



# Soil Microflora and its Role in Diminution of Global Climate Change

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## Abstract

From the last two decades, the issue of climate change and its potential impacts on air, water and soil health has consistently been reminding us of the biggest scientific and political challenges of twenty-first century at global level. There are a number of strategies initiated to reduce the adverse effect of climate change on biodiversity, interaction between hosts and pathogens, population dynamics of microbiomes, aquatic ecosystem and several abiotic factors, namely temperature, rainfall, moisture status of air and soil, etc. Majority of these strategies are emphasized upon the technologies based on chemical and biological conversions. Microbial biodiversity of soil and its potential exploitation towards the mitigation of global climate change is a matter of utmost importance that needs to be explored. The proper utilization of beneficial microorganisms present in soil could fix the major dilemma related to the uncertainty of agricultural production happened due to erratic environment and natural calamities. The maximum exploration of soil microbial community could be employed in various arenas of sustainable agriculture such as suppression of soil-borne plant pathogens, enhancer in plant growth and development, biofertilizer cum symbiotic nitrogen fixer, inducer of systemic acquired resistance, alleviation of biotic and abiotic stresses in plants, remediation of heavy metals from contaminated soils, soil resilience, degradation of polyethylene component from soil. Considering the importance of soil microflora and its role in nature, there is a need to promote the investigations on these aspects with possible modifications which can improve the ecology and environment for better life in the world.

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**13.1 Introduction**

In modern world, change in climate and environment due to human activities is a well-discussed topic when it comes to the point of research about extinction in plant and animal species and change in biodiversity. Extinction of species, communities and habitats are considered as a subject of detailed research, thus well understood and documented compared to microorganisms. The role of microorganisms are usually less discussed in the context of climate change, as well as the influence of climate change on the general mechanisms of microbial activity remains hardly analysed (Cavicchioli et al. 2019). Despite being invisible to the naked eye, the microbial abundance (total  $\sim 10^{30}$  bacteria and archaea) and diversity perform their role in maintaining a healthy global ecosystem and account for the life support system of the biosphere. The terrestrial ecosystems undergo a principal role in such climate-feedbacks as they both release and absorb greenhouse gases, precisely carbon dioxide, methane and nitrous oxide, while acting as a significant carbon sink by storing in soil and living plants (Bardgett et al. 2008). The net effect of climate change on total amount of ecosystem carbon budgets is dependent on the equilibrium between photosynthesis (autotrophic respiration) and respiration (heterotrophic soil microbial respiration). Thus, the immense diversity of soil microbes constitutes a significant role in emission of greenhouse gases and in elevation of environmental warming due to their biological processes involved in plant–microbe interaction on carbon-nitrogen cycling. All these observations confirm the need of including the study and research on terrestrial microorganisms especially soil microbes, for the microbial mitigation of soil to maintain the agricultural sustainability, their interactions with autotrophic and heterotrophic living organisms, as well as their biological mechanisms related to climate changes (Cavicchioli et al. 2019).

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**13.2 Terrestrial Microbiome**

Terrestrial plants account for a significantly large biomass and also act as the source of roughly half of the net global primary production (Cavicchioli et al. 2019). Different microbial communities reside in different terrestrial ecosystems depending on their distribution over space and time, different land use types and disturbances introduced by human (Singh et al. 2010). The plant–microbe interaction with mycorrhizal fungi and nitrogen fixing bacteria is well understood in the terrestrial ecosystem whereas the involvement of heterotrophic microbial communities in climate change is still somehow unclear (Singh et al. 2010). The soil ecosystem is a significant reservoir of dynamic carbon and for this reason is an efficient

determinant of pattern in climatic changes. Soil carbon comprises two-third of the total Carbon content of terrestrial ecosystem, i.e. more than the total combined amount of Carbon in atmosphere and vegetation. The microbial exercises have been one of the basic determinants of convergences of ozone harming substances, for example, Carbon dioxide (CO<sub>2</sub>), Nitrous oxide (N<sub>2</sub>O) and Methane (CH<sub>4</sub>) in environment. Microorganisms have been major players in the cycling of ozone depleting substances and after their development to earthly condition also since their advancement in the sea more than 3.5 billion years ago. Microorganisms are probably going to get influenced by the climatic changes just as they can control the atmosphere through their association with the motions among soil and environment in ozone harming substances (Dutta et al. 2016). As per the IPCC environmental change report (IPCC 2007), in 2005, the normal worldwide convergence of CO<sub>2</sub> in the air was almost 380 ppm which outperformed the past most extreme focus for the past 6.5 million years by around 80 ppm. The Special Report on Global Warming of 1.5 °C (SR15) published by IPCC on the year 2018, depicted that limiting the warming close to 1.5 °C would require to decrease the net emissions by around 45% by 2030. As the worldwide increment in ozone depleting substance outflow has got one of the most fundamental logical and political difficulties, the better comprehension of the natural components occurring between land, sea and environment liable for worldwide carbon trades has got one of the greatest imperative.

Both immediate and aberrant impacts have been applied by environmental change on the mechanisms of soil microorganisms that discharge ozone depleting substances to the air and award their commitment on a worldwide temperature alteration. The immediate impacts grasp the effect on soil organisms and creation of ozone harming substance bringing about rise in temperature, changing precipitation cycles and other outrageous climatic occasions. Atmosphere driven changes may result in plant profitability just as decent variety in vegetation that may adjust soil conditions, particularly the stock of carbon to soil and the action of microbial networks occupied with arrival of carbon (Singh et al. 2010). Soil microorganisms largely affect plant efficiency which could be characterized in two primary recognizable systems as immediate consequences for plants by means of root-related living beings that structure mutualistic or pathogenic associations with plants, and backhanded impacts by means of the activity of free-living organisms that change the paces of supplement supply (Van der Heijden et al. 2008).

