Uncovering The Hidden World Beneath Our Feet: How Soil Microbes are Key Players in Mitigating Climate Change; A Review

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Abstract; The most significant problems with the current environmental situation are global warming and climate change. Higher levels of greenhouse gases in the atmosphere, which cause warming, are to blame for these issues. Although anthropogenic sources and the effects of these gases have received much attention, microorganisms and their relevance still need to be discussed. Microorganisms perform a wide range of tasks, but they are utilized particularly in the processes that treat and reduce greenhouse gases by recycling nutrients. Depending on the case, it efficiently uses or produces these gases by reducing environmental risks brought on by both natural and human activity. It tries to evaluate the processes that drive bacteria to release and absorb greenhouse gases using the available literature. Moreover, research has been done on the feedback and subsequent impacts. The importance of bacteria in climate change was later discovered. Hence, bacteria should always retain their significance in models and debates about climate change. In the present review, we also discussed how different cycles like the carbon, methane, and nitrogen cycles, help mitigate climate change. In addition, the review also identified the necessity of proper research and future prospect.

Keywords; Climate change, microbial diversity, soil microbes carbon cycle, methane cycle, nitrogen cycle and carbon sequestration

1. Introduction

Climate change is now widely recognized as humanity's most serious contemporary challenge. Indeed, a new report from the Intergovernmental Panel on Climate Change (IPCC) states that the situation has grown even worse, with 3.3 billion of the world's population highly vulnerable to climate change, and that current unsustainable development patterns are increasing exposure of ecosystems and people to climate hazards (IPCC, Climate change, 2022). For more than 12,000 years, the world's climate has been steady, which is essential to humanity's survival (NASA, 2015). Yet over the past century, the average global temperature increased by 1.5 °F; in the next 100 years, it is expected to rise by another 0.5-8.6 °F. This is a critical problem since even little changes in the average global temperature can result in dramatic changes in the climate and weather (US EPA, 2015). As soil microorganisms are largely responsible for the cycling of soil organic carbon (SOC) and other nutrients, they have a key role in climate feedback, including the production or consumption of greenhouse gases such as CO_2, CH_4 and N_2O. However, whether the soil will become a source or sink of greenhouse gases under future climate scenarios has been difficult to predict due to unknown changes in soil carbon and nitrogen pools and differences in microbial responses between soil locations (Friedlingstein et al., 2006; Wang et al., 2017). Thus, although the importance of soil microbial ecology for predicting future climate impacts has been recognized, it remains a challenge to integrate with landscape-scale climate models (Wieder et al., 2013).

One major concern with climate change is that soil microorganisms will mineralize more SOC and contribute substantially to greenhouse gas (CO_2 and CH_4) emissions, thus exacerbating warming trends. This is a concern because the total amount of soil carbon, including within permafrost, is estimated to be ~3,300 petagrams (Pg), approximately five times larger than the current atmospheric pool of CO_2 (Tarnocai et al., 2009; Birdsey et al., 2018). However, climate models have considerable uncertainty on whether this soil carbon pool will increase or decrease in the future. Most empirical data from climate change studies in the field have relied on measuring changes in soil respiration. In order to improve models of soil carbon–climate feedback, there is also a need to determine how to bulk soil carbon stocks change with changes in climate (Bradford et al., 2008). Soil microorganisms carry out the dichotomous roles of mineralizing SOC and stabilizing carbon inputs into organic forms. The balance between these two processes governs the net flux of CO_2 and CH_4 to the atmosphere. The proportion of carbon substrate retained in the microbial biomass compared with that respired as CO_2 is called the microbial carbon use efficiency. SOC's heterotrophic respiration has globally increased due to climate change, thus contributing to increased atmospheric inputs of CO_2 (Bond et al., 2018). However, soil carbon losses to the atmosphere could be countered by increased soil carbon inputs due to increased plant growth and autotrophic fixation by soil microorganisms (Rustad et al., 2001). Also, the temperature sensitivity of the decomposition of SOC varies with the quantity and chemistry of plant litter and pre-existing SOC (Nottingham et al., 2015). Thus, the local biogeochemical environment strongly influences microbial metabolic responses to climate, even within specific biomes. Developing a mathematical understanding of the microbial ecology that drives ecosystem carbon use efficiency and the feedback with climate forcing is a pressing need for improving climate change models. Nitrogen cycling also strongly influences climate change because nitrogen availability is closely correlated to the production of CO_2, N_2O and CH_4 (Vitousek et al., 1997). In particular, management of N_2O emissions remains a pressing issue because N_2O is a potent greenhouse gas, with 298 times the warming potential of CO_2 and emissions from soil represent 56–70% of all global N_2O sources (Syakila & Kroeze, 2011). Managing N_2O emissions within soil ecosystems has been a formidable challenge due to the microbial communities' complexity and the soil environment's spatial and temporal variation (Groffman et al., 2006; Butterbach et al., 2013). Recently, microorganisms were discovered that can completely oxidize ammonia to nitrate (common) without generating N_2O as a by-product, which is abundant in soil (van Kessel et al., 2015).

