Review

Impact of Soil Bacteria on Biochemical Cycles

Nisha Kishor Prasad, Loveleen Kaur, D.R. Modi*

Department of Biotechnology, Babasaheb Bhimrao Ambedkar University, Lucknow, India

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Soil bacteria play a vital part in the biochemical cycles, impacting nutrient availability, ecosystem functioning, and global biogeochemical processes. This abstract explores the significance of soil bacteria in biochemical cycles, focusing on their roles in carbon, nitrogen, sulfur cycle, phosphorus, iron cycle and manganese cycles. Soil bacteria, responsible for fixing nitrogen, nitrify and denitrify also mineralize organic phosphorous into soluble form. These correlations are essential for implementing sustainable soil management techniques and reducing ecological deterioration. These interactions can be disturbed by anthropogenic activity, which calls for more investigation to comprehend their processes along with responses to environmental changes. Overall, soil bacteria are essential regulators of biochemical cycles, and maintaining environmental balance. Understanding the intricate interactions between soil bacteria and biochemical cycles is crucial for effective soil management, ecosystem conservation, and sustainable development practices. The aim of the paper is to identify and characterize the bacterial communities involved in these cycles and to determine their contributions to soil health and plant growth. We conducted a comprehensive analysis of soil samples from various ecosystems, using both culture-dependent and culture-independent methods. High-throughput sequencing and metagenomic approaches were employed to identify bacterial taxa and their functional genes related to biochemical cycles. We found that certain bacterial taxa, such as *Rhizobium, Pseudomonas*, and *Bacillus,* play pivotal roles in nitrogen and phosphorus cycling. Our data indicated that microbial diversity and activity are closely linked to soil organic matter. These findings can inform sustainable land management practices and enhance our ability to predict and mitigate the impacts of environmental changes on soil ecosystems.

Keywords*:* ammonification, biochemical cycle, decomposition, denitrification, microbial activity

1 Introduction

Soil consists of 25% of all species worldwide, which are extremely biologically diverse settings. One gram of soil contains ten million of bacteria and fifty thousand species of bacteria, respectively. Through their actions, soil organisms contribute to a variety of ecosystem services (de Vries *et al.,* 2013) and are essential to the functioning of the soil (Wagg *et al.,* 2014). In addition to providing nutrients, bacteria also promote plant development, reduce disease activity, enhance the structure of the soil, and bioaccumulate inorganic material (Hayat *et al*., 2010). Numerous studies have shown that they also help with bioremediation of contaminated soils by reducing organic contaminants. The lack of biodiversity has made soil an extremely vulnerable ecosystem (Trap *et al*., 2015). Threats to soil organism abundance, distribution, and activity include erosion of soil, land use modification, overexploitation, pollutants, and biological invasion (Gardi *et al.,* 2013; Trap *et al*., 2015). The biochemical cycle is greatly influenced by soil bacteria, which mediate activities related to soil fertility and plant growth and aid in the cycling of vital elements such as sulfur, phosphorus, and nitrogen (Basu, S. *et al.,* 2021). Because of their diverse metabolic makeup, soil bacteria can either source or sink large amounts of greenhouse gasses, which has a substantial impact on climate regulation (Mohanty *et al.,* 2021). Soil bacteria are central players in these cycles, driving transformations that impact soil fertility, plant nutrition, and environmental quality. According to research, organic matter is the main source for carbon along with other nutrients in soil (Rousk, J., & Bengtson, P. (2014**)**.

* **Corresponding Author:** Prof. D.R. Modi; Department of Biotechnology, Babasaheb Bhimrao Ambedkar University, Raibareli Road, Lucknow-226025, India; E-mail: drmodilko@gmail.com; ORCID: https://orcid.org/0009-0006-6707-951X

Microbial communities and environmental parameters, such as pH, temperature, and soil water capacity, impact the breakdown of organic matter in soil, and biogeochemical activity rates are reliant on these variables.

Decomposition of organic matter, carbon compound recycling, fixation of nitrogen, nitrification, denitrification, ammonification, phosphorous solubilization, and sulfur mineralization are all significantly aided by soil bacteria. They contribute to the synthesis of organic carbon, break down complex carbon molecules, and exhale carbon dioxide. They also aid in the solubilization and mineralization of phosphorus for plant uptake, as well as fixing nitrogen, nitrification, denitrification, and ammonification. They also take part in sulfur mineralization, sulfide oxidation, and sulfate reduction. In order to create nitrogen-fixing symbiosis with leguminous crop plants, *Rhizobium* species—including *Rhizobium* and *Mesorhizobium*, *Bradyrhizobium*, *Azorhizobium*, *Allorhizobium*, and *Sinorhizobium*—have been productively employed worldwide (Hayat *et al*., 2010). Non-symbiotic nitrogen fixing bacteria like *Azotobacter, Azospirillum, Bacillus,* and *Klebsiella sp*. are used to inoculate arable land globally to boost plant productivity. To increase the phosphorus status of plants, phosphate-solubilizing bacteria such as *Bacillus* and *Paenibacillus* have been added to soils. They support environmental safety and health by assisting in the removal of polluted soils through processes like biodegradation, biosurfactant synthesis, and toxic element detoxification (Fatima *et al., 2022;* Srivastava *et al.,* 2022). The capacity to improve the biodegradation of organic contaminants and the extraction of heavy metals from soil has been shown in bacteria such as *Pseudomonas, Bacillus, and Acinetobacter* (Srivastava *et al.,* 2022). The ability of soil bacteria to adapt to different soil environments, preserve soil quality, and take part in worldwide biogeochemical cycles is attributed to their metabolic versatility and phenotypic plasticity. Overall, soil bacteria's functional traits and interactions with the soil environment are fundamental in shaping global element cycles and ecosystem functioning.

2 Review

2.1 Soil Bacterial Diversity and Composition

With its unrivaled richness of bacteria, soil represents one of the most diversified biosphere segments (Bickel, S., & Or, D. (2020). One common explanation for soil's enormous diversity is that it has a variety of chemical and physical microenvironments (Bach, E. M. *et al.,* 2018; Vos, M. *et al.,* 2013). The complex structure of soil pores offers a multitude of habitats for a wide variety of bacterial species. Bacterial species with low abundance play an important role in biochemical cycles and serve as the "seed pool" for species richness. Fluctuations in microbial biomass are frequently seen; these fluctuations are affected by the availability of resources and have an effect on bacterial diversity across all sizes (Bickel, S. *et al.,* 2020; George, P. B. L. *et al.,* 2019). Because they accentuate low-abundance species in resource-rich environments, observations of microbial abundance fluctuations with soil depth may mislead conclusions about bacterial richness (Bickel, S. *et al.,* 2020). According to recent empirical research, comprehending bacterial abundance and diversity requires assessing soil properties such as texture, porosity, and hydrated conditions in connection to climate and vegetation cover (George, P. B. L. *et al.,* 2019). Diversity is also influenced by the nature of the soil, which includes the pH, texture, organic matter level, and mineral makeup. Different types of vegetation offer different niches for soil bacteria; different bacterial communities can be found in forests, grasslands, marshes, and deserts. Soil bacterial diversity can be changed by human activities such as agriculture, urbanization, deforestation, and pollution. The functional diversity of bacterial communities in soil can be quantified using a variety of diversity indices with the Biolog® EcoPlatesTM approach. To unravel the genetic diversity of soil microorganisms, including unculturable bacteria implicated in nitrogen fixation and bioremediation processes, molecular techniques such as 16S rDNA sequencing and Sanger sequencing are applied. Techniques including FISH, denaturing gradient gel electrophoresis, and terminal restriction fragment length polymorphisms are used to examine the genetic diversity and structure of soil microorganisms (Dubey *et al.,* 2020). To comprehend the complex nature of microbial communities in soil and their essential function in maintaining soil fertility and fostering plant health, researchers employ a variety of techniques (Yaman *et al.,* 2022).

