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REVIEW

Unravelling the secrets of soil microbiome and climate change for sustainable agroecosystems

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Abstract

The soil microbiota exhibits an important function in the ecosystem, and its response to climate change is of paramount importance for sustainable agroecosystems. The macronutrients, micronutrients, and additional constituents vital for the growth of plants are cycled biogeochemically under the regulation of the soil microbiome. Identifying and forecasting the effect of climate change on soil microbiomes and ecosystem services is the need of the hour to address one of the biggest global challenges of the present time. The impact of climate change on the structure and function of the soil microbiota is a major concern, explained by one or more sustainability factors around resilience, reluctance, and rework. However, the past research has revealed that microbial interventions have the potential to regenerate soils and improve crop resilience to climate change factors. The methods used therein include using soil microbes' innate capacity for carbon sequestration, rhizomediation, bio-fertilization, enzyme-mediated breakdown, phyto-stimulation, biocontrol of plant pathogens, antibiosis, inducing the antioxidative defense pathways, induced systemic resistance response (ISR), and releasing volatile organic compounds (VOCs) in the host plant. Microbial phytohormones have a major role in altering root shape in response to exposure to drought, salt, severe temperatures, and heavy metal toxicity and also have an impact on the metabolism of endogenous growth regulators in plant tissue. However, shelf life due to the short lifespan and storage time of microbial formulations is still a major challenge, and efforts should be made to evaluate their effectiveness in crop growth based on climate change. This review focuses on the influence of climate change on soil physico-chemical status, climate change adaptation by the soil microbiome, and its future implications.

Keywords Soil microbiome · Crop resilience · Soil ecosystem · Sustainable agriculture · Stress tolerance

Introduction

To foster the rising population, the urge for increased agricultural production is of utmost importance. The growing population requires continuous food production while taking food safety and environmental sustainability into account (Lykogianni et al. 2021). The achievement of this goal must be made against a background of widespread and pervasive land degradation (Kaur et al. 2023a, 2023b; Montanarella et al. 2015) and mounting difficulties brought on by a changing climate. Soil acts as a prospective cradle for essential ecosystem services that meet the demands of an increasing global population (Kopittke et al. 2019; Greiner et al. 2017). However, it is still unclear how much soil can be exploited in order to produce enough food without contributing to environmental damage and climate change (MacLaren et al. 2020). Also, the present state of climate change and other catastrophes have a significant impact on biotic and

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abiotic factors that manage the operations of the agroecosystem, consequently influencing the discussion of worldwide food security (Rodriguez and Durán 2020; Raza et al. 2019). In light of this perspective, a fresh green revolution is imperatively needed for food security, thus, fresh ideas and thoughts are sought to boost sustainable agricultural development (Hartmann and Six 2023).

According to Poore and Nemecek (2018), 14% of the global greenhouse gases (GHGs) like CO_2, N_2O, and CH_4 are produced by agriculture, making it a significant contributor to anthropogenic climate change (Parajuli et al. 2019; Swaminathan and Kesavan 2012). Additionally, the intensive agricultural practices of today, which include clearing land, overusing fertilizers and irrigation, and using fossil fuels to power agricultural machinery, result in a high carbon footprint because they continuously release large amounts of greenhouse gases at a comparable volume to those produced by industrialization, household warming, and energy production (Blattner 2020). Although there are relatively few swings in precipitation and temperature over long periods of time due to climate change, the slow variations in climate have an influence on several soil techniques, particularly those related to soil health. As a result, modern-day agriculture-based techniques necessitate addressing two significant problems (mitigation and adaptation): combating the effects of climate variations and developing sustainable methods connected with the offsetting of detrimental effects on food quality and yields. It can be done by cautiously utilizing natural resources and decreasing the quantity of pollutants and waste (Singh et al., 2012). The release or retention of soil carbon into the environment depends on a number of factors at the landscape scale, and soil ecosystems are incredibly diverse (Jansson and Hofmockel 2020). The competency of the soil to carry out the various natural processes (chemical, physical, as well as biological) under particular climatic and topographical conditions governs its capability to provide ecosystem services and is indicated by the emerging notion of “soil health” (Guo 2021). To address food security concerns, farming methods that ignore the many benefits of soil and soil health have resulted in soil degradation and eventual crop degradation, which is expected to degrade ecosystem services (Bagnall et al. 2021). To avoid the breakdown of organic matter and altering the nutrient cycle, exposure to synthetic fertilizers and pesticides will pollute soil ecosystems, leading to reduced fertility, reduced soil biodiversity, and finally, the deterioration of clean soil health (Bisht and Chauhan 2020).

Soil health management and sustained nutrient cycling become more difficult with the use of conventional farming techniques. Soil-dwelling microorganisms with traits that encourage plant growth present a potential alternative to artificial fertilizers for these serious issues (Bargaz et al. 2018). Furthermore, long-term use of these possibly beneficial bacteria is a major player in green agriculture. The main drivers of nutrient cycling and soil organic carbon (SOC), as well as those responsible for the synthesis and utilization of GHGs including CO_2, CH_4, and N_2O, are soil microbes. Apart from performing similar functions, the soil microbiome also controls the efficiency of many agriculture-based ecosystems (Van Der Heijden et al. 2008). The exploitation of microbes intends to improve soil health and recycle crop leftovers, forming a dynamic strategy for the sustainable production of food and energy. According to predictions, the vast majority (90%) of microbial variety is still hidden, and this ground-breaking diversity is comparable to the riches of soil health sustainability. Finding the key drivers that drive the ecosystem is still the most difficult assignment, and using these drivers to create value is even harder (Dubey et al. 2019). There is also an increase in the combination of overall changes that have a beneficial impact on the persistence and reactivity of the soil microbiome in response to weather changes (Norby et al. 2016).

Archaea, bacteria, fungi, and protozoa live on top of each other in what is called the “soil microbiome,” and soil makes up the most distinct ecosystems on the earth. The abiotic atmosphere of soil is also varied; It is about water-containing air, water-filled pores, and probable hot spots for bacteria (Kuzyakov and Blagodatskaya 2015). The soil atmosphere is quite vibrant when paired with the impact of plants and soil fauna, in addition to alterations in temperature, soil moisture, and shifting redox states. However, the impact of a change in climate on the resilience and stabilization of microbial health in soil is still unknown. These changes are more extensive and more dramatic (Norby et al. 2016). To predict and manage ecosystem responses to climate change, a clear definition of the ability of microbial communities to adapt ecosystems to climate change is required.

Agriculture and climate change

Agriculture is especially susceptible to climate change because of its vast scope and weather-related sensitivity, which will have a major economic impact. Weather-related factors, like rainfall and temperature, have a big impact on crop yields. Increasing temperatures, erratic precipitation, and CO_2 fertilization all affect the crop, location, and degree of parameter. Rising precipitation is anticipated to offset or mitigate the effects of rising temperatures, which have been reported to reduce yields (Adams et al. 1998). Crop type, crop adaptability, climate scenario, and CO_2 fertilization effect are some of the elements that affect crop productivity in Iran. Climate change affects agricultural production differently depending on the region and irrigation method. Crop production can be amplified by expanding irrigated regions, although doing so could harm the ecology (Kang et al. 2009). Because of their shorter growth seasons brought on by rising temperatures, many crops would likely yield less. A 2 °C increase in temperature is expected to cause a decrease in the overall yield of wheat, rice, and maize in both the temperate and tropical zones (Rosenzweig and Liverman 1992). Climate change typically affects tropical regions more because tropical crops remain closer to their high-temperature optima and hence experience high-temperature stress under rising temperatures.

Furthermore, warmer, humid climates are more conducive to the growth of pest insects and diseases. Temperature, precipitation, humidity, and wind speed all affect crop yields; in the absence of these variables, it is possible that the effects of climate change have been overstated. Additionally, studies show that until 2100, China's yields of rice, wheat, and corn are predicted to decrease by 18.26 ± 12.13, 45.10 ± 11.55, and 36.25 ± 10.75%, respectively, due to climate change (Zhang et al. 2017). Since the turn of the twentieth century, the Netherlands has experienced a rise in the frequency of extreme weather events, which has had a major impact on the region's wheat production. In the near future, most portions of the world are likely to experience more frequent droughts due to climate change; by 2100, the area impacted by drought is predicted to rise from 15.4 to 44.0% (Powell and Reinhard 2016). Africa is listed as the area most at risk. Major crops in drought-prone areas are predicted to yield less by around 90% by 2100 and less than 50% by 2050 (Li et al. 2009).

