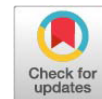


Review Article



Exploring the Unseen: Novel Microbes and Their Impact on Biogeochemical Cycling

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Abstract | Our study will expand in the small world of the unseen microbes, where the dark matter is created and the biogeochemical cycling is done. The introductory paragraph reveals why it is crucial to determine the roles of newly discovered microbes in making the microbial community more complex and important in ecosystem function. The central mention throughout the paper clarifies the value of the microbes for the biogeochemical processes and allows the resilience of the ecosystem. In the study, there are various types of novel bacteria being subdivided and their phylogenetic diversity, metabolic functionality and ecological features are discussed in details. Techniques of isolating microbes that are not cultivable is discussed especially the culture-independent approaches like metagenomics, single-cell genomic, and metatranscriptomics which have changed the way we study microbes that are never before grown and isolated outside. Biogeochemical cycling basing on either nitrogen or carbon are put under attention here so that the effects of novel microbes on carbon fixation, organic matter decomposition, nitrogen fixation, nitrification, denitrification and ammonification are expressed. Novel microbes' capacities for biogeochemical cycling models are explored, including demonstrating increased species refinement, environmental changes influence microbial response prediction, and microbial omics data integration into the models. To sum up, this research has illustrated the need to discover new bacteria in the lift of study of biogeochemical cycles and its implication for ecosystems' dynamics, the environment, and biotechnologies. As a result of unveiling the secrets of the microbial dark matter, we shall enhance our understanding of the complexity of life on this planet and it shall be revealed to be a system of interconnected ecosystems.

Received | March 16, 2024; **Accepted** | May 30, 2024; **Published** | June 07, 2024

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Citation | Abd, R.A. 2024. Exploring the unseen: novel microbes and their impact on biogeochemical cycling. Hosts and Viruses, 11: 45-55.

DOI | <https://dx.doi.org/10.17582/journal.hv/2024/11.45.55>

Keywords: Microbes, Biogeochemical cycling, Nitrogen, Carbon, Ecosystems



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Introduction

The frontier of microbial ecology - which is, now, is represented by an unstructured cluster composed of empirical data, visionary proposals, and hy-

potheses that are rooted in constructivist thinking - can be, someday, a systematic, strong discipline. The new approach will be based on the identification of the microbial diversity as well as the understanding of the ecophysiological activities that are the governors

of the microbial processes. With the manipulation of environmental controls, we will be in a much better situation to enhance or to depress the microbial activities in beneficial ways for specific ecosystem processes. Although these statements could appear as extravagant, this gives an idea of what is involved in microbial activities in the biogeochemical significance so that we can use the necessary steps to understand the process. In order to accomplish that, the study of all the key elements of the Earth's ecosystem will be pursued onsite and in a laboratory environment in order to be able to accurately predict the result of specific human-caused or natural events on the quality of Earth and human life. For the moment, considering that we are still in the process of building microbial ecology and microbial processes and microbial communities are extremely diversified and complicated, therefore, there is no way to groups of prediction. Consequently, now is the era where the microbial ecologists who have different views and perspectives need to come up with a resolution, learn and build a plan on how to move on (Sokol *et al.* 2022).

The key message of this paper is to discover the novel microbes, provide the critical role the microbes play on the environment, and enhance our understandings of the interactions between biogeochemical cycles and microbes. The places which these microbes are found generally are either in the deep earth crust, in the extreme arctic or even in the space stations, which in turn is most of the time ignored and never to be remembered deeper because it is hard to see or imagination their existences. Microbes contribute greatly in maintaining the biogeochemical cycling through ecosystem processes in the biosphere which is essential for the life support system: humans, the other animal species that live on mother earth. However, a few areas of microbial ecology - especially those dealing with open microbial communities and biogeochemists - are beginning to identify emerging themes that will lead to a new approach to microbial ecology and an increased understanding of microbial processes and their methods (Martínez-Espinosa, 2020).

Importance of Novel Microbes

Microbs are the quiet protagonists that tirelessly maintain Earth's biogeochemical cycles by assuring that each element has its particular piece of acting in the play of life on the planet. Actually within these cycles, the carbon cycle appears to be the most crucial,

and microbes are the ones who are the real partakers of it. Photoassynthetically active microbes of the realm like cyanobacteria and algae enable the cut back of extra CO₂ that is usually from the atmosphere into carbon compounds through the process of photosynthesis. Such dynamics not only enhance their own livelihood but also become the roots of the trophic chain, where these compounds often are taken as food by the other living things. Though microscopic, decomposer organisms digest organic matter, resulting in the carbon dioxide being eventually released via their breathing (Selhub *et al.*, 2014).

In terms of the nitrogen cycle, microorganisms remain the key players capable of nitrogen transformations that have great significance for life on Earth. Dinitrogen-fixing bacteria, for example those that have formed roots nodules of leguminous plants or freely live in the soil, are the organisms that nitrate ammonia gas that comes from the air to ammonia, the form usable by plants through a process called nitrogen fixation. Beyond nitrifying of nitrogen, other microbes are involved in nitrite production which further changes into nitrate, a nutrient that is easily used by plants. The cycle is completed by nitrifying bacteria that convert nitrates back into gaseous nitrogen, hence, returning this form back into the atmosphere. Through these, microbes control the accessibility of nitrogen in the ecosystem which stimulate the growth of plants, promotes soil fertility and eventually, impacts on the aquatic environment (Marchesi *et al.*, 2016).

Through metabolic pathways in all kinds of microorganisms, many essential elements for life on Earth undergo changes, and sulfur is one of them. Sulfate reducing bacteria are the only organisms that have the ability to thrive in anaerobic environments, the environments without oxygen. They reduce sulfate to hydrogen sulfide, which is a component of the sulfur cycle in the wetlands and marine sediments. However, sulfur-oxidizing bacteria oxidize sulfide to sulfate through oxidation in aerobic environment and thus it is seen as one of the oxidizing factors of sulfur in the soils and aquatic ecosystems. Microbial transformