Climate Change Extenuation by Greenhouse Gas Quenching Microflora

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Abstract

The major cause of climate change is global warming, which refers to an increase in the concentration of three most important greenhouse gases such as CO_2, CH_4, and N_2O in the atmosphere. Climate change has become a hot topic because of its pervasive detrimental impacts globally. World over, the high level think tanks suggest the remedial measures to the policy makers so as to ameliorate the ramifications of climate change but till now, no suitable method has been devised which can mitigate the effects of climate change. The world is in need of a strategy that will be cost-effective and sustainable. Such techniques can now be used by harnessing the ability of microbes to sequester the greenhouse gases in an irreversible manner, thus aiding in climate change mitigation. The varied biogeochemical processes on earth are wholly and solely dependent upon the metabolic activities of microbes, without which our planet would have been packed with debris. Microbes thriving in the extreme conditions have an inherent ability to sequester CO_2, CH_4, and N_2O. Microorganisms such as Methylobacillus and Methanotrophs are important carbon recyclers as they use the greenhouse gases as their sole carbon and nitrogen sources which are consequently needed for their metabolic activities. Such bacteria are found in abundance in paddy fields, landfill sites, extreme alkaline environments and geothermal areas. There are some microbes which can convert CO_2 to $CaCO_3$ that can fetch minerals of economic value. Thus microorganisms have a great potential to fight against global

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warming and also for combating pollution. This chapter primarily focusses on the role of microbes in mitigating the effects of climate change.

Keywords

Bacteria · Climate change · Microorganisms · Global warming

3.1 Introduction

A thick layer of gases encapsulates the planet Earth, which work like a blanket and aid in keeping the planet warm in addition to allowing the flora and fauna to survive and sustain. The atmosphere is so pivotal in a way that in its absence, the planet would have been much colder (20–30 °C), thus rendering it inhospitable. Climate change has become a global phenomenon and its evidence can be exemplified by the increasing overall surface temperatures worldwide by a process called global warming. Even if, there is a minuscule alteration in earth's temperature, it can have disastrous consequences such as melting of glaciers and flooding. The atmosphere becomes warmed up because of the absorption of heat by the constituent gases. Consequently, the primary reason of such warming is the heat energy absorption by greenhouse gases (methane, carbon dioxide, ozone and nitrous oxide) that are reflected by the surface of Earth. The source and sink of these gases are the microbes which have an important part to play because of the recycling and transformation capability of essential elements, particularly carbon and nitrogen, which make up the cells. Of all the microorganisms, bacteria and archaea are concerned with the cyclic transition of every essential element. For example, in the process of methanogenesis, the concerned bacteria convert carbon dioxide into methane in Carbon cycle; the nitrogen-fixing bacteria such as Rhizobium fixes nitrogen, thus helping in the conversion of nitrogen in atmosphere into the form of nitrogen that can be taken up by plants in usable form. Photosynthetic algae and cyanobacteria are also involved in these cycles and form a major component of phytoplanktons. Different microorganisms (bacteria and fungi mostly) residing in soil are known for their decomposition ability as they break down complex organic matter into simpler ones, thereby releasing carbon dioxide back into the atmosphere (Panikov 1999). This chapter primarily focusses on the ability of microbes in mitigating the effects of climate change.

3.2 Soil Microbes and Climate Change

The microorganisms residing in the soil form an indispensible component for maintaining various ecological processes such as cycling of nutrients, decomposition of detritus, utilization and the making of trace gases, ultimately the biotransformation of metals (Panikov 1999). As per the IPCC report, there has been an unprecedented warming of climate systems plus the basic cause has been found out to be of anthropogenic origin. Additionally, the human activities, particularly the disposal of waste and intensive agricultural practices have paved a way for the production of greenhouse gases by microorganisms (IPCC 2007). There is an immense need to contemplate upon the role, soil microbiota has both as contributors and pacifiers with regard to climate change. Soil has been considered as a living, fertile and a substance for it is a home for varying life forms ranging from microorganisms to higher animals. When there is an increase in the temperature of Earth, the metabolic activities of microbes are enhanced, thereby expediting the biodegradation processes which further results in the release of more carbon dioxide into the environment. It has been shown experimentally that there has been an increase in soil respiration and carbon dioxide emission with the increase in temperature. The mass release of CO_2 is directly proportional to the global warming, that in turn augments the pace of microbial activity in soil (Briones et al. 2004). Nitrous oxide, another deadly greenhouse gas being 300 times more dangerous which depletes the ozone layer. Fortunately, mother nature has a substitute for combating the greenhouse effect (Sanford et al. 2012). There are various groups of microorganisms known as denitrifying bacteria which have the ability to convert nitrous oxide into harmless nitrogen. Scientists opine that other than the denitrifying bacteria, there are other microbes which have the same potential of using nitrous oxide, thereby mitigating the emissions (Willey et al. 2009). Researchers have estimated that *Prochlorococcus* and *Synechococcus* (single celled cyanobacteria) eliminate almost 10 billion tons of carbon from atmosphere every year (Willey et al. 2009). Microbes with such capabilities are found in most of the sediments and soils, implying that large microbiological masses contribute actively to nitrous oxide utilization (Willey et al. 2009).