With a 0.3% annual loss of future global GDP by 2100, crop yield declines have the potential to drive up food prices and have a major effect on agricultural wellbeing globally. Nevertheless, Bosello and Zhang 2005 discovered that while climate change won't have a big impact on the world's food supply, it would negatively affect underdeveloped nations significantly. Expected temperature increases in India range from 2.33 to 4.78 °C, which will double the amount of CO_2 in the atmosphere and prolong heat waves. These factors could have a negative impact on the country's agriculture industry (Kumar and Gautam 2014). Farmers in Pakistan's dry Rawalpindi region will have to pay INR 4180/acre yearly for every 1 °C increase in temperature by the year 2100. On the other hand, an 8% or 14% increase in rainfall can result in a net income gain of INR 377.4 and INR 649.21, respectively (Shakoor et al. 2011). Three cereal cereals (rice, maize, and wheat) are expected to have yield losses of 10 to 25% more severe with a 1 °C increase in the world mean surface temperature (Deutsch et al. 2018).

Changes in temperature and precipitation have a major effect on the relationship between plants and water, and sudden changes in these variables are more likely to have an impact on physiological changes than changes in the typical climate. The way different plant species and developmental stages react to climate change is evident. Different plant species respond to these thresholds in different ways, and different plant species have varied threshold values. Yield loss, root elongation, and root growth angle perturbation are a few examples of these reactions (Gray and Brady 2016). It has been demonstrated that when plant transpiration increases, the amount of CO_2 in the atmosphere decreases and the air temperature rises by 0.42 ± 0.02 K. On terrestrial surfaces, an increase in temperature of 3.33 ± 0.03 K can be caused by the direct radiative effect combined with the indirect physiological effect of increased CO_2 (Cao et al. 2010). Harvestable agricultural yields are predicted to rise in response to rising atmospheric CO_2 levels, and crop-specific variations in plant development occur.

A sensitivity study utilizing CERES (crop estimating via resources and environmental synthesis) suggests that at double the levels of CO_2, wheat and rice yields in northwest India may increase by 28% and 15%, respectively. Nevertheless, the positive impact is nearly neutralized by the enhanced thermal stress brought on by the higher temperatures associated with high CO_2 (Lal et al. 1998). Furthermore, the current irrigation scheduling will enhance wheat and rice yields by 21% and 4%, respectively, even with the combined effects of increasing CO_2 and thermal stress (Long et al. 2006).

These observations can help mitigate the large economic losses that are expected to come from climate change, both on a micro and macro level. The extreme unpredictability of climate change and its effects adds a little complexity to the planning of adaptation and mitigation. This demands the use of a transdisciplinary approach tailored to the unique region in the creation of climate-resilient technology.

Impact of climate change over soil health

The alteration in climate can be defined as the change in climate over time because of the anthropogenic activities of humans (Karmakar et al. 2016). These alterations in climate have slow impacts on the soil, in part due to the fact that soil acts as a source of climate change-causing greenhouse gases and is also impacted by these gases itself (for example, the decomposition temperature of soil organic matter and changes in soil moisture). The outline of the direct and indirect effects of climate change on soil productivity is given in Fig. 1. Moreover, the loss of soil carbon would alter multiple soil properties like soil texture, water holding capacity, aggregate stability, nutrient accessibility, and erosion (Hussain et al. 2021; Cavicchioli et al. 2019). Furthermore, the rapid loss of soil carbon is explained by the increased temperatures. Increased nutrient release, on the other hand, could lessen these impressions and boost plant output in comparison to litter inputs. Yet, higher temperatures encourage the breakdown of organic matter in soil and

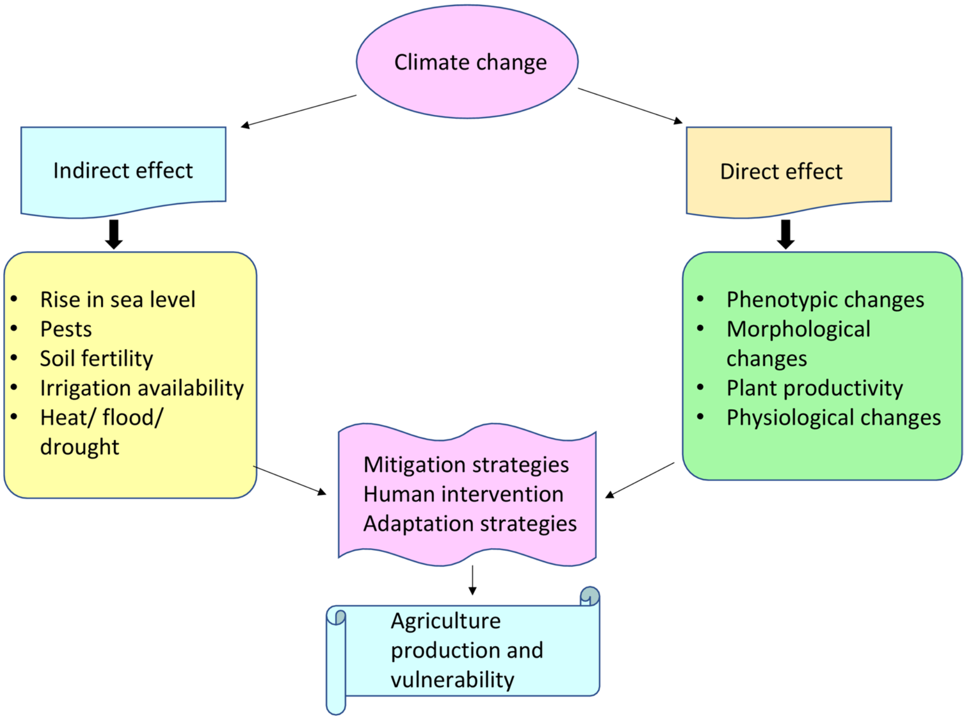

Fig. 1 Direct and indirect effects of climate change on soil productivity

accelerate the loss of soil organic matter (Karmakar et al. 2016). Increased precipitation could predict an increase in peat formation and methane production, while regions receiving lower amounts of rainfall could encounter losses of peat, CO_2, and soil moisture for forests and arable crops, which would disrupt the survival, scavenging habits, and reproduction of soil invertebrates (Chander 2012). Droughts brought on by climate change are known to raise the possibility of shrink-swell in clay soils; the higher temperatures may further aggravate foundations through chemical attack, potentially amplifying leachate generation and landfill gas release (DEFRA 2005). The interactions of the environment with pesticides, diseases, and pests can be tightly regulated under climate change. For example, increased temperatures hasten soil degradation, drier climes encourage pesticide persistence, and augmented precipitation enhances mass flow rate along with downward movements (Yi et al. 2021).

A change in climate impacts soil processes both directly and indirectly, with soil moisture playing the most significant role. It controls soil heat regimes, the availability of nutrients and moisture to plants, and the microbiological activity of the soil (Medhi et al. 2021). Increased temperature causes the soil structure to be disrupted, diminishing the soil's ability to retain moisture, which reduces soil efficiency and functions (Cai et al. 2016). The loss of food cations in salinization-triggered areas with increased evapotranspiration or reduced rainfall, irrigation, washing, or net upslope water are examples of rapid mineral and chemical changes due to climate change in the soil. (He et al. 2018). With the exception of Al and Mn, plant nutrients are inaccessible at low pH levels, while at high pH levels, the presence of critical plant nutrients like Fe, Mn, Cu, or Zn gets reduced due to a reduction in the solubility of many metals and trace elements (Delgado and Gómez 2016; Kaur et al. 2023a, 2023b). Also, the climate change scenarios have an immediate effect on the mobility and flux of harmful pollutants in the environment, particularly in the areas of the atmosphere, soil, sediment, water, and biota (Bardgett et al. 2008). Extreme weather conditions disrupt pollutant transport routes such as surface runoff, precipitation, volatilization, degradation, and transformation (Alava et al. 2017). Metal concentrations in crops will increase due to rapid evaporation, rapid release of soil particles and diffusion to roots, rapid decomposition of soil organic matter, or a combination of these variables (Biswas et al. 2018). Moreover, increased rainfall intensity and frequency can increase surface runoff and erosion, which can increase the transfer of pollutants outside of the parent soil (Alava et al. 2017).