Hence, as they store and release enormous amounts of carbon, microbial reactions are a major part of the carbon flow on Earth (Weiman, 2015; Naylor et al., 2020). It is important to emphasize that most greenhouse gases, including CO_2, CH_4, and N_2O, are produced by bacteria (Singh et al., 2010). The microbial world is an essential component of the carbon cycle and other biogeochemical cycles, and it is important to pay attention to how they relate to climate change. Yet, bacteria are rarely included in conversations on climate change (Dutta, 2016). Most climate change models do not adequately consider microbial activity due to a lack of information in this area (Dutta, 2016). Consequently, this review focuses on the role of soil microbes in reducing climate change.

II. Climate change and its causes

The climate is the long-term weather conditions of a place over many years, including temperature, humidity, atmospheric pressure, wind, precipitation, etc. The climate of a place depends on its latitude, altitude, terrain, and the presence of nearby water bodies and their currents. A climate system is a complex system formed due to the interaction of variable factors such as oceans, ponds, the earth's environment, atmosphere, glaciers and living organisms that determine the place's climate. Climate change occurs over decades to millions of years due to plate tectonics, volcanic activity, thermohaline ocean circulation, changes in ocean currents, rainfall, vegetation types, and coverage density. These changes in the number of atmospheric greenhouse gases result in global warming (Werk & Mulder, 2007). The result of climate change leads to extreme weather events like floods, droughts, temperature elevation, storms, etc. The climate may be associated with both natural and anthropogenic factors. However, it mostly altered 150 years ago. Therefore, it is important to understand the key factors responsible for changes over such a short period. Many studies confirm that the earth's temperature is increasing by global warming due to the emission of greenhouse gases and human activity since the beginning of-20th century (Melillo et al., 2014). Most greenhouse gases (e.g., carbon dioxide, methane, water vapor, and nitrous oxide) are released naturally, but some (e.g., synthetic halocarbons) are added in the atmosphere due to human activity. Human activities, such as the combustion of fossil fuels in the electricity generation, transportation sectors, agriculture, land-use change, waste treatment, and various industrial processes, further increase carbon dioxide, methane and nitrous oxide (Table 1).

Table 1 Major greenhouse gases, CO_2, methane, nitrous oxide, synthetic chemicals generation sources (U.S. greenhouse gas emissions 2017).

Greenhouse gasses	**CO_2 generation**	**sources Methane generation**	**sources Nitrous oxide generation**	**sources Synthetic chemicals generation sources**
Carbon dioxide (82%)	Electricity (37%)	Natural gas and petroleum systems (29%)	Agricultural soil management (74%)	Substitution of ozone-depleting substances (90%)
Methane (10%)	Transportation (31%)	Enteric fermentation (26%)	Stationary combustion (6%)	Electrical transmission and distribution (3%
Nitrous oxide (6%)	Industry (15%)	Landfills (18%)	Industry or chemical production (5%)	Production and processing of aluminum and magnesium (3%
Fluorinated methane (3%)	Residential and commercial (10%)	Coal mining (10%)	Transportation (5%)	HCFC-22 production (2%)
Other	Other non-fossil fuel combustion (6%)	Manure management (5%)	Manure management (10%)	Semiconductor manufacture (2%)

III. Soil Microbial Diversity

Soil microbiome refers to the diverse communities of microorganisms, including bacteria, fungi, archaea, protozoa, and viruses, that inhabit the soil. These microorganisms are crucial in nutrient cycling, plant growth, and soil health. In recent years, advances in high-throughput sequencing technology have enabled researchers to explore the diversity and function of soil microbiomes in unprecedented detail. One of the key functions of soil microbiomes is nutrient cycling. For example, nitrogen-fixing bacteria such as Rhizobia can convert atmospheric nitrogen into a form that plants can use. Similarly, phosphorus-solubilizing bacteria such as *Bacillus* and *Pseudomonas* can release phosphorus from organic matter and minerals, making it available to plants. Despite the importance of soil microbiomes, many aspects of their diversity and function are still poorly understood. However, recent studies have shed light on the complexity and diversity of soil microbiomes. For example, a study by Fierer et al. (2012) used high-throughput sequencing to analyze the bacterial and fungal communities in soils across North and South America. The researchers found that soil microbial communities are highly diverse, with different soils having unique communities of microorganisms. Another study by Delgado-Baquerizo et al. (2018) used a meta-analysis to examine the global distribution of soil microbiomes. The researchers found that soil microbial diversity is strongly influenced by soil pH, with acidic soils having lower microbial diversity than neutral or alkaline soils. In addition, the researchers found that microbial diversity is negatively correlated with soil nitrogen availability, suggesting that nutrient-rich soils may have lower microbial diversity.

Soil microbial diversity is a crucial component of soil health and ecosystem functioning. One of the earliest studies to examine soil microbial diversity using high-throughput sequencing was conducted by Roesch et al. (2007). The study analyzed soil microbial communities from different ecosystems, including grassland, forest, and wetland, using pyrosequencing of 16S rRNA gene sequences. The researchers found that soil microbial diversity was highly variable across ecosystems, with forest soils having the highest diversity and wetland soils having the lowest. In another study, Janssen (2006) used culture-dependent and culture-independent techniques to examine soil microbial diversity. The study found that culture-dependent methods underestimated microbial diversity, with up to 99% of soil bacteria being unculturable. The study also found that soil microbial diversity was influenced by environmental factors such as pH, moisture, and nutrient availability. A recent study by Bahram et al. (2018) used high-throughput sequencing to examine soil microbial diversity across various ecosystems, including forests, grasslands, and deserts. The study found that soil microbial diversity was strongly influenced by local and regional factors, with soil pH being the strongest predictor of microbial diversity. In addition to examining soil microbial diversity, researchers have also explored the functional diversity of soil microorganisms. For example, Philippot et al. (2013) used a meta-analysis to examine the functional diversity of soil microbial communities involved in nitrogen cycling. The study found that microbial functional diversity was positively correlated with ecosystem productivity, suggesting that microbial diversity is essential for maintaining ecosystem functioning.