3.3 Microbes and Global Warming

The technical and scientific world can enhance its comprehension on global environmental roles of the emissions of nitrous oxide and for enhancing the cycle models of greenhouse gases by the innovation of microbial diversification and its aid in nitrous oxide utilization (Sanford et al. 2012). This will pave a way for better understanding the ramifications of anthropogenic activities on climate change. One cannot accurately predict the global nitrous oxide emissions by analysing the microbial populations which are responsible for denitrification. Cellulose is the structural support and framework of plant cell wall, which being insoluble cannot be broken down by animals because of the lack of cellulase enzyme. Nature has solution for everything and in this perspective a specific group of animals known as ruminants are able to digest cellulose because of their four chambered stomach in which the largest compartment being the rumen is replete with millions of microorganisms which in turn are able to digest cellulose. Methanogens, living in rumen can break down complex food substance into methane, consequently, ruminants belch the gas out of digestive system. Methane is potent than carbon dioxide as it traps about 20 times more heat than it, resulting in the warming of planet

20 times more than CO_2. About 20% of global methane emanation is from farm animals as per the estimation of scientists (Panikov 1999) and they are now looking at ways of reducing the amount of methane emissions from ruminants. A vaccine has been developed in Australia which prevents the microbes present in the rumen from producing methane and it was tested on sheep and to our surprise it belched 8% less methane in a 13 h test. Currently, this vaccine is only effective against 20% of the microflora which produces methane. It is imperative for scientists to manufacture such vaccine which is effective against most of the microbes producing methane (IPCC 2007). *Methylokorus infernorum*, the methanotrophic bacteria, found in geothermal sites has the ability of consuming methane gas (11 kg/year) as the sole energy source, ultimately converting it to carbon dioxide during the digestion process. It is hoped that this bacterium can be very helpful in reducing methane emission from various sources (Jenkinson et al. 1991). Similarly other forms of bacteria known as *Methylobacillus*, found in astonishing numbers in all water ecosystems are of most important carbon recyclers of Earth. Generally, methylotrophs use greenhouse gases for fulfilling their energy needs. Recently, a microbe has been developed by Indian that can convert carbon dioxide into calcium carbonate that can fetch minerals of economic value. The enzyme that is used for such conversion can be installed in any industrial for the conversion. The discovery has been seen as a cornerstone which can go a very long way to fight global warming (Jenkinson et al. 1991).

3.4 Microbes as Carbon Sink

A cluster of oceanic microorganisms play a fundamental role in combating climate change and the task of oceans in absorbing carbon dioxide is crucial to comprehend. The photosynthetic activity taking place in the oceans by phytoplanktons is the main way that CO_2 is absorbed by the ocean. This is where the concept of food chain sets in starting from algae to the larger animals is followed by the death, sinking and decomposition of these creatures to the ocean floor. Such remains are known as particulate organic matter (POM). The organic compounds are contained within the dead creatures. Most of which is dissolved, which was not thought to be an important component of the total carbon dioxide (Anisimov et al. 1999).

