Paradigm Ecological Shift and Succession in Microbiomes: A Climatic Advent

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Abstract

Surge in the global mean annual temperature a resultant of the significant rise in CO_2 concentration and other greenhouse gases have become a serious concern internationally due to their unfavourable impacts on the physical and biological entities. Throughout Earth's history, microbiomes are known to play important roles in changing climate and are in turn being continuously changed by the climate. Certain recent studies are even pointing towards changes within the Earth's diverse microbiome as the causality of the warming Earth. Amongst all the factors, climate change has taken over as the most important determinants of the alterations in diversity, distribution and abundance of species in both artificially managed as well as natural terrestrial and marine ecosystems. Understanding microbial ecology of different ecosystems on earth, whether terrestrial or aquatic, is essential for assessing the relationship between various biogeochemical cycles with climate, its responses and feedbacks. But the microbial communities are very complex in their organization and function and are easily influenced by the changes in climate. Several studies have revealed the extent to which the shifts in microbial species interactions due to changing climatic scenario lead to alterations in biodiversity and function of both terrestrial and aqueous ecosystems. In fact, the interactions of soil microbes within their community and as well as rhizoplanes and root-rhizosphere of plants can directly or indirectly reform landscape patterns and abundance, diversity and composition of flora and fauna. Events such as ecological succession are also of prime importance in this context, as acute climatic changes could result in faster succession of a microbial community by another within a particular ecosystem.

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5.1 Introduction

Ecological succession of a microbial community is defined as the change in the species abundance and microbial population within an ecological niche over the time. The microbial community in an ecosystem is shaped by the environmental factors in nature, and the ecological succession of the microbial community in the particular space occurs when these environmental factors are modified. For example, climatic elements like rainfall, moisture and temperature have a direct impact on the biology of freshwater fungi responsible for the shifts in various important components of heterotrophic food webs in woodland streams. Similarly, ocean acidification rising temperature and seawater threaten the survival of marine ecology involving marine microbial diversity, coral physiology, etc. Microbiomes are the pioneers in mineralization of litter carbon and conversion of complex, dead, organic matter into simpler biomass, due to which even a minimal change in climatic elements could indirectly deliver a large scale impact on agriculture, fresh water and marine ecology. Microbiomes respond, adapt, and evolve to their surroundings at much higher rates than any other higher organisms. This property allows scientists to correlate and derive scalable assessments in a little span of time on the impacts of changing climatic factors on the nature of microbiomes. This may in turn be used to understand and forecast imminent effects on all forms of life in changing climatic scenario. Hence, the chapter puts some efforts in explaining the effects of changing climate on the diverse microbiomes under different ecosystem.

Microbes are the main decomposers of organic materials existing in environment. Changes in microbial community or microbial succession are occurred due to their adaptation in various habitats. Due to global change, the species distribution is also altering and thus interactions among organisms within the specific ecological niche. In a niche, microorganisms are living with thousands of other different species. Of them few are beneficial to each other and helping them to live in community, whereas some are pathogenic and have effects on other species. But some microbes have no effect to the other microbes within the community either positive or negative. Since in natural conditions the microbial community is made up with several microorganisms with having different characters and dispersal ability, it can be assumed that the organisms present within the same econiches will react in dissimilar way under changing climatic conditions. The microorganisms take a major role in regulating nutrient transformation in a macroecological system and allow the co-existence of higher organism. When changes come to the microorganisms or their surrounding environment at large spatial scale due to the climate change, the patterns of abundance, distribution and diversity of the species are altered within the niche where it belongs, and not only a single community, rather than whole ecosystem could be affected. Thus, the species are altered permanently; and the gradual microbial succession is taken place. In this chapter, we provide information about succession of different microbial community existing in different natural habitat. We elucidated in this chapter that how microbes are being stimulated with changing climatic factors and discussed the real consequences of changes in microbial interactions which are the main functional composition in a frame of microbial ecosystem.

5.2 Responses of Soil Microbial Community Under Changing Multiple Climatic Factors

Recycling of nutrients and carbon (C) in ecosystems soil microbial communities have a big role to play, where all activities are influenced by two main external factors (Hector et al. 2010), abiotic components, e.g. quantity and quality of the litter in the soil, soil moisture conditions, soil temperature, temperature of the open environment, humidity, CO_2 concentration and even other gaseous components of the open air; and biotic factors, e.g. microbiome of the soil, plant diversity and activity of the other higher organisms. Sudden or gradual but stable changes in surrounding atmospheric or climatic conditions always have influential role on both abiotic and biotic components of an ecosystems directly and indirectly by modification in their responses in ecosystems (Fig. 5.1). Again, the co-responses of the ecosystem from the opposite side to the environment as feedback may also be regulated by microbial populations present in the soil (Bardgett et al. 2008). It has

Fig. 5.1 Unusual precipitation results either low soil moisture stress (drought) or off time high soil moisture stress (water lodging/flood)

been shown in some previous research that changes in climatic factors, e.g. raising temperature and elevated CO_2 would act together to alter the overall process and common properties of the ecosystem. But the core process of the ecosystem that known to be regulated by the general responses generated from the microbial communities is very unpredictable, and it is often unanswered how the composition and abundance of microbial communities associate with the upshot of ecosystem processes and climatic perturbations. Till date, the research conducted related to climate change had intended on microscale responses to climate change, e.g. much of the research to date related to climate change generally focused on the effect and response at microscale level such as alteration of compositions in the plant community (Bakkenes et al. 2002; Lloret et al. 2009), plant growth (Norby et al. 2001, 2004) and coarse scale soil processes (Garten et al. 2008; Franklin et al. 2009), and interestingly all of which are indirectly effects of microbial processes. In response to single climatic factor, some gross parameters of microbial process like the basic microbial community profile, microbial biomass, and enzymatic activity may also be changed. In a study, the direct and interactive effects of single or different combinations of several climatic factors on fungal and bacterial communities (composition and abundance) present in soil were observed in an old-field ecosystem, where different environments were created on the basis of changing climatic scenarios by altering and simulating the multi-factor of the climate. The environments of old-field ecosystem were stimulated and exposed it to different atmospheric CO_2 concentration (ambient and elevated), rainfall precipitation (dry and wet) and temperature (ambient and elevated up to +3 °C). The old-field ecosystem was left for interaction and alteration in abundance and community structure of soil microorganisms, e.g. fungus and bacteria. In that study, it was found that (a) in warmed conditions, fungal abundance increased; (b) bacterial abundance decreased under ambient atmospheric CO_2 with warmed conditions; (c) bacterial abundance increased under elevated CO_2 with warmed conditions; (d) the distribution of the fungal and bacterial spp. in phylogenetic cluster was varied among treatments; (e) the composition of fungal community changed with the alteration in precipitation; (f) the ratio of Proteobacteria and Acidobacteria was altered with the change in rainfall precipitation. The results of the study indicated that change in climatic factors and their interactive effects in turn to changes in overall abundance of soil microorganism, i.e. fungal and bacterial population in an ecosystem. But changes in precipitation, the overall effect is too high to establish a stable alteration in community composition.

