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# The Use of Microbial Community to Produce the Green House

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**ABSTRACT:** Climate warming is predicted to increase heterotrophic metabolism in northern peatland soils leading to enhanced greenhouse gas emissions. However, the specific relationships between temperature and the greenhouse gas producing microbial communities are poorly understood. Thus, in this study, the temperature dependence of carbon dioxide (CO<sub>2</sub>) and methane (CH<sub>4</sub>) production rates along with abundance and composition of microbial communities were investigated in peat from a Sphagnum-dominated peatland, S1 bog (Minnesota, United States). Whereas CH<sub>4</sub> production rates increased with temperature up to 30°C, CO<sub>2</sub> production did not, resulting in a lower CO<sub>2</sub>:CH<sub>4</sub> ratio with increasing temperature. CO<sub>2</sub> production showed both psychrophilic and mesophilic maxima at 4 and 20°C, respectively, and appears to be mediated by two anaerobic microbial communities, one that operates under psychrophilic conditions that predominate for much of the year, and another that is more active under warmer conditions during the growing season. In incubations at 10°C above the ambient range, members of the Clostridiaceae and hydrogenotrophic methanogens of the Methanobacteriaceae dominated. Moreover, a significant negative correlation between temperature and microbial diversity was observed. Results indicate that the potential consequences of warming surface peat in northern peatlands include a large stimulation in CH<sub>4</sub> production and a significant loss of microbial diversity.

**KEYWORDS-** green house, microbes, climate, warming, diversity

## I.INTRODUCTION

Covering approximately 3% of the land surface while storing up to one-third of global soil carbon, boreal peatlands are effective carbon sinks. At the same time, boreal peatlands represent one of the main natural sources of the greenhouse gas methane (CH<sub>4</sub>) (Gorham, 1991; Tarnocai et al., 2009; Dlugokencky et al., 2011). Climate models predict an increasing contribution of these ecosystems to climate change due to an estimated 6–10°C temperature elevation by the end of the 21st century that will likely stimulate microbial activities, CO<sub>2</sub> and CH<sub>4</sub> production (Collins et al., 2014; Wu and Roulet, 2014; Schuur et al., 2015; Schadel et al., 2016). However, most existing climate models lack detailed input parameters specifically defining the temperature effect on microbial community composition and activity.

Boreal peatland soils are saturated with water and anoxic conditions prevail belowground (Limpens et al., 2008). Anaerobic decomposition of organic matter in peat is mediated by a complex web of metabolic interactions between many microbial groups (Drake et al., 2009). Plant-derived organic matter (cellulose, hemicellulose, pectin) is first hydrolyzed into sugars, fermented to organic acids (acetate, propionate, butyrate, etc.) or alcohols, and then terminally metabolized to CO<sub>2</sub> and CH<sub>4</sub>. Since the majority of peatlands harbor low concentrations of inorganic electron acceptors such as nitrate manganese (Mn [IV]), ferric iron (Fe [III]), or sulfate methanogenesis is considered to be the predominant terminal electron accepting process in peatland soils (Conrad, 2009; Bridgman et al., 2013). [1,2,3]Methanogenesis is an anaerobic process carried out by archaea, mainly those taxonomically affiliated with the Euryarchaeota group; however, methane production has been observed in aerobic soils (Angle et al., 2017). In addition, some saprotrophic fungi, taxonomically affiliated with the Basidiomycetes, and bacteria affiliated with Cyanobacteria are able to produce CH<sub>4</sub> under oxic conditions (Lenhart et al., 2012; Bizić-Ionescu et al., 2018). These recent findings challenge the dogma that methanogenesis is exclusive to strictly anaerobic Archaea. Under anoxic conditions, methanogenic archaea produce CH<sub>4</sub> through three major pathways (1) from CO<sub>2</sub> and H<sub>2</sub> (hydrogenotrophic pathway), (2) acetate disproportionation (acetoclastic pathway), and (3) cleavage of methylated compounds (Whitman et al., 2006; Thauer et al., 2008; Borrel et al., 2013, 2016; Offre et al., 2013). Peat temperature, water table depth, and microbial community composition are among the major factors that control methanogenesis (Dunfield et al., 1993; Schulz and Conrad, 1996; Metje and Frenzel, 2005, 2007; Tveit et al., 2015; Peltoniemi et al., 2016; Wilson et al.,