3.5 Combating Global Warming Through Biofuels

Entire world is struggling to address the issues related to global warming and primarily the basis for this is industrial revolution which played a major role in the emission of greenhouse gases. This issue is such that it cannot be addressed in 1 day, rather it will take years altogether and the involvement of each and every individual, both at the local and the global level. Undoubtedly these emissions can be lowered by shifting to low carbon fuels and other sources of alternate energy. Important to mention that a hefty cluster of microorganisms have played a pivotal role to reduce these gases. The responsibility of microbes in determining the concentration of GHGs is commonly acknowledged (Singh et al. 2010). Ocean and forest ecosystems have been presumed to act as sinks for carbon and their protection through green technologies is considered to be another way of mitigation. The United Nations Environment Program (UNEP) is mainly involved in sustaining an international low carbon planet through climate change mitigation approaches. Techs such as geothermal power, hydrogen fuel cells, tidal energy, solar and wind power have been used to reduce greenhouse gas pollution (Edenhofer et al. 2012). Microorganisms such as methanotrophs already have propensity at using methane as a carbon and energy sources and moreover help to restrict the volume of GHG inside the system. There seems to be myriad studies that demonstrate microbiome can play a critical role in controlling global climate change (Singh et al. 2010). Earth's microbial ecological communities too are sensitive to man made climate change in two ways. First by manipulating the morphology of prevailing microbial species and then reshaping the makeup of microbial communities. Modifying the microbial communities provides a powerful effective method for mitigating global climate change.

3.6 Volatile Organic Carbon Mitigation and Methylotrophs

The chemical composition of the environment is changed directly by the volatile organic carbons (Cappellin et al. 2017). The intermediates of global carbon cycling such as methane and methanol are plentifully present in the earth. The bidirectional exchange of volatile organic compounds between red oaks and atmosphere was reported as per the recent research, that also emphasized the role and effectiveness of microbiota in curbing volatile components. The exchange was such that methanol in addition to the deposition in fumigation experiment, methanol was also deposited in trees and in soil (Wohlfahrt et al. 2012) Mainly, methanol generation can be linked to plant decay associated with degradation of lignin and pectin. Few facultative methanotrophs have been determined in earlier investigations to use organic compounds such as ethanol and acetate, although most of them are effective utilizing sole and various carbon compounds (Kolb 2009; Dunfield et al. 2010). Gout (2000) suggested that methanol is taken up by leaf stomata through leaf pores followed by transforming it into formaldehyde. Even though methylotrophic bacteria glossily appear on the surface of leaf, they are susceptible of using methanol by means of metabolic pathways (Subhaswaraj et al. 2017; Meena et al. 2012; Holland and Polacco 1994) or by chemical modification reactions (Elliot and McCracken 1989), while further lowering the volatile compound to certain magnitude.

3.7 Carbon Cycling and Climate Change

The global carbon perturbations are actually stated by the global carbon cycling of the natural ecosystems. Carbon is amongst the most complex elements on earth, a functional life support, and hence plays a fascinating role in weather, its reliability and human energy wealth.

The microbial transformation of damaged cells and organic matter lead to the elimination of CO_2 into the atmosphere as a consequence of their respiration and finally CO_2 is used by plants for photosynthesis. Methylotrophs are the pivotal class of bacteria which utilize greenhouse gases. Furthermore, the influence of global warming is greatly reduced (Kumar et al. 2016). As well as the various autotrophs such as vegetation and photosynthetic bacteria, methanogens utilize CO_2 for their energy demand. Heterotrophs additionally utilize organic compounds and transform them into CO_2 for their development. Several chemical transformations such as carbon dioxide fixation, methanotrophy, methanogenesis, fermentation, and anaerobic respiration maintain the stability of carbon cycling. A squad of bacteria named methylotrophs oxidize the single most significant and active greenhouse gas, i.e. methane and its equivalents (Meena et al. 2012; Kumar et al. 2015; Kumar et al. 2016; Holland and Pollacco 1994). There is the process of methylotrophic bacteria degradation and decomposition which sustains carbon cycling in the environment. Biological degradation of organic molecules results in CO_2 generation in the atmosphere (Allison et al. 2010). In conjunction, prokaryotes which include Actinomycetes, Fermicutes, Arthrobacters and Pseudomonads also have a huge role to play in perilous carbon biodegradation and its equivalents. The distinct soil microbiomes are climate change variables that enhance our insight of how articulately they adapt to climatic changes (UCAR 2011). Numerous human activities, such as habitat destruction, development of mills, automotive combustion of carbon fuels, air and water pollution, affect climate change (UCAR 2011). The above entanglements have precipitated changes in the concentration of carbon and nitrogen throughout the world. The rapid expansion of greenhouse gases as well as other atmospheric changes simultaneously affects the environment. Humanity has a considerable part to play in improving the architecture of the environment and the energy cycle which has been influenced by microbial communities for so many years (Udakis 2013).