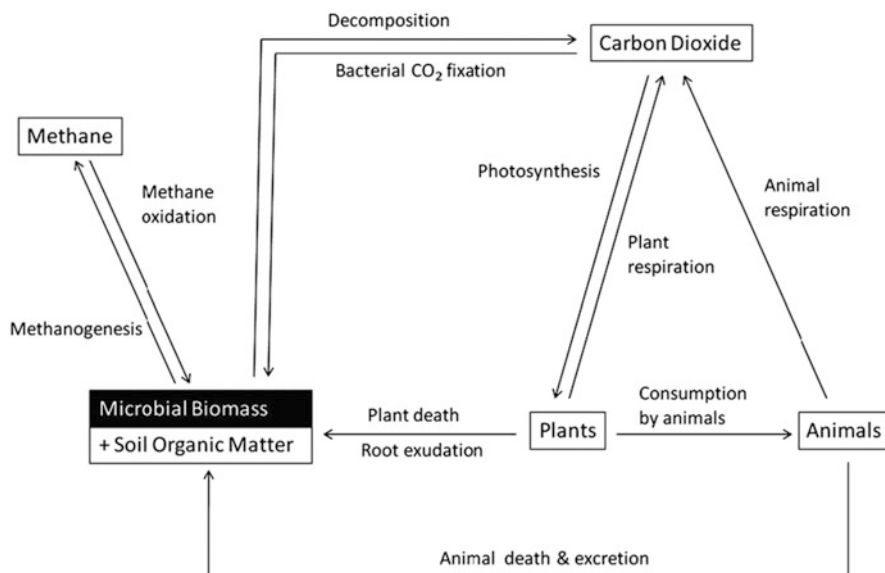
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### 13.3 Changes in Climate Affect Soil Microflora

Numerous studies have shown that shifts in species interactions according to climate change are likely to alter biodiversity and the function of terrestrial ecosystems, but very few studies have focused on soil communities (Singh et al. 2010). Soil microbes interact with one another as well as with plants in a myriad of ways that shape and maintain ecosystem properties which can shape landscape patterns of plant and animal abundance, diversity and composition.

### 13.3.1 Temperature and Thermal Adaptation on Soil Microbes

The relative plentitude and capacity of soil networks get adjusted due to climatic changes as soil community individuals differ in their physiology, growth rates and temperature lability. Worldwide climatic changes, for example, warming is directly altering the microbial soil respiration rates, and the temperature sensitive procedures interceded by the soil organisms. The job of elevated temperature in microbial metabolism has got critical consideration in some on-going investigations (Bradford 2013; Frey et al. 2013; Hagerty et al. 2014). The inherent temperature sensitivity of microbial action bringing about little changes in microbial network creation is characterized as the factor by which microbial metabolic action raises with a 10 °C elevation in temperature. In any case, utilizing just the factor to clarify temperature affectability in models may lead to poor forecasts as this relationship covers a lot of considerable interactions that have influence on the temperature sensitivity of microbial mechanisms, for example, decomposition. Further, while decomposition of soil organic matter, soil respiration and growth of microbial biomass are up-regulated with temperature, these reactions to experimental warming are frequently brief in field studies. The brief impacts of warming on soil microbial networks have been recognized to happen, as labile soil carbon substrates are depleted by expanded microbial action in soil and as a result of adjusting the microbial networks either adapt and move in synthesis or limit their biomass in light of the modified condition (Van der Heijden et al. 2008; Bradford 2013). As far as long term effect of increasing high temperature on soil microbiome is concerned, the combustion of fossil fuel could be proven as the most threatening ailment to the living world. The burning of fossil fuel derived from the degradation of biomass of microbes, plants and animals over millions of years is now considered as the prime factor of rising in atmospheric CO<sub>2</sub> concentration and liberation of greenhouse gases. As a result, the increasing rate of global warming phenomenon is not only altering the physical and chemical properties of soil but also the complex network association among various microorganisms and with plants and animals. These changes are clearly experienced by the behavioural response of microbiomes to the surrounding environments (e.g. rising rate of microbial respiration and acidification of soil micro-climate) (Cavicchioli et al. 2019). Experimental evidences of induced warming showed an alteration in microbial community abundance of Gram-positive and Gram-negative bacteria (Van der Heijden et al. 2008). Often short term laboratory experiment and long term field studies showed contradictory results on thermal compensation prompting in debate on thermal acclimation (Van der Heijden et al. 2008). Laboratory experiments demonstrate on more than 15 years old mid-latitude forest showed soil microbial respiration thermally adapting to seasonal variation in temperature supported by the contribution of substrate depletion and reduced soil biomass (Bradford et al. 2008) (Fig. 13.1).



**Fig. 13.1** The major processes mediated by soil microorganism of terrestrial carbon cycle (Adapted from Gougoulias et al. 2014)

### 13.3.2 Precipitation

As indicated by some on-going experiments, it has been discovered that warming had a differential impact on both bacterial and fungal community structures under every precipitation system. In the meantime, the warming effect on the diversity and assorted variety of bacterial and fungal communities fluctuated among precipitation treatments. These discoveries show that the impact of warming on the development and structure of a soil microbial community might be controlled by controlling the precipitation and the adjustments in the microbial community structure, which were influenced by treatment-incited changes in soil moisture. Certain microbial groups may have special adaptive characteristics to desiccation, for example, thickened cell walls, coming about in greater resistance to variances in soil moisture. As the soil is anaerobic and that moisture controls nutrient diffusion, soil moisture could be a basic factor influencing microbial community structure by means of connecting moisture based mechanistic processes.

The alteration of diversity and structure manipulated by precipitation or total soil moisture is much more prominent in fungal communities (Singh et al. 2010). As the fungal communities show more interaction with plants due to their symbiotic behaviour, the effect of changes in soil properties due to alteration in precipitation tends to manipulate the fungal communities which might emerge as a reason for a combined 34% soil diversity. An acidic soil condition under increased precipitation may act as environmental stress for fungal communities which may consequently alter soil fungal diversity (Li et al. 2018). The major alterations in bacterial

communities were observed in specific dominant phyla (e.g., *Proteobacteria* and *Acidobacteria*), occupying unique niches. Some climate change studies suggested that climate change drivers could change the structure and composition of soil microbial communities by selecting species that can thrive in the new environments (Zhang et al. 2016). As actual climate change can be more gradual than the changes observed in short term experiments, these studied results might not reflect the long term changes in the soil microbial communities and for that, further monitoring is required to confirm whether the detected changes in pattern will persist under more gradual climate changes over a longer time scale.