5.3 Development and Evolution of Microbial Ecosystems and Its Gradual Succession

The development of ecosystem in an area is usually called ecological succession. So under climatic change scenario the major questionable area related to evolution of ecosystems or ecological succession is (a) the parameters on which stability of the community depends even after disturbance of the environment; (b) for community

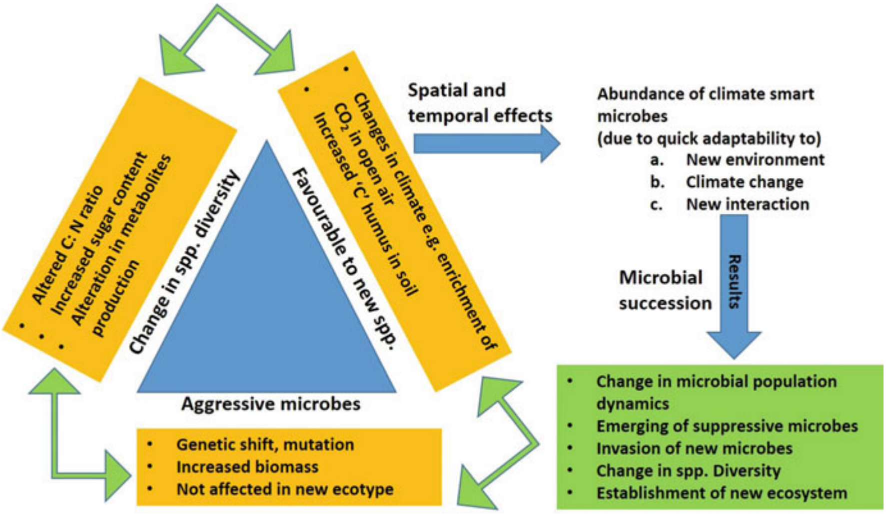

Fig. 5.2 The spatial and temporal effects of climate change on establishment of new or altered ecosystem

dynamics, what are the driving forces; (c) what is the relation between ecosystem functions and community functions. The true microbial succession is happened when a better adapted and best fitted microbial population is stabilized in an ecological niche with an altered environment and climatic conditions by replacing previous stabled any microbial population. The development of the microbial ecosystem in a particular geographical area is brought by a slow but a continuing and steady changes within the main composition of a microbial and climax characteristic (Fig. 5.2). The changes in community composition of a microbial ecological niche are seasonal and multiyear dynamic process which is cyclic and random because of fluctuations. On the contrary, the microbial ecological succession is an irreversible, unidirectional and orderly process. Usually, the succession in a microbial community started by intense change within abiotic environmental conditions, e.g. desertification, heavy rain and flooding, cooling or warming climate, volcano eruption, forest fire, etc. We can easily differentiate between a primary and a secondary succession. The primary succession assumes the development and establishment of initial microbial community within a land that bared originally, e.g. suddenly released rock, magma rock of lava-stream or sand dune where the ecosystem starts from zero. But the process and establishment of secondary microbial succession are much faster than a primary microbial succession. Generally the secondary microbial succession is occurred when the soil is already been improvised naturally by the heavy deposition of organic matter. Again, the succession of a microbial community is a continuous and concomitantly process with the evolution of the entire microbial ecosystem as the microbial microenvironment affects by the orderly and gradual replacement of higher organisms, especially plant and species. The ecologists view the whole mechanisms of succession in two competing

Table 5.1 Evolution of microbial community and role of holistic and meristic paradigm as a driving force

	Paradigm	
Components	Holistic	Meristic
Community arrangement	Persistent, specifically determined by resilient interspecific links	Non-persistent, be influenced by emigration and immigration, local conditions and past history
Boundary ecosystem	Definite and clearly expressed	Indefinite and not clearly expressed
Risk in forecast	High	Low
Pioneer stages of succession	Inappropriate abiotic atmosphere for starting of life. The ecology begins when stress resistant species start to colonize which advance the environment for other species	Begins due to ecological vacuum, where environment is suitable but little saturation of organisms within the community. Opportunistic species colonize first without any severe stress and competition
Transitory short-live community	Edification improves abiotic environment for the community; the productivity increases. The organisms are not emphasized although not rejected by the reverse effect of environment	The organisms are selectively chosen by the strong environmental effects. Progressive increase of competition for resources. Edification improves abiotic environment for the community; the productivity increases. The organisms are not emphasized although not rejected by the reverse effect of environment
Climax community	Symbiotic association within the maximum organisms helps community to be stabilized	In similar econiches, the maximum microorganisms are interacted each other competitively, but the community become stabilized

paradigm: holistic and meristic (Table 5.1). In holistic paradigm concept, the first biotic component (e.g. microbial organisms) of econiches acts as a kind of superorganisms. In the beginning of ecology in a bare area, the superoganisms are stress resistant and start to colonize in an inappropriate abiotic atmosphere and make a favourable ecosystem to grow other organisms. This paradigm has steady structure with non-selective and strong deterministic interactions among the different econiches, similar to interaction between cells and specialized tissues within the higher organisms (Table 5.2). According to this concept the previous microbial population amend the habitat and physical state which improve the living conditions for successive organisms. The meristic paradigm approaches give freedom to some independent organisms for making biotic interaction with the other organisms living within the same econiches. As the species are independent and community is open, the organisms can freely enter or leave the community by immigration or emigration. The replacement of the species occurs when two species compete each other within the same econiche (Fig. 5.3).