3.8 Methylotrophs Mitigating Methane

Methane is next just to carbon dioxide, amongst the most important greenhouse gases as far as their role in climate change is concerned. Frequent discharge of methane from various sources may pose a potential temperature threat in near future. Therefore, a well-developed mechanism should be put in place to reduce the methane emissions. A wider array of mitigation strategies have also been introduced that address different human sources, which need to be customized for subsequent use. The use of methylotrophs and a thorough explanation of soil methanotrophy may be a very valuable method for resolving the natural release of methane from closed landfills and a major reduction in waste-related GHG pollution from methanotrophic processes (Hettiaratchi and del Castillo Sternenfels 2013). Methanotrophs have an incredible ability to flourish and adapt and change aerobically on CH_4 as a common source of carbon and energy, and these microorganisms play a central role in the conversion of CH_4 into organic compounds available as CO_2 to autotrophs (Large 1983). In addition, methane oxidation occurring under environmental conditions in the presence of hydroxyl radicals is the key component disintegration that occurs from a variety of photochemical reactions. A successful research was performed on methane biodegradation and consequential agglomeration of poly-β-hydroxybutyrate (PHB) using only a methanotrophic conglomerate and an independent strain, culminating in significant methane remediation outcomes. Lately, the straightforward spectrophotometric test for methane screening using microbial strains has been investigated, reviewed thoroughly with the different methods available; i.e. the methylotrophs that reduce methane, traditional gas liquid chromatographic methods, monitoring of specific enzymes, and molecular characterization/detection of MMO and mxaF encoding genes (methane monooxygenase and methanol dehydrogenase). Jhala et al. (2015) however successfully engendered the strains of bacteria, deteriorating methane by boosting soil with methane as the principal energy source and water as the basal medium. In conjunction, colorimetric assay plates established their presence in evacuated tubes containing methane and the nature of soluble methane enzyme monooxygenase (sMMO). The potential of the isolates to breakdown methane was subsequently developed by the identification of enzyme gene encoding (methane monooxygenase and ethanol dehydrogenase) along with the detailed evaluation of the isolate enzyme function (Jhala et al. 2015). A research on slurry content captured from the Herman Pit (once a mercury mine) demonstrated the key role of methanotrophic bacteria in extracting methane from the sediments under anaerobic environment. The methanogenic operation was also conducted in artificial acid environments that demonstrated the presence of acidophilic or acid-tolerant methanotrophs. Furthermore, the acid-resistant methanotrophs were conclusively proven using incubated slurries to achieve optimum operation at pH 4.5. In conjunction, certain methanotrophs were subjected to sterol and hopanoid lipid extraction (methanotrophic characteristic), and their prevalence was exacerbated with expanded use of methane sediments. A sequence enriched for pmo A gene that associated with methanotrophic members of the Gammaproteobacteria has also been seen by the genomic DNA engendered by certain supplementation cultures that oxidize the methane gas. An enrichment culture was formed under acidic conditions (pH 4.5), by methane oxidation (Baesman et al. 2015). Strengthening the amount of CO_2 in the atmosphere is yet another concern for the global scientific establishment, and consideration is now being given to tracking the role of methylotrophs in carbon dioxide prevention and management. Carbon emissions from most biomass or biomass-based waste depletion are usually not included in the national or international greenhouse gas list, as biomass linked with waste is anticipated to be produced on sustainable basis and no net carbon dioxide emissions are forecasted, as it is assumed that carbon dioxide emitted from the decay of food waste can be absorbed by next year's crop.