IV. Carbon Cycling and Soil Microbes

Carbon cycling in soil refers to the movement of carbon between different forms and reservoirs in the soil ecosystem. Carbon is an essential element for plant growth and microbial activity, and carbon cycling through the soil system is a critical process that supports the functioning of terrestrial ecosystems. The carbon in the soil exists in different forms, including organic carbon in living and dead plant and animal material and inorganic carbon in the form of carbon dioxide (CO_2) and bicarbonate (HCO_3^-) ions. Carbon cycling involves different steps; the first step is carbon fixation. The carbon fixation process is the first step in the carbon cycle, whereby plants absorb carbon dioxide (CO_2) from the atmosphere and convert it into organic compounds through photosynthesis. Plants can then use these organic compounds as a source of energy and growth, or they can be stored in the plant's biomass. Soil respiration is when soil microbes break down organic matter, releasing CO_2 into the atmosphere. This process is also known as soil carbon loss and is influenced by temperature, moisture, and soil nutrient availability. Soil organic matter (SOM) is a complex mixture of partially decomposed plant and microbial material that can persist in the soil for centuries. Carbon sequestration is the process whereby carbon is removed from the atmosphere and stored in soils for long periods. Carbon sequestration can occur through SOM formation, root biomass accumulation, and biochar addition. The balance between carbon fixation, soil respiration, and carbon sequestration determines the net carbon flux in a given ecosystem. Suppose the rate of carbon fixation exceeds the rate of soil respiration. In that case, the ecosystem is considered a net sink for carbon, meaning it removes more carbon from the atmosphere than it releases. However, if the rate of soil respiration exceeds the rate of carbon fixation, then the ecosystem is considered a net carbon source, meaning it releases more carbon into the atmosphere than it removes (Six and Paustian, 2014).

Soil microbes play a crucial role in the global carbon cycle as they decompose organic matter in the soil, which releases carbon dioxide (CO_2) into the atmosphere. However, soil microbes also have the ability to store carbon in the soil, which can offset some of the carbon dioxide emissions from decomposition. The balance between carbon storage and emissions depends on various factors, including temperature, moisture, soil type, and land use (Bardgett et al., 2008). One way that soil microbes affect the atmosphere is through respiration, where they break down organic matter to release CO_2. This process is essential to the carbon cycle, allowing nutrients to cycle through the ecosystem and supporting plant growth. However, soil respiration also releases carbon dioxide into the atmosphere, which can contribute to global warming and climate change. On the other hand, soil microbes can also sequester carbon in soil through carbon fixation. This process involves converting atmospheric CO_2 into organic matter, which can be stored in the soil for long periods (Six et al., 2002). This carbon sequestration helps mitigate climate change's effects by reducing the amount of carbon dioxide in the atmosphere. The ability of soil microbes to store carbon depends on several factors, including the type of microbes present, the quality of organic matter in the soil, and the environmental conditions. For example, certain bacteria and fungi are more effective at breaking down organic matter and releasing carbon, while others are better at storing carbon in the soil. Also, soil moisture and temperature can affect the balance between carbon storage and emissions, as dry or cold soils may reduce microbial activity (Lehmann and Kleber, 2015).

V. Soil Microbe's carbon fixation and Climate Change Mitigation

Most microbes potentially fix CO_2 from the air through various mechanisms and pathways (Table 2). Photosynthetic and non-photosynthetic pathways are the microbial mechanism involved in sequestering atmospheric CO_2 into biomass and energy. The benefits of CO_2 captured by microbes include the following; high pro- duction maximum rate of bio fixation, high ability to bioremediate atmospheric CO_2, the capabilities to produce several additives are extreme, no difficulties in genetic augmentations, the capability of being used in bioprocessing at industries, rapid growth and continuous culture in bioreactors, no competition and food scarcity. It includes bacteria, fungi, yeast and algae etc.

V.I Bacteria

Bacteria are unicellular, microscopic organisms with 19 groups. Most of them fall under the following groups: *Actinomycetes, Mycoplasma, Rickettsia's, Archaebacteria, Cyanobacteria* and *Eubacteria,* etc. Among these six groups, the Archaebacteria, Cyanobacteria, and Eubacteria are autotrophic, which fixes CO_2 for organic carbon production.