2016; Zalman et al., 2018). While peat temperature and the availability of thermodynamically preferable terminal electron acceptors have a direct effect on methanogenesis, the microbial community response to temperature may have broader ecosystem consequences. Nevertheless, the response of peat microbial communities to rising temperatures is poorly understood.

The consensus of previous work is that climate warming is likely to result in an acceleration of organic matter decomposition, and stimulation of CO<sub>2</sub> and CH<sub>4</sub> emissions in peatlands (Davidson and Janssens, 2006; Weedon et al., 2013). Since CH<sub>4</sub> has a sustained global warming potential of 34-times that of CO<sub>2</sub> over a 100-year time frame, enhanced CH<sub>4</sub> emission is likely to result in a positive feedback to climate warming (Myhre et al., 2014; Neubauer and Magonigal, 2015). Thus, understanding the temperature dependence of microbially-mediated organic matter turnover and CH<sub>4</sub> production is critical for predicting ecosystem responses to climate change drivers (McGuire and Treseder, 2010; Wallenstein and Hall, 2012; Schimel, 2013; Wieder et al., 2013; Ma et al., 2017). [4,5,6]

## II.DISCUSSION

Greenhouse gas (GHG) emission from agriculture contributes significantly to the global climate change. The major greenhouse gases emitted from agriculture are methane (CH<sub>4</sub>) and nitrous oxide (N<sub>2</sub>O). These two greenhouse gases have higher global warming potential than carbon dioxide (CO<sub>2</sub>). The manuscript embodies biogeochemical cycling of CH<sub>4</sub> and N<sub>2</sub>O. Microbial pathways of methanogenesis, CH<sub>4</sub> oxidation, nitrification, and denitrification are outlined. Information on the agricultural strategies to mitigate GHG emission from soils are discussed. The review highlights significance of low-affinity methanotrophs that can be activated by repeated enrichment of high CH<sub>4</sub> concentration, as global climate regulators. Iron redox cycling is also linked with soil CH<sub>4</sub> uptake as repeated Fe<sup>3+</sup> reduction and Fe<sup>2+</sup> oxidation decline crystalline Fe fraction that enhances CH<sub>4</sub> consumption by stimulating *pmoA* gene of methanotrophs. Studies suggested alternate flooding and drying as a potential approach to mediate atmospheric CH<sub>4</sub> uptake in flooded soil. N<sub>2</sub>O emission from soil is the outcome of both nitrification and denitrification. However, in upland soil N<sub>2</sub>O emission occurs through nitrification and through denitrification from flooded soil ecosystem. Nitrogen-fixing *Rhizobium* sp. also produces N<sub>2</sub>O, and these bacteria can be manipulated to mitigate N<sub>2</sub>O emission by activating N<sub>2</sub>O reductase (*nosZ* gene). It is concluded that apart from regular agricultural resource management strategies, there is need of genetically manipulated soil microorganisms to effectively mitigate climate change.

Climate change impacts many aspects of our lives and almost every environment on earth. Industrial activity is widely accepted to be the main driving force behind this. The presence of microbes and their role in the climate is of paramount concern to scientists working in the field of climate science. Knowledge of this “unseen majority” is vitally important to fully understand their function and how they can be used in technological applications that combat climate change itself. [7,8,9]

## III.RESULTS

Micro-organisms are involved in many environmental processes including the nitrogen and carbon cycle. They are abundant in nearly all environments including the air, soil, the abyssal depths of the ocean, deep underneath the Earth’s surface, and in environments that range widely in temperature, pressure, and chemical composition. It is estimated that there is something in the region of  $\sim 10^{30}$  total bacteria and archaea on Earth.