Climate change has a direct and indirect impact on soil microbial functions, which provide feedback on the release of carbon monoxide into the atmosphere, which causes global warming. Climate change in plant diversity and productivity has direct effects on soil physicochemical properties, soil carbon availability, the activity and structure of related microbial communities, decomposition processes, and soil carbon emissions. Precipitation, temperature, and tremendous climatic actions have a direct impact on greenhouse gas production and soil microbes (Haines et al.

2006). Generalizing the soil microbiome is very difficult because it depends on biotic and abiotic parameters such as pH, aeration, moisture, soil structure, vegetation type, and microbe-microbe interaction. The soil microbiome is largely determined by plants, as they influence the community structure by attracting the appropriate players (Santoyo 2022; Jacoby et al. 2017). Xie et al. 2022 emphasized the regulatory behavior of minor peptides in plant responses to abiotic and nutritional factors. Plants secrete small peptides to adapt to various environmental challenges. These minor peptides are sensed by co-receptors and/or co-receptors and induce cell signaling pathways that produce cellular and physiological activity.

Exudates from the roots help the plant share its photosynthates with the below-deck team, thereby changing the microbiome in tandem with exudates. In addition to abiotic factors such as humidity, temperature, and soil structure, these changes can result from minor changes in area, such as the external radial distance between root teeth or parts of the roots themselves (Christy 2021). The influence of climate change on the functionality and stability of the soil microbiome is a key cause of concern (Shah et al. 2022; Allison and Martiny 2008; Griffiths and Philippot 2013). One or more of the key stability criteria, including resistance (remaining unaltered in the face of disturbances), resilience (recovering to a steady state), and functional redundancy (maintaining functional profiles despite taxonomic shifts), define the stability of a community (Griffiths and Philippot 2013). We can better understand the way microbial community structure and the associated ecosystem services are subjected to this combined pressure by observing the response of microbes to anticipated climate changes, such as increased carbon dioxide levels, increased temperatures, exacerbated droughts, erratic precipitation, and increased fire frequency (Wahl et al. 2018; Naylor et al. 2020).

Impact of high temperatures

Although topography, vegetation type, age of the soil, parent material, texture, climate, and soil community composition all have an impact on soils' capacity to store carbon, decomposing microorganisms largely regulate the rate-determining phases in the breakdown process (Classen et al. 2015). Warming alters the physiological processes of decomposers, affecting the CO_2 outflow from soil (Schindlbacher et al. 2011). The physiological changes that organisms experience in response to temperature comprise alterations in the lipid constituents of the plasma membrane that reduce membrane fluidity and the appearance of heat shock proteins (Jansson and Hofmockel 2020). An increase in temperature is anticipated to speed up the breakdown of fungal matter, increasing the amount of carbon dioxide released from the soil (Hannula and Morriën 2022). On the other side, higher temperatures increase the soil nitrogen level, which slows the pace of fungal breakdown. Higher temperatures have the potential to directly or indirectly affect the efficiency of nitrification by altering the metabolic processes of bacteria (Hu et al. 2016) or altering the properties of soil, such as soil oxygen levels and substrate accessibility (Bai et al. 2013).

An early labile carbon depletion was noted by the warming experiment at Harvard Forest in the soil, followed by the decomposition of less resistant carbon reservoirs (Melillo et al. 2017). Long-term warming is caused by organic carbon depletion in the soil and the consequent loss of microbial biomass, thus indicating that long-term warming has long-term effects on soil (Melillo et al. 2017). According to DeAngelis et al. (2015), low carbon levels were associated with a decrease in fungi and actinomycetes and an increase in oligotrophic bacteria, supporting the idea that microbial behavior may be linked to changes in ecosystem respiration. Depletion of the available substrate might also result from the changing composition of the microbial community due to warming (Schindlbacher et al. 2011). This is substantial, as particular microbes govern ecological processes like methanogenesis, nitrogen fixation, nitrification, and denitrification. Hence, changes in their relative abundances have an immediate impact on the speed of the aforementioned processes (Dutta and Dutta 2016).

Impact of high CO_2 levels

The effect of increased CO_2 on soil ecosystems has largely been studied through the free air CO_2 enrichment experiment (FACE), which shows the soil microbes response to added CO_2. However, the effects on microbial function and composition with respect to the carbon and nitrogen cycles have been unequivocal (Jansson and Hofmockel 2020). The metabolically active microbiome that predominates in rhizospheric soil was strongly impacted by elevated CO_2 levels, in contrast to the bulk soil microbiome, which essentially remained unchanged (Rosado-Porto et al. 2022). Microbial gene networks involved in denitrification, methanogenesis, nitrogen mineralization, carbon fixation, and carbon decomposition all evolved in hays exposed to high CO_2 (Yu et al. 2018). Increased accumulation of rhizo deposits in response to more CO_2 will act as a catalyst for microbe-mediated decomposition of available soil organic carbon (Qiao et al. 2014). It is difficult to distinguish it from the combination of CO_2 added by warming because the increase in CO_2 can increase humidity while the thermal effect can increase, causing the soil to dry out. Despite an increase in total mushroom abundance in Australian grasslands, total mushroom abundance decreased as CO_2 increased with warming (Hayden et al. 2012). Hence, it is crucial to understand how variations in CO_2 concentration connect to important environmental factors like rainfall, temperature, soil moisture, and nutrients in order to forecast the response of microbiome soil ecosystems.

Impact of drought

Future climate change is expected to cause more droughts, which will affect crop health, development, productivity, and quality, as well as microbial community structure and related activities (Abdul Rahman et al. 2021; Siebielec et al. 2020). Microbial processes, which are essential for the sustainability of ecosystems, are predicted to deteriorate due to drought (Sheik et al. 2011). The negative impact of drought on soil microbes leads to decreased enzyme activity, decreased nutrient availability (e.g., nitrogen, carbon), and decreased soil fertility, affecting crop yields, particularly drought-sensitive crops, and affecting economic recovery (Nguyen et al. 2018). Drought stress affects the root penetration of soil microbiota, particularly with prolonged drought stress (Bogati and Walczak 2022; Breitkreuz et al. 2021). Network analysis in mesocosm studies (Upton et al. 2018) and temporal field studies (De Vries et al. 2018) showed that bacteria are much more susceptible to dryness in grasslands in contrast to fungi. Therefore, fungi can significantly contribute to maintaining nitrogen and carbon cycling in environments with limited water resources (Treseder et al. 2018). Also, in physically secured soil pores, where fungal hyphae may help in linking the spatially dissimilar resources (Guhr et al. 2015), microbial dispersion grows into more confined ones under drier soil conditions, aiding the overall microbiome. Therefore, it is important to understand how interactions between kingdoms affect society's response to stress. Sadhukhan et al. (2022) stated that short-term drought memory is controlled by abscisic acid (ABA) and other plant hormones, capable of signalling the transcriptional memory behavior found in many genes. Drought causes demethylation of DNA near the genes (drought-response genes) that control this process. The offspring of drought-stricken plants are better adapted to drought because they inherit certain methylation patterns. Small RNAs play an important role in regulating drought memory by altering the levels of drought-responsive genes.

Impact of increasing rainfall

Climate change is expected to increase precipitation in the north, causing heavier rainfall and more frequent freeze–thaw cycles (Sorensen et al. 2016). As soil moisture increases, water fills soil pores, creating anaerobic conditions that are ideal for methanogenesis and denitrification, with probable emissions of CH_4 and N_2O, respectively. Different moisture and vegetation conditions brought on by different precipitation patterns can have different effects on microbial community responses. This is significant because fluxes caused by rainfall are a major factor in determining whether ecosystems serve as CO_2 generators or sinks in the environment (Shim et al. 2009). Indeed, moisture and respiratory distribution are greatly affected by precipitation (Aanderud et al. 2011). Past studies have shown reduced fungal populations in soil due to flooding, which promotes anaerobic bacteria in the soil while creating unfavorable conditions for the fungal community (Grzyb et al. 2020). Microbial activity has been shown to decrease during extended periods of flooding as resources are depleted in a "burst and subsidence" pattern (Sjogaard et al. 2018). Alterations among soil microbial communities and the presence of organic carbon and electron acceptors in the soil (which maintain carbon and nutrient balance during greenhouse emissions) will eliminate the sadness of the end of marine air.