A. Clostridium

Anaerobic gram-negative bacteria substantially degraded organic carbon materials, acid synthesis, and the carbon cycle (Migliardini et al., 2014). Various species are chiefly involved in the bio-fixation of CO_2, such *as Clostridium autoethanogenum, Clostridium pasteurianum, C. formicoaceticum, Acetobacterium woodi, Clostridium thermoaceticum* incorporates atmospheric carbon dioxide into acetyl-CoA through Wood–Ljung-dahl pathway/Reductive acetyl CoA pathway which is the direct and most effective thermodynamic pathways (Tracy et al., 2012). The energy required for the fixation of CO_2 is obtained from the hydrogen molecules. Carbon monoxide dehydrogenase and acetyl-CoA synthetase are the two enzymes that play a chief role in acetyl-CoA synthesis by converting carbon monoxide into carbon dioxide (Liew et al., 2016; Fast and Papoutsakis, 2012; Ezeji et al., 2007; Ni and Sun, 2009). This bacterial sp. cannot survive atmospheric CO_2, a major disadvantage (Qureshi et al., 2007). Clostridium thermoaceticum was the first model used to study this pathway.

B. Proteobacterium

Proteobacteria are large phyla capable of incorporating atmospheric carbon dioxide via various biological mechanisms such as the Calvin cycle/reductive pentose phosphate cycle, TCA cycle/Krebs cycle and also directly in the cytoplasm (Paoli &

Tabita, 1998; Ding & Yokota, 2004). Calvin cycle is used by the following species *Oligotropha carboxidovorans*, *Rhodobacter sphaeroides*, *Xanthobacter flavus*, *Rhodobacter capsulatus*, *Beta proteobacter*, *Ralstonia eutropha*, *Herbaspirillum autotropicum*, and Gama proteobacter, Acidithiobacillus ferrooxidans, Acidithiobacillus thiooxidans, *Hydrogenovibrio marinus*, etc. (Wang et al., 2008; Brigham et al., 2011; Albuquerque et al., 2011). Some of the bacterial spp. are used to synthesize commercial products such as biopolymers and medicine (Willey et al., 2008). In the cytoplasm of R. eutropha, polyhydroxy alkanes are produced by utilizing CO_2. Sulfur-reducing bacteria such as *Desulfobacter hydrogenophilus* (delta-proteobacteria) and *Thiomicrospira denitrificans* (epsilon-proteobacteria) utilize CO_2 and H_2O to produce organic materials through the TCA cycle in which the ATP-citrate lyase splits acetyl-CoA and oxaloacetate.

V.II Archaea

Archaea is a unicellular, prokaryotic microbe termed as extremophiles and surviving under intense ecological extremities such as high fluctuating temperature, pH, and absence of O_2. Archaea has three groups: halophiles (ability to withstand higher salt), thermoacidophiles and methanogens. The methanogens produce biofuel-methane under an anaerobic environment by utilizing CO_2 as raw material and energy obtained from hydrogen for the bioconversion process (Rittmann et al., 2015; Demirel & Scherer, 2008). Two types of methanogens are commercially used to produce methane; they are acetoclastic and hydrogenotrophic methanogens. These methanogens potentially bioremediate wastewater and capture CO_2; hence, they can generate methane from the sludge by recycling CO_2 and bioremediate wastewater. It includes *Methanobacteriaceae*, *Methanospirrillaceae*, and *Methanosarcinaceae spp* (Yasin et al., 2013, 2015). The 3-hydroxy propionate 4-hydroxybutyrate cycle pathway is used to fix atmospheric CO_2 by *Cenarchaeum*, *Archaeoglobus*, and *Metallosphaera* and *Sulfolobus*, *sp* (Berg et al., 2007). Two acetyl-CoA and one bicarbonate molecule are used to produce succinyl-CoA, which undergoes a 4-hydroxybutyrate pathway to generate two molecules of acetyl-CoA. In this pathway, Acetyl-CoA/Propionyl-CoA carboxylase is the enzyme that actively fixes atmospheric CO_2 into biomolecules. Thermophilic methanogens produce carbonic anhydrase enzymes to produce methane, which can be used in large-scale industries (Smith & Ferry, 2000; Henstra et al., 2007).

V.III Cyanobacteria

Cyanobacteria are prokaryotic, blue-green bacteria or algae that serve as a connecting link between bacteria and green plants. They are photoautotrophic gram-negative bacteria present in both microscopic and macroscopic forms. They possess carboxysomes in their cytoplasm for carbon fixation. Some microorganisms, such as photoautotrophs and chemoautotrophs, have carboxysomes, e.g., Bacteria and all cyanobacteria, resulting from an adaptation called the Carbon dioxide Concentration Mechanism (CCM). It is involved in the Calvin-Benson cycle. The two enzymes RuBisCO and carbonic anhydrase are enclosed in bacterial microcompartments called carboxysomes located in the cytosol. There are two carboxysomes: alpha carboxysomes with RuBisCO form IA and beta carboxysomes with RuBisCO IB. The alpha carboxysomes exist in all alpha-cyanobacteria, most of the chemoautotrophs, and some purple bacteria, but the beta carboxysomes are only seen in beta-cyanobacteria.

Table 2 Microbial carbon sequestration through various pathways.