### 13.3.3 Elevation of Carbon Dioxide

Arrival of progressively powerful ozone harming substances, for example, Methane and Nitrous oxide by soil organisms is supported by expanded barometrical degree of CO<sub>2</sub> (Pathak et al. 2012). Truth be told, higher CO<sub>2</sub> levels increment efflux of methane as well as down direct the take-up of methane up to 30% by soil microorganisms (Dutta et al. 2016). Nonetheless, raised degrees of carbon dioxide prompt significant modifications in the microbial networks of tree leaves which are an intense wellspring of supplements for the little phytophagous creatures, may have results on the natural way of life all things considered microorganisms. Also, increment in microbial respiration happens due to up-regulated plant efficiency that happens because of raised carbon dioxide, particularly under nutrient rich conditions (Curtis and Wang 1998). This expands the carbon transition to roots, their symbionts and heterotrophic microorganisms through effectively degradable sugars and amino acids as root exudates (Zak et al. 1993). The outcomes of quickened carbon motion from roots to soil and carbon exchange for microbial networks are complicated to anticipate, due to their generous variety with factors like plant character, soil ripeness, soil nourishment web associations and a scope of other biological system properties (Bardgett et al. 2005). In any case, some potential results in connection to the soil microorganisms and carbon exchange incorporate the up-regulation of soil carbon as simplified natural carbon by respiration, because of stimulated microbial action and their abundance, which consequently gives more carbon substrate to soil microbial networks. A key component by which carbon cycle criticism is impacted by microorganisms and their digestion for atmosphere driven adjustments in vegetation synthesis is through changes in the quality and amount of natural issue going into the soil as plant litter. Slow-developing plants, for example, evergreen bushes, produce low quality litter which is poor in supplements and wealthy in headstrong mixes, for example, lignin and phenolic acids, decay gradually because of weakening of microbial movement; though, quickly developing plants, for example, graminoids and N-fixers, produce generally top notch supplement rich litter which breaks down quickly because of expanded degree of microbial action. The view of the significance for carbon trade of such connection between change in atmosphere, vegetation and related soil microbial working is poorly understood and therefore requires further research (Bardgett et al. 2008).

### 13.3.4 Resistance Development in Several Harmful Plant Pathogens

The predominant view is that natural changes including rising air CO<sub>2</sub> concentration, warming, and altered precipitation designs will build the frequency of plant invasions and worsen the negative impacts of these factors on the environment. As talked about before (Wolfe and Klironomos 2005), migration of plant species into novel territories may adjust the capacity of native soil food webs by (1) changing the quality, amount and timing of litter deposition and rhizodeposition; (2) causing direct release of novel antimicrobial substances; (3) by essentially modifying food relations by introducing alternate methods of nutrient acquiring, for example, nitrogen fixation; or (4) by modifying soil structure or physical properties because of novel or prevailing rooting habits.

Dispersal of organisms into new environments could bring about change in the abundance and elimination of taxonomic groups in soil. These impacts could affect environment diversity and functionality and could make both wild and maintained plant systems increasingly vulnerable to invasive pathogens or may decline subterranean challenge, permitting pathogenic soil organisms to thrive. In any case, the functional redundancy of soil taxonomic groups common to many soil communities may buffer against critical shifts in the productivity of wild and maintained plant systems. This implies that huge changes to various groups of soil organisms may eject each other out, but still these soil community movements will have no net impact on ecosystem productivity (Bradford et al. 2002).

Notwithstanding indirect effects on soil life forms caused by invasive plant species, ecological changes may also legitimately elevate the potential for distribution of soil organisms (Pariaud et al. 2009). The oomycete *Phytophthora cinnamomi*, an invasive root pathogen endemic to New Guinea-Sulawesi, for example, has as of now invaded in at least 76 countries, that too as the dominant part of worldwide biodiversity hotspots. *P. cinnamomi* has caused massive elimination of *Quercus* spp. also, *Castanea* in the USA and *Eucalyptus* spp. in Australia over critical geographic regions (Dunstan et al. 2010). Models show that expansion in soil temperature related with climate change is probably going to expand the decent variety of *P. cinnamomi* in both Europe (Bergot et al. 2004) and Australia. Warming of soil is likewise likely to cause comparable directional dispersal of plant parasitic nematodes, worms and numerous other soil life forms.

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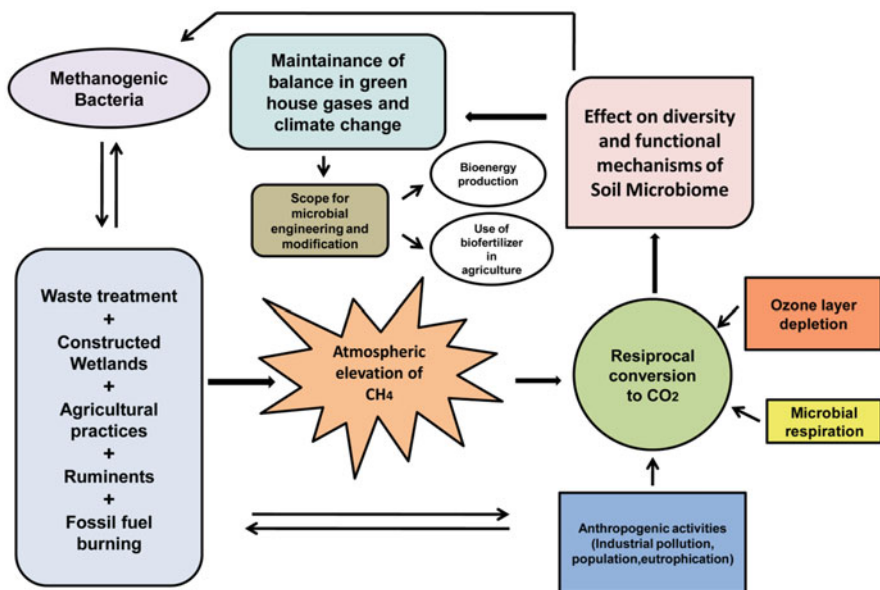
## 13.4 Effects of Soil Microflora on Climate Change