Adaptation during climate change and the soil microbiome

Soil microbial populations often change in response to changes in resource availability. Changes in the environment often lead to mutations, dormancy, or the death of infectious organisms (Kumar et al. 2022). The level of agitation and amount of time needed to accumulate mutations, as well as the regulation of gene transcription and translation together with gene amplification via horizontal gene transfer, all together influence the adaptation of microorganisms. In order to adapt to changing environmental conditions, resident microorganisms in soil ecosystems, which are diverse dynamic systems, have evolved phenotypic strategies. The adaptation of soil bacteria to stresses brought on by climate change assures that resource allocation, from growth to survival strategies, is altered (Schimel et al. 2007). The interrelationship between climate change adaptation and the soil microbiome is depicted in Fig. 2. However, the underlying mechanisms that enable organisms to manage ecosystem responses to climate change are still in their infancy. Therefore, deciphering the physicochemical changes that alter the physiology and metabolism of important microbiomes in soil remains important for reducing atmospheric greenhouse gas emissions (Bertini and Azevedo 2022). The investigations carried out in recent years have revealed the possibility of microbial involvement in soil regeneration or the assurance of boosted resilience for crops. Methods covered include exploiting the carbon monoxide storage ability of soil microbes, enhancing the role of autotrophs such as algae to convert carbon into lipids, regulating adenosine triphosphate into their numerous carbon sequestration capacities, and regulating various metabolic processes in photosynthetic organisms. The direct processes of specific soil bacteria revolve around phytostimulation (Babalola and Glick 2012), biofertilization (Kalayu 2019), rhizomediation,

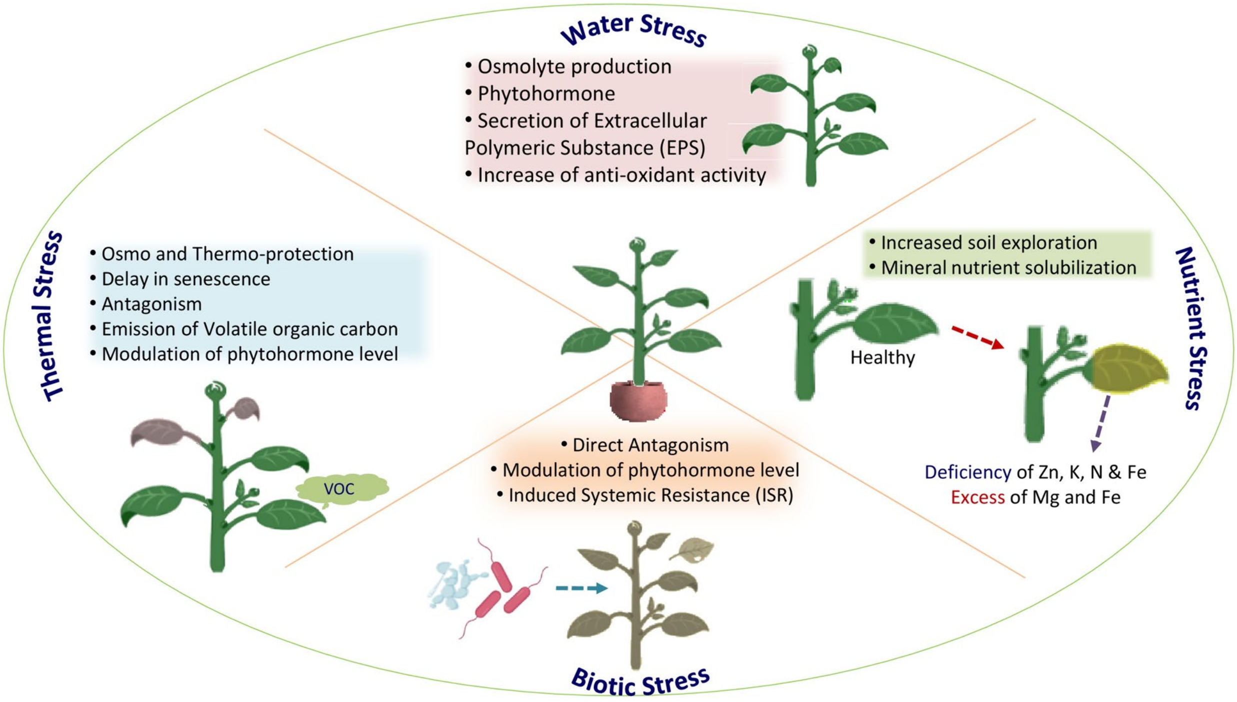

Fig. 2 Climate change adaptation and soil microbiome

or stress regulation (Stamenković et al. 2018). Indirect strategies include the removal of volatile organic compounds (VOCs) (Sun and Tang 2013), enzyme-mediated decomposition, antibacterial treatment, competition for soil nutrients, stimulation of antioxidant defense mechanisms (Malik et al. 2020), and systemic host plant stimulation (Heil and Bostock 2002). However, the effectiveness of soil microbiome restoration under climate change depends on the inherent qualities of the soil as well as environmental and agronomic management factors. The alleviation of abiotic stresses mediated by potential beneficial bacteria is illustrated in Table 1. The main factors affecting the survival and performance of soil bacteria that promote plant growth are nutrient availability, temperature, soil area, hydrology, plant genotype, and management (Gupta et al. 2019).

Salinization

Extremely harmful salt stress disrupts practically each feature of a plant's physiology and biochemistry, which contributes to a discernible decline in crop output and efficiency (Singh et al. 2015). Examples of plant regulators are phytohormones, which promote crop's growth and development (Delgado et al. 2021). These organic components function as signaling molecules under diverse environmental conditions (Phour et al. 2020; Enagbonma et al. 2023). For instance, auxin has been linked to the cytokinin hormone and has been credited with stimulating adventitious root growth, enhancing cell proliferation, and delaying the aging processes of plants (Mukherjee et al. 2022; Neina 2019). Plants prefer to produce more of the ABA and ethylene, contrary to indole-3-acetic acid (IAA), salicylic acid (SA), cytokinin, and jasmonic acid (JA), whose synthesis is decreased by salinity stress (Gul and Nawaz 2023). Under stress conditions, hormone deficiency or insufficient exudation may prevent plants from growing as they should. Contrarily, increasing hormone levels tends to improve stress tolerance (Mukherjee et al. 2018). Microorganisms that are halotolerant and halophilic respond to such conditions by producing unique enzymes with polyextremophilic structures that function in salinity environments, such as celluloses, lipases, proteases, amylases, and xylanases (Mukhtar et al. 2019a, 2019b). These enzymes include notable biological compounds, namely phytohormones and exopolysaccharides, that are essential for plant-microbiome association, maintain the integrity of soil aggregate, and help soil separate to retain water (Mukhtar et al. 2019a, 2019b). It has been shown that a variety of rhizosphere-dwelling bacteria aid plants in adapting to salt stress by absorbing nutrients from the soil, which enhances plant growth and development (Otlewska et al. 2020). In addition, improvements in disease resistance, root architecture, biomass, chlorophyll content, and seed germination may result from increased metabolic activity and microbial enzyme performance under salt stress. Strategies for mitigating the effects of salt include both direct and indirect methods that encourage plant development and