Table 5.2 Type of ecological interactions within the microbial community and its effect on population growth

Interactions	Group I organisms	Group II organisms
Competition	Negative effect; compete with group II organisms	Negative effect; compete with group I organisms
Mutualism	Positive effect; helping to survival of group II organisms	Positive effect; helping to survival of group I organisms
Parasitism/ predation	Positive effect; dominant over Group II organisms	Negative effect; dominated by group I organisms
Commensalism	No effect	Positive effect; benefited from group I organisms
Amensalism	No effect	Negative effect; inhibition of survival by group I organisms
Neutralism	No effect	No effect

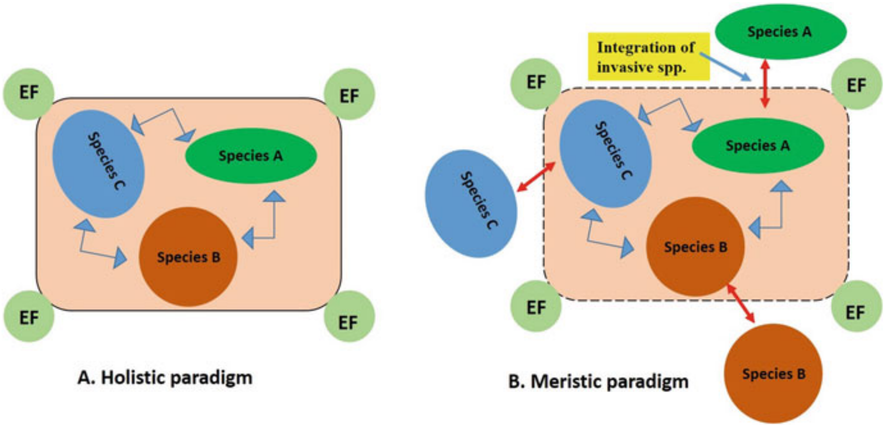

Fig. 5.3 Establishment of stable microbial community in an econiche through a holistic or meristic paradigms succession. "EF" is denoting environmental factors

5.4 Role of Microbes in Global Warming and Recycling the Essential Elements

The grazing animals like cattle, sheep, camel, goats, etc. have a special chamber in stomach called rumen. This part is swarming with billions and billions of microorganisms like moulds, yeasts, bacteria and protozoa. Those microbes are essential for digesting cellulose that is consumed by animals. Animals cannot produce cellulose degrading enzymes, so they absorb the cellulose directly. The microbes break it down the complex food into simpler organic substances. On the other hand, some methane loving archaea bacteria live in the rumen, which are specialized in producing methane by breaking down the animal's food. The methane, a very powerful greenhouse gas then is out from their digestive system. The methane can trap about 20 times more heat than CO_2. It means that the methane can warm the atmosphere 20 times more than same volume of CO_2 gas can. But the question of worry is that the cattle and farm animals are producing around 20% of total global methane. Nowadays, scientist are concerned about to stop or decrease the methanogenesis inside the rumen of grazing animals, but that results in the animal being smaller. Some researchers are finding certain additives for their diet which can reduce emission of methane. The soil microbes have also a big role in changing climate. Soil is the immense collection of a range of diversified microbes. In changing climate scenario, it is predicted that the emission of CO_2 will be increased and carbon-based materials in the soil will be broken down very swiftly because of changing activity of microbes due to climate heats up. If this happens then global temperature will increase because release of CO_2 in the environment will be more as a waste product due to increased microbial activity and their respiration.

Microbes play an important role to recycle and transform the essential elements, e.g. organic carbon and nitrogen as either generators or users of these vital gases in the atmosphere. Since beginning of the life lower organisms like bacteria and archaea is recycling of all the essential elements. During methanogenesis, methanogenic microbes convert CO_2 to methane through carbon cycle. Again, nitrogen-fixing bacteria fix nitrogen by the process of nitrogen cycle, by which they convert atmospheric nitrogen into biological nitrogen that can be used by higher organisms. In spite of those microbes, other microbes, e.g. cyanobacteria and photosynthetic algae are also involved in these cycles. The taxonomically higher algae capable to photosynthesis and cyanobacteria are the major component of marine plankton which play a major role in carbon cycle through photosynthesis and the basis of food chain in the marine ecosystem. On the other side, soil microorganisms, e.g. fungi and bacteria are the main decomposer of organic matter and they break down the complex organic matter to simple compound and bring back CO_2 into the atmosphere.

But the question is that the microbes can help to solve the planet from global warming. Photosynthetic microorganisms have big power to convert atmospheric CO_2 into O_2. Some single-celled blue green algae (BGA), e.g. *Prochlorococcus* and *Synechococcus* are very small in size but most abundant BGA the ocean. Near about 10×10^7 cells of *Prochlorococcus* are present in 1 litre of marine water. It was estimated that *Synechococcus* and *Prochlorococcus* can eliminate about 10×10^9 tons of carbon from the atmosphere every year; i.e. almost 66.66% of the total C fixation succeeds in the sea water. If we are able to use power of such microbial organisms, the level of greenhouse gases including CO_2 could reduce from the atmosphere and eventually could slow down the global climate change.

5.5 Acceleration of the Spatial Turnover of Soil Microbial Communities Under Elevated CO_2

Elevated CO_2 considerably affects the function, composition, dynamics, interaction and diversity of soil microbes. The impacts of elevated CO_2 on geographic distribution of microbial community at regionally or globally are little known. The research on climate change showed that elevated CO_2 shifted the structure, interaction and composition of microbial community present in soil (Deng et al. 2012; He et al. 2012a, b; Van Groenigen et al. 2014). Generally elevated CO_2 increases the total biomass of plants and productivity leading more deposition of organic carbon in soil (He et al. 2014), the soil microenvironment (Van Groenigen et al. 2014; Xiong et al. 2015), and the microbial growth and activity (Kelley et al. 2011; Van Groenigen et al. 2014) but these responses seemed to be largely inconstant among the different econiches. So many studies were carried out, but effect of elevated CO_2 on geographic distribution like soil microorganisms and their association with different habitats and associated ecosystems is still unclear.

The distance–decay relationship (DDR) is a model to understand the mechanisms help in forming community assembly and biodiversity across a range of organisms in different geographical patterns at different spatial scales (Hanson et al. 2012). This model is shown the relationship between decline patterns of community similarity and increasing distance of geographical location. According to hypothesis, with the increase of geographic distance the similarity within microbial community will be declined, and the changes of DDR would be greatly determined by the niche assembly theory. The niche assembly theory predicts the stability of the community biodiversity and how a certain number of microbial species coexists in a close proximity by segregating themselves to a specific econiche (Webb et al. 2002). For predicting the response of microbial communities in a particular econiches to future climate change, understanding the mechanisms of maintaining biodiversity is needed. In some study it has been proved that the turnover rate of a soil microbial community at a spatial scale under elevated CO_2 is higher. Where the soil C: N ratio could be prime contributor to DRR, C: N ratios have a close relation with microbial growth and total biomass (Fierer et al. 2009). In point of fact, environmental selection has a major role in structuring the microbial community, where four evolutionary and/or ecological processes, i.e. selection, mutation drift and dispersal would construct biogeography of microbial ecosystem (Hanson et al. 2012).