Input	**Pathways**	**Enzymes**	**Organism**
CO_2	Calvin-Benson-Bassham cycle (CCB) or Reductive pentose phosphate cycle mycobacteria	RuBisCO	Plants, algae, cyanobacteria, proteobacteria,
CO_2	Reductive tricarboxylic Acid cycle (rTCA)/ Reductive citric acid cycle/Reverse Krebs cycle/Arnon Buchanon cycle	PEP carboxylase 2-Oxogluteratesynthase, Isocitrate Dehydrogenase Pyruvate synthase	Proteobacteria, green, sulfur, bacteria, quaficae bacteria
CO_2	Wood-Ljungdahl pathway (W-L) or Reductive acetyl-CoA pathway	Ormate dehydrogenase, Carbon monoxide dehydrogenase (CODH) Formylmethanofuran Dehydrogenase (FMFD)	Euryarchaeota, proteobacteria, planctomycetes, spirochaetes
CO_2	3-Hydroxypropionate 4- hydroxybutyrate cycle (3HP-4HB)	Acetyl-CoA/ Propionyl CoA carboxylase	Aerobic crenarcheota
CO_2	Dicarboxylate 4-hydroxybutyrate cycle (DC-4HB)	Pyruvate synthase PEP carboxylase	Anaerobic crenarcheota
CO_2	3-Hydroxypropionate bi-cycle (3-HP)/Fuchs-Holo cycle	Acetyl-CoA carboxylase Propionyl-CoA carboxylase	Green non-sulfur bacteria

V.IV Algae

Algae is the most efficient photosynthetic bio-factory incorporating CO_2 into biomass and energy. They range from macro to micro size. Macroalgae produce high lipid content; hence they are directly used to extract for biodiesel production. Micro-sized algae include cyanobacteria, diatoms, euglenoids, green, blue, red, brown, golden, yellow colored algal species. They have huge potential to fix CO_2 enzymatically using RuBisCO in the Calvin–Benson cycle. e.g., About 1 kg of micro-sized algae fixes 1.84 kg of atmospheric carbon dioxide. The carbon dioxide fixed by Anabaena is 1.46 g/L/d and 6.24 g/L/d by Chlorella vulgaris. They utilize CO_2 to produce biomass and bioenergy (Chen et al., 2010). Cultivating these algae very close to the emitting sources can reduce elevated CO_2 levels and produce huge quantities of biomass and bioenergy (Cheah et al., 2015). Selection of algal species, optimal growth parameters and proper feedstock are the factors that should be considered before cultivation practices to obtain the maximum yield (Ghorbani et al., 2014). Perfect algal species should possess the following characteristics to achieve maximum CO_2 bio fixation and yield. The ability to capture carbon and the rate of incorporation should be extreme. It should tolerate maximum CO_2 stress, properly utilize limited nutrients, and tolerate fluctuation in thermal and H^+, OH^- parameters (Abd-Rahaman et al., 2011). Algae, ideal for maximum carbon capture and fuel production, like *Botryococcus braunii*, *Scenedesmus obliquus*, *Nannochloropsis oculate*, and *Chlorella vulgaris* (Pires et al., 2012; Brilman et al., 2013; Singh & Ahluwalia, 2013). The algae *Scenedesmus dimorphus* tolerated up to 20% (v/v) of CO_2 stress even though its optimal level to biofix CO_2 was only 2%(v/v). This indicates that the amount of

CO_2 the algae were exposed to would significantly reflect the bioconversion rate and yield. This clearly showed that the tolerance to high CO_2 content by *Chlorella sp* is remarkably extreme (Jiang et al., 2013). They show extreme tolerance to CO_2 content, up to 40–41% under the temperature and pH of 30 °C and 5–6, respectively (Chen et al., 2014). *Nannochloropsis spp*. was found to be grown at a rate of 58% with a CO_2 stress of 15% (v/v) (Jiang et al., 2011). It has been reported that a high concentration of carbon dioxide can significantly endorse the rate of photosynthetic CO_2 bio fixation in a short duration and more than 5% (v/v) becomes toxic. Also, the Continuous injection of an elevated level of CO_2 in the culture media inhibits algal growth (Lee et al., 2000). Calvin Benson pathways are used for carbon fixation in algae. Production of 3- phosphoglycerate occurs through the carboxylation of ribulose 1,5-biphosphate by the catalytic activity of RuBisCO enzyme there by two molecules from which one enters the central metabolism and the other is exploited to continue the cycle.

V.V Fungi

Fungi are eukaryotic, multicellular organisms with a rigid cell wall. They are heterotrophic and serve as primary decomposers and chief organisms to capture carbon in the terrestrial ecosystem. Based on decomposing organic matter, they are categorized into two groups, saprophytic and mycorrhizal fungi. Saprophytic fungi produce enzymes to decompose substances such as cellulose, hemicellulose, pectin and lignin, etc. which are responsible for the mineralization and carbon cycle and the decomposition by mycorrhizal fungi is low due to the lack of an enzyme (Ahmed et al., 2019). Mycorrhizal fungi form a symbiotic association with plants and exist in three forms, including ectomycorrhizal, arbuscular mycorrhizal form and ericoid mycorrhizas only found in plants belonging to the order Ericales.

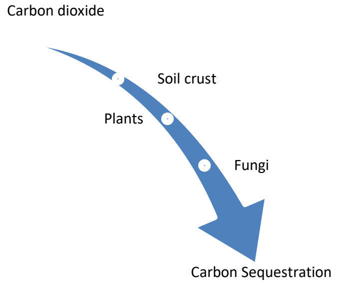
A. Mechanism.