Table 1 Abiotic stress alleviation by beneficial soil microbes

Microbiome	Type of stress	Beneficial plant species	Reference
Pseudomonas fluorescens, *Bacillus subtilis*	Drought	*Vigna radiata*	Saravanakumar et al. (2011)
Bacillus licheniformis	Drought	*Capsicum annuum*	Lim and Kim (2013)
Achromobacter xylosoxidans, *Bacillus pumilis*	Drought	*Helianthus annuus*	Castillo et al. (2013)
Bacillus spp.	Drought	*Sorghum bicolor*	Grover et al. (2011)
Bacillus thuringiensis, *Pseudomonas polymyxa*	Drought	*Triticum aestivum*	Timmusk et al. (2014)
Pseudomonas aeruginosa	Drought	*V. radiata*	Sarma and Saikia (2014)
Burkholderia sp.	Drought	*Zea mays*	Fan et al. (2015)
Azospirillum brasilense	Drought	*A. thaliana*	Cohen et al. (2015)
Osmotolerant bacteria	Drought	*Oryza sativa*	Yuwono et al. (2005)
Achromobacter piechaudii	Drought	*L. Esculentum,*	Mayak et al. (2004a, 2004b)
Azospirillum	Drought	*T. aestivum*	Creus et al. (2004); Creus et al. (2005)
Azospirillum brasilense	Drought	*P. vulgaris*	German et al. (2000)
Rhizospheric microbial community	Drought	*Acer saccharum*	Kannenberg and Phillips (2017)
Reprogramed Rhizospheric microbial community	Drought	*Hordeum vulgare*	Ye et al. (2022)
High microbial diversity community	Drought	*Pisum sativum*	Prudent et al. (2020)
Rhizobacterial microbial consortia	Cold Stress	*Solanum lycopersicum*	Vega-Celedón et al. (2021)
Marine plant growth-promoting rhizobacteria consortia	Temperature	*Vitis vinifera*	Carreiras et al. (2023)
Thermophilic plant growth promoting consortium	Temperature	*Vigna radiata*	Verma et al. (2018)
Burkholderia phytofirmans	Temperature	*Vitis vinifera*	Ait Barka et al. (2006)
Burkholderia phytofirmans	Temperature	*Solanum tuberosum*	Bensalim et al. (1998)
Aeromonas hydrophila, *Serratia proteamaculans*	Temperature	*Glycine max*	Zhang et al. (1997)
Arthrobacter sp.	Osmotic (45% PEG)	*C. annuum*	Sziderics et al. (2007)
Azospirillum	Osmotic (20% PEG) in the dark	*T. aestivum*	Pereyra et al. (2006)
Azospirillum brasilense	Osmotic (20% PEG)	*T. aestivum*	Creus et al. (1998)
Halotolerant microbial consortia	Salinity	*Lycopersicon esculentum*	Kapadia et al. (2021)
Root-derived bacteria	Salinity	*Cucumis sativus*, *Cucurbita moschata*, *Cucurbita maxima*, *Cucurbita ficifolia*, and *Lagenaria siceraria*	Li et al. (2021)
Dietzia natronolimnaea	Salinity	*T. aestivum*	Bharti et al. (2016)
Sphingomonas sp.	Salinity	*Solanum pimpinellifolium*	Khan et al. (2017)
Halobacillus dabanensis, *Halobacillus* sp.	Salinity	*Oryza sativa*	Rima et al. (2018)
Pseudomonas putida, *Novosphingobium* sp.	Salinity	*Citrus*	Vives-Peris et al. (2018)
Curtobacterium albidum	Salinity	*O. sativa*	Vimal et al. (2019)
Bacillus halotolerans, Lelliottia amnigena		*T. aestivum*	El-Akhdar et al. (2020)
Azotobacter sp.	Salinity	*T. aestivum*	El-Nahrawy and Yassin (2020)
Acinetobacter bereziniae, *Alcaligenes faecalis*	Salinity	*Pisum sativum*	Sapre et al. (2022)
Azospirillum brasilense	Salinity	*Phaseolus vulgaris*	Dardanelli et al. (2008)
Pseudomonas syringae, *Enterobacter aerogenes*	Salinity	*Zea mays*	Nadeem et al. (2007)

Table 1 (continued)

Microbiome	Type of stress	Beneficial plant species	Reference
Pseudomonas fluorescens	Salinity	*Arachis hypogaea*	Saravanakumar and Samiyappan (2007)
Azospirillum	Salinity	*Lactuca sativa*	Barassi et al. (2006)
Achromobacter piechaudii	Salinity	*Lycopersicon esculentum*	Mayak et al. (2004a, 2004b)
Bacillus sp.	Salinity	*Triticum aestivum*	Ashraf et al. (2004)
Azospirillum	Salinity	*Z. mays*	Hamdia et al. (2004)
Azospirillum brasilense	Salinity	*Cicer arietinum, Vicia faba* L	Hamaoui et al. (2001)
Bacillus subtilis, *Arthrobacter protophormiae*, *Dietzia natronolimnaea*	Drought and Salinity	*T. aestivum*	Barnawal et al. (2017)
Variovorax paradoxus	Drying soil	*Pisum sativum*	Belimov et al. (2009)
Pseudomonas putida	Flooding	*L. esculentum*	Grichko and Glick (2001)
Bacillus polymyxa, *Pseudomonas alcaligenes*	Nutrient deficiency	*Z. mays*	Egamberdiyeva (2007)
Bacillus subtilis	Iron toxicity	*O. sativa*	Asch and Padham (2005); Terré et al. (2007)
Bacterial consortia	Water shortage and salt stress	*Persea americana*	Barra et al. (2017)
Microbial consortia	Oxidative damage and cold Stress	*Zea mays*	Moradtalab et al. (2020)

raise agricultural yields in salty soils. The direct mechanisms involved in this process are as follows: (a) increasing the accumulation of osmoprotectants like glycine, betaine, trehalose, and proline (Mehta and Vyas 2023); (b) increasing the production of antioxidant enzymes to protect against oxidative stress (Ali et al. 2023); (c) It reduces stress levels caused by hormones (ethylene) by increasing ACC deaminase activity (Choudhury et al. 2023); (d) synthesizing exopolysaccharides and forming biofilms to bind to excess Na + ions and stop them from moving through xylems to plant leaves (Sarraf et al. 2023); (e) keeping stomatal conductance and photosynthetic activity high (Bhardwaj et al. 2023).

As per Jiang et al. (2023), other indirect ways in which plant growth–promoting rhizobacteria (PGPR) have been employed to reduce salt stress along with increasing nutrient accessibility and absorption, creating nutrients for iron absorption, solubilizing phosphate, controlling plant growth hormones to stimulate roots and shoot growth, and promoting disease resistance via promoting systemic tolerance, manufacturing of organic acids and NO (nitric oxide), and release of extracellular polymers increase soil aggregation.

They also contribute to the bioremediation of contaminants in salty soils (Bergi and Trivedi 2020). Bacteria and plants can accumulate osmolytes in response to low osmotic pressure. However, osmolyte generation through intricate pathways consumes a lot of energy with the help of a massive carbon skeleton, leading to a fall in growth and activity (Chakraborty et al. 2020). The most common organic osmolytes of halotolerant bacteria are proline, betaine, and glycine; the most common inorganic osmolytes are potassium ions (Csonka 1989). High salinity, which is similar to dry conditions, causes oxidative stress. Reactive oxygen species (ROS) are typically created as a consequence of numerous alterations in the metabolism and physiology of plants (Mansoor et al. 2022). In stressful situations, the concentration of ROS enhances the effects of stress. Certain features like pathogen defence, plant-programmed cell death, and stomata closure may have been regulated through these signalling molecules (Dos Santos et al. 2020). To reduce the damage caused by this stress, plants have evolved antioxidant mechanisms, including antioxidant enzymes and other non-enzymatic antioxidant mechanisms (Wu et al. 2017). Superoxide dismutase (SOD) produces H_2O_2 and O_2 predominantly as an O_2 scavenger. As a result, H_2O_2 can be removed by catalase, ascorbate peroxidase, and guaiacol peroxidase (Aslam and Ali 2018). Malondialdehyde (MDA) is an important product of the peroxidation of polyunsaturated fatty acids and is one of the biomarkers of oxidative stress. MDA can act far from its source due to its strong biological activity and capacity for long-distance transport. This organic substance manages to deactivate enzymes and indirectly influences the processes involved in the synthesis of proteins (He et al. 2018).

Drought

It is known that phytohormones play a vital function in regulating how various plants react to different types of drought. Additionally, key plant hormones to deal with drought stress include auxin (indole-3-acetic acid, IAA), gibberellins (GAs), cytokinins (CKs), salicylic acid (SA) brassinosteroids (BRs), and ethylene (ET), (Vaishnav and

Chowdhury 2023). According to Jing et al. (2023), auxins are phytohormones that are critical for the growth, development, and stress response of the plants. Numerous investigations carried out by many experts have discovered that auxin plays a beneficial effect in the development of drought resistance. Studies have shown that Aux/IAA genes are present in rice and many genes are activated under stress (Sun et al. 2023).

