658184

104. Smith P, Martino D, Cai Z, Gwary D, Janzen H, Kumar P et al (2007) Policy and technological constraints to implementation of greenhouse gas mitigation options in agriculture. Agric Ecosyst Environ 118(1–4):6–28. https://doi.org/10.1016/j.agee.2006.06.006

105. Lal R (2004) Soil carbon sequestration impacts on global climate change and food security. Science 304(5677):1623–1627. https://doi.org/10.1126/science.1097396,PMID15192216

106. FAO (2009) Food Security and agricultural mitigation in developing countries: options for capturing synergies. Rom

107. Smith P, Smith P (2004) Soils as carbon sinks: the global context. Soil Use Manag 20(2):212–218. https://doi.org/10.1079/SUM2004233

108. Houghton RA (2007) Balancing the global carbon budget. Annu Rev Earth Planet Sci 35(1):313–347. https://doi.org/10.1146/annurev.earth.35.031306.140057

109. Luo Y, Wan S, Hui D, Wallace LL (2001) Acclimation of soil respiration to warming in a tall grass prairie. Nature 413(6856):622–625. https://doi.org/10.1038/35098065,PMID11675783

110. Raich JW, Potter CS (1995) Global patterns of carbon dioxide emission from soils. Global Biogeochem Cycles 9(1):23–36. https://doi.org/10.1029/94GB02723

111. Wilson PDG, Brocklehurst TF, Arino S, Thuault D, Jakobsen M, Lange M et al (2002) Modelling microbial growth in structured foods: towards a unified approach. Int J Food Microbiol 73(2–3):275–289. https://doi.org/10.1016/s0168-1605(01)00660-2,PMID11934035

112. Dens EJ, Van Impe JF (2001) On the need for another type of predictive model in structured foods. Int J Food Microbiol 64(3):247–260. https://doi.org/10.1016/s0168-1605(00)00472-4,PMID11294347

113. Kirschbaum MUF (2004)Soil respiration under prolonged soil warming: are rate reductions caused by acclimation of substrate loss? Glob Change Biol 10(11):1870–1877. https://doi.org/10.1111/j.1365-2486.2004.00852.x

114. Ruess L, Michelsen A, Schmidt IK, Jonasson S (1999) Simulated climate change affecting microorganisms, nematode density and biodiversity in subarctic soils. Plant Soil 212(1):63–73. https://doi.org/10.1023/A:1004567816355

115. Liski J, Palosuo T, Peltoniemi M, Sievänen R (2005) Carbon and decomposition model Yasso for forest soils. Ecol Modell 189(1–2):168–182. https://doi.org/10.1016/j.ecolmodel.2005.03.005

116. Kirkby KJ, Smart SM, Black HIJ, Bunce RGH, Corney PM, Smithers RJ (2005) Long term ecological change in British woodland (1971–2001). In: English nature research report, vol 653. Peterborough: English Nature

117. Sleutel S, De Neve S, Hofman G (2003) Estimates of carbon stock changes in Belgian cropland. Soil Use Manag 19(2):166–171. https://doi.org/10.1079/SUM2003187