Fungi facilitate carbon sequestration in soil by forming organic humus and maintaining the carbon balance, thereby contributing CCS largely in the terrestrial ecosystem when compared to bacteria (Fig. 1); three methods involved in soil carbon storage, including recalcitrant biomass and their secondary products, producing soil aggregate and incorporation of atmospheric CO_2 into fungal biomass. The mycelium acts as a storage site for the carbon. Thus, a large amount of biomass is produced by efficiently incorporating CO_2 at a higher percentage.

B. Role of mycelia in carbon capture

The vegetative tissue produced in fungi, the so-called mycelia, has a rapid growth rate and spreads much faster in the soil by facilitating access to nutrients and H_2O. Fungal contribution to sequester carbon from CO_2 is achieved through biomass formation and their secondary products and degradation of their necromass. The rate of carbon sequestered will depend upon the type of fungal species present in the soil and its biomass produced- i.e. the higher amount of mycelia produced, the greater the percentage of carbon incorporated. Thus, the amount of fungal biomass produced will directly reflect the percentage of CO_2 utilized. The mycelia serve as a carbon sink in the soil. Fungal necromass contributes up to 71% of humus production compared to bacteria, with only 26%. The degradation of fungal necromass is directly affected by the concentration of soil nutrients such as nitrogen and chitin; the mycelial necromass is decomposed within 8 days when the nitrogen and chitin are concentrated in the soil. Simultaneously, the decomposition of mycelia is resisted in cells filled with melanin pigment. Therefore, the carbon is locked up within the cells for a prolonged period depending upon its melanin concentration. Therefore, the amount of necromass protected directly correlates to the amount of carbon sequestered (Fernandez and Koide, 2014). Even soil aggregates also possess fully functional fungal necromass contributing in soil carbon storage.

Fig 1 Carbon sequestration of fungi in soil



C. Role of glomalin protein and soil aggregate in carbon capture

The mycorrhizal fungi produce a glomalin protein, secreted from the fungal hyphae and spores as a thermal adaptation. The glomalin is thick, sticky, and recalcitrant to resist decomposition. Glomalin promotes carbon capture via two processes, making the fungal hyphae resist decomposition and endorsing soil aggregation. Thus, the carbon is ceased within the hyphae and soil aggregate for a prolonged period. Glomalin is found to be the principal substance responsible for the formation of stable soil clumps along with permeability to H_2O and air (Pal & Pandey, 2014). Its hydrophobic nature protects the soil clump from microbial degradation and erosion. Hence, the organic carbon and nutrients within the clump remain protected for over 50 years. Thus, glomalin act as a carbon sequester in the terrestrial carbon pool and promotes soil quality. Fungal species present in the following genera secretes glomalin protein: *Entrophospora*, *Gigaspora*, *Acaulospora*, *Scutellospora*, *Glomus*, etc. (Pal & Pandey, 2014).

VI. Microbial Methane Cycle

Since it lies at the bottom of the redox scale, methane is essential to the global carbon cycle. Methane is a powerful greenhouse gas with a warming potential 34 times greater than that of carbon dioxide over a period of 100 years (Myhre et al. 2013). The carbon exchange between carbon dioxide and organic molecules is seen as having ecological significance. The carbon atom in the methane molecule is completely reduced; it can no longer take electrons but is a potential electron donor. Carbon dioxide, the most oxidized form of carbon in the cycle, is located at the other end of the redox scale. Although it cannot provide electrons, carbon dioxide may receive them. These substrates can be converted to methane under strongly reducing circumstances without other possible electron acceptors like nitrate, sulfate, or ferric iron. Certain methane-producing bacteria may create methane by combining carbon dioxide reduction and hydrogen oxidation, while others can do so by further reducing the tiny organic substrates they consume during fermentation. Microbial activity is primarily responsible for methane (CH_4) entering the atmosphere, which sources gas. Microbes that consume methane are essential to preserving the Earth's climate. Bacteria use methane as an energy source for metabolism (Semrau et al., 2010; Bousquet et al., 2006). Methanotrophic bacteria use methane as their only energy source, breaking it down into carbon dioxide.

These bacteria can absorb extremely high amounts of methane, which lowers methane emissions from landfills and facilities that produce methane (Gupta et al., 2014; Shindell et al., 2012). Methanotrophic bacteria oxidize CH_4 to CO_2 when oxygen is present. The oxidation of CH_4 finishes the carbon cycle to CO_2. Microorganisms consume many ubiquitous CH_4 molecules (Zimmerman & Labonte, 2015). Methanogenic bacteria efficiently convert carbon dioxide into methane in anaerobic environments, such as deep compacted muck. Hydrogen is required for the conversion process, which produces water and energy for the methanogens. Methane oxidizing bacteria, often known as methanotrophs (literally, "methane eaters"), are another class of methane bacteria that may carry out the recycling pattern. Water and energy are also produced during this aerobic conversion. Methanotrophic bacteria oxidize CH4 to CO_2 when oxygen is present. The oxidation of CH_4 finishes the carbon cycle to CO_2.