Plant–Microbe Interaction and the Temporal Turnover of Soil Microbial Community.

The number of species replaced or eliminated per unit of time is called species temporal turnover (Hatosy et al. 2013). Another common model for describing species temporal turnover is the time–decay relationship, where the changes in number of the species in a community similarity over time are used to explain (Nekola and White 1999). The rates of temporal turnover depend on local environmental factor, ecosystem types (Korhonen et al. 2010), disturbances (Svensson et al. 2009) and temporal scale (Hatosy et al. 2013). The temporal turnover of animals and plants is well documented, but temporal turnover of microbial world is yet to be known. Only few researches have been conducted on microbial temporal turnover for a short period, i.e. only few months, which were mainly based on microbial growth under a controlled engineered system. Recently a study on temporal beta-diversity of three bacterial communities from three different marine environments showed that different factors are involved in appearance of dissimilarity in turnover at different time scales (Hatosy et al. 2013). The variations in temporal turnover of soil microbial community with changing climatic scenario and related mechanisms remain largely unknown.

The soil microbes can remain active potentially or dormant for a long period within an econiche and those microbes have a role in shaping of soil microbial ecosystem. As, the soil microbial populations can evolve within the short period of time scale, it can shift the plant–microbe interactions quickly (Chave 2013); for example, in a micro-ecosystem like plant rhizosphere, the microbial communities change their composition time to time throughout the plant's growing season (Cregger et al. 2012; Kumar et al. 2016). The changes in microbial communities due to seasonal variation are more imperative than ecosystem C-fluxes during inter-annual variations. In a study, it was observed that background microbial variation was constantly higher when precipitation is unchanged since few years then altered precipitation (Gutknecht et al. 2012). In a community, microbial acclimation and adaptation are often alluding to elucidation that climate manipulation for the shorter period has no influence at long time scales (Bradford et al. 2008). Rapid adaptation of microbial communities may allow the modern plant species which are resilient and up-to-date to new climate, as the longer generation times of host plant lag behind the dynamic microbial communities (Lau and Lennon 2012). Evolution may swamp long-term impacts of climate and background microbial community variations may overcome climate treatments on seasonal timescales.

5.6 Few Example of Microbial Community Succession Under Changing Environment Stimulated Through Soil Transplant

The transplantation of soils from one geoclimatic zone to another geoclimatic zone gives an effective method to examine the response of microbial organisms in an econiche due to alteration of multiple climatic factors under changing climatic scenario (Sun et al. 2014; Zhao et al. 2014). It is reported that the soil transplantation has an impact on composition of microbial communities, but till now it is debatable. For instances, transplantation of soil from cooling area to warming area resulted in a change of microbial biodiversity and loss in total biomass. These functional and structural changes in microbial community in warmer condition indicated that exposure in higher temperature for few years could alter the soil microbiome (Vanhala et al. 2011). The microbial composition, biomass, respiration and enzymatic activities found to be decreased, after transplanting of soils under oak canopies to an open environment of grassland with lower soil water content and higher temperature (Waldrop and Firestone 2006a, b). The bacterial and fungal community structures of a forest soil were found to be significantly changed after 2 years of incubation subsequently transplanting the soil to meadows (Kageyama et al. 2006). Similarly, transplanting the black soil to warmer areas and red soil to colder regions (Zhao et al. 2014) caused huge alterations in the activities of microbial populations.

5.7 Influence of Climate Change in Shifting Plant Diseases from Minor to Major

To develop any disease in plants, infection, establishment and colonization of pathogen into the host tissue are the most important steps. Again, the infection of pathogen to host is completely depended on environmental factors (Madgwick et al. 2011; Sharma et al. 2015, 2019). Environmental stress plays an important role on community interaction between plants and pathogens (Chobe et al. 2016; Tarafdar et al. 2017, 2018). If any of three factors (host × pathogen × environment) in disease 'Δ' is altered, the disease progression would change. Elevated temperature and CO_2, ozone depletion, high or low humidity all are events of imperious deviances in climatic components. Alteration in above climatic components plays important roles in expression and pathosystems. The diversity of pathogens, e.g. nematode, protozoa, phytoplasma, mycoplasma, fungi, oomycetes, bacteria, virus and viroids (Tarafdar et al. 2012; Singh et al. 2013; Biswas et al. 2014; Padaria et al. 2016) infecting crops is overwhelming and becoming more pathogenic by continuous expanding themselves through mutation, adaptation, evolution and dissemination of new strains/variants/pathotypes/races (Table 5.3). Recently emerged fungi, *Puccinia striiformis* and *P. graminis* are among the utmost destructive and swift spreading pathogens. For instances, other late blight genotypes of potato have been displaced and rapidly emigrant by a new lineage of *P. infestans*. Another example,

Table 5.3 Effect of elevated CO_2 on pathogenic microbes causing plant diseases

No effect	Positive effect (increase)	Negative effect (decrease)
• Sudden death syndrome (*F. virguliforme*) in soybean. • *Phytophthora* root rot (*P. parasitica*) in tomato	• *Fusarium* rot (*F. verticillioides*) in maize. • *Fusarium* wilt (*F. oxysporum* f. sp. *lactucae*) in lettuce. • *Phytophthora* blight in pigeonpea by *P. cajani*, chilli pepper by *P. capsici* and potato by *P. infestans*. • Crown rot (*F. pseudograminearum*) in wheat. • Brown spot (*Septoria glycines*) in soybean. • Sheath blight (*Rhizoctonia solani*) and blast (*Pyricularia oryzae*) in rice	• Downy mildew (*Peronospora manshurica*) in soy bean. • Anthracnose (*Colletotrichum acutatum)* and two bacterial diseases, viz. bacterial wilt (*Ralstonia solanacearum*) and bacterial spot (*Xanthomonas campestris* pv. *vesicatoria*) in chilli paper. • Powdery mildew (*Erysiphe graminis*) in barley and wheat. • Rust (*Puccinia sparganioides* Ellis & Barth) in C3 sedge