### 13.4.1 Carbon Dioxide Emission

The measure of environmental carbon discharged because of microbial disintegration of soil, which is exceptionally delicate to climatic patterns, is 7.5–multiple times in contrast with what is yearly radiated because of anthropogenic capacities overall (Crowther et al. 2015). Additionally, microorganisms in soil contribute  $5.5 \times 10^{12}$  kg (55 billion tons) of carbon dioxide yearly through the deterioration

of plant organic matter, which is itself far more than what is discharged by people. Soil biotic collaborations are along these lines considered huge on the grounds that they are critical in intervening soil microbial relationship to environmental change (Weiman 2015). Plants discharge ~50% of fixed carbon into the soil, which is experiment in woods accessible for microbial development. Notwithstanding microorganisms utilizing exudates as a vitality source, exudates can free natural mixes from minerals that are utilized for microbial respiration, consequently expanding carbon discharge disturbing natural incorporation of minerals (Cavicchioli et al. 2019). Anthropogenic environmental changes may support a good uprising in carbon discharge which can be anticipated by transient variety happened in deterioration of natural processes and generation of CO<sub>2</sub>, resulting in prompt changes in microbial network and carbon use. This may further bring about decreased microbial biomass and thus diminished free carbon for microbial processes as shown in a 26-year soil warming experiment in woods (Weiman 2015). Overhauled information on reactions in microbial network and practical systems is required for better understanding over-the-ground plant-biomass reactions to CO<sub>2</sub> levels (Fig. 13.2).

The polar permafrost, known as the greatest earthly repository of carbon mixes (Zimmerman and Labonte 2015), should be particularly referenced with regard to environmental change. Regardless of possessing just 9% of the landmass of the earth, the permafrost contains about 25–50% of worldwide soil natural carbon. Around  $1.7 \times 10^{15}$  kg of carbon remain caught in permafrost, though the environment contains roughly  $8.50 \times 10^{14}$  kg (Atkin et al. 2015). Be that as it may, a



**Fig. 13.2** Generation of Carbon dioxide and Methane and their impact on soil microbiome



worldwide temperature alteration starts the softening of the idle permafrost layers and subsequently, the microbial network which stayed lethargic for a considerable length of time inside these layers is activated, and their biotic exercises, for example, respiration, methanogenesis and multiplication are provoked (Zimmerman and Labonte 2015). Microbes that are available in the defrosting soil layer along these lines produce a few chemicals and proteins associated with disaggregation of enormous carbon atoms, for example, plant cellulose into monosaccharides that can fill in as wellspring of vitality for the microorganisms. Every step of these procedures realizes the emanation of ozone depleting substances (e.g., CO<sub>2</sub> and CH<sub>4</sub>) by change of soil carbon (Zimmerman and Labonte 2015).

### 13.4.2 Methane Emission

Worldwide discharge of CH<sub>4</sub> is all the more straightforwardly related to microorganisms when contrasted with CO<sub>2</sub> (Singh et al. 2010) (Fig. 13.2). Microorganisms are liable for about 85% of worldwide methane discharge determined by rise of temperature (Steffen et al. 2015). In this unique circumstance, an uncommon notice must be given to springy marsh soils, as enormous number of microbial qualities and proteins are liable for arrival of methane which can be exemplified by the catalyst methyl-coenzyme M reductase, engaged with change of CO<sub>2</sub> into methane. Microorganisms are equipped for disposing of air methane even at low focuses and expend about 60% of methane delivered internationally and happen in both land and sea (Steffen et al. 2015). In such manner, the microorganisms of local prairie fields merit a notice, which assume the significant job of settling carbon transition. Modification in examples of precipitation emerging because of environmental change influences these organisms. This thus has the potential for influencing soil carbon store, along these lines invigorating significant outcomes on the carbon balance in such environments (Zimmerman and Labonte 2015). Dissolving and decrease of permafrost permit microbial decay of recently solidified carbon, radiating CO<sub>2</sub> and CH<sub>4</sub> (Cavicchioli et al. 2019). Seaside permafrost scraped area can prompt the preparation of huge amounts of carbon to the sea, consequently bringing about conceivably more prominent CO<sub>2</sub> discharges happening through expanded microbial remineralization causing a positive input circle that goes about as a trigger of environmental change. Anaerobic CH<sub>4</sub> creation by methanogens and CO<sub>2</sub> generation by a scope of microorganisms through expanding water-soaked soils are advanced by dissolving of permafrost (Dutta et al. 2016). An investigation of 7 years' laboratory analysis shows more prominent measure of CO<sub>2</sub> and methane emanation by methanogens engaged with permafrost defrosting in anoxic condition than oxic condition foreseeing climatic change before the finish of century (Knoblauch et al. 2018).

### 13.4.3 Role of Ruminants, Earthworms and Herbivores

The measure of natural issue that is cycled back to soil is influenced by herbivores (invertebrates and mammals). Consequently microbial biomass and movement additionally get influenced, for example, grasshoppers bring about expanded microbial cell movement by lessening plant biomass and plant nitrogen request. Environmental change may crumble herbivory, winding up in generally speaking adjustments to worldwide carbon and nitrogen cycles. Detritivores (for example, Earthworms) can impact the arrival of ozone depleting substance by implication influencing plants by expanding soil fruitfulness and decent variety of soil microorganisms. Earthworms guarantee alteration of soils through bolstering, tunnelling and affidavit of waste materials. The anaerobic condition of the night crawler gut sustains microorganisms that experience denitrification and produce nitrous oxide (Cavicchioli et al. 2019).

Worms expand soil fertility, despite the fact that the consolidated impacts of raised temperature and lightened precipitation on detritivore bolstering and microbial respiration may decrease emanations, their quality can bring about net ozone harming substance outflows. Ruminant creatures are considered as the biggest single wellspring of anthropogenic CH<sub>4</sub> discharges, as 19–48 times more noteworthy emanation of carbon dioxide is started from ruminant meat generation contrasted with plant-based high-protein nourishments. Ventures for non-ruminant meat creation (for example, pigs, poultry and fish) may discharge 3–10 times more methane than high-protein plant nourishments (Cavicchioli et al. 2019).

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## 13.5 Agriculture

As 40% of terrestrial land has been used as agricultural fields, elevation of such lands may increase substantial changes in Carbon, Nitrogen and Phosphorus cycles, leading to significant changes through loss in biodiversity of microorganisms. Use of both plant associated and animal associated microorganisms for increasing sustainability in agriculture and to alleviate the effects of climate change on agriculture has become a burning topic of research and for this, the better understanding of effect of climate change on microbes is required.

