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Effect of Climatic Change on Soil Microbial Community

Debasmita Das¹ and Kumar Chiranjeeb^{2*}

¹Assistant Professor, Department of Agronomy, GIET University, Gunupur, Rayagada, Odisha-765022

^{2*}Ph.D. Scholar, Department of Soil Science, CSK HPKV, Palampur, HP-176062

*Corresponding Author E-mail: kumar.chiranjeeb3@gmail.com

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ABSTRACT

Climate change is the most severe problem that adversely affects crop productivity and negatively impacts soil microbial biodiversity, which is considered the key component of soil fertility indicators. Microbial biodiversity regulates all necessary functions to strengthen and maintain the stability of the ecosystem. Climate change primarily affects the crop microclimate, which in turn destroys the ecological balance and disrupts the ideal growth conditions for the crops and hampers the proliferation of microorganisms in the environment, thus decreasing crop production over a particular region. Climate change conditions such as higher temperature, rainfall and other abrupt conditions destroy the equilibrium between microbes, plants and the environment to a large extent, altering the plant-microbe interactions. Higher Carbon dioxide concentration favours the crop in photosynthesis and helps achieve higher productivity. Microbial respiration also enhances the carbon dioxide concentration in the atmosphere, leading to global warming and other potentially hazardous conditions. Mitigation strategies on crop, soil and land management measures are important to counteract the negative impact of climate change.

Keywords: Climate, Microbes, Mitigation, Temperature, Carbon dioxide.

INTRODUCTION

The global climate is prognosticated to change drastically over the coming century, and colourful parameters will be affected in this changing terrain (Houghton et al., 2001). This is the case for atmospheric CO₂ attention that increases continuously (IPCC Climate Change, 2007). Also, global face temperatures are prognosticated to increase between 1.8 and 3.6°C by the time 2100, driven by increased

atmospheric CO₂ situations deduced from natural and anthropogenic sources (IPCC Climate Change, 2007). In recent decades, climate-changing situations on the earth have been influencing the functionality of soil micro biomes present. The global change pressures like elevated temperatures, rush, and CO₂ emigrations are affecting the soil dynamics and, accordingly the soil – microbe relations (Vanisree et al., 2022).

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The microbial community present in the soil is an important natural element of soil function. It is valued for perfecting soil quality and regulating nutrient vacuity, thereby impacting factory product for husbandry and other purposes (Kennedy & Smith, 1995; Papendick & Parr, 1992). Soil microorganisms could important part in potentially play an contributing to the development of ecosystem resistance to abiotic stresses, similar to increased temperature and rush, and adding resiliency in agrarian systems (Pankhurst et al., 1996). Soil microbial community and its functions are sensitive to changes in both temperature and water vacuity (Hartel, 2005). The mechanisms controlling temperature acclimation situation of microbes present in soil could be acclimations in terms of physiological in case of single species (Malcolm et al., 2008) or species shifts within the microbial community. They can also affect between the commerce shops and aboveground macrofauna. For illustration, the presence of nematodes and microorganism inoculants has been proven to reduce aphid populations, significant beasties and vectors of complaint (Bezemer et al., 2005). Singh et al. (2011) reviewed the part of microbes in the development of sustainable husbandry and showed that factory growth promoting rhizobacteria (PGPR) and cyanobacteria frequently affect increased crop product and ecosystem health. Soil organisms also provide a broad range of services essential to the sustainability function of all the ecosystems by becoming the primary driving agents for nutrients cycling, controlling the dynamics of variability in organic matter, soil carbon insulation and hothouse gas emigration, modifying soil physical parcels and water administrations, enhancing the quantum and effectiveness of nutrient accession by the foliage and enhancing factory health. Grampositive and Gram-negative bacteria showed variable patterns in terms of substrate Gram-positive preference. bacteria dominant in soils with low substrate material

vacuity and found more in deeper soil layers (Fierer et al., 2003), while Gram-negative bacteria were set up to dominate in soils with high vacuity of the fluently decomposable substrate(Kramer & Gleixner, 2006). Archaea were set up abundantly in numerous soils and are important in methane (CH4) and nitrogen (N) dynamics (Leininger et al., 2006). Soil microbes are anticipated to be impacted by colorful global climate change angles, similar increased atmospheric CO2, temperature and rush patterns, and increased frequency of extreme climate events (IPCC, 2007). Soil is also a suitable habitat for many microorganisms like bacteria, fungi, actinomycetes, protists and numerous other organisms that may be salutary, neutral or pathogenic. It's a well-honoured fact that these microbiomes are crucial pointers of factory health and play an important part in productivity and growth (Berg et al., 2016). The microbiome is a contributor of multiple aspects of the factory system. They regulate factory health through their antagonist and synergistic geste in association with the shops. They impact factory system through metabolic cooperation, converting signalling responses and microbial symbiosis. Studies made regarding the miracle by which shops acquire pathogenic defence medium against microorganisms and get advantaged from salutary bones have gained important attention in recent many times. numerous experimenters explored introductory principles of commerce with factory and microbiota, signalling process of factory defense and symbiotic responses toward microbes (Jones et al., 2016), a inheritable system of microbes that transport signalling patch to regulate functions of host cells (Hwang et al., 2017) and specific double and community position conflict in factory and microbial relations (Hacquard et al., 2017).