Through interactions with other organisms, such as symbiosis, competition, and predation, soil bacteria shape variety through ecological processes. Diversity of soil bacteria can also differ at different spatial scales within the same ecosystem. Comprehensive sampling, molecular analysis methods, and ecological modeling are necessary to comprehend this diversity.

2.2 Techniques for studying Soil Bacterial diversity

2.2.a Plate Counts*:* The quick, low-cost, culture-dependent plate count approach gives direct information about the population's heterotrophic, active component (Bing-Ru *et al.,* 2006). Approximately five thousand different species of bacteria have been identified; however, only 0.1 percent to 1 percent of the soil's bacteria can be cultivated in a laboratory setting using conventional methods. Growth circumstances are limited by factors such as light, pH, and temperature. There are about 1.5 million species of fungi in the world, yet many of them cannot be cultured like bacteria in typical laboratory settings. Colony-forming unit (CFU) assays, sometimes referred to as culture-based methods or plate count techniques for soil bacteria, are used to quantify viable bacterial populations in soil samples. Sample preparation, serial dilution, inoculation, incubation, colony enumeration, and data analysis are all included in these approaches. To lower the microbial load, soil samples are gathered, homogenized, and diluted with sterile diluents. Using aseptic methods, aliquots of the diluted soil solutions are plated onto solid agar substrate. To encourage bacterial growth, incubation is carried out for 24–48 hours at a temperature of 25–30°C. Following incubation, colonies are counted by hand or with the use of automated counters. The bacterial count is computed using the number of colonies counted as well as the plating dilution factor. By using data analysis, one can compare the bacterial populations in various soil samples.

2.2.b Community level physiological profiles (CLPP) and sole carbon source utilization (SCSU) patterns*:* The CLPP approach analyses the physiological diversity of soil to uncover probable patterns of carbon substrate usage by microbial communities. Variances are interpreted as corresponding to variances in the principal active microbial members. To generate the metabolic profile of microorganisms, the BIOLOG system makes utilization of 95 carbon sources. The analysis and interpretation of automated measuring techniques can be difficult, despite their popularity in the study of the functional properties of microbial communities (Bing-Ru *et al.,* 2006). The culturable bacterial metabolic diversity is assessed by the BIOLOG systems; the microbial metabolic activity is not significantly affected by soil fungi or slow-growing bacteria. Partial microorganisms' ability to adapt to these soils may be limited by the plate neutral pH, in contrast to some acidic or alkaline soils. Numerous variables have impacted the composition of soil microbial communities, many of which have been detrimental.

A useful method for determining the functional diversity of microbial communities in research publications is metatranscriptomics (Adekoya *et al.,* 2023*;* Mukherjee *et al.,* 2020*;* Taj *et al.*, 2023). By analyzing the complete set of transcripts from environmental samples, metatranscriptomics enables the study of various functions and pathways in microorganisms, shedding light on biogeochemical cycles, pathogenic processes, metabolism, and development. This approach goes beyond traditional culture-based techniques, providing a comprehensive understanding of microbial activities and interactions within complex ecosystems. Metatranscriptomics not only identifies uncultured organisms but also allows for the exploration of gene expression profiles, offering insights into how microbial communities respond to environmental changes and drive essential processes within their habitats.

2.2.c The analysis of FAME (Fatty acid methyl ester) and PLFA (phospholipid fatty acid): By grouping fatty acids, the FAME technique offers information about the makeup of microbial communities (Bing-Ru *et al.,* 2006). Signature fatty acid composition, which comprise a stable fraction of cell biomass, have been shown to be able to distinguish between the main taxonomic categories within a community. A change in the composition of fatty acids indicates a change in the community structure and microbial biomass. The techniques that microorganisms use to adapt to a variety of environmental variables, such as soil type, management methods, climate, and disturbances, have been investigated through the application of the PLFA approach (Bing-Ru *et al.,* 2006). It suggested grouping PLFAs into chemically distinct subgroups to streamline assessment processes and enhance the evaluation of the soil microbial population by examining important mechanisms.

2.2.d Molecular-Based Techniques: To identify and cultivate soil bacteria and ascertain their variety, molecular methods such as PCR-dependent procedures and indirect DNA cultivation are frequently used. A growing number of microbial ecologists are use molecular techniques, such as DNA cloning, FISH, PCR-based techniques, and nucleic acid hybridization, to investigate the distribution and activity of environmental microorganisms. A quick and effective way to research biodiversity is through metagenomics, which makes it possible to identify bacteria that cannot be cultured (Chaudhari *et al.,* 2023*;* Yaman *et al.,* 2022*;* Hussein, A. 2021). However, each molecular technique has its limitations, leading to knowledge gaps in microbial ecology. To address these gaps, a combination of methods can be utilized. For instance, while metagenomics provides a broad view of microbial diversity, metatranscriptomics can offer insights into functional diversity by analyzing gene

expression within these communities. By integrating metagenomics with metatranscriptomics, researchers can bridge the gap between microbial composition and activity, providing a more comprehensive understanding of microbial ecosystems and their interactions with the environment. This synergistic approach helps overcome the individual limitations of each method, leading to a more holistic assessment of microbial diversity and function.

2.2.e Nucleic acid hybridization and fluorescent in situ hybridization (FISH)*:* Nucleic acid hybridization is a vital analytical tool in genomic bacterial ecology (Bing-Ru *et al.,* 2006). Techniques for hybridization can be used on extracted RNA and DNA or in situ within cells. The FISH method has been successfully utilized to study the spatial distribution of bacteria in biofilms, as noted by (Bing-Ru *et al.,* 2006). Due to sensitivity limits, low ribosome content cells cannot be detected using the usual FISH approach. Slow-growing or hungry cells could go undetected because low ribosomal content per cell is frequently associated with poor physiological activity (Bing-Ru *et al.,* 2006). Detecting FISH-stained cells, auto fluorescence interference, and changes in detection rates brought on by soil microbe activity are some of the drawbacks associated with using DAPI for counterstaining. The inability of most nucleic acid-based technologies to establish a direct connection between phylogeny and processes restricts the inferences that can be made from the produced data. In order to overcome these constraints, hybridization chain reaction (HCR) with FISH has been modified to increase signal intensity and specificity in environmental samples such as sea sediments. Standardizing procedures and analytical techniques is advised to increase the comparability of soil eukaryotic marker gene sequencing results.