Microbes play an important role in the production and consumption of powerful greenhouse gases including CO<sub>2</sub> and methane, have negative and positive feedback responses to temperature changes, and play a vital function in the regulation of ocean acidity. All of these can suffer perturbations due to anthropogenic climate change. They also have important functions in agriculture and the food web.

Loss of habitat and the biodiversity of animal and plant species and communities is relatively well-publicized. However, the role of microbial communities is still poorly understood as they live in diverse communities that interact with the environment and other organisms in a complex way. Therefore, including microbial activity in climate models is gaining prominence in the field of climate science.



Microbial communities support all higher lifeforms and any significant perturbation to them (for example, rising levels of ocean acidity and the sensitivity of marine microbes to these changes) has a knock-on effect on the existence of all life. Undoubtedly, as we come to understand more about how micro-organisms respond to environmental disturbances, data gathered by studies will help us to elucidate the overall impact of climate change itself.

#### Using Micro-organisms to Limit the Impact of Climate Change

Climate science is not just about studying the impact of climate change itself, though that does contribute a large part of the field, it also is about developing technological solutions that can ease the burden of human activity on fragile ecosystems. [10,11,12]

#### Using Microbes to Absorb CO<sub>2</sub>

The best way to combat climate change remains the mitigation and reduction of greenhouse gases. The main greenhouse gas that most people know about is carbon dioxide and for years scientists have been researching ways to mitigate the levels of this gas in the atmosphere.

A team at the Weizmann Institute of Science in Rehovot, Israel, has used a combination of lab evolution and genetic engineering to create a strain of E. Coli which uses CO<sub>2</sub> as its sole source of carbon.

It is hoped that systems can be developed to use this modified form of E. Coli to consume atmospheric CO<sub>2</sub> and either store it or produce biofuel and foodstuffs. However, the team is still working on increasing the efficiency of the bacteria in consuming atmospheric CO<sub>2</sub>.

#### Reducing Nitrous Oxide Emissions

Another critical greenhouse gas is nitrous oxide. It is the third most important GHG and is also a major ozone-depleting substance. One of the major routes of production of this harmful gas, which is also a major pollutant responsible for numerous deaths worldwide, is car exhausts. Another significant contributor is the agrochemical industry.

Recently, several mitigation techniques based upon microbiological methods have been the subject of research. These include the manipulation of microbiomes in diverse environments and integrating microbiome-based knowledge of nitrous oxide sources and sinks. There has also been research into using bacteria-based systems for directly removing nitrous oxide from car exhausts and power stations.

Soil microbes play an important part in regulating greenhouse gas emissions, as well as productivity and sustainability of agricultural systems, and degradation of soil and water. All this has a real impact on climate change. Climate-smart agriculture (CSA) is an integrative approach to agriculture that aims to limit the impact of the agricultural industry upon the long-term viability of the climate.

Understanding the specifics of how these soil microbiomes respond to agricultural practices and climatic pressures such as temperature and extreme weather events is an integral part of this discipline. Increased knowledge of microbial ecology and the interactions between plants and microbes in soil is essential for the use of microbial biotechnology for climate change adaptation and mitigation.[13,14,15]

#### Living Concrete

The construction industry has a huge impact on climate change. According to some studies, the contribution of construction projects contributes to 40% of total energy use globally. One innovative use of micro-organisms to combat this issue is the use of “living concrete” which utilizes photosynthetic cyanobacteria called *Synechococcus* sp. PCC. Held in a biosynthetic gel. Another benefit of this technology is that it can be used to absorb CO<sub>2</sub> from the atmosphere.[16,17,18]

#### IV.CONCLUSION

Climate change is, without a doubt, the most pressing concern for humanity. It affects the long-term viability of not only our civilization but for all life on Earth.[19]

To maintain a healthy global ecosystem, microbes are vitally important. Understanding the complex interactions of microbial biomes with higher organisms (especially plants) and how these communities of microbes can be affected by climate change is therefore critical. Microbial-based applications for climate-mitigation technology are also an increasingly important area of research.[20]

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