Temperature effect on interaction of cropmicrobes

Weather parameter "Temperature" is the factor that's decisive in the growth of factory, phenology, distribution and circumstance of microbes population (Angilletta, 2009; & Kashyap et al., 2017). The cause of rise in average global temperature is due to an increase in mortal interventions and the emigration of GHGs like CO₂, water vapour and methane. The mean temperature is expected to increase by $1.8 - 3.6 \circ C$ by the year 2100, which might lead to insufficient water and failure in numerous corridor of the world (Compant et al., 2010). This increased average temperature influences the exertion and morphology of shops. Many research has been done showing the demonstration of effect of elevated temperature on different species of crops (Chen et al., 2021). This elevated temperature imparts an implicit request effect on factory-associated microbial communities' composition, conditioning and circumstance. This may also affect in quicker growth of microbes with altered respiration. Also, elevated temperature and failure conditions factorysignificantly affect microbe association, exertion and cornucopia. The respiration rates of microbes in the rhizosphere are directly influenced by elevated temperature and Global (Classen et al., 2015). It has been proved that with the increase in temperature, soil respiration also increases exponentially (Karhu et al., 2014). The organic matter application by soil microorganisms depends on temperature (Frey et al., 2013). Vela squez et al. (2018) reported that changes in climatic conditions and microorganism pathogenicity could also be observed with temperature differences, the concentration of CO₂ and other environmental conditions. Newsham et al. (1995) reported that warming of soil and failure conditions causes an impact on factory nutrient uptake and exchange of carbohydrates in the rhizosphere by AFM. High temperature enhances acridity of bacteria Pecto bacterium atrosepticum causing soft spoilage and some other seed borne microbes causes declination of cell wallenzyme and increase complaint prevalence in shops (Hasegawa et al., 2005). High temperature leads to ocean warming that causes phonological shifts in ocean weeds