2.2.f PCR - based techniques: Polymer chain reactions (PCR) is a useful tool for ecology and environmental study since it is being used in studies of diversity to address the drawbacks of culture-based methodologies. Although 18s rDNA as well as ITS regions are being increasingly utilized to research fungal communities, 16s rDNA PCR is commonly used to study prokaryotic bacteria diversity and identify prokaryotes (Bing-Ru *et al.,* 2006). To obtain particular community information, the target DNA has been amplified using universal or particular primers, segregated, and hybridized with primers.

2.2.g Denaturing gradient gel electrophoresis (DGGE) and temperature gradient gel electrophoresis (TGGE): Two techniques for examining microbial diversity are DGGE and TGGE. The advantages of using these two techniques are the analysis of large number of samples can be done simultaneously and these techniques are reliable, reproducible and rapid to observe changes in the sample (Gałązka, A., & Grządziel, J. (2016). Point changes in DNA sequences can be found using the TGGE and DGGE methods, where temperature is employed as the gradient instead of chemical denaturants. DGGE has limitations due to its reliance on PCR, necessitating careful selection of conditions and suitable polymerase. The majority of issues with this method arise from errors made during this stage. Polymerase chain reactions can introduce errors by altering the genetic profile of the samples being studied. PCR products with distinct nucleotide sequences from different organisms can occasionally have the same melting point. There are the greater chances of some bands on the gel being missed. PCR can lead to false results due to non-specific products, such as amplification of chloroplast or mitochondrial DNA. Several step PCRs and touchdown PCRs can be used to improve the reaction's specificity and avoid such circumstances.

2.2.h Restriction fragment length polymorphism (RFLP) and terminal restriction fragment length polymorphism (T-RFLP)*:* The RFLP banding pattern must be fully digested and repeatable in order to be used as a DNA sequencer-based technique for evaluating the diversity of the microbial population. Community's analysis uses agarose or non-denaturing electrophoresis of polyacrylamide gel (PCGE) to detect various lengths. Each PCR primers is marked with a dye that is fluorescent in the T-RFLP approach, which is widely used to monitor shifts in microbial diversity over time and space (Bing-Ru *et al.,* 2006).

2.2.i Single-strand conformational polymorphism (SSCP): The separate extraction of PCR-amplified rRNA or rDNA molecules is a technique known as SSCP, and it has been effectively used to the study of the dynamics and composition of microbial communities. The technique is based on the variation in the intra-molecular fold of single-stranded genetic material, which is impacted by changes in DNA sequences and influences the movement of PCR amplifications on the electrophoresis. SSCP is used to differentiate between undeveloped rhizospheric microbial communities and pure soil microorganism cultures from various plants. Since there is no need for a gradient gel or GC-clamp, SSCP analysis is less complicated than DGGE or TGGE. However, because of different operons or conformations, it might produce several bands.

3 Biochemical Cycle

Through the process of biogeochemical cycling, which combines chemical and biological processes, microorganisms work together to change the chemical and physical properties of nutrients such as nitrogen, phosphorus, carbon, and sulfur, iron, and manganese. While gaseous components are absent from sedimentary cycles like those containing phosphorus and iron, they are present in both nitrogen and carbon cycles and are frequently fixed by soil, water-based, and marine microorganisms. A brief explanation of biochemical cycle is in Figure I.

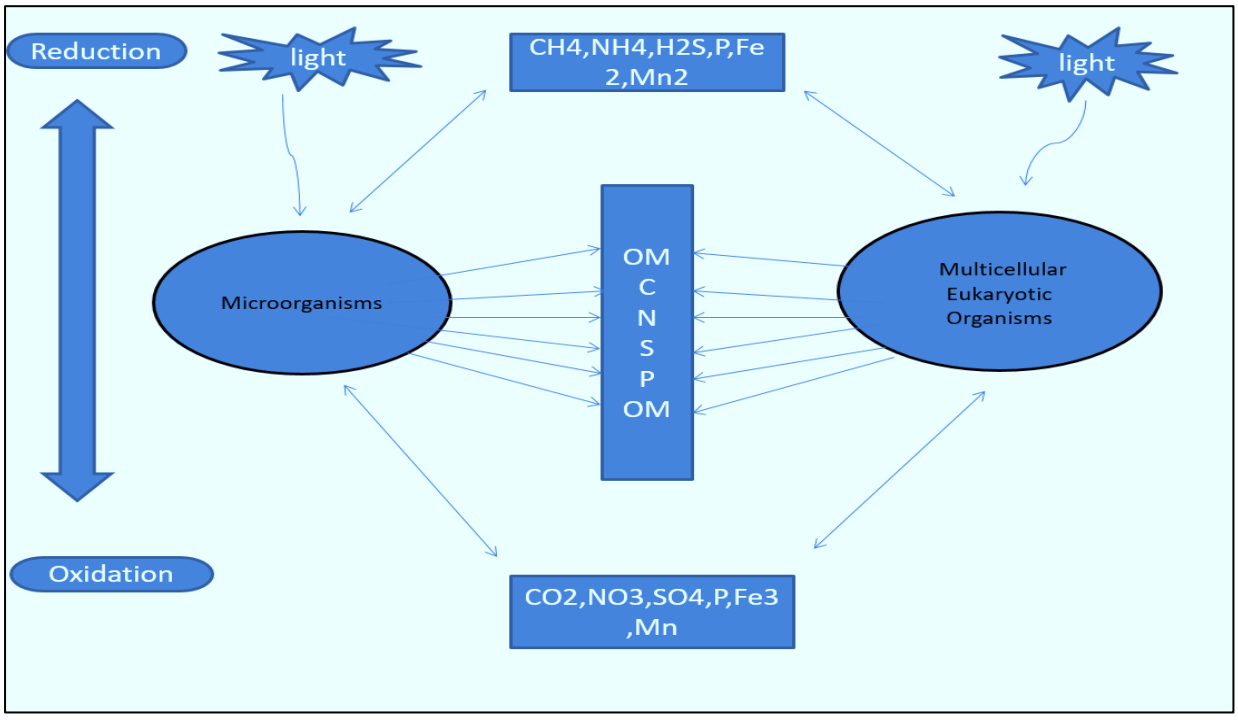

Fig. 1 Biogeochemical cycles, which involve light energy and reduced/oxidized molecules, are interrelated. Major fluxes include organic substances, lithogenic sources, biotic components, including microbes and multicellular creatures (Prescott *et al.,* seventh edition page 666)

4 Carbon Cycle

Plant development can be improved by soil bacteria which will increase the amount of carbon retained in plant biomass (Dathe, A. *et al.,* 2023). By releasing and sequestering carbon dioxide, bacteria in soil contribute to the creation and decomposition of organic matter, which in turn affects carbon storage (Bertini, S.*et al.,* 2022). Particularly in less productive soils, actinobacteria, a soil-living bacteria, are essential to the breakdown of plant waste (Bao, Y. *et al.,* 2021). High concentrations of carbohydrate-active enzyme (CAZymes) and comparatively steady presence throughout decomposition are two characteristics of these bacteria.