Fusarium head blight, a damaging disease of wheat at anthesis period is emerging again in the USA for warm and wet condition. As pathogen aetiology and growth are often dependent on soil moisture, the availability of water, the infection development and colonization establishment to plants can greatly affect either positively or negatively (Ghosh et al. 2016, 2017; Tarafdar et al. 2017, 2018). For instance, under low soil moisture conditions, the susceptibility of host plants to bacterial pathogen can increase (Mohr and Cahill 2003). Similarly, low soil moisture stress significantly increases the incidence and severity of dry root rot disease (*Rhizoctonia bataticola*) in chickpea (Tarafdar et al. 2018) but on contrary lowering the collar rot disease (*Sclerotium rolfsii*) in similar condition. Although till now very limited information is available about the effect of elevated CO_2 in developing plant diseases and their pathogens, whether the incidence and/or severity of the diseases are remaining unaffected or it may increase, or decrease. The studies of Sharma et al. (2015) and Ferrocino et al. (2013) showed that the elevated CO_2 enhanced the colonization of *Phytophthora cajani* (*Phytophthora* blight) in pigeon pea and *Fusarium oxysporum* f. sp. *lactucae* (*Fusarium* wilt) in lettuce roots, respectively. On the other hand, the study of Thompson and Drake supported the reduction of disease severity in wheat by *Erysiphe graminis* (powdery mildew) severity and in C3 sedge (*Scirpus olneyi*) by *Puccinia sparganioides* (Ellis & Barth) Grey (rust). Thus the real interest in our study to decipher how elevated CO_2 level would influence the chickpea–Foc interactions which may help to better understand the change in *Fusarium* wilt disease dynamics and aetiology in chickpea under elevated CO_2. Again sheath blight (*Rhizoctonia solani*) and blast (*Pyricularia oryzae*) in rice, and higher threats of late blight (*Phytophthora infestans*) in potato are increasing day to day due to elevated temperature and CO_2.

5.8 Effect of Climate Change on Marine Microbial Succession

The microbial ecosphere is frequently left out from the dialogues in changing climate scenario. But microbial world is one of the acute contributors in the biogeochemical cycles, e.g. carbon and nitrogen (Fig. 5.3). So, the attention is needed to be given on microbial responses to global warming. About 93% of total CO_2 in world is accumulated in oceans, out of this 90 billion tons of CO_2 cycles per year. The mechanism of carbon cycle in the ocean is mostly dominated by microbial species existing in it. Earth's climate is regulated by the oceans so the small change in oceans is responsible for the change in earth's climate. On the other way, the ocean is increasing temperature of the climate by continuous depositing and distributing heat around the globe and transferring heat within the atmosphere. The exterior part of the stratum warms very swiftly, when the atmosphere heated up and so does ocean. The acidification within the ocean water is a natural phenomenon. Although acidification and warming are different singularity, the elevated CO_2 is increasing acidification in ocean by raising temperature of the surrounding atmosphere of ocean. Both the phenomenon are interacting and becoming detrimental for the marine ecosystem and associated microbial community. The CO_2 level of the ocean surface and the atmosphere was constant since millions of years. From past few centuries due to human interference, e.g. land-use practice and burning fossil fuels, the level of CO_2 significantly augmented and reached to serious concern level. As an effect, the ocean absorbs about 29% of more carbon as compare to normal. This extra CO_2 has substantial effects on water of ocean, make it 30% more acidic. Every drop of seawater contains thousands upon thousands of small and single-celled microorganisms which are the part of ocean ecosystem.

Since past century, the temperature of coastal water has been upsurge, and estimated to be increased by 4–8 °F in the twenty-first century (US EPA 2015). The ocean ecosystems are dependent on so many properties of the water, which are vital and critical. But those properties are being now affected when the fluctuation of the water temperature occurs. As a result, the dramatic changes in the ocean life happen (NASA 2015). These environmental situations are likely to be favourable for some microbial species which are adapted to that condition. This is specifically understood in the case of two species of common oceanic nitrogen fixers, viz. *Trichodesmium* and *Crocosphaera* (Michaels et al. 2001).

Microbiomes retort, alter and evolve to their ecosystem at much higher rates than any other higher creatures. This property permits scientists to associate and originate scalable assessments in a short period of time on the effects of changing climatic factors on the nature of microbiomes. This may in turn be used to recognize and predict the future repercussions of climate change on all forms of biodiversity. Microbiomes are the forerunners in mineralization of litter carbon and alteration of complex dead organic matter into simpler biomass, due to which even a trifling change in climatic elements could secondarily deliver a large scale impression on marine ecology. 70% of earth surface is covered by marine biomass including mangroves, coral reefs, costal estuaries and the open ocean. During photosynthesis the phototropic microorganisms use sun in the top 200 m of the water column, whereas marine ecosystem in deeper zones uses organic and inorganic compounds for energy. In addition to sunlight, the accessibility of other energy forms and water temperature stimulates the composition of marine communities. In marine environments, microbial prime production provides significantly to CO_2 sequestration.

Marine microorganisms recycle nutrients to use them in CO_2 release process and ultimately in marine food web. In accumulation, CO_2 accretion is prominent to its acidification. The expansion of oxygen-depleted zones has also been ascended due to stratification of oceans. Alterations like this are likely to have impacts on the microbial food pyramid and ultimately on the biogeochemical cycles (Walsh et al. 2016). Although distinct from sure, the repercussions of global warming on marine microbial populations were projected in several studies.

Similarly, bacterio-plankton plays a key function in the marine food pyramid. These microorganisms are accountable to an activity known such as re-mineralization. Complex organic matter breaks down to CO_2 and vital inorganic nutrients. So this answer that ocean does not stink but at some places it does. Stinky organic matter and by-products of organic matter decay are the product of slow re-mineralization of microscopic organisms from which plenty of nutrients are brimmed up from some highly fruitful coastal locations. While on the huge clear surface of water of the ocean, preliminary production of these organic matters is closely attached to re-mineralization.

Bacterio-plankton obscuring and restraining energy and carbon transfer up the food chain rapidly guzzle organic matter directly released from phytoplankton. Plenty of carbon goes into organization of new bacterio-plankton cells, and rest of reverted to water and atmosphere as CO_2. Hence to generate the energy essential for endurance and reproduction the cells ‘burn’ the carbon. At the same time by regenerating the nutrients required to sustain primary production bacterio-plankton plays an acute role.

In addition, the ocean-bacteria grown on phytoplanktons and break them into molecules such as lipids and fats. This may become airborne to link aerosols as the ocean agitates. Ultimately the further process is cloud condensation where the further progress into a context where the clouds made by the conversion of moisture droplets. The total volume of oceanic microbes can significantly be altered by the alterations of climatic elements, and this alteration can directly disturb the amount of partially water soluble organic materials such as lipids (Iacurci 2015). Change in climatic element can also be the major range in extension of detrimental microbes and causes biodiversity. These facts can be evaluated through parasite *Perkinsus marinus* has responsible for causing huge oyster deaths.