### 13.5.1 Methane Emission from Different Agricultural Activities

Methane is the second most significant anthropogenic greenhouse gas simply after CO<sub>2</sub> regarding complete atmosphere controlling and microbial use, accurately known as methanotrophy, which is the largest terrestrial sink. Hence, to more readily foresee methane emissions, it will be fundamental to comprehend the reaction of CH<sub>4</sub> flux to atmosphere change. Natural emanations (~250 million tons of CH<sub>4</sub> every year) are ruled by microbial methanogenesis, a process that is completed by a group of anaerobic archaea in wetlands, sea, rumens and termite guts. Be that as it may, these common sources are enlarged by emissions from human activities

(unequivocally rice cultivation, landfill, petroleum derivative extraction and live-stock cultivation) (about 320 million tons of  $\text{CH}_4$  every year), which aside from certain emanations from non-renewable energy source extractions are additionally determined by microorganisms. Methanotrophic microorganisms fill in as a critical buffer to sublimate the gigantic measures of methane delivered in a portion of these conditions. The alleged 'low-affinity' methanotrophs, which are active just at a  $\text{CH}_4$  concentration of under 40 ppm; belonging to class Gamma-proteobacteria, can regularly devour a huge extent of  $\text{CH}_4$  released in soil before discharged into the environment. For  $\text{CH}_4$  as of now in the atmosphere, the 'high affinity' methanotrophic microorganisms, belonging to the class Alpha-proteobacteria, (active at a concentration of under 12 ppm) may likewise act as a net  $\text{CH}_4$  sink and expel roughly 30 million tons  $\text{CH}_4$  from the climate every year. Rice is considered as a prime food source for half of the overall population and rice paddies are considered as a wellspring of around 20% of cultivating  $\text{CH}_4$  surges, paying little heed to covering just generally 10% of arable land. Anthropogenic ecological change has been foreseen to two-fold  $\text{CH}_4$  outflows from rice fields before the end of the century.

One truth that must be referenced with respect to this territory is that farming is considered as a gigantic wellspring of the strong ozone harming substance Nitrous oxide ( $\text{N}_2\text{O}$ ) outflow, discharged by oxidation and decrease of nitrogen interceded by organisms. The compound  $\text{N}_2\text{O}$  reductase in rhizobacteria living in vegetable root knobs and other soil microorganisms may likewise change over  $\text{N}_2\text{O}$  to Nitrogen. The rate at which microbial nitrogen cycle happen and Nitrogen is discharged (deterioration, mineralization, nitrification, denitrification and fixation) can be activated by environmental change (Cavicchioli et al. 2019).

### 13.5.2 Fossil Fuel Combustion and Use of Fertilizers

Emissions of black carbon and organic carbon from cooking and heating with biofuels and from diesel transportation, and emission of sulphates and nitrates from fossil fuel combustion, can increase seasonal mean AODs (aerosol optic density) to as high as 0.4 (larger during volcanic periods), tends to decrease 10–15% of incident solar radiation at the surface. In addition to this, elevated utilization of fertilizers in fields together increases availability of environmental nitrogen, leading to a severe threat on ecosystem sustainability (Cavicchioli et al. 2019; Nisbet et al. 2019).

### 13.5.3 Eutrophication

The combined effects of climatic change and use of fertilizers in agricultural fields might imply unpredictable potential effects on microbial competitiveness (Cavicchioli et al. 2019). In a study in deep lake of Zurich revealed that reducing the use of phosphorus rich fertilizers increases non-nitrogen fixing cyanobacterial

growth, elevation of annual warming might also result in persistence of toxic cyanobacteria in lake due to absence of predation and reduction in annual mixing (Posch et al. 2012). Human activities that have direct effect on microorganisms include greenhouse gas emissions (CO<sub>2</sub>, methane and N<sub>2</sub>O), pollution (precisely eutrophication), use of land in agriculture and growth in population which positively manipulates climate change, pollution, various agricultural practices and the multiplication of pathogenic microbes. In small lakes, located in climate sensitive regions, eutrophication causes elevated emission of methane, raises the need of considering lake microorganisms on greenhouse gas emission (Cavicchioli et al. 2019).

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## 13.6 Microbial Mitigation of Climate Change

The ecological community of all types of microorganisms present in soil microflora, termed as 'soil microbiome', has a great level of changes in their population, diversity and functionality due to the continuous effect of climate change. So, the microbial shifting in various directions due to the alternation of climate is still under the subject of research for most scientific communities. Due to higher potentiality level of evolution, they can stably modify their ecological response as the climate deviates from its native state. For example, the consistent elevation of temperature leads to the reduction of respiration rate in soil microbes (Bradford et al. 2008) or the changes in precipitation pattern now make the microbial community much more tolerant to adverse condition than earlier time (Wallenstein and Hall 2012). These kind of incidents now make us to think that the maximum buffering capacity of terrestrial living communities with the continuous change could be utilized in practical only by monitoring and exploiting microbial processes undergoing on soil microbiome under soil. Therefore, it is necessary to discuss and open a third eye of knowledge that could explore a number of approaches dealing with microbial modelling for minimizing the effect of global climate change in sustainable manner. There are number of approaches concerned with the engineering of microbial communities through bioremediation with a great potential under complex environment. Here, we are highlighting some physical literature of most promisable and convenient techniques to suggest a way out that scientists can imply to.

### 13.6.1 Management of Soil-Borne Plant Pathogens

Soil microbial diversity is a mixture of heterogenous population of fungi, bacteria, viruses, algae, nematodes, protozoans and actinomycetes representing a great variability in a single microflora. Since last 50 years of science and research discovery, several types of beneficial effects of soil microbes have been studied and implemented in agriculture and plant health management (Subba Rao and Gaur 2000). As per as management of plant pathogen is concerned, some specific suppression of mechanisms among microbes and plants are well established and that includes (1) Plant-microbe (Biocontrol agent) interaction; (2) Microbe (pathogen)-

microbe (Biocontrol agent) interaction; (3) Plant metabolites (Biocontrol agent)—microbe (pathogen) interaction; (4) Induced systemic resistance. Release of biocontrol products in efficient way is dependent not only on its types or structural configuration, but also on switching on or off of the complex interactions of microbes and plants as mentioned (Sangeetha et al. 2012).