Carbon is present in reduced forms like methane (CH_4) and organic matter, as well as more oxidized forms like carbon monoxide (CO) and carbon dioxide (CO_2). The carbon cycle begins with carbon fixation, where at least half of the Earth's carbon is fixed by microbes such as *Cyanobacteria, Prochlorococcus* and *Synechococcus*. Organic matter can be reduced anaerobically to methane (CH_4) or oxidized back to CO_2 through aerobic or anaerobic respiration and fermentation. Methane production is influenced by factors such as nutrient availability, abiotic conditions, and the presence of microbial communities. Nutrients may not be completely recycled into living biomass due to the environment's deficiency in certain nutrients. For example, chitin, protein, and nucleic acids contain nitrogen in large amounts, which can be released to the environment through mineralization. Some carbon substrates can be degraded easily with or without oxygen, but hydrocarbons and lignin are unique in that they require the initial addition of molecular oxygen. Anaerobic degradation of

hydrocarbons with sulfate or nitrate as electron acceptors can occur, but this process proceeds more slowly and only in microbial communities exposed to these compounds for extended periods Fig. II (Prescott *et al.,* seventh edition page 665). Influenced by elements such as microbial count, richness of species, diversity of bacterial species, and enzyme activity, soil bacteria play a major role in the breakdown and sequestration of carbon in the soil ecosystem.

The global C cycle and the N cycle interact, with the nitrogen supply initially lowering CO_2 emissions but raising them when there is an excess, underscoring the complex interplay in the dynamics of climate change. Cyanobacteria, a type of bacteria, play a crucial role in CO_2 fixation through both photosynthetic and chemosynthetic assimilation processes (Angel *et al.,* 2022). In order to control atmospheric carbon levels and mitigate the impacts of global warming, microbial activity is essential. Gas emissions in the nitrogen and carbon cycles are a major cause of climate change caused by microbial processes (York, A. (2018). Biogeochemical cycles and bacteria are essential for preserving planetary habitability and resolving climate change-related environmental problems. It is essential to comprehend the various metabolic capacities of bacteria in order to analyse how gas emissions affect cycles and how this affects climate change.

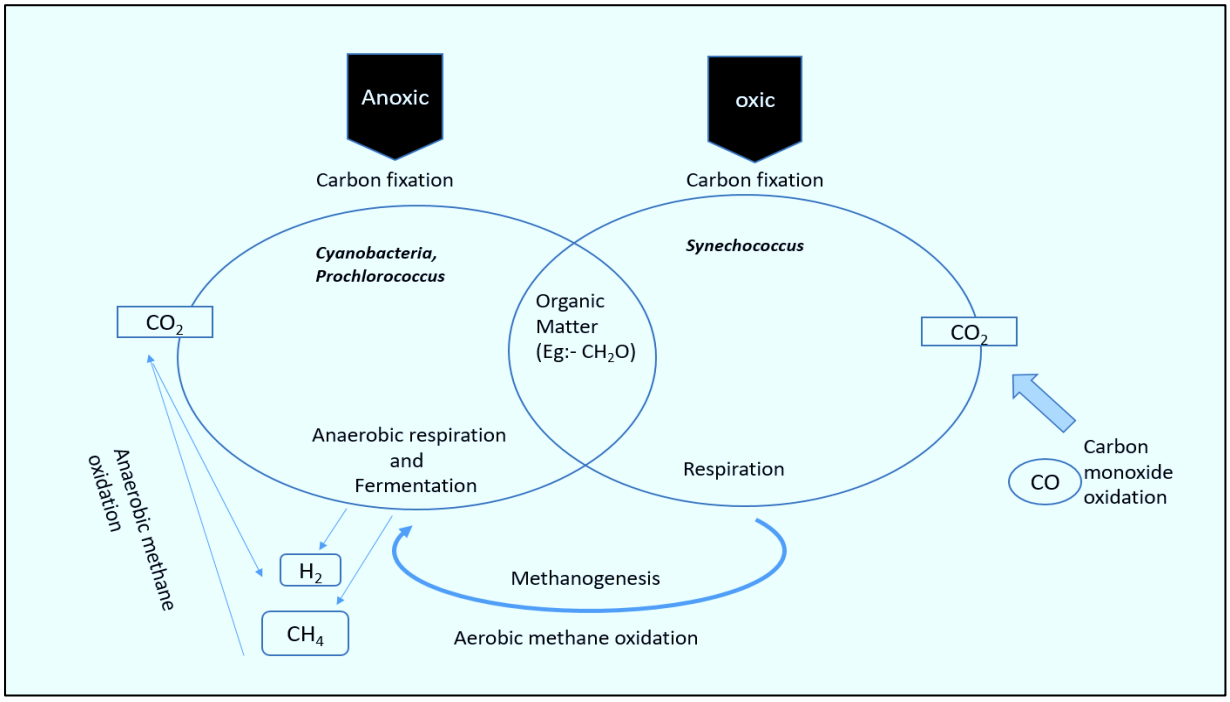

Fig. 2 Carbon Cycle in the environment by the soil bacteria (Prescott *et al.,* seventh edition)

5 Nitrogen Cycle

New PCR-free meta-omics studies cast doubt on the traditional nitrogen fixation population and identify *Deltaproteobacteria*—a hitherto underappreciated group—as the main diazotrophic microbiome in soils (Mauda, Y. *et al.,* 2022). Free-living nitrogen-fixing bacteria called *Azotobacter* species are known to play a significant role in biological nitrogen fixation and have the potential to be used as biofertilizers to improve soil fertility and plant nutrition. Prokaryotic microorganisms like *Azotobacter, Trichodesmium*, and anaerobes like *Clostridium* are the main hosts of the nitrogen fixation process. Although bacterial symbionts that live inside of leguminous plants have been the subject of the most research, other bacterial symbionts such as *Frankia* and *Anabaenea* have also been shown to fix nitrogen in water ferns and woody shrubs. Ammonia is created during nitrogen fixation and is then absorbed by organic materials as an amine. Because they are O_2 sensitive, nitrogenase enzymes need to be kept away from oxidizing environments. Heterocysts are a tactic used by aerobic and microaerophilic bacteria to distinguish between fixation and photosynthesis. The nitrogen cycle proceeds, nitrifying ammonium to produce nitrate. The second stage, which involves oxidizing ammonium ion, is carried out by *Nitrobacter* as well as associated chemolithoautotrophic bacteria, whilst *Nitrosomonas* and *Nitrosococcus* bacteria are crucial in the first step. The process of assimilating nitrate, or reducing it by combining it with organic nitrogen, depends on nitrate generation. This procedure can accumulate as a temporary intermediary and is costly. Through

denitrification, which yields the gases nitrogen and nitrous oxide, dissimilatory reduction uses nitrate as an electron receiver during anaerobic respiration. One consequence of nitrosamines that might cause cancer is nitrite. Bacteria in dissimilatory reduction include *Desulfovibrio spp., Clostridium spp.,* and *Geobacter metallireducens.* Marine microorganisms have discovered a new method of converting nitrogen: the anammox process. Nitrite serves as the terminal electron acceptor in this anaerobic process, which reduces ammonium ion to nitrogen gas (N_2). Since planctomycete bacteria convert NH_4 to N_2, this discovery has caused a re-evaluation of the nitrogen cycle in the open ocean Fig. III (Prescott *et al.,* seventh edition). In agricultural ecosystems, soil bacteria—such as diazotrophs, nitrifiers, and denitrifiers—play a crucial role in the cycling of nitrogen. Their activity and abundance are determined by many soil variables.

