OPINION

Importance of monitoring soil microbial community responses to climate change in the Indian Himalayan region

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Increasing emission rate of carbon dioxide (CO_2) and other greenhouse gases is the major driver of global temperature increase. Soil microbial respiration is accelerating the release of CO_2 in the environment, but the mechanistic understanding of this process is still at its nascent stage. In this note, we discuss the importance of understanding the microbial responses to climate change and associated respiration process in the Indian Himalayan region. We also discuss the goals of microflora component of the ongoing National Mission for Sustaining the Himalayan Ecosystem project in tracking climate change impacts in this fragile, mountainous ecosystem.

Global climate change is currently a major challenge for modern science and society. Increasing emission rate of carbon dioxide (CO_2) from both natural and anthropogenic sources, along with other greenhouse gases is playing a major role in global warming. CO_2 emission from soil respiration (both autotrophic root respiration and heterotrophic microbial respiration) is known to be the second largest natural terrestrial flux of carbon[1]. Conversely, rising temperature leads to depletion of soil organic carbon (SOC) stocks through enhanced microbial decomposition and rapid release of CO_2, providing a positive feedback to climate change[2]. Although recent climate-carbon models support such positive feedback responses, the detailed process is still unknown due to our limited understanding of temperature sensitivity of microbial SOC decomposition[3]. Despite soil microbial decomposition of SOC results in emitting up to 25% natural CO_2 each year[4], the process of microbial community respiration with regard to climate change under varying soil environment has not been studied globally.

Soil microbial communities mediate global biogeochemical cycles (carbon, nitrogen), and any climate-driven physiological changes can affect the rates of these cyclic processes[5]. To understand patterns of temperature-induced microbial respiration at the level of ecosystems, there is a need for paradigm shift from earlier climate models which focused mainly on soil carbon pool size[6]. Particular emphasis is needed on understanding soil microbial community diversity, composition and functions for mechanistic insight into their feedback responses to climate warming[5]. A number of studies suggest that soil microorganisms either undergo functional modifications of their existing populations, or changes in their community composition in response to environmental changes, leading to altered temperature sensitivity of SOC decomposition[5,7]. Functional modifications might happen in the short-term temperature rise scenario, resulting in an increasing soil microbial respiration from faster microbial growth and physiological processes[5,7]. However, in the long-term climate change scenario, the increase or decrease in microbial respiration rate will depend on the environmental conditions and resource availability (substrate) for the existing microbial community[5,7]. Similarly, shift in microbial community composition can also be driven by environmental changes and consequently may affect soil respiration rates[5,7]. If the changed community has higher carbon efficiency (i.e. it stores more carbon than it metabolizes), then SOC decomposition will decrease along with microbial respiration rate[5]. However, in the event of community shifts towards greater diversity with microbes capable of degrading complex soil carbon, SOC decomposition will increase favouring CO_2 emission from soil and provide positive feedback to climate change[7]. Therefore, identifying different functional groups of microbes is essential in understanding the feedback responses, as they have varying capacities to decompose SOC[8]. Since such feedback responses will vary across ecosystems and regions, a clear understanding on which of these mechanisms is prevalent and how microbial diversity will affect the responses is critical in quantifying them. Although a number of studies have focused on addressing these issues in different parts of the world[9,10], data from the Indian subcontinent are completely lacking.

The Himalayan region comprising diverse and fragile ecosystems offers an excellent opportunity to study the response of changing climate on soil microbial environment, and is considered most vulnerable to increasing temperature. Harbouring a gradient of environments and ecosystems from extremely low carbon stock such as morainic soils to carbon-rich peatlands, this region plays a significant role in global carbon cycle[11]. A perusal of the literature on the Indian Himalayan region (IHR) reveals that it retains about 33% of the country's SOC[12] that changes along elevation gradient[13]. However, very few attempts have been made to quantify the rates of microbial respiration and short-term impacts of temperature and precipitation variations on SOC storage across different forest types[14]. There is a need to establish baselines on these parameters and initiate long-term monitoring. To address the information gap and also understand the impacts of climate change on the Himalayan ecosystems, the Department of Science and Technology, Government of India has initiated a dedicated National Mission for Sustaining the Himalayan Ecosystem (NMSHE) in the IHR in 2015. As part of this mission, studies on soil microflora and fauna have been initiated along an elevational gradient in the Gangotri National Park and adjoining regions to generate baseline data on soil microbial community diversity and their SOC degrading potential. With specific focus on soil bacteria, fungi, lichens and nematodes along with soil physico-chemical properties and SOC degrading enzyme activities, this component will provide valuable insights into the microbial control of soil CO_2 emission and a rapid method to track climate change impacts at ecosystem level.

Baseline data generated on soil properties, microbial biodiversity, activity and respiration in the IHR will assist in understanding the mechanisms and controlling factors of SOC decomposition in the region. Through modeling of these soil microbial community data along with other climate factors, the results will help us in developing long-term strategies to monitor climate change impacts and propose policy briefs/management strategies to manage microbial systems for mitigation of climate change.

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Declaring the commercial source and grade of chemicals, and equipment, in a scientific paper

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Scientific biomedical papers widely use chemicals, reagents and/or equipment. These are described in the materials and methods section. The source of these methodological props needs to be precisely defined for scientific and proprietary reasons. The commercial source or grade of a chemical can affect the quality and outcome of an analysis, e.g. in plant tissue culture. Failure to recognize the commercial source deprives a company of its due proprietary investment in a product, reduces reproducibility and thus constitutes an incomplete or erroneous methodology. Such errors should be corrected, which should be the responsibility of authors, editors and publishers.

A methodological prop or tool (MPT) is defined here as any chemical, utensil, or equipment (CUE) that serves to support a methodology within a scientific manuscript. Not only do MPTs serve as important and fundamental tools for completing a method, their commercial source can, in select cases, also influence the outcome of a scientific manuscript. This note aims, using plant tissue culture, to (a) highlight the importance of specifying the commercial source and grade of CUEs; (b) show through select and concrete examples, how specific CUEs from different sources, or of different quality, can lead to qualitative and quantitative differences in the outcome of an experiment; (c) encourage authors, editors and publishers to correct the literature, to correct the weaknesses of traditional peer review[1], through post-publication peer review (PPPR), in a bid to make the methodological sections as accurate and precise as possible. In doing so, reproducibility of weak, unclear or unstated methodological flaws might increase. However, efforts to increase reproducibility will be in vain, unless all parties are involved[2].

Using select examples of plant tissue culture, a branch of plant biotechnology, we demonstrate how differences in the choice of MPTs and CUEs can influence the outcome of an experiment. Thus, defining these elements is a central aspect of reproducibility of a protocol. This concept is fortified by a respectable leading Society in the plant science community – The American Society for Horticultural Science[3], which states that 'In general, refer to trade or brand names only parenthetically with the active ingredient, chemical formula, purity, and diluent or solvent stated clearly in the text and emphasized in preference to the commercial product; also, include the name, city, and state/country of the company that produces the product.'

The effect of chemicals, vessels, or medium components on analytical and developmental outcome in plant tissue culture

Plant cells and tissues can grow and develop *in vitro* on different media containing inorganic and organic nutrients and plant growth regulators that are added, creating an artificial growth environment, and either benefiting or negatively affecting growth. However, such nutrients may also contain impurities in the