### 13.6.1.1 Exploitation of *Pseudomonas*, *Bacillus* and Other Rhizobacterial Species

Majority of the Gram-negative *Pseudomonads*, namely *P. fluorescens*, *P. syringae*, *P. aeruginosa*, *P. putida*, *P. aureofaciens*, *P. chlororaphis*, *P. brassicacearum*, *P. varvalensis* are well known for their biocontrol activity against a wide range of plant pathogens. The typical colonization level touching  $10^5$ – $10^6$  CFU (colony forming unit)/g value at root region is sufficient enough to shield the plant against *Pythium spp.* attack. Though the laboratory based *Pseudomonas* culture growth reached to root up to  $10^7$ – $10^8$  CFU/g, but no longer preserve the colonization rate with equal potential (Landa et al. 2003).

Another report confirmed that the combinatorial application of *P. fluorescens* (Pfbv22) and *Bacillus subtilis* (Babv57) was highly effective to suppress the nematode population in banana plant significantly. In that case, the active antibiotic compound (2,4-DAPG) is the prime agent to suppress the pathogenic invasion after its introduction where suppression is almost lost when *Pseudomonas spp.* is eliminated. In similar way, the microbial formulations of *Pseudomonas* and *Bacillus spp.* were proved to be highly challenging against various *Phytophthora*, *Fusarium* and *Pythium spp.* in some vegetables and flowering plants (Sangeetha et al. 2012). In other hand, the Gram-positive rod shaped bacteria, *Bacillus sp.* is highly efficient for its antagonistic activities against several fungal pathogens as their endospores are inherently tolerant to desiccation and heat. Besides their defensive actions (such as parasitism, antibiosis or induced systemic resistance), some species of these Rhizobacteria are highly capable of promoting plant growth by releasing specific volatiles (Ryu et al. 2003) and even acquisition of photosynthetic energy by *B. subtilis* (GB03) in *Arabidopsis thaliana* (Zhang et al. 2008).

### 13.6.1.2 Exploitation of Rhizobacteria Against Other Biotic Stresses

The prime hormone related to biotic and abiotic stress is ethylene, mainly derived from the precursor of 1-amino cyclopropane-carboxylic acid (ACC) and that also act as a plant growth inhibitor. But another key enzyme, ACC-deaminase (1-amino cyclopropane-1-carboxylate deaminase) is reported for its blocking mechanism on ACC in stressed plant and this noble enzyme is interestingly higher in several PGPR strains of fluorescent *Pseudomonads* (Wang et al. 2000; Mayak et al. 2004). In addition to the disease suppression by narrowing down the deleterious enzyme activity, some rhizobacteria known as endo-mycorrhizae/vesicular arbuscular mycorrhizal fungi (VAM) are also suppressing the pathogen attack by strengthening structural defense mechanism. VAM fungi basically develop a complex network of fungal arbuscules or vesicles (hyphae) and thus prevent pathogenic entry through root in the host plant. Beside this, VAM fungi also restricts the pathogen growth by

different ways including by enhancement of nutrient supply to plant and boosting host immunity, development of root lignification and sometimes altering the chemical composition of defense responsive enzymes, namely chitinase and isoflavonoids (Garcia-Garrido and Ocampo 1989).

### 13.6.1.3 Induction of Systemic Resistance

It has been reported that several strains of root colonizing microbes are potentially acting as an elicitor to induce hypersensitive response for host plant defense (Haas and Defago 2005). The development of this type of resistance in host plant due to the interaction between plant roots and some rhizobacteria is known as induced systemic resistance (ISR). It is very promising that a number of chemical elicitors are synthesized in PGPR strains after immediate induction triggered by pathogens and they are mostly salicylic acid, siderophores, cyclic lipopeptides, lipopolysaccharides, 2,4-diacetyl phloroglucinol (PhI) and other volatile substances (Ongena et al. 2004).

## 13.6.2 Microbial Exploitation for Sustainable Agriculture and Plant Growth Enhancement

As a part of natural ecosystem, microbial diversity is solely depending on the internal network between microbial growth and development with several biotic and abiotic factors influencing the microbiota. In other way, microbial diversity has a great impact on the quality and quantity of various plant derived metabolites. For instance, the synthesis principle of different flavon precursors in cocoa beans and tea leaves are influenced by development of microflora in and out of the reaction centre. In similar way, some rhizobacteria (PGPR) are tremendously helpful in stable supply of major nutrients to plant roots by means of asymbiotic, symbiotic or associative fixing mechanisms. Some of the important areas of implications of microbial diversity in the development of agriculture and plant metabolism can be drawn for literature exploration.

### 13.6.2.1 Development of Biofertilizer or Nitrogen Fixer

A spectrum of plant growth promoting rhizobacteria are responsible for fixing atmospheric and terrestrial nutrient component by various mechanisms. Some notable microbial members are Cyanobacteria, Actinomycetes, free-living diazotrophic bacteria (*Azospirillum* and *Azotobacter*) and phosphate solubilizing bacteria (*Microbacterium*, *Pseudomonas*) (Peoples et al. 1995). Microbial exploitation for enhancement of biological nitrogen fixing (BNF) bacteria (*Rhizobium* and *Bradyrhizobium*) from nodules of legume crops is currently of great concern. As the abundance of these microbial communities in the rhizosphere not only increase the availability of nitrogen and phosphorus by expanding the root surface area but also suppress the harmful effects of incoming plant pathogenic microbes, these beneficial functions, majority of rhizobacteria are also reported to synthesize auxin

series phytohormones and indole acetic acid inside their cell, which is considered to have an implicit role in promoting plant growth (Wani et al. 2007).