Natural equilibrium is upset by the greenhouse gas releases from the carbon and nitrogen cycles, which include methane and nitrous oxide (N_2O has a radiative force 298 times larger than CO_2) (Mande *et al.,* 2016). While nitrogen deposition affects sources and sinks of N_2O, CH_4, and CO_2, it also affects nitrogen cycling mechanisms, which directly affect radiative forcing through N_2O emissions and carbon sequestration in forests. Human activity affects soil health and climate change by increasing nitrogen deposition, increasing N_2O emissions, and influencing the cycling of carbon and nitrogen on land. The global C cycle and the N cycle interact, with the nitrogen supply initially lowering CO_2 emissions but raising them when there is an excess, underscoring the complex interplay in the dynamics of climate change.

6 Phosphorus Cycle

In living cells, phosphorus is essential for lipids, polysaccharides, and nucleic acids. It is found in soil both in organic and inorganic forms and is produced by the weathering of rocks that contain phosphate. Microbial activity recycles organic phosphorus, transforming it back into its organic state. Between pH 6 and 7, inorganic phosphorus forms complexes with cations such as calcium, iron, and aluminium, which makes it available to microorganisms and plants. All organic forms of phosphorus maintain their 5 valence state. Simple orthophosphate is transformed into more complex forms by microorganisms (*Actinomycetes, Pseudomonas*) during the phosphorus transformation process (Prescott *et al.,* seventh edition). The breakdown and solubilization of phosphorous in soil, which transforms insoluble phosphorus into soluble forms suitable for plant uptake, depends on phosphorus solubilizing bacteria (PSB) (Kiprotich *et al.,* 2023). Tricalcium phosphate (TCP) along with other inorganic phosphates can be dissolved by the production of organic acids and the acid phosphatases by bacteria (Donglan He and Wenjie Wan 2022) and (Wang, C. *et al.,* 2023). Additionally, they help organic phosphates become mineralized so that plants can use them (Nguyen, T. T., & Trung, Q. (2022). The quantity of PSB and phosphorus-cycling-related genes has been discovered to be influenced by fertilization treatment and aggregate fractions in soil aggregates (Jilani*et al.,* 2021). PSB highlights their function in phosphorous mineralization and solubilization processes, as well as their prospective applications in sustainable agricultural and soil remediation. It enhances soil phosphorus availability, plant development, and phosphorus uptake. Explained in Fig. IV

7 Sulphur Cycle

Sulfur is converted by microorganisms such as sulphur-oxidising bacteria (SOB) of the *Thiobacillus* genus, *Campylobacter, Desulfuromonas acetoxidans* from organic into inorganic forms and back again. Sulfide is broken down into elemental sulfur and sulfate, which are used as electron sources by photosynthetic and chemolithoautotrophic organisms. Sulfate is used by microorganisms such as *Desulfovibrio* to receive electrons during anaerobic respiration. Assimilatory sulfate elimination is utilized in the creation of proteins and amino acids, whereas dissimilatory sulfate reduction builds up sulfide in the environment. Many microbes can convert another intermediary, sulfite, to sulfide. Deep water columns are home to photolithotrophic sulfur oxidizers such as *Chlorobium* and *Chromium*, while a wide range of bacteria use carotenoid and bacteriochlorophyll a pigments to carry out aerobic anoxygenic photosynthesis. Small sulfur cycle chemicals, like as DMSP, are essential to life as they are converted into volatile sulfur, which influences atmospheric processes, and are utilized by bacteria for protein synthesis. Important sulfur cycle changes, such as sulphide oxidation to elemental sulfur, which has a quick half-life of 10 minutes at room temperature, happen without the presence of microbes under ideal pH and oxidation-reduction conditions Fig. V (Prescott *et al.,* seventh edition).