VII. Microorganism and Nitrogen Cycle

There is an elemental form of nitrogen. It makes up the majority of air, accounting for around 78% of the gases in the Earth’s atmosphere. The atmosphere also contains several nitrogen-gaseous molecules, such as NH_3, NO, and N_2O. The highly stable molecule (N_2) representing nitrogen is inaccessible to plants and animals without fixation. Nitrogen The conversion of atmospheric nitrogen into chemical forms that living beings may utilize is known as fixation. The biosphere receives N_2 through biological fixation. For intensive agriculture, biological nitrogen fixation will never fully replace industrial fixation. Rhizobium bacteria are responsible for developing nodules on the roots of legumes like alfalfa and soybeans. For instance, the bacteria are extremely specific to particular plants; a type that infects soybeans will not infect alfalfa.

The plant creates a hollow thread leading into the root due to the bacteria attaching to one of the plant's root hairs. Along this infection thread, bacteria develop and finally cause the creation of a nodule on the root. Bacteria may comprise as much as 30% of a nodule's weight. By fixation, the plant transfers energy from the air into a form it can use. This illustrates symbiotic nitrogen fixation (Bernhard, 2010; Vitousek et al., 2013). As part of the symbiotic relationship, certain bacteria (Rhizobium Trifolium) possess nitrogenous enzymes that can fix atmospheric nitrogen into a form (ammonium ion) chemically useful to higher organisms. The plant converts the "fixed" ammonium ion to nitrogen oxides and amino acids to form proteins and other molecules, such as alkaloids (Jama et al., 2013). The major function of the nitrogen cycle is the transformation of nitrogen. Most of the time, bacteria push the system to gather energy or build up nitrogen in a form necessary for their growth and development.

The major transformations of nitrogen are involved through the following steps.

A. Nitrogen fixation

The initial stage is converting nitrogen into a form that plants can use or absorb. the microbes that turn nitrogen into ammonium. Two recognized varieties of bacteria fix nitrogen. Cyanobacteria, also known as blue-green algae, Anabaena, Nostoc, Azotobacter, Beijerinckia, and Clostridium, are among the free-living (non-symbiotic) bacteria. The second kind is the mutualistic (symbiotic) bacteria, primarily Rhizobium, connected to leguminous plants. Microorganisms that are symbiotic and free-living do an excellent job of fixing nitrogen. These bacteria possess the nitrogenase enzyme, which turns ammonia produced by the reaction of gaseous nitrogen and hydrogen into other organic compounds (Bernhard, 2010; Orr et al., 2011).

B. Nitrification

The process by which living things convert ammonium into nitrates. What the organisms can absorb are nitrates. Soil-dwelling bacteria and other nitrifying bacteria finish the conversion of ammonia to nitrate. Bacteria like the Nitrosomonas species oxidize ammonium (NH_4^+) during the first stage of nitrification, turning it from ammonia to nitrites (NO_2). The conversion of nitrites into nitrates (NO_3^-), carried out by other bacterial species like Nitrobacter, is necessary for life. Since ammonia gas is poisonous to plants, ammonia is changed into nitrates or nitrites. Ammonium ions are helpful to the system's bacteria that utilize them as a source of energy. Both plants and animals are poisoned by nitrite. Different species must instantly transform it into nitrate (Ward, 2011; Wunderlin et al., 2012). Assimilation: This process shows how a plant’s system absorbs nitrogen. Using their root hairs, plants may absorb nitrates from the soil. Ultimately, it manufactures cellular components like amino acids, nucleic acids, and chlorophyll. Plants directly take up some nitrogen with a symbiotic connection with rhizobia in the form of ammonium ions from the nodules. Other living forms use the structure of the food chain to find nitrogen (Singh & Kundu, 2014).

C. Ammonification

Is the stage of decay? While living things die, decomposers like fungi and bacteria turn nitrogen into ammonium. Later it can reenter the normal nitrogen cycle. In the N_2 process, nitrogen is released, usually in the form of ammonia. The process is termed as ammonification or mineralization. Many enzymes are involved, for example, Gln Synthesis (Cytosolic and Plastid), Glu 2-oxoglutarate aminotransferase (Ferredoxin and NADH dependent) and Glu Dehydrogenase. In soil, this takes the form of the ammonium ion (NH_4^+), which has a positive charge. This charge tends to bind the nitrogen to soil clay minerals, an advantage in that the nitrogen is not readily lost by leaching or runoff. It has the disadvantage that it cannot easily migrate to reach plant roots for uptake (Bernhard, 2010; Singh & Kundu, 2014).

D. Denitrification

At the end of the cycle, extra nitrogen molecules in the soil move out to the atmosphere. Denitrification is the reduction of nitrates back into the largely inert nitrogen gas (N_2) to complete the cycle. A special and unique group of bacteria like Pseudomonas and Clostridium performs this task. They use nitrate as an electron acceptor in place of oxygen during respiration. The denitrifying bacteria use nitrates in the soil to carry out respiration and produce nitrogen gas, which is inert and unavailable to plants. The process is taken without oxygen, commonly in waterlogged soils. Eventually, nitrate is converted to nitrogen gas and reenters the atmosphere (Bernhard, 2010; Groffman, 2012).