Same as in coral reefs are the most distinct and parsimoniously important ecosystem in the marine ecology as well as on earth. They are in danger due to change in various climate related marine ecosystem like raising sea level, ocean acidification and raising ocean temperature. Coral reefs require $CaCl_3$ to build frames, but the ocean acidification is driving its availability downwards. Near about 14.2% great barrier coral reefs has been lost due to calcification.

A significance of change in physiognomies, death rates and uniform allele rate of recurrence is all dependent on degree of change in climate is that the development and resilience of whole populations. If the population size changes, it interfaces among the species may also disturbed and eventually regimen shift may occur with undergoing rapid and irrevocable transition from one phase to another in biodiversity. For example, propagation of micro algae can be led by underlying damage and death to coral reefs due to bleaching and storms. As corals are dwelling for many marine microbial species loss of coral will lead to change in biodiversity and amount of such species and it may be responsible for extension of reef specialties. In addition to it change in reef specialties may adversely affect the fishes and invertebrates and may have large scale implications on fisheries, tourism and other human uses of reefs.

Covering 65% of earth surface benthic deep-sea ecosystems are the major ecosystems on the earth. A critical share of global biogeochemical cycles is played by microorganisms dwelling in these huge biomes at all water depths which has a significant share of biomass and biosphere. As benthic deep-sea ecosystem is not much explored till now they received a less attention. Hence the shift in benthic deep-sea biota remains mysterious. But the deep-sea ecosystem directly or indirectly affecting by the global climate changes (Gooday et al. 2008; Goineau and Gooday 2017). This predominantly applies to deep-sea microorganisms like micro eukaryotes their viruses, bacteria and archaea. Unexplored information on the response of deep-sea microbes to these alterations limits our ability and study to forecast the enormousness of the repercussion of global climate changes on the deep-sea microbial biodiversity. These repercussions may lead to regime shifts, shifting of deep-ocean life amenities like carbon sequestration capacity and nutrient regeneration, which is mostly dependent on microbes (Danovaro et al. 2017). The maintainance of the ocean ecosystems depends mostly on the functioning and distribution of benthic deep-sea microorganisms. The effect on the functioning of the ocean interior is a main concern to better forecast the potential implications at global scale.

There are various effects of human interference, agriculture, rivers and local environmental factors, including light and soil type affects the existing complex network for microbial exchange significantly, that occur with other microorganism. These exchanges facilitate how microbes retort to change in climatic elements and affect climate change and how climate change in turn affects microbial responses.

In conclusion, studies are going on in commencement for demonstration that marine microorganisms can be useful as watchdogs to assess the effect of climate change on marine ecosystem. Hence there is an acute necessity in lasting phase sequence biotic assessment of marine ecosystem. We may exactly foresee the change? But still the microbial ocean leftover is cryptic.

Importance of microorganisms in influencing the greenhouse gases concentration in atmosphere is worthy, but till now it is not properly recognized and praised by the scientists. Keeping in mind the observed suspicions, it is obvious that considering the straight and secondary repercussions of climate change on the microorganisms and their consistent lasting and temporary reactions can capture the major influences of these microbes. So, for variable climate change, hitched appropriately microorganism could be the potential natural resources. Conversely, proper attention is needed to stop to be turn as most incipient accelerator to hitch. Now it is a time to study this facet, to act and understand the mechanism more exactly. Hence use it appropriately to draw some solutions (Fig. 5.4).

5.9 Conclusion

Ecological succession of a microbial community provides conceptual framework in which many ecological topics of concern can be examined. In future, the microbial succession could be the major indicator or a central concept in ecology that would provide the information that makes critical contribution to understand the environmental changes as well as environmental challenges. Use of modern tools like mathematical modelling, meta-analysis of multi-site data and expert systems could be the medium to better understanding of microbial succession due to climate change, biodiversity loss, restoration and species invasion. Indirect influence of climate change on microbial populations can be facilitated via plants which may be stronger and durable than direct impact, as the community compositions and microbial activities can be influenced by the climate configuration. The novel

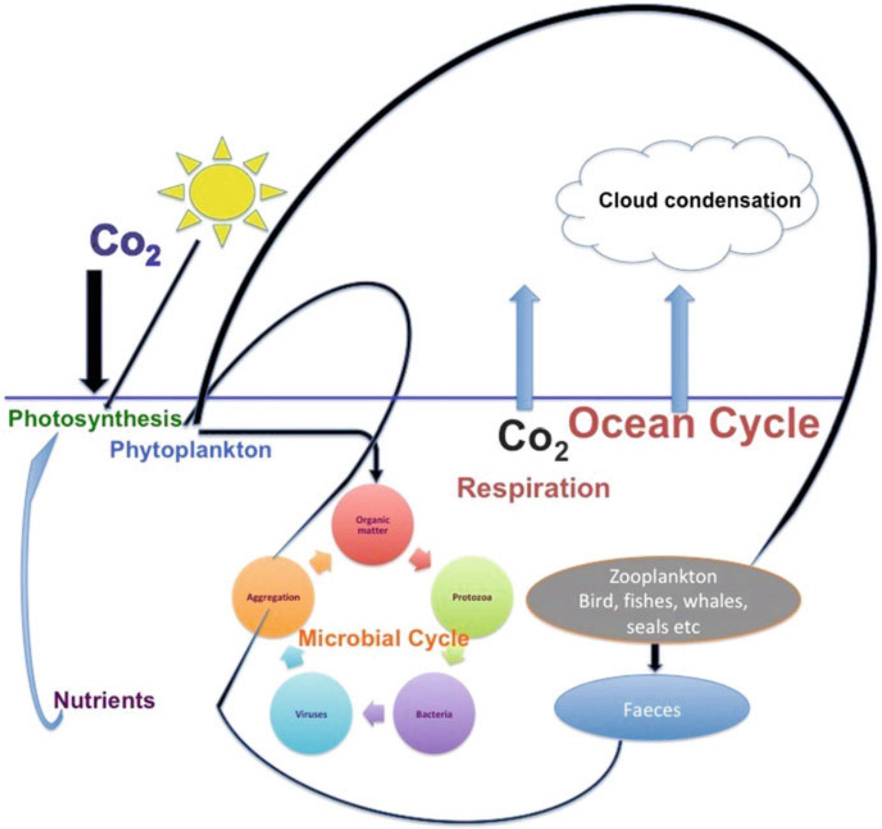

Fig. 5.4 The role of climatic factors on marine ecosystem

technologies will be essential to gather knowledge on microbe-centric information to identify the climate sensitive taxa whose response leads to shift in population dynamics of microbial community and alter in microbial activities. So, for predicting future ecosystem under changing climate scenario, we need best approaches and model for quantifying, observing and scaling the microbes–microbes interactions.