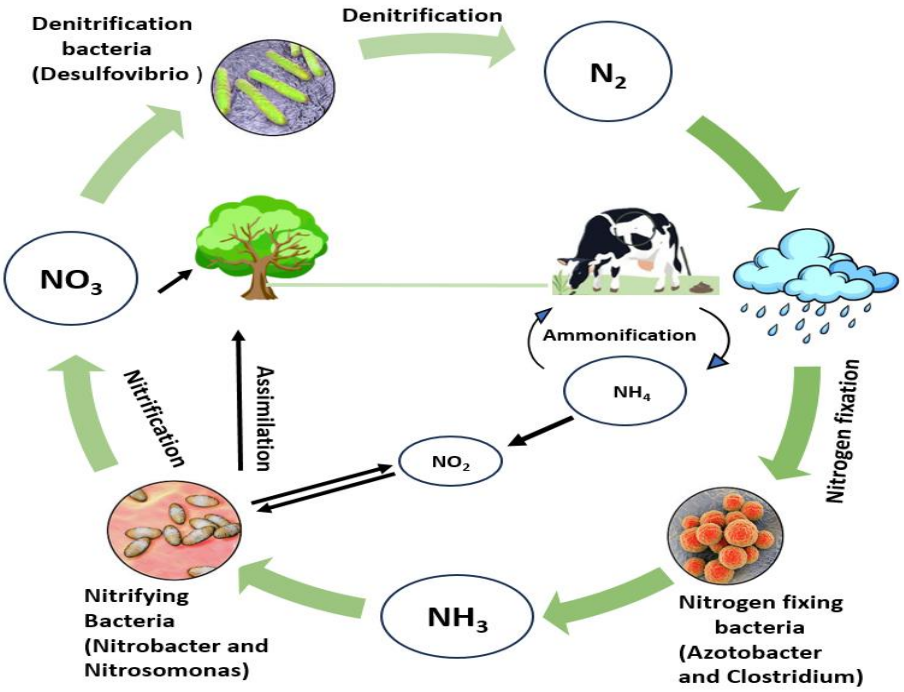

Fig. 3 Nitrogen Cycle done by Microorganisms in Environment

8 Iron Cycle

Thiobacillus ferrooxidans and *Sulfolobus* oxidize iron in acidic environments, while *Gallionella spp.* oxidize iron in neutral pH circumstances. Other genera, such as *Leptothrix* and *Sphaerotilus*, which were formerly categorized as "iron bacteria," have been identified as chemoorganotrophs because of their chemical oxidation. A mixotrophic microbe called *Dechsoma suillum* uses nitrates as an electron receiver to oxidize Fe^2. It can also make use of perchlorate and chlorate, which are contaminants found at military sites and weapons plants. This mechanism can lead to the accumulation of oxidized iron zones in sediments from waters with oxygen levels that are low. Under anoxic conditions, specialist bacteria such as *Ferribacterium limneticum, Geobacter sulfurreducens, Shewanella putrefaciens* and *Geobacter* metallireducens are primarily responsible for iron reduction. They use ferric iron to get the energy they need to thrive on organic materials. Certain bacteria convert extracellular iron to magnetite, which helps them build magnetic compasses inside their cells. Magnetotactic bacteria, such as *Aquaspirillum magnetotacticum*, build intracellular magnetic devices and accumulate magnetite as an external product by converting extracellular iron to the mix valence oxide of iron mineral magnetite (Fe_3O_4). Sediments include magnetite, which contributes throughout time to activities related to the cycling of iron. To create new magnetically sensitive microbes, bacteria have cloned the genes responsible for the creation of magnetite. Using magnetic fields, magnetotactic bacteria move to the ideal oxygen concentrations. Anoxic oxidation/reduction cycles are produced by iron-oxidizing bacteria when they create ferric ions, which enable chemotrophic-based iron reduction