encyclopaedically (de Bettignies et al., 2018). Also, the activity of coralline algae gets affected by elevated temperature (Page et al., 2021). Research studies proved that extreme temperature has considerable goods on the growth and development of cyanobacteria (Deng et al., 2021). Elevated temperature in addition to heat swells, enhances the exertion of microbes for mineralization of microbial necromass, Carbon and Nitrogen recycling and thus, amplifies warming goods in mountainous soil (Donhauser et al., 2020). The increased microbial necromass N and development of microbes with weather parameters temperature, relative humidity and UV radiation were studied by (Wang et al., 2020). Low humidity and failure conditions affect microbes present in the soil, root endosphere and rhizospheric conditions (Cheng et al., 2019). Due to failure conditions, there is a reduction in the population of bacteria present in the rhizosphere and root endosphere in the sludge root microbiome (Xu et al., 2018). Drought conditions drop AMF colonization. AMF could not populate factory under failure (Schellenbaum et al., 1998; & Staddon et al., 2004). Querejeta et al. (2009) revealed in studies that the colonization capability of ectomycorrhiza has decreased in oak under failure than AMF colonization under moisture stress conditions are more desirable for unborn climatic scripts. Effect of CO2 on Plant-Microbe Interaction The atmospheric CO₂ is veritably pivotal in maintaining allocation of carbon and root exudates composition in the soil environment, which imparts effect on the rhizospheric environment with salutary microbes (Berendsen et al., 2012) Microbes plays important role in net exchange of carbon through colourful ways, i.e., respiration, organic matter decomposition, pathogenic or symbiotic association with shops, and by changing the soil nutrient status (Williams et al., 2018). Elevated CO₂ situations not only changes factory physiology and metabolism but also stimulate direct and circular effect on the microbial community in rhizospheric and phyllosphere conditions. Due to elevated CO₂ conditions, reshaping of root exudates composition along with differences in nutrient vacuity occurs (Ostle; Company et al., 2010). More carbon assimilation effectiveness has been noticed in fungi as compared to bacteria and has a higher chance for carbon storage than rallying. Hence, the carbon emigration increases through roots that stimulate microbe growth in the soil, thereby minimizing soil nitrogen available for crop due to soil nitrogen immobilization. There is an increased soil respiration due to elevated CO₂ in the atmosphere (Korner & Arnone, 1992; & Hungate et al., 1997). The composition of CO₂ is more in soil than in the atmosphere. Soil Microbial populations (fungi, bacteria, actinomycetes) show different responses to elevated CO₂conditions. Gavito al. (2000) observed that in Pisum sativum cv. Solarasignificant effect of elevated CO₂, i.e., 700 ppm was found on the colonization of AMF where asin case of Barnyard lawn, rise in CO₂ (7 ppm) gave a significant rise in the colonization of mycorrhiza with relation to Nitrogen and Phosphorus uptake(Tang et al., 2009). Increased CO₂ conditions in atmosphere also influence the biodiversity of ectocommunity. Elevated mycorrhizal conditions resulted in a triple enhancement in biomass of ECM myceliain P. sylvestris (Fransson et al., 2005). Rather than AMF and ECM, PGPB growth and sustainability have also been observed to support factory growth. Other microbes that belong tothese rubrics include Azospirillum, Azotobacter, Bacillus, Erwinia, Proteus, Pseudomonas, Arthrobacter and Rhizobium etc. Bacterial diversified communities connected with the factory biome shows the outstanding impact on CO2 situations. According to Schortemeyer et al. (1996) studies demonstrated inFree- air CO₂ enrichment, shown thatthere is a massive increase in the microbial population of R. Leguminosarum by trifolli in rhizosphere of white clover under elevated CO₂ (600 ppm). Multitudinous experiments have been performed about the influence of CO2 in factory of bacteria in many species which were growth promoting in nature (Lipson et al., 2006; Haase et al., 2007; Lesaulnier et al., 2008; & Xu et al., 2013). An increase in CO₂ concentration in the generalized atmosphere also significantly affects the ocean's microbial population. The seaweeds in terms of their growth and survival in high CO2 terrain are remarkable as increased organic attention helps seaweeds for proper proliferation. Singh and Singh, (2014) research in algae exploration determines that with increased CO2 attention, there is also an increase in biomass and lipid of microalgae species. Thus, higher CO₂ concentration microbial communities, influence biological, and physiological systems and thereby play an important role in future conditions of climate. Haase et al. (2007) demonstrated that higher CO₂ levels change soil microbes activity associated with nutrient addition, Yáñez-López et al. (2012) noted that it affects responses of the pathogens towards the plants and help in carbon sequestration in soil. The role of rhizosphere microorganisms under increased CO₂ level is mostly needed to be evaluated for performing climate-resilient agriculture in addition with remarkable effort in exploring the long-term effect of soil microbe dimension to elevated CO₂ conditions and efficient sequestration conditions by the processes of plant-microbe interaction (Malmstrom & Field, 1997; & Grover et al., 2015).

Other Factors Influencing Plant-Microbe Interaction

The ever changing climatic situations cause a major impact on types of structures with associated functions as well as variable changes regarding plant- microbe association in the environment (Dastogeer et al., 2020). Elevated climatic conditions lead to increased levels of radiation to the plants, which also changes ozone concentrations in the atmosphere. Rise in UV-radiations destroys ozone concentration in the stratosphere of the

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atmosphere, thus changes the climate. These changes have negative effects on crops grown and on associated microbiome. Higher concentration of UV- radiations alters oxygen yield of cell, photosynthetic mechanisms along with proliferation of cyanobacteria (Zeeshanand Prasad, 2009). However, not much considerable effects of UV-B radiations are found on lichen organisms (Bjerke et al., 2005). Radiation-sensitive fungi show retarded growth as an indication of damaged cell condition and low proliferation rate by a higher concentration of infrared radiation. There is evidence of adverse effects on conidia germination rate, hyphal growth control and chemical production in response to UV radiation (Braga et al., 2015; & Thind & Schilder, 2018). Similarly, UV radiation level negatively affects growth factors and the survival rate of bacterial communities (Vanhaelewyn et al., 2020). The microbial communities residing in the phyllosphere are comparatively more prone to rising radiations of UV as compared to rhizospheric microbial communities and are associated to constant and major changes with alteration in the related climate. Alteration in the associated climatic conditions influenced the rise in the occurrence of stresses in the environment. Variability in climatic conditions control the functions of pathogens and other microorganisms, transferring helpful microbes from one niche to another in the ecosystem. Rainfall is a key controller of different plant associated microbes functions interactions. Adequate precipitation enhances the functionality of soil microbes thus rising microbes-based biomass carbon. The level of precipitation is positively correlated with below ground biomass carbon (Zhang & Xi, 2021). Drought stress is correlated with the other phenomena such as global warming and climatic instability. The development of mycelium in mycorrhizal association is severely affected by scarcity of moisture in rhizosphere zone (Singh et al., 2019). There are different drivers of plant microbial

connections aboveground and below-ground communities.