Cytokinins (CKs) are one of the major phytohormones that must control the plant's growth, development, and ability to respond to environmental stressors such as stress (Prasad 2022). According to numerous research, CKs can affect drought tolerance in both positive and negative ways (Asif et al. 2022; Mandal et al. 2022). The length and severity of the drought can also affect the amount of CK in the blood. In transgenic plants harboring an isopentenyl transferase gene, endogenous CK levels were elevated. The transgenic plants exhibited enhanced drought tolerance as a result of delayed senescence and suppressed drought-induced leaf senescence. A variety of microbe-produced drought-sensitive metabolites function as plant hormone precursors, including phenylalanine, which is required for the production of salicylic acid (SA), and other secondary metabolites that are responsive to drought stress (Lephatsi et al. 2022).

Due to the stress conditions created by drought and salt, ABA, the so-called stress hormone, is a vital molecule and occupies one of the key positions as regulators of drought mitigation strategies (Vishwakarma et al. 2017). The hormone levels have a strong relationship with the level of stress present, making them an effective indicator of its extent (Sah et al. 2016). Only plants can produce the soluble receptor ABA. A rise in hormone levels causes the cells to react to this abiotic stress. To this end, the stomata of the plant get close, and the expression levels of genes related to stress change. Subsequently, the plant attempts to adapt to the changing conditions, but ABA is crucial for controlling the ratio of shoot to root growth and encouraging root expansion. The most well-known osmo-protectants are those containing proline, glutamine, glutamic acid, volatile organic compounds, taurine, and extracellular polymeric molecules. They can aid in the survival of both plants and microorganisms under a variety of stress conditions, notably in high-salinity environments (Oteino et al. 2015). The accumulation of osmo-protectants, electrically neutral, non-toxic, and low-molecular-weight metabolites lowers the osmotic stress. Their effectiveness depends on ion transport across the plasma membrane and supplementary turgor pressure in cells (Chen et al. 2020). Proline continues to play a crucial role as a plant osmoprotectant in drought-like conditions (Fiodor et al. 2021).

Soil fertility

Sequestration of carbon

Through both biotic and abiotic processes, atmospheric carbon stocks can be reduced by sequestering them into stable, non-gaseous forms (Averill et al. 2014). The assimilation of atmospheric CO_2 by plants and autotrophic soil microbes facilitates the release of carbon into the soil. Approximately 20% of the photosynthetic material transported to the rhizosphere by plants is released through various means such as mycorrhizal fungi, sloughed root cap cells, or root exudation (Averill et al. 2014). Carbon inputs stimulate symbiotic and free-living organisms, leading to the dispersion of carbon throughout the soil matrix. Microbial biochemical modifications and the subsequent exchange among communities enable bioavailable carbon forms to cycle and persist in non-bioavailable forms (Lal 2004). Soils with greater biodiversity exhibit an increased capacity to store carbon (Lal 2004). Soil fungi and bacteria collaborate in the production of carbon polymers, which contribute to the formation of soil aggregates and the occlusion of soil carbon. Researchers are currently exploring the untapped biochemical potential of the soil microbiome for novel reactions that accelerate carbon deposition in the soil (Hicks et al. 2017). These processes can be facilitated by interacting members of consortia, influencing carbon breakdown pathways towards more resistant and stable end products (Hicks et al. 2017). Alternatively, the soil microbiome can be modified in situ by incorporating amendments that enhance the soil's carbon absorption and storage capabilities. For example, residual microbial products that yield persistent carbon may be preserved in deeper soil layers (Schmidt et al. 2011). Microbial residues such as macromolecules from deceased biomass (necro-mass) or extracellular polymeric substances have been identified as surviving components in the soil (Kapilan et al. 2018). To achieve relatively stable sequestration of soil carbon, pyrolyzed carbon, also known as biochar, can be utilized as an amendment (Elkhlifi et al. 2023). The stability of biochar depends on whether its components are respired by soil microbes. Additionally, it is possible to regulate plant-soil rhizosphere interactions to promote soil carbon storage (Jansson et al. 2018). For instance, enhancing the allocation of carbon from plants to the rhizosphere, where it is converted into stable metabolites and/or retained in microbial biomass, can improve the deposition of root exudates (Jansson et al. 2018). In such cases, genetic modifications in plants may be employed to favor specific root-colonizing bacteria that capture the particular carbon exudates released by the plant (Chauhan et al. 2023). Future techniques may enable genetic control over photosynthetic allocation to optimize the plant–microbe-soil system for maximum plant production and soil carbon deposition (Jansson et al. 2018).

Achieving this outcome will necessitate collaboration between soil microbiologists and plant breeders to identify the most beneficial combinations of useful bacteria and plant genotypes without resorting to the field use of genetically engineered plants (Lakshmanan et al. 2017).

Microbes as advantageous plant inoculants

Beneficial bacteria and fungi living in the rhizosphere, called plant growth-promoting (PGP) bacteria, can help reduce the negative effects of drought by enabling plants to grow under increased demand (Naylor and Coleman-Derr 2018). PGP bacteria can be incorporated to plants in the field as a liquid or granular supplement or as a top coat for seeds. Rhizobium species used in legume bionitrogen-fixing inoculants are examples of PGP species. Besides the use of pesticides and biofertilizers, there is now interest in the use of PGP bacteria to reduce the impact of climate change (Kumar et al. 2022; Kumar et al. 2023; Chaudhary et al. 2023; Compant et al. 2010). The PGP gene has been studied in many ways to help plants cope with stress (Lakshmanan et al. 2017). For example, some soil bacteria produce polymeric extracellular materials that form hydrophobic biofilms that protect plants from desiccation (Naylor and Coleman-Derr 2018).

Beneficial soil bacteria can increase crop resistance to stress by producing plant hormones that promote plant growth, recruiting osmotic regulators or other resistance chemicals, or detoxifying reactive oxygen species (Lakshmanan et al. 2017). For example, some bacteria produce indole-3-acetic acid, which promotes root growth in the rhizosphere and reduces water stress (Armada et al. 2015). Research also shows that compounds released by rhizosphere bacteria can be stored in plants and reduce osmotic stress (Koza et al. 2022). Integration of beneficial arbuscular mycorrhizal fungi can lead to resistance to stress and nutrition, for example by controlling plant production of certain molecules called aquaporins to reduce water stress (Kapilanet al. 2018; Quiroga et al. 2017). Arbuscular mycorrhizal fungi can also come into direct contact with water by spreading through the mycelium into the soil through pores inaccessible to plant roots. Ability to reduce microbial N2O production in synchronizing plant needs with microbial nitrogen supply. For example, arbuscular mycorrhizal fungi can be used to obtain ammonium and reduce N_2O production (Zhang et al. 2023). Inoculating communities that consume N_2O or preventing nitrification by utilizing biological inhibitors of the ammonia oxidation pathway are two more biological methods for reducing N_2O emissions (Subbarao et al. 2009). Combined, these examples show how the advantageous functions performed by soil microbes might be used to support the maintenance of ecosystem services in a changing environment.

The National Academy of Sciences recently released the report "Science Advances in Food and Agriculture 2030," which advocates altering the soil microbiome to increase crop yields in response to climate change (National Academies of Sciences, Engineering, and Medicine 2019). In order to develop more effective strategies to stop soil carbon loss, it is also necessary to comprehend the biogeochemical mechanisms underlying SOC degradation and greenhouse gas generation.

For example, although the redox chemistry of electron donor molecules is well established, the thermodynamics and energetics of organic carbon electron acceptors that power microbial metabolism from soil are not well understood. The physiological response or metaphenome of the soil microbiome is our current area of research (Azeem et al. 2022). This information will make it easier to predict how climate change will affect soil performance and use characteristics of the soil microbiome to mitigate its effects.