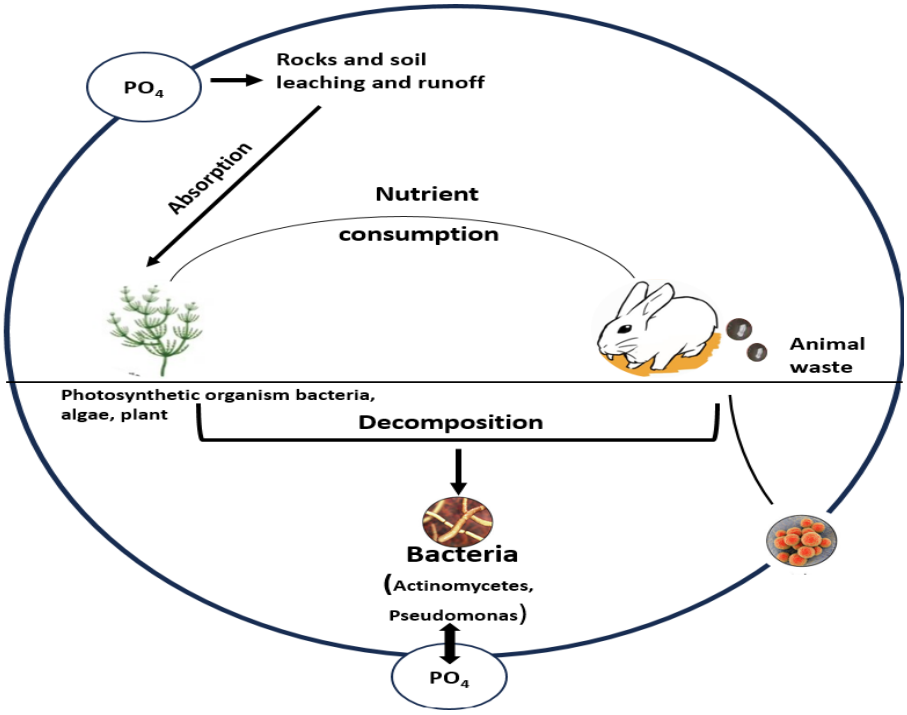

Fig. 4 Phosphorus Cycle by Microorganisms in the Environment

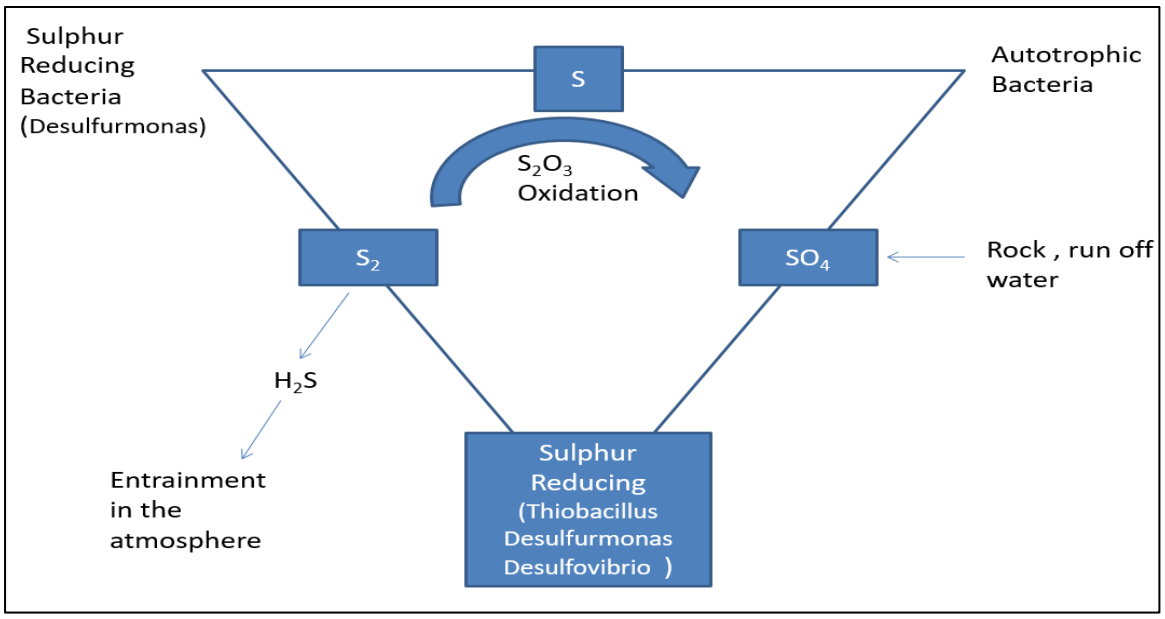

Fig. 5 Sulphur cycle by Microorganisms in the Environment

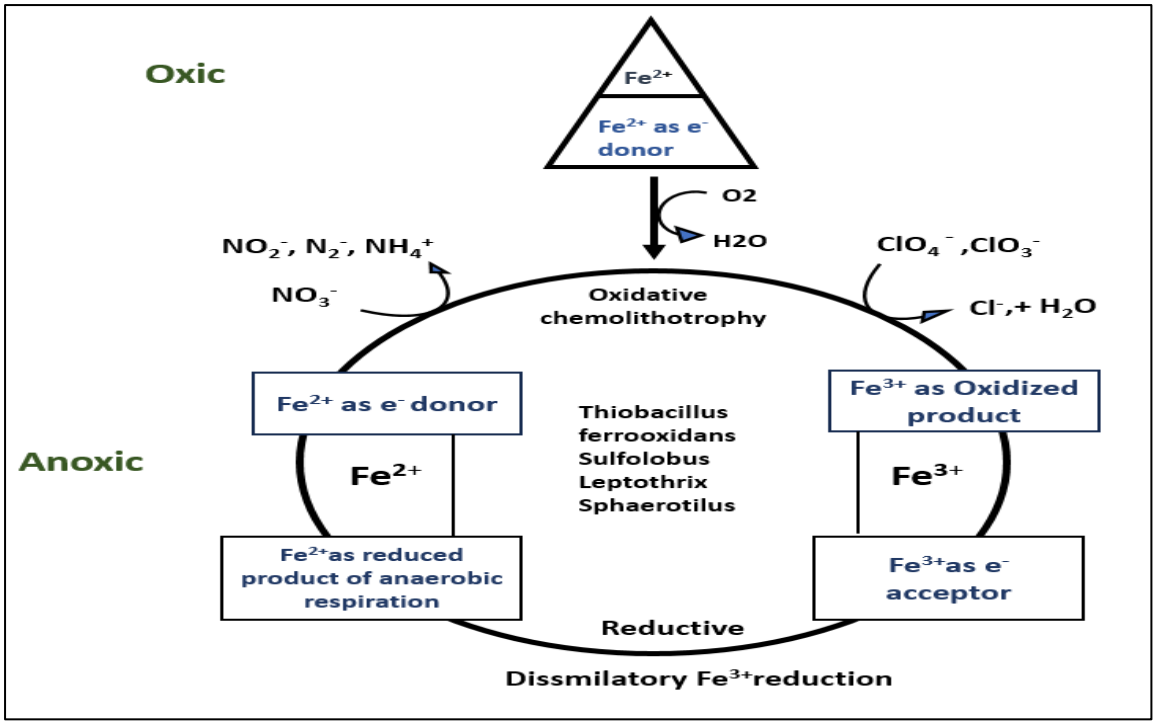

Fig. 6 Iron Cycle by Microorganisms in the Environment

9 Manganese Cycle

Microorganisms, including *Pedomicrobium, Arthrobacter, Shewanella, Leptothrix, Geobacter*, and others, are essential to the manganese cycle because they convert manganous ion (Mn2) into MnO_2 (Prescott *et al.,* seventh edition). In order to control biogeochemical cycles and affect the mobility of Mn in soil environments, this mechanism is essential (Javier Velaza, 2022). Research reveals that bacteria, in specific, are the principal microorganism responsible for the breakdown of soluble Mn (II) in natural environments (Lorenz, C. *et al.,* 2012). Reactive oxygen compounds (ROS), which are produced in reaction to Mn(II) exposure, are involved in the bacterial non enzymatic Mn(II) oxidation displayed by soil-borne bacteria such as *Providencia sp. LLDRA6*. The oxidation and mobilization of manganese (Mn) in soil environments, that in turn affects Mn's transit and destiny in biogeochemical cycles, is largely dependent on soil bacteria Fig. VII.

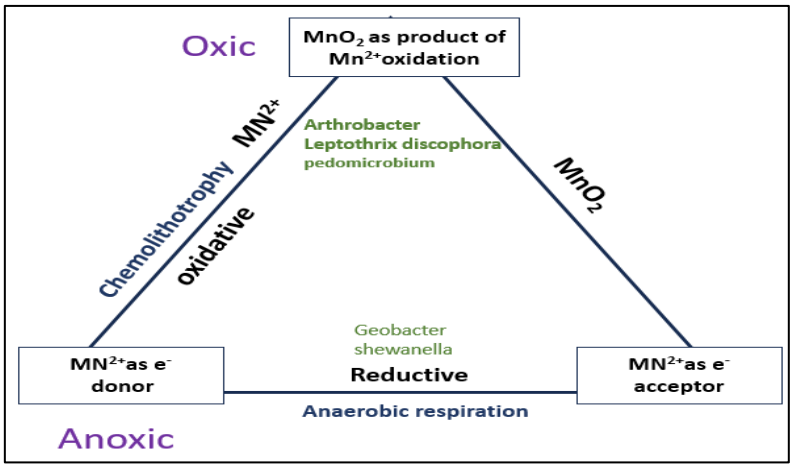

Fig. 7 Manganese Cycle by Microorganisms in the Environment

10 Ecological Implications and application

Microorganisms found in soil serve a vital role in the cycling of nutrients, the breakdown of organic matter, and the maintenance of soil structure (Basu, S. *et al.,* 2021). The biochemical cycle of vital elements, such as phosphorus, nitrogen, and sulphur, which are crucial for the development and growth of plants, is greatly aided by soil microbial communities. Agrochemical fertilizers and pesticides have the potential to suppress microbial activity, whereas soil management techniques such as organic and biobased technologies can support microbial populations and the cycling of nutrients. Understanding the metabolic cycles mediated by soil bacteria is essential to preserving soil fertility and advancing sustainable agriculture.

11 Potential applications of soil bacterial manipulation for agricultural and environmental management

Manipulating soil microorganisms may have uses in environmental and agricultural management. The application of microorganisms in microbial remediation has demonstrated promise in repairing soil contamination brought on by pesticides, heavy metals, and petroleum (Miaorong Yu and Jinbo Li, 2023). Microbes have a crucial part in the breakdown of petroleum and pesticides (Abo-Alkasem *et al*., 2023), as well as in the absorption of heavy metals and the subsequent decrease in the rhizosphere's concentration (Shylla *et al*., 2021). The main method for removing heavy metals from fields is phytoremediation, in which plants take up and eliminate the metals (Atuchin *et al.,* 2023). Field trials involving microbial applications in agricultural and environmental management have been conducted to combat heavy metal contamination. In an effort to enhance phytoremediation effectiveness in agricultural soils and remove contaminants from experimental media, a collaboration of technogenic microorganisms conducted a study that produced encouraging finding (Zhu, Y. (2022). Biofertilizers encompass a variety of nitrogen fixation processes: phosphate solubilization by *Pseudomonas*, *Bacillus*, and *Enterobacter*; potassium solubilization by *Bacillus mucilaginosus* and *Frateuria aurantia*; organic matter decomposition by *Bacillus subtilis* and *Cellulomonas*; and symbiotic nitrogen fixation by *Rhizobia* and *Frankia*; free-living nitrogen fixation by *Azotobacter* and *Azospirillum*. Both the structure of the soil and the availability of vital nutrients are improved by these bacteria. Plant growth-promoting rhizobacteria (PGPR) stimulate root elongation, nutrient uptake, cell division, shoot growth, gibberellin production, iron acquisition, and stress resistance. They produce auxins, cytokinins, gibberellins, siderophores, and stress-resistance compounds, enhancing growth and preventing iron deficiency. These bacteria also aid in abiotic stress mitigation. Antagonistic bacteria can be used to biocontrol plant diseases by inhibiting their growth via antibiotics or resources outcompetition. Plant tolerance to pathogen attacks can be strengthened via induced systemic resistance (ISR). Moreover, competitive exclusion, biofilm development, pathogen predation, and antifungal agents can be used. These advantageous bacteria have the ability to suppress pathogen populations, erect physical obstacles, and outcompete dangerous diseases for resources and available space. Thus manipulating soil microbes can improve agricultural methods and combat pollution.