### 13.6.2.2 Phytohormone Synthesis

A number of scientific literatures reported that several phytohormones are (Auxin, GA, Cytokinin, Ethylene) produced in higher rate in plant when their root rhizosphere is associated with PGPRs. For instance, some bacteria like *Comamonas acidovorans*, *Alcaligenes piechaudii* and *Agrobacterium sp.* are associated with increased production of Indole-3-acetic acid (IAA) in lettuce (Salisbury 1994), where *Aeromonas veronii* and *Enterobacter cloacae* are related to enhance IAA production in *Oryza sativa* (Mehnaz et al. 2001). On other hand, the synthesis of natural cytokinin is induced when *P. fluorescens* and *Rhizobium leguminosarum* are associated with the growth factor in soybean (de Salamone et al. 1996) and in rape or lettuce (Noel et al. 1996). As per as the increased production of gibberellin is concerned, *Penicillium corylophilum*, *Penicillium corylophilum*, *Penicillium funiculosum*, *Penicillium cyclopium*, *Aspergillus flavus* and *Aspergillus niger* are mostly reported PGPRs found in plant rhizosphere (Hasan 2002). Besides the magical production of phytohormones by these rhizobacteria, some of them are capable of synthesizing ACC-deaminase, a component that actively breaks down the precursor of ethylene biosynthetic pathway, called ACC. The most discussed rhizobacteria of such category are *Variovorax paradoxus*, *Pseudomonas sp.*, *Enterobacter cloacae*, *Bacillus pumilus*. The secretion level of Ethylene, the main villain of root lengthening and overall plant growth could be reduced by naturally culturing these PGPR groups (Saleh and Glick 2001). As per as economic and ecological point of view, the beneficial application of a major groups of Rhizobacteria and PGPRs can be considered to replace the excessive use of agrochemicals.

### 13.6.3 Bioremediation

The demand of pure drinking water is increasing day by day worldwide. But the mode of ground water contamination with the help of spreading pollution in soil, namely lands filter, mining and agrochemicals making the drinking water hardly reachable in an adequate quantity to a majority of world population. But the activity of microflora available in soil is quite promising in degrading harmful pollutants and decreasing the impact of poor sanitation, For instance, exploration of *Enterobacter cloacae* by any effective technique of bioremediation could drastically reduce the contamination of selenium in agricultural and industrial waste water (Schlanger 2017).

Bioremediation by using microbial communities deals with biological cleaning by recycling the waste materials into non-toxic or useful forms, with the help of metabolic activities of microbes rather than other potent organisms. On the other way, microbial bioremediation is mostly involved with single or multiple microbial events like eradication, detoxification, degradation, immobilization of different chemicals or biological wastes or physical hazardous materials which are

continuously generated or deposited in environment by the activity of human or other organisms.

### **13.6.3.1 Microbial Bioremediation: Overview and Types**

In this context, we will discuss about some most promising approaches or strategies, that are coming into the light of scientific perception and some of the notable approaches are bioaugmentation, bio-stimulation, bio-attenuation, biopiling and bioventing. In a brief, the potential approaches of microbial bioremediation need to be addressed before entering into the area of possibilities of bioremediation in relation to soil microbes.

As per as bio-stimulation is concerned, a specific concentrated nutrient medium or a combination of media is supplied to the site of soil or ground water area where beneficial microorganisms are in action and it is performed to stimulate their growth and development which escalate their bioremediation activity. In addition to this medium, several other factors like oxygen, temperature, pH and a little amount of pollutant suitable for optimum microbial activity are provided to the microbiome to accelerate their enzyme or biomass production (Adams et al. 2015). Bio-attenuation is the natural eradication process of pollutant concentration of surroundings by means of biological (biodegradation), physical (dispersion, dilution) or chemical (ion exchange) forces. Some of the tiny bugs or microbes have the ability to uptake harmful chemicals or pollutants from soil or ground water and metabolize them into less toxic or harmless gasses or solvents. Another term, bioaugmentation is also popular in relation to bioremediation that is one form of biodegradation. Basically it is the addition of a natural population of microbes to the natural microbial population exist in soil or ground water contaminated with organic or inorganic pollutants and thereby enhance their degradation capacity to reduce pollution rate (Malik and Ahmed 2012). This strategy is much more convenient and realistic way of constructing bioengineering microbes in order to completely destroy the complex pollutant. The genetically engineered microorganisms can be customized through DNA manipulation and are highly efficient than microorganisms of natural species to breakdown certain compounds or pollutants with a faster rate.

### **13.6.3.2 Bioremediation of Heavy Metals**

The heavy metals directed contamination in soil and waterbodies is getting special attraction because persistent accumulation and impact on human body are quite dangerous than the efficacy of other available contaminants in ecosystem. Among them, cadmium (Cd), arsenic (As), nickel (Ni), cobalt (Co), caesium (Cs), strontium (Sr), chromium (Cr), mercury (Hg), lead (Pb), silver (Ag), zinc (Zn), copper (Cu), vanadium (V), tin (Sn) and thallium (Tl) are considered as the most potent toxic heavy metals dangerous to ecosystem (Wang and Chen 2006). The deleterious impact of heavy metals is quite high because its ionic form have a high electrostatic affinity with cellular components and causing severe damages in the form of destabilization in the molecular structure of vital biomolecules (RNA, DNA and enzymes), which results mutagenesis, cancer or genetic disorders at extreme stage (Abatenh et al. 2017). Several studies reported that a number of microorganisms



have an inherent capacity to reduce or neutralize the efficiency of most of the potentially toxic heavy metals by activating certain phenomena such as bioaccumulation, bioaugmentation, biosorption, biodegradation, combating resistance to heavy metals, etc. (Table 13.1). Therefore in conjugation of phytoremediation, microbial efficiency to block the negative effect of heavy metals could be enhanced by adopting various feasible genetic engineering approaches in future scientific studies.