Microbial phytohormones to mitigate abiotic stress

Studies have shown that microbes produce phytohormones, which enhance plant growth and stress tolerance in various environments like heat, salt, drought, and metal toxicity. These microorganisms reduce abiotic stress in plants. Plant-associated bacteria and IAA synthesis also promote plant development in abiotic stress. For example, *Curtobacterium flaccumfaciens* E108 and *Ensifer garamanticus* E110 from *Hordeum secalinum* increased barley's resilience to salt stress and increased plant biomass (Cardinale et al. 2015). Under saline soil conditions, the root-colonizing halotolerant bacteria *B. licheniformis* HSW-16 was able to reduce damage caused by salt stress and promote wheat development by producing IAA (Singh and Jha 2016). Similar findings were documented by Upadhyay et al. (2012), that observed that the plant tissue's sodium content was lowered and wheat biomass and total soluble sugars were raised by the salt-tolerant bacterial strains *Bacillus subtilis* and *Arthrobacter* sp. *Pseudomonas* spp. isolated from harsh settings (near volcanic sites) produced IAA at high temperature (40 °C) and salt stress (500 mM NaCl) in research. They were also able to drive increases in maize biomass in the roots and shoots (Mishra et al. 2017). Plants that are protected by IAA from the harmful effects of abiotic stress have stronger cellular defense mechanisms, as per the findings of Bianco and Defez (2009). Cucumber biomass and yield in greenhouse conditions have been enhanced by salt-tolerant strains synthesizing IAA in culture medium. IAA-producing bacteria linked with roots help plants under drought stress. In nutrient-poor soil, IAA-producing bacteria enhance plant growth and development. In chickpea grain production, IAA-producing bacteria from *Serratia* sp. increased chickpea grain production. Fungal species can modify plant physiology and root systems, creating growth regulators for plants. Inoculating *Arabidopsis thaliana* with *Trichoderma virens* led to enhanced lateral root production, root hair growth, and improved root system architecture, all contributing to increased plant biomass. Overall, these findings highlight the potential of IAA-producing bacteria in improving plant growth and development (Zaheer et al. 2016).

Root-associated microorganisms use osmoregulation, hormonal balancing, biochemical processes, and modifications to metabolic interfaces to interact with symbiotic microbes and host plants, therefore promoting plant development under stress. Under salt stress, IAA-producing bacteria, like *B. subtilis* NUU4 and *Mesorhizobium ciceri* IC53, increase nodule formation and biomass in the roots and shoots of chickpeas. Under salt stress, cytokines such *Arthrobacter*, *Bacillus*, *Azospirillum*, and *Pseudomonas* enhance the biomass of soybean shoots and roots as well as the amounts of proline and cytokinin in plant tissue (Egamberdieva et al. 2017). By triggering ABA synthesis, *Bacillus licheniformis* and *Pseudomonas fluorescens*' production of ABA promotes grapevine plant growth under water stress. Under circumstances of salt stress, bacterial inoculation greatly boosts the development of roots and shoots as well as the concentration of SA in rice plant tissue. By encouraging plant biomass and nodule number, *Bacillus aryabhattai* strain SRB02 from the soybean rhizosphere increases the drought stress tolerance of soybeans by causing stomatal closure in hot weather (Liu et al. 2013). In drought-prone environments, the endophytic bacteria *Achromobacter xylosoxidans* and *Bacillus pumilus* that produce SA increase the biomass of sunflower seedlings. Salt-tolerant *Serratia marcescens* NBRI1213 enhances plant stress tolerance to salt and promotes root and shoot development as well as maize's uptake of nutrients (Lavania and Nautiyal 2013). Important physiological processes, such as hormonal balance, are modulated by the interaction of phytohormones generated by bacteria in plant tissue. IAA, which is produced by *Sphingomonas* sp. LK11 and *Serratia marcescens* TP1, increases the amount of ABA and gibberellin, lowers the quantity of jasmonic acid, and promotes the development of soybean roots and shoots. When exposed to salt stress, *Trichoderma asperellum* Q1, which produces IAA, GA, and ABA, increases the biomass fresh weight of cucumber seedlings (Park et al. 2017). These investigations show that plant-associated microorganisms that promote stress tolerance are involved in phytohormone regulation in plant tissue.

Harnessing the soil microbiome to achieve agricultural sustainability under the scenario of climate change

In polluted soils, dangerous chemicals can be broken down or detoxified by soil bacteria. Soil microorganisms can be employed in the following ways to reduce pollution:

Biodegradation Organic contaminants and heavy metals in the soil can be detoxified and immobilized by microbially driven degradation processes, which will stop them from moving (Zheng et al. 2023). Microbes in soil have the ability to decompose into less toxic forms. Pollutants are broken down by specific enzymes in a process called biodegradation (Bisht et al. 2015).

Bioremediation Using soil microorganisms, heavy metal pollutants are broken down and transformed to lessen their bioavailability and potential absorption by plants (Zheng et al. 2023). Certain types of soil bacteria have the ability to eliminate heavy metals from polluted soil, including lead, cadmium, and mercury. Microbes that may immobilize, convert, or volatilize the heavy metals are used in this procedure, which is referred to as "bioremediation of heavy metals" (Tarfeen et al. 2022).

Phytoremediation It is possible to reduce the hazards related to heavy metal pollution in crops by using a technique called phytoremediation, which combines the skills of plants and soil bacteria (Zheng et al. 2023). This method reduces environmental pollution by having plants absorb and collect toxins from the soil, whereupon soil microorganisms then try to convert down into less dangerous compounds (Pilon-Smits 2005; Salt et al. 1995).

Utilizing soil microorganisms to offset environmental disruptions is becoming more and more important as we deal with the effects of climate change on soil microbiomes. This includes using microbial inoculants as environmental probiotics, modifying land management techniques, or directly modifying soil microbial populations. It becomes clear that the soil microbiome is an important instrument for reducing the negative consequences of climate change. As a new way to reduce stress, bacteria can produce extracellular polymeric substances, which clog soil pores and increase soil moisture. Bacteria can also serve as carbon by consuming carbon from plants and storing it as cellular biomass or stable metabolites. Either biotically or abiotically, soil microorganisms aid in the absorption of carbon into stable, non-gaseous forms. Transport of photosynthates to the rhizosphere, promotion of free-living and symbiotic soil organisms, and distribution of carbon throughout the soil matrix are all accomplished by plants. We may use the soil microbiome's latent biochemical potential to improve carbon deposition into the soil even more. By changing the routes that carbon breaks down into more stable and resistant end products, we may be able to modify the carbon breakdown process (Kumari et al. 2023).

As an alternative, we can add naturally occurring microbial species or consortia that have the appropriate metabolic pathways to soil ecosystems in order to sequester carbon (Kaur et al. 2024). Another possible strategy is to modify the soil microbiome in situ by improving the ability of soil bacteria to absorb and store carbon. An important strategy to reduce the effects of climate change is to promote the deposition of microbial material in deep underground layers and produce carbon monoxide. Soil organisms contribute to soil organic matter because they produce stable metabolites or dead matter (dead biomass).

Current advances involving genetic engineering of microbes for improving agricultural production and environmental sustainability

Increased microbial diversity in the rhizosphere and soil may contribute to the sustainability of ecosystems (Trivedi et al. 2020). However, careless use of agrochemicals disrupts the variety of beneficial bacteria in the soil and the soil environment, which has detrimental effects on crop yield, quality, and soil fertility (Huang et al. 2019). In response to different biotic and abiotic stress restrictions, plants have evolved a range of strategies to modify the rhizosphere microbiome (Li et al. 2022). Under salt stress conditions, Wang et al. (2022) detected a considerable shift in rhizobacterial diversity and rhizosphere metabolites of Sea rice 86 (SR86) using genome sequencing and transcriptome analysis. Using co-occurrence and correlation analysis, keystone taxa were found for the use of certain PGPR in the reclamation and use of salty soil. A number of processes are involved in the modification of the microbial population in the rhizosphere to enhance plant health and production, according to recent research on plant–microbe interactions and microbial metabolism (Kandasamy et al. 2021). By manipulating microbial populations and plant ecosystems, or by employing stress-tolerant bacteria as biostimulants or fertilizers, we can lessen our need on agrochemicals (Lau et al. 2022).

By adding stress-tolerant microbes through soil/seed treatments, the rhizosphere may be modified to increase nutrient exchange, plant-crop growth promotion, disease resistance, and/or reduction of abiotic stress (Orozco-Mosqueda et al. 2022). Rhizosphere engineering has become a feasible method for boosting microorganisms' cellular stress resistance for sustainable agriculture as metagenomic analysis makes it possible to identify the variety of rhizospheric microorganisms more quickly (Babalola et al. 2021). In genetically engineered plants, activating a stress-response signal transduction pathway may improve plant tolerance to environmental stresses, which may be a powerful and promising strategy (Sanghera et al. 2011).