12 Considerations for sustainable soil management practices

Sustainable soil management techniques require an all-encompassing strategy that considers a number of variables. It is essential to assess how different management strategies affect different soil services and functions at different geographical scales and under different local conditions (Gin Garland, 2023). In order to avoid harm and advance social and environmental advantages, the building and urban development industries would proactively plan and manage soil (Davies *et al.,* 2023). Soil management strategies that are climate-smart are essential for adapting to changing environmental conditions. To close the knowledge gap in sustainable soil management, scientists and policymakers should work together.

Table 1 Correlation of Soil bacteria with the Biochemical cycle

BIOCHEMICAL CYCLE	SOIL BACTERIA	CORRELATION	REFERENCES
Carbon cycle	*Cyanobacteria Prochlorococcus Synechococcus*	Soil bacteria significantly influence the global carbon cycle, affecting carbon sequestration, plant growth, organic matter decomposition, carbon storage, and greenhouse gas emissions.	Bertini, S.*et al.,* 2022
Nitrogen Cycle	*Azotobacter Trichodesmium Clostridium Nitrosomonas Nitrosococcus*	Through their effects on nitrification processes, soil microbial populations, genetic capacity, and the dynamics of bioavailable nitrogen, soil bacteria including diazotrophic and archaea contribute significantly to the nitrogen cycle.	Shukla, S*. et al.,* 2021
Phosphorus Cycle	*Actinomycetes Pseudomonas*	The study shows a correlation between the quantity of phosphate-solubilizing bacteria and the abundance of phosphorus-cycling genes in soil aggregates.	Donglan He and Wenjie Wan 2022
Sulphur Cycle	*Thiobacillus Campylobacter Desulfuromonas Desulfovibrio*	Soil bacterial activity correlates with the sulfur cycle, influencing carbonyl sulfide (OCS) exchange rates, especially at moderate moisture levels, impacting soil atmosphere gas exchange dynamics.	Behrendt, T. *et al*., 2019
Iron Cycle	*Thiobacillus ferrooxidans Sulfolobus Leptothrix Sphaerotilus Geobacter*	Soil bacteria that oxidize, nitrify, and denitrify iron are linked to metal corrosion, enhancing nitrogen cycling and electron transfer pathways, thus affecting the iron cycle in the environment.	Huang, Y. *et al.,* 2021
Manganese Cycle	*Pedomicrobium Arthrobacter Shewanella Leptothrix Geobacter*	Soil bacteria significantly contribute to manganese cycles by promoting oxidation and reduction processes, affecting groundwater quality and potentially enhancing water treatment applications.	Javier Velaza, 2022

13 Future Directions and Research Needs

Subsequent investigations have to center on comprehending the function of soil bacteria in biochemical cycles, their reaction to alterations in the environment, and an analysis of their worldwide dispersion. The purpose of the study is to investigate how soil multifunctionality is related to variations in the organization of bacterial communities in different types of soils. Microbial ecophysiology, which includes methods for reducing energy, producing exudate, and bacterial turnover in responses to famine, should be studied in research. Fertilization is essential for altering bacterial populations and managing the cycle of nutrients in the soil. To comprehend the implications of changing climates on biochemical cycling, research should examine the relationship between soil bacteria and abiotic elements in addition to their multitrophic interactions. New instruments, such as 13C metabolic flux analysis, should be developed in the future to measure microbial functionality in intact soils directly.

To understand the dynamics of bacterial communities and how they affect biogeochemical cycles, it is essential to investigate predator-prey relationships between bacteria and bacterial viruses. An understanding of the genetic repertoire and function of soil microbes in the cycling of carbon and nitrogen can be gained by investigating soil metagenomes vertically. It is vital to take into account the function of biochemistry in soils and the environment, particularly as it relates to microbial activity and soil carbon cycling.

14 Conclusion

In conclusion, the impact of soil bacteria on biochemical cycles is profound and multifaceted, influencing the cycling of nutrients essential for ecosystem function. Throughout this exploration, it becomes evident that soil bacteria play pivotal roles in the carbon, nitrogen, phosphorus, sulfur, iron and manganese cycles driving processes essential for the sustainability of life on Earth. Biochemical cycles and a variety of living forms depend on the diversity and composition of soil in terrestrial ecosystems. These cover a wide range of ecosystems that have distinct plant species, soil creatures, and microbial communities. Environment, geography, vegetation, and human activity all have an impact on the composition of soil. While minerals maintain the structural integrity of the soil, organic matter supplies nutrition. The cycling of nutrients, decomposition, and fertility are all significantly impacted by the soil microbiome. To manage land sustainably, conserve natural resources, and lessen the effects of climate change, one must have a thorough understanding of soil variety. Important services including agriculture, carbon sequestration, and filtration of water can be protected by maintaining soil biodiversity, fostering healthy ecosystems, and improving soil fertility. The variety of soil microorganisms is investigated by both conventional and contemporary methods. Although they can capture some basic information, traditional culture-based methods such as enrichment cultures and plate counts are not able to fully capture the diversity of microbes. By directly evaluating DNA from environmental samples, molecular tools such as PCR, FISH, denaturing gradient gel electrophoresis (DGGE) and temperature gradient gel electrophoresis (TGGE), Restriction fragment length polymorphism (RFLP) and terminal restriction fragment length of polymorphism (T-RFLP) and Single-strand conformational polymorphism (SSCP).

Global biogeochemical processes, ecosystem function, and nutrient dynamics are all impacted by soil bacteria, which are essential to many biochemical cycles. By converting organic matter into synthetic molecules and breaking down organic matter, they affect soil fertility, emissions of greenhouse gases, and carbon sequestration. By fixing nitrogen and developing symbiotic interactions with plants, they contribute to the nitrogen cycle by increasing nitrogen availability and stimulating plant development. Additionally, they have an impact on soil fertility and ecosystem production through their participation in the cycling of iron, sulfur, and manganese. It is crucial to comprehend these relationships in order to address environmental issues and manage land sustainably. Moreover, the interactions between soil bacteria and plants further amplify these effects, as symbiotic relationships and microbial communities influence nutrient availability and plant health. Understanding the intricate dynamics of soil bacterial communities and their impact on biochemical cycles is crucial for sustainable agriculture, ecosystem management, and mitigating global environmental challenges such as climate change and nutrient pollution. In essence, soil bacteria serve as the invisible architects of terrestrial ecosystems, orchestrating biochemical processes that sustain life and regulate the Earth's biogeochemical cycles. Recognizing their significance underscores the importance of preserving soil biodiversity and fostering practices that promote soil health and resilience in the face of ongoing environmental change.

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