References

Bakkenes M, Alkemade JRM, Ihle F, Leemans R, Latour JB (2002) Assessing effects of forecasted climate change on the diversity and distribution of European higher plants for 2050. Glob Chang Biol 8:390–407

Bardgett RD, Freeman C, Ostle NJ (2008) Microbial contributions to climate change through carbon cycle feedbacks. ISME J 2:805–814

Biswas KK, Tarafdar A, Sharma SK, Singh JK, Biswas K, Diwedi S (2014) Status of disease incidence and distribution of *Citrus tristeza virus* in Indian citrus growing geographical zones. Indian J Agric Sci 84:184–189

Bradford MA, Davies CA, Frey SD, Maddox TR, Melillo JM, Mohan JE, Reynolds JF, Treseder KK, Wallenstein MD (2008) Thermal adaptation of soil microbial respiration to elevated temperature. Ecol Lett 11:1316–1327

Chave J (2013) The problem of pattern and scale in ecology: what have we learned in 20 years? Ecol Lett 16:4–16

Chobe DR, Gupta O, Pawar M (2016) Radiation induced mutation for resistance against races/ pathotypes of *Fusarium oxysporum* f.sp *ciceris* in chickpea (*Cicer arietinum* L.). Indian Phytopathol 69:260–265

Cregger MA, Schadt CW, McDowell NG, Pockman WT, Classen AT (2012) Response of the soil microbial community to changes in precipitation in a semiarid ecosystem. Appl Environ Microbiol 78:8587–8594

Danovaro R, Rastelli E, Corinaldesi C, Tangherlini M, Dell'Anno A (2017) Marine archaea and archaeal viruses under global change. F1000 Res 6:1241

Deng Y, He Z, Xu M, Qin Y, Van Nostrand JD, Wu L, Roe BA, Wiley G, Hobbie SE, Reich PB, Zhou J (2012) Elevated carbon dioxide alters the structure of soil microbial communities. Appl Environ Microbiol 78:2991–2995

Ferrocino I, Chitarra W, Pugliese M, Gilardi G, Gullino M, Garibaldi A (2013) Effect of elevated atmospheric CO_2 and temperature on disease severity of *Fusarium oxysporum* f.sp. *lactucae* on lettuce plants. Appl Soil Ecol 72:1–6

Fierer N, Strickland MS, Liptzin D, Bradford MA, Cleveland CC (2009) Global patterns in belowground communities. Ecol Lett 12:1238–1249

Franklin O, McMurtrie RE, Iversen CM, Crous KY, Finzi AC, Tissue DT, Ellsworth DS, Oren R, Norby RJ (2009) Forest fine-root production and nitrogen use under elevated CO_2: contrasting responses in evergreen and deciduous trees explained by a common principle. Glob Chang Biol 15:132–144

Garten CT, Classen AT, Norby RJ, Brice DJ, Weltzin JF, Souza L (2008) Role of N_2-fixation in constructed old-field communities under different regimes of [CO_2], temperature, and water availability. Ecosystems 11:125–137

Ghosh R, Tarafdar A, Sharma M (2016) Rapid detection of Fusarium oxysporum f. Sp ciceris from disease infested chickpea fields by loop-mediated isothermal amplification. Indian Phytopathol 69(4s):47–50

Ghosh R, Tarafdar A, Sharma M (2017) Rapid and sensitive diagnoses of dry root rot pathogen of chickpea (*Rhizoctonia bataticola* (Taub.) Butler) using loop-mediated isothermal amplification assay. Sci Rep 7:42737

Goineau A, Gooday AJ (2017) Novel benthic foraminifera are abundant and diverse in an area of the abyssal equatorial Pacific licensed for polymetallic nodule exploration. Sci Rep 7:45288

Gooday AJ, Nomaki H, Kitazato H (2008) Modern deep-sea benthic foraminifera: a brief review of their biodiversity and trophic diversity. In: Austin WEN, James RH (eds) Biogeochemical controls on palaeoceanographic environmental proxies, vol 303. Geological Society of London, London, pp 97–119

Gutknecht JL, Field CB, Balser TC (2012) Microbial communities and their responses to simulated global change fluctuate greatly over multiple years. Glob Chang Biol 18:2256–2269

Hanson CA, Fuhrman JA, Horner-Devine MC, Martiny JBH (2012) Beyond biogeographic patterns: processes shaping the microbial landscape. Nat Rev Microbiol 10:497–506

Hatosy SM, Martiny JBH, Sachdeva R, Steele J, Fuhrman JA, Martiny AC (2013) Beta diversity of marine bacteria depends on temporal scale. Ecology 94:1898–1904

He Z, Piceno Y, Deng Y, Xu M, Lu Z, Desantis T, Andersen G, Hobbie SE, Reich PB, Zhou J (2012a) The phylogenetic composition and structure of soil microbial communities shifts in response to elevated carbon dioxide. ISME J 6:259–272

He Z, Van Nostrand JD, Zhou J (2012b) Applications of functional gene microarrays for profiling microbial communities. Curr Opin Biotechnol 23:460–466

He Z, Xiong J, Kent AD, Deng Y, Xue K, Wang G, Wu L, Van Nostrand JD, Zhou J (2014) Distinct responses of soil microbial communities to elevated CO_2 and O^{-3} in a soybean agro-ecosystem. ISME J 8:714–726

Iacurci J (2015) Ocean microbes: how they may directly impact climate change. http://www.natureworldnews.com/articles/14761/20150519/oceanmicrobeshowtheymaydirectlyimpactclimatechange.htm

Kageyama SA, Posavatz NP, Jones SS, Waterstripe KE, Bottomley PJ, Cromack K Jr, Myrold DD (2006) Responses of soil bacterial and fungal communities to reciprocal transfers of soil between adjacent coniferous forest and meadow vegetation in the Cascade Mountains of Oregon. Plant Soil 289:35–45

Kelley AM, Fay PA, Polley HW, Gill RA, Jackson RB (2011) Atmospheric CO_2 and soil extracellular enzyme activity: a meta-analysis and CO_2 gradient experiment. Ecosphere 2:96