Bridging the gap with innovation through microbes in models

Under scenarios of global warming, metagenomics and other omics technologies have a significant ability to supply the data inputs required to support pathogen surveillance efforts and climate models (American Academy of Microbiology 2011). Using large-scale sequencing to retrieve microbial genomes directly from a specific environment has given researchers a comprehensive understanding of the diversity and functional potential of microbes (Gupta et al. 2023; Nayfach et al. 2021). Although the application of climate science and combating the direct impacts of climate change has not yet been established, significant and creative steps need to be taken to extend mathematical models to the development of tools that measure microbial functions and metabolic rate along with changing data infrastructure and data sharing practices to assist the rapid dissemination, application, and extraction of microbiome data.

Little knowledge exists regarding the phenotypic characteristics and metabolic dynamics of microbial communities. Despite the fact that bacteria mediate crucial processes in all biogeochemical cycles, this information gap has restricted the inclusion of microbial factors in climate models. Understanding how microorganisms actively cycle nutrients, interact with other species, and react to disruptions (such as fire or extreme weather events) may help us quantify traits that are important for metabolism. The way we monitor the microbiome may change as a result of new molecular assays to assess metabolic rates in situ and at high-throughput resolution. Similar to this, novel experimental and statistical methods to link the metabolic characteristics of community-level microbial isolates to their genomes have the potential to use metagenome data to infer dynamic processes (Gowda et al. 2022). The conventional and advanced techniques used to uncover hidden black box of soil are shown in Fig. 3a and b). Beyond a descriptive approach, hypothesis-driven, mechanistic studies will promote predictive knowledge of how bacteria affect ecosystem processes (Prosser and Martiny 2020). Another difficulty for climate modeling is the size at which bacteria work (Bar-On et al. 2018). To explicitly link geographical, temporal, and phylogenetic aspects with microbial size and community assembly, a theoretical framework and mathematical methods must be created. Different

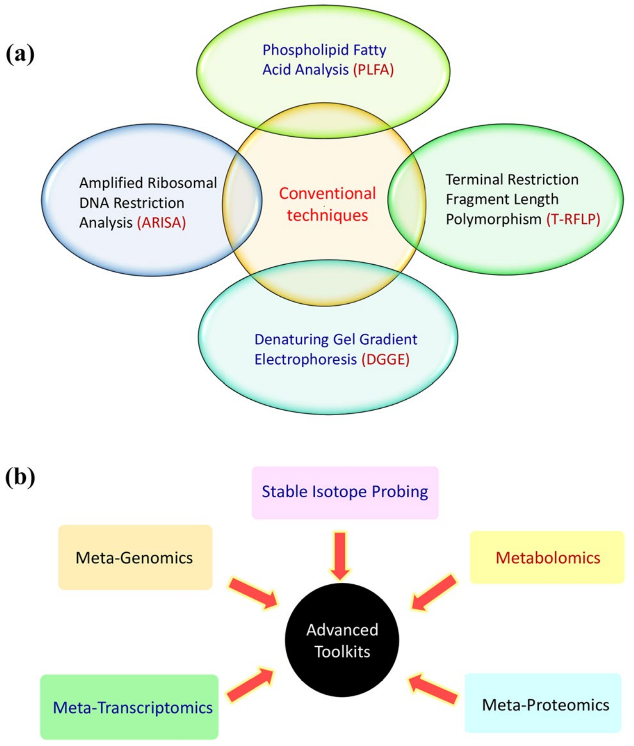

Fig. 3 **a** Conventional methods for uncovering soil's hidden black box. **b** Advanced methods for uncovering soil's hidden black box

mechanisms predominate at various scales in the assembly of microbial communities, which is thought to be a combination of deterministic processes (such as selective pressures imposed by abiotic and species interactions) and stochastic processes (such as neutral dispersal, colonization, or extinction events). The ability to translate microbial metabolic dynamics to ecosystem and global models will be made possible by the development of new mathematical approaches to identify mechanisms impacting assembly and scale. A set of "microbial indicators" of climate change can be created by using these new mathematical tools to determine what microbiome data are required for long-term environmental monitoring. The imperative requirement for data infrastructure and support for open data sharing methods is fundamental to developing innovative new tools. The National Science Foundation (NSF) LTER Program and NEON, the Department of Energy (DOE) Next-Generation Ecosystem Experiments (NGEE)-Arctic and Spruce and Peatland Responses Under Climatic and Environmental Change (SPRUCE), and the International Consortium of Ocean Observatories are just a few examples of long-term research programs that have made significant investments in environmental monitoring. While microbiome measurements and experiments are a part of all of these research initiatives, there is a lack of coordination for standardized procedures and data streams across different institutions, which creates extra obstacles to integrating across studies and ecosystems. Creating a framework for coordinated microbiome protocols and data sharing infrastructure, similar to what was done as part of the global, interdisciplinary Tara Oceans project, would be a step in the right direction (Sunagawa et al. 2020). The research community may more easily offer the necessary data inputs for climate models by moving quickly and immediately to standardize microbiome data creation (Banerjee and Heijden 2023). The integration of microorganisms into climate models will advance with the help of a data-driven strategy and a strong shared data infrastructure, resulting in better climate projections and perhaps new mitigation tactics that will always be advantageous to society.

Conclusion and future prospects

Soil, a non-renewable resource, is often overlooked due to its importance in maintaining healthy soil for future generations. Soil microbiomes play a crucial role in retaining carbon and providing nutrients to plants. Understanding the impact of climate change on soil microorganisms' biogeochemical processes is essential for improving climate predictions and designing microbial strategies to combat warming and soil degradation. Climate change-related agitations alter soil microorganisms, providing feedback on ecosystem health and climate limits. Despite uncertainties, soil microbial communities can be managed for monitoring, adaptation, and mitigation. A deeper understanding of the effects of climate change on soil microbes' biogeochemical processes is needed to make more accurate climate change impact estimates and design microbial strategies for addressing future climate impacts and soil degradation. Soil should be appreciated as a living component and future concerns should be raised.

The future prospects are as follows

The ideas that follow can be the focus of future study to better understand and manage soil microbial populations and their potential uses to enhance soil health.

Additional research is required to examine the variety of soil microbial communities and how they operate in various habitats. To identify and characterize particular microbial taxa and their active genes, this may involve sophisticated molecular techniques like metagenomics and meta transcriptomics. It is essential to comprehend the intricate relationships between various microbial species and how they impact soil processes. In order to understand the mechanisms behind microbial-mediated soil activities, future study might examine the dynamics of microbial communities, including competition, cooperation, and synergistic connections.

With the development of high-throughput sequencing technologies, the successful analysis and interpretation of large-scale microbial information requires the use of computational models and bioinformatics tools. Deeper understandings of microbial communities and their roles may be gained by combining machine learning methods, network analysis, and multi-omics data integration. Investigating cutting-edge methods for influencing the microbial populations in the soil might enhance plant development and soil health. In order to increase both the number and the activity of beneficial microbial groups under various soil types and situations, this may entail investigating certain microbial inoculants, amendments, and management techniques.

More research should be done to determine whether soil bacteria may be used for bioremediation. This entails investigating the synergistic impacts of microbial and plant-based remediation techniques for contaminated soil restoration as well as the microbial processes involved in the breakdown and detoxification of different pollutants. In order to convert scientific discoveries into useful applications, microbial-based technologies that are easily implemented in environmental and agricultural contexts must be developed. Subsequent investigations may concentrate on expanding the scope of microbial therapies, refining their delivery techniques, and evaluating their enduring efficacy under various field circumstances.

Forecasting the resilience and stability of ecosystems in the future requires examining how soil microbial populations and their roles are affected by climate change. The effects of changes in temperature, precipitation patterns, and other climatic variables on soil microorganisms, nutrient cycling, and general soil health should be the focus of research efforts. In order to further research in this sector, a multidisciplinary and comprehensive approach is essential. Comprehensive insights into soil microbial populations and their applications may be obtained through collaborative investigations that integrate ecology, agronomy, engineering, microbiology, and environmental sciences. In general, the goal of future study should be to expand on our knowledge of the ecological roles played by soil microbial communities and the possible uses of these communities in enhancing soil health. This information may support ecological restoration, sustainable farming methods, and the creation of creative responses to environmental problems.

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