### 13.6.3.3 Other Scopes and Possibilities: Synthetic Biology Approach

Besides several genetic engineering approaches, the recent advancement of synthetic biology to reprogramming microorganisms in order to divert their genetic potential towards the remediation of pollutants is considered as a steady strategy at global level. To adopt such strategies, it is very important to know the key signals generated and circulated through a complex network established by several genes in microbial metabolism. To precisely and accurately control the candidate genes or gene cluster during their switching on and off moment, understanding the entire map of regulatory network involved with a number of genes, enzymes and proteins in microbial biosystem is extremely necessary. To customize such synthetic regulatory networks, major challenges appeared; of them designing of several well characterize regulatory parts sensitive to genetic and environmental factors, constructing of circuits require large DNA fragments with many cellular regions and finally debugging of circuit to evaluate the cellular response when exposed to abiotic stress under subject are of great importance. By building and reprogramming such internal gene circuits, it is quite possible to deploy a specific bacterial species or community (e.g. *Pseudomonas*) naturally associated with plants having phytoremediation potential (e.g. legumes) and accelerate the bioremediation process in much faster rate from waste contaminated areas. This type of bio-programming approach could be proven as a most indispensable leading bioremediation technique in the areas of plastic degradation, reduction of use of industrial chemicals, biofuel production, heavy metal detoxification and even minimizing the effect of agrochemicals used in agriculture (McAdams and Shapiro 1995).

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## 13.7 Conclusion

The existence of soil microbial diversity is the most powerful and secret weapon to explore its potentiality for combating continuously elevating and most threatening global climate change. As most of the techniques related to bioremediation driven by soil microbial communities are not so old, but it is very essential to imply this technology up to a maximum level by flourishing our knowledge on microbial reactions and possible modifications to restore adverse climate change. The increasing rate of climate change in terms of precipitation, irregular happening and shifting of seasons, global warming, raising of sea water level are directly or indirectly influencing the frequency of disease development and plant health. The severe effect of changing climate can damage our soil to extreme level and that can further depress

**Table 13.1** Major soil microorganisms used in bioremediation

Organisms	S. no.	Genus/species	Application in bioremediation
Bacteria	1.	<i>Bacillus subtilis</i> strain NAP1, NAP2, NAP4 (Abatenh et al. 2017)	Used to degrade contaminants which are taken as food by the bacteria in oil-based paints to negligible level in environment. Optimum levels of nutrient and other chemical substances are supplied for fast activation of microbial enzymes
		<i>Bacillus spp.</i> ETL-2012, <i>B. pumilus</i> HKG212 (Abatenh et al. 2017)	Used for textile dye, Sulphonated di-azo dye and RNB dye degradation
		<i>Bacillus cereus</i> , <i>B. Coagulans</i> , <i>B. Brevis</i> (Abatenh et al. 2017)	Diesel, crude oil degradation from ocean and terrestrial environment
	2.	<i>Pseudomonas aeruginosa</i> , <i>P. fluorescens</i> , <i>P. putida</i> , <i>P. cepacia</i> (Abatenh et al. 2017)	Monocyclic aromatic hydrocarbons (e.g. benzene, xylene) in diesel, crude oil and oil-based product; textile dye, heavy metal (Fe <sup>2+</sup> , Cu <sup>2+</sup> , Pb <sup>2+</sup> , Mn <sup>2+</sup> ) degradation
	3.	<i>Staphylococcus aureus</i> , <i>Klebsiella oxytoca</i> (Abatenh et al. 2017)	Contaminants in vat dyes and textile effluents degradation
	4.	<i>Enterobacter cloacae</i> (Banerjee et al. 2015)	Heavy metal (Pb <sup>2+</sup> , Cd <sup>2+</sup> , Ni <sup>2+</sup> ) in soil and waste water and agricultural waste degradation
	5.	<i>Citrobacter sp.</i> (Abatenh et al. 2017)	Diesel, crude oil degradation
Fungi	6.	<i>Cupriavidus metallidurans</i> (Perpetuo et al. 2011)	Heavy metal mainly cadmium degradation
	7.	<i>Acinetobacter sp.</i> , <i>Arthrobacter sp.</i> , <i>Photobacterium sp.</i> , <i>Flavobacterium sp.</i> , <i>Achromobacter sp.</i> (Abatenh et al. 2017; Perpetuo et al. 2011)	Heavy metals and pesticides (Chlorpyrifos and methyl parathion), polycyclic aromatic hydrocarbons (e.g.-toluene) degradation
	8.	<i>Penicillium chrysogenum</i> , <i>P. funiculosum</i> , <i>Penicillium ochrochloron</i> (Abatenh et al. 2017)	MAHs and PAHs, industrial dyes degradation
	9.	<i>Aspergillus niger</i> , <i>A. Fumigates</i> (Abatenh et al. 2017; Perpetuo et al. 2011)	Hydrocarbon in industrial waste degradation
	10.	<i>Cunninghamella elegans</i> (Abatenh et al. 2017)	Heavy metals degradation
	11.	<i>Fusarium sp.</i> (Abatenh et al. 2017)	Oil degradation
Yeast	12.	<i>Saccharomyces cerevisiae</i> (Abatenh et al. 2017; Perpetuo et al. 2011)	Heavy metals degradation (Lead, Mercury and Nickel)
	13.	<i>Candida sp.</i> (Abatenh et al. 2017; Perpetuo et al. 2011)	Hydrocarbons in industrial waste

(continued)

**Table 13.1** (continued)

Organisms	S. no.	Genus/species	Application in bioremediation
Algae	14.	<i>Chlorella vulgaris</i> (Zeraatkar et al. 2016)	Uranium, nickel degradation
	15.	<i>Chlamydomonas reinhardtii</i> (Zeraatkar et al. 2016; Chekroun et al. 2014)	Cadmium, chromium; herbicide (Prometryne, Fluroxypyr) degradation
	16.	<i>Scenedesmus sp.</i> (Zeraatkar et al. 2016; Chekroun et al. 2014)	Chromium, organic pollutants in oil degradation
	17.	<i>Cladophora sp.</i> (Zeraatkar et al. 2016)	Cu <sup>2+</sup> degradation

our ability to grow food and our good health, wildlife ecosystem and our planet's sustainability. Taking into consideration of above serious matter, microbial bioremediation tailoring with the use of modern genetic engineering and synthetic biology tools adopted with soil microbiota could only can tackle environmental pollution and replenish the green planet with clean air, water and soil. So, the better understanding on the microbial diversity and its role in plant disease suppression could be the most promising weapon to defeat the adverse effect of global climate change in near future. Molecular microbiology has disseminated its implication to uncover the qualitative and quantitative accounts of soil microbiota. Therefore, disseminating the highest level of applications of soil microbiota by studying its qualitative and quantitative accounts at molecular level would be taken with highest priority for restoring the native state of global climatic change.

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