Korhonen JJ, Soininen J, Hillebrand H (2010) A quantitative analysis of temporal turnover in aquatic species assemblages across ecosystems. Ecology 91:508–517

Kumar R, Pankaj VP, Tarafdar A, Biswas K, Kumar S (2016) Soil microbes and their interaction with plants. In: Mitra R, Barman A (eds) Plant pathogen interaction: recent trends. Sharma Publications, New Delhi, pp 1–46

Lau JA, Lennon JT (2012) Rapid responses of soil microorganisms improve plant fitness in novel environments. Proc Natl Acad Sci USA 109:14058–14062

Lloret F, Penuelas J, Prieto P, Llorens L, Estiarte M (2009) Plant community changes induced by experimental climate change: seedling and adult species composition. Perspect Plant Ecol Evol Syst 11:53–63

Madgwick J, West J, White R, Semenov M, Townsend J, Turner J, Fitt BL (2011) Impacts of climate change on wheat anthesis and *Fusarium* ear blight in the UK. Eur J Plant Pathol 130:117–131

Michaels AF, Karl DM, Capone DG (2001) Element stoichiometry, new production and nitrogen fixation. Oceanography 14:68–77

Mohr P, Cahill D (2003) Abscisic acid influences the susceptibility of Arabidopsis thaliana to *Pseudomonas syringae* pv. Tomato and *Peronospora parasitica*. Funct Plant Biol 30:461–469

NASA (2015) Responding to climate change. http://climate.nasa.gov/solutions/adaptation-mitigation

Nekola JC, White PS (1999) The distance decay of similarity in biogeography and ecology. J Biogeogr 26:867–878

Norby RJ, Cotrufo MF, Ineson P, O'Neill EG, Canadell JG (2001) Elevated CO_2, litter chemistry, and decomposition: a synthesis. Oecologia 127:153–165

Norby RJ, Ledford J, Reilly CD, Miller NE, and. O'Neill EG. (2004) Fine-root production dominates response of a deciduous forest to atmospheric CO_2 enrichment. Proc Natl Acad Sci USA 101:9689–9693

Padaria JC, Tarafdar A, Raipuria R, Lone SA, Gahlot P, Shakil NA et al (2016) Identification of phenazine-1-carboxylic acid gene (phc CD) from *Bacillus pumilus* MTCC7615 and its role in antagonism against *Rhizoctonia solani*. J Basic Microbiol 56:1–10

Sharma M, Ghosh R, Tarafdar A, Telangre R (2015) An efficient method for zoospore production, infection and real-time quantification of Phytophthora cajani causing Phytophthora blight disease in pigeonpea under elevated atmospheric CO_2. BMC Plant Biol 15:90

Sharma M, Ghosh R, Tarafdar A, Rathore A, Chobe DR, Kumar AV, Gaur PM, Samineni S, Gupta O, Singh NP, Saxena DR, Saifulla M, Pithia MS, Ghante PH, Mahalinga DM, Upadhyay JB, Harer PN (2019) Exploring the genetic cipher of chickpea *(Cicer arietinum* L.) through identification and multi-environment validation of resistant sources against *Fusarium* wilt (*Fusarium oxysporum* f. sp. *ciceris*). Front Sustain Food Syst 3:78

Singh JK, Tarafdar A, Sharma SK, Biswas KK (2013) Evidence of recombinant *Citrus tristeza virus* isolate occurring in acid lime cv. Pant lemon orchard in Uttarakhand terai region of northern Himalaya in India. Indian J Virol 24:35–41

Sun B, Wang F, Jiang Y, Li Y, Dong Z, Li Z, Zhang X (2014) A long- term field experiment of soil transplantation demonstrating the role of contemporary geographic separation in shaping soil microbial community structure. Ecol Evol 4:1073–1087

Svensson JR, Lindegarth M, Pavia H (2009) Equal rates of disturbance cause different patterns of diversity. Ecology 90:496–505

Tarafdar A, Ghosh PD, Biswas KK (2012) *In planta* distribution, accumulation, movement and persistence of *Citrus tristeza virus* in citrus host. Indian Phytopathol 65:184–188

Tarafdar A, Rani TS, Chandran USS, Ghosh R, Sharma M (2017) Impact of moisture stress on collar rot (Sclerotium rolfsii Sacc.) development in chickpea (Cicer arietinum L.). in: Proceedings of ISMPP International Conference on “Plant health for human welfare.” Organized by Indian Society of Mycology and Plant Pathology, (Jaipur), 119

Tarafdar A, Rani TS, Chandran USS, Ghosh R, Chobe D, Sharma M (2018) Exploring combined effect of abiotic (soil moisture) and biotic (*Sclerotium rolfsii* Sacc) stress on collar rot development in chickpea. Front Plant Sci 9:1154

U.S. EPA (2015) Greenhouse gas emissions and fuel efficiency standards for medium- and heavy-duty engines and vehicles—phase 2. Fed Regist

Van Groenigen KJ, Qi X, Osenberg CW, Luo Y, Hungate BA (2014) Faster decomposition under increased atmospheric CO_2 limits soil carbon storage. Science 344:508–509

Vanhala P, Karhu K, Tuomi M, Björklöf K, Fritze H, Hyvärinen H, Liski J (2011) Transplantation of organic surface horizons of boreal soils into warmer regions alters microbiology but not the temperature sensitivity of decomposition. Glob Chang Biol 17:538–550

Waldrop MP, Firestone MK (2006a) Response of microbial community composition and function to soil climate change. Microb Ecol 52:716–724

Waldrop MP, Firestone MK (2006b) Seasonal dynamics of microbial community composition and function in oak canopy and open grassland soils. Microb Ecol 52:470–479

Walsh EA, Kirkpatrick JB, Rutherford SD, Smith DC, Sogin M, D'Hondt S (2016) Bacterial diversity and community composition from seasurface to subseafloor. ISME J 10:979–989

Webb CO, Ackerly DD, Mcpeek MA, Donoghue MJ (2002) Phylogenies and community ecology. Annu Rev Ecol Syst 33:475–505

Xiong J, He Z, Shi S, Kent A, Deng Y, Wu L, Van Nostrand JD, Zhou J (2015) Elevated CO_2 shifts the functional structure and metabolic potentials of soil microbial communities in a C4 agroecosystem. Sci Rep 5:9316

Zhao M, Xue K, Wang F, Liu S, Bai S, Sun B, Zhou J, Yang Y (2014) Microbial mediation of biogeochemical cycles revealed by simulation of global changes with soil transplant and cropping. ISME J 8:2045–2055