VIII. Challenges and Limitations of Using Soil Microbes for Climate Change Mitigation

Although there are many opportunities to leverage carbon stock and sequestration potential in the soil of different ecosystems, numerous challenges are making this difficult in reality. Some of these challenges include:

A. Measurement and verification: carbon stock in soils is difficult, time-consuming, and expensive. Changes within the range of 10% are very difficult to detect due to sampling errors, small-scale variability and uncertainties with measures and analysis (Sparling et al., 2006). The annual incremental carbon stock in the soil is very small, usually within 0.25–1.0 t/ha (Ravindranath and Ostwald, 2008). It is even more difficult to account for little gains or losses in soil carbon at various scales due to methodological difficulties such as monitoring, verification, sampling and depth (Trumbore, 2003). Even if these small changes (gains or losses) are detected, linking such changes to management or land use practices in a given context is not easy. The capacity of the soil to sequester and retain carbon is also finite as it reaches a steady state after some time.

B. Carbon pools: sequestered carbon in the soil in different pools with varying degrees of residence time in the ecosystem. These pools include a Passive, recalcitrant, or refractory pool: organic carbon held in this pool has a long residence time ranging from decades to thousands of years. Active, labile, or fast pool: carbon held in this pool stays in the soil for a much shorter period due to fast decomposition. The residence time normally ranges from 1 day to a year. Slow, stable or humus pool: carbon held in this pool has a long turnover time due to a slow decomposition rate. The residence time typically ranges from 1 year to a decade.

C. Permanence: another challenge of carbon sequestration in soil is the non-permanence of the sequestered carbon, as it can be released back into the atmosphere as easily as it is gained due to decomposition or mineralization. For this reason, sequestered carbon is considered a short-term option for removing carbon from the atmosphere. The rate of carbon loss depends on several climatic, land use, and management factors.

D. Separation: it is very difficult to isolate and differentiate the portion of carbon sequestered in the soil due to management activities or land use and that which occurred naturally. The principle of separation requires that the carbon sequestered or GHGs emission prevented due to management intervention be distinguished from that which would have occurred due to natural causes. Therefore, methods are needed to differentiate naturally sequestered carbon from that captured due to human management (Swift, 2001).

IX. Future prospect

By 2100, it is predicted that the average worldwide surface air temperature would rise by 1.4 to 5.8 C. (World Meteorological Organization Web site). According to predictions, a 2° C rise in global temperatures would result in an increase in soil carbon release of 106 kg (10 petagrams) of CO_2 and other greenhouse gases (Raich and Potter, 1995; Luo et al., 2001; Pendall et al., 2004). This would result in a vicious loop of increased temperature rise and environmental changes. Climate change is predicted to result in more precipitation throughout the winter months in northern medium and high latitudes and Antarctica. Instead of being spread out across multiple moderate occurrences, greater amounts of precipitation will likely be delivered in a few huge outbursts (World Meteorological Organization Website). As a result, several ecological factors in terrestrial and aquatic environments are anticipated to alter, significantly influencing bacteria. Many models foresee how environmental changes may affect bacteria (Dens and Van Impe, 2001; Wilson et al., 2002). However, the most recent modeling approaches and research have shown that long-term soil warming implies favorable feedback between global warming and atmospheric release of soil organic matter, more so than first thought (Kirschbaum, 2004). Terrestrial ecosystems in the arctic are predicted to be particularly hard hit by the issue. Hence, the Arctic has been emphasized as a crucial area for identifying climate change (Ruess et al., 1999). But few mechanistic models forecast how soils will respond to climate change (Liski et al., 2005). Various ecosystems are probably going to react to the problem in different ways. For instance, it has been predicted that European forest soils will behave as CO_2 sinks in reaction to climate change, whilst agricultural soils will lose organic matter and emit CO_2 (Sleutel et al., 2003; Kirkby et al., 2005). On the other hand, higher atmospheric carbon dioxide levels are anticipated to result in an up to 39% increase in marine phytoplankton consumption. Although the global climate system can be expected to benefit, the increased oxygen consumption caused by the breakdown of the increased biomass would pose a serious threat to deep ocean marine life. Moreover, the pace of ocean acidification may increase (Leibniz Institute of Marine Sciences, 2007).

X. Conclusion

Global warming and climate change are major problems worldwide, affecting almost every ecosystem on earth, including plants, animals, and microbes. It causes changes in microbial community structure and their important metabolic activities associated with the alteration of the biogeochemical cycle on earth. Microbes may speed up global climate change by releasing greenhouse gases through the breakdown of organic matter. However, they can also prevent climate change by reducing the emission of greenhouse gases by converting them to organic form usable for themselves. Microorganisms, through nutrient cycling, play a dual role in GHG production and utilization. They utilize GHG for their energy requirements which reduces global warming and climate change. Soil bacteria show a modest response to global climate change and heating, but soil and root-related fungi show more profound changes. Biological carbon sequestration is important to consider for improving the condition of climate change. Among the various carbon sequestration microalgal fixation methods, CO_2 has many advantages over others, as biomass can produce energy, which is considered beneficial due to economic gains. This method is also considered to be a permanent sequestration technique. Microorganisms make a major contribution to carbon sequestration. By denitrification, methanogenesis (CH_4), and heterotrophic respiration (CO_2), microorganisms also significantly contribute to greenhouse gas emissions (N_2O). It is impossible to ignore the part that microorganisms play in regulating the level of greenhouse gases in the atmosphere, but more research in this area has to be done.

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