3.9 Methylotrophs Mitigating Methane in Paddy Fields

The disproportional balance of methane has led to the wide range of changes in the properties of climate at the physical and chemical levels. The wide fields of rice epitomizes the same as an acme of methane source. (Dubey 2005). The methane as such in the vast rice fields is biodegraded and reduced, with methanotrophic bacteria playing a major role of catalysing the same..The ample presence of water in the paddy fields activates the methanogens thereby generating methane gas and thereby leads to trapping of methane gas by methanotrophic bacteria and subsequently the methane gets converted to methanol and biomass. Methane monooxygenase (MMO) enzyme and oxygen as a triggering agent are preconditions for any methanotrophic action. This enzyme mechanism triggers to destroy the methane methanotrophs. This aerobic condition is exacerbated by the green algae prevalent over the water-filled rice paddies surface (Singh and Dubey 2012). The methylotrophic isolates with functioning enzyme systems were obtained from Gujarat wetland paddy fields, and through biochemical and molecular characterization they transformed out to be separate species of *Bacillus* and *Penibacillus*. The active enzyme mechanism indicates the existence of the genes of particulate methane monooxygenase (pmoA), encoding the gene cluster α subunits. The involvement of the gene pmoA clearly indicates the use of methane by microbiota such as *P. illinoisensis, B. Aerius, B. Subtilis* and *Rhizobium sp.,* whereas in *Methylobacterium extrorquens* the existence of mmoX gene encrypts (α subunit of the hydroxylase component). Where as in another analysis, methane effectively exploits communities such as *P. illinoisensis* and *Rhizobium sp*. Prevalence of the mxaF coding gene α subunit of methanol dehydrogenase enzyme was identified. Communities with a propensity to degrade methane were baptized from wetland rice fields which revealed the presence of methane depletion enzymes and genes within a recognized plant growth facilitating microbial community (Jhala et al. 2014). In the paddy fields there is a structured structure of certain unique methylotrophic groups with a latent propensity and capability to absorb greenhouse gas methane, culminating in aerobic conditions on the surface of the ground in paddy fields. This systemic structured film is linked to the algal colonies commonly seen in rice fields. Algal ecosystems play a key role in reducing global greenhouse gas emissions by influencing methane gas oxidation activity. In yet another trial, in the isolation of rice plants, a small quantity of algae minimized the methane emission (Wang et al. 1995). The algae on the exterior of waterlogged paddy fields also engendered the methanotrophs and halted the generation of methanogen. Peng et al. (1995) showing that, in the availability of rice, CH_4 emissions are mainly from aerenchyma. Studies thus reveal and illustrate the relationship and role of methylotrophs in the removal of greenhouse gases in the atmosphere.

3.10 Conclusions

Methylotrophic bacteria use and disrupt condensed carbon compounds such as methane, which have an unprecedented function in combating climate change. This community of bacteria is exceptional in mitigating emissions of greenhouse gases. The rice field, where enzymatic operations are facilitated by various species such as algae and methanogens, is the most suitable habitat for methanotrophs. Rice production makes a significant contribution up to 15% of global methane emissions. Methylotrophs, furthermore which degrade many methane equivalents in the atmosphere, also assist in reducing CO_2. Such conditioned response of methylotrophs thus facilitates the climate latently. Varying bacterial species with methylotrophic properties as observed in soil, water and plant habitats contribute immensely to reduction of greenhouse gases. Therefore fundamental science cannot neglect the significance and role of methylotrophs in combating climate change. Together with recent perspectives, the role of methylotrophic ecosystems in addressing climate change has led us to investigate their function in global carbon cycling and minimize the impact of greenhouse gases such as methane and implicitly carbon dioxide on the landscape.

We attempted to explain the methylotrophic community‘s position in the rice environment as well as climate change. Also stressed was their role in sequestration of carbon or release of climate-active metabolites as a result of climate change. Methylotrophs represent a practical microbe community that uses decreased carbon substrates that don’t even contain carbon–carbon bonds. Methylotrophic bacteria include methanotrophs (which digest methane) and methylotrophs besides the methanotrophs (which eat non-methane-reduced carbon substrates). This comprehensive functional group can use different compounds like formaldehyde methanol, methylamine, dimethylamine, as well as methane. In addition to methane, this systematically integrated group will use different compounds such as formaldehyde methanol, methylamine, dimethylamine as the sole source of carbon and energy and is a persistent stakeholder in the global carbon cycle. Methanotrophs also oxidize greater than 90% of the methane contained in the soil prior to evaporating into the atmosphere (Oremland and Culbertson 1992). Methanotrophic biological oxidation of methane contributes for just approximately 5% of the global dump of atmospheric Methane (Hanson and Hanson 1996).

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