Mitigation Strategies

On larger context, the same practices that increase productivity and adaptability to climate change also give positive co-benefits with respect to agrarian mitigation of GHGs. There are three main mechanisms for mitigating GHGs in husbandry a) reducing emigrations, b) Increasing atmospheric carbon removal and c) avoiding emissions through the use of bioenergy or agrarian intensification rather than expansion (Smith et al., 2007). There is a positive correlation between soil organic carbon and crop yield; practices that increase soil fertility and crop productivity also alleviate GHGs emigrations, particularly in areas where soil declination is a major challenge (Lal, 2004). There is little research on the solidarity and trade-offs between agrarian adaption, mitigation and productivity impacts. FAO (2009) distinguishes between activities with higher level versus lower mitigation eventuality and those with higher level versus lower food security prospects.

- 1. Mulching: Mulching practice adopts covering of soil surface to protect the soil surface against erosion and to enhance fertility level. Mulch in general applied on the soil surface initially during the crop growing seasons. Mulch supply the necessary temperature and conserved moisture for crop germination and growth. Different materials can be used as mulching like organic residues (e.g. crop residue, hay, bark), manures, sewage sludge, compost and rubber or plastic films.
- 2. Application incorporation and of organic residues (compost/manure/sludge): Animal manure, compost from waste materials, sludge, cereals and legumes enhances the organic matter content of the field decomposition On incorporation of organic residues is important for agricultural purposes. This is

- because the addition of carbon-rich compounds temporarily immobilizes available N in the soil as the microbes accumulate carbon and nitrogen for their growth.
- 3. **Fertilizers:** High levels of some inorganic nitrogenous fertilizers provide microbes nutrients for their body growth and cell maintenance, thereby increasing their activity. The higher microbial activities in soil deplete the organic matter content in soil and thus lower soil fertility and degrade soil structure.

Crop management factors

Selection of the crop cultivars: The availability of habitat for soil fauna depends on the choice of different cultivated crops. For example, legume crop can may act as a source of nutrients, improving the N concentration in soil by establishing a symbiotic relationship with rhizobia. Application of nitrate fertilizers as calcium ammonium nitrate in crops with aerobic conditions and ammonium fertilizers as ammonium sulphate, urea, in wetland crops also helping to reduce the nitrous oxide (N₂O) emission (Pathak & Nedwell, 2001).

Rotation of Crop Cultivars: Rotation of crops may help to avoid the colonization up of various phytopathogens and associated pests, as the alteration of cultivars of different crops changes the related biological communities. Proper crop management practices that lead to enhanced nitrogen use efficiency, yield, and capture the factor to decrease nitrous oxide emission.

Management of Landscape Component Hedgerows and grassy field margins: Establishing hedgerows or grassy strips at the edge of arable fields offer a stable habitat, source of food and a secured environment for soil fauna as compared to the heavily managed fields. Hedgerows are even more favourable to soil micro organisms, in particular biological key regulators than grassy field margins. Low mobility of the soil organisms will be limited to their dispersal into the fields.

Associated Microbial Communities and Mitigation Options

Microbial communities management to decrease carbon dioxide emissions: Currently, soils contain about 2,000 Pg of organic carbons, which is twice the amount of carbon in the atmosphere and three times the quantity found in vegetation (IPCC 2007 & Smith, 2004). The potential of different land types (for example, woodland, pasture and arable land) to store carbon differs which provided the fact that land use can be managed to store a further 1 Pg of carbon per year in soils (Smith 2004 & Houghton, 2008), this potential has received considerable scientific attention (Lal 2008 & Busse, 2009).

Methane emissions reduction: emissions of methane are directly controlled by microorganisms than emissions of CO₂. In case of natural emissions (~250 million tonnes per year) are dominated by methanogenesis, a process that is carried out by a group of anaerobic archaea microbes in wetlands, oceans, rumens and termite guts. Human activities (mainly rice cultivation, landfill, fossil fuel extraction and livestock farming) contribute more methane emissions than natural release in the environment. Methanogenic bacteria species serve as a crucial influencer to release the huge amounts of methane produced in some of these environments. The class Gammaproteo bacteria consume a major part of the CH₄ produced in soils before it escapes to the atmosphere and in this class low affinity type methanotrophs are present, which get activated in the concentration of range >40 ppm.

CONCLUSION

The microbial communities and their impact on soil with respect to climate change are dynamic in nature and the associated studies are still in progress. Rhizospheric and phyllosphere microbial association with crops positively improves the crop yield of the crop thus ensuring food security in a sustainable manner. Adverse climatic conditions hamper the microbial growth by changing the global crop production pattern to mitigate the food crisis worldwide with lowering soil fertility status around the globe. The microbial structure and ecological niche are affected by climate change, which can change the microbiome's status with its association with plants. The suitable micro-climate over the crops can sustainably increase the crop production and ensuring global food security with providing an eco-friendly environment.

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Conflict of Interest:

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Author Contribution:

Both author have participated in critically revising of the entire manuscript and approval of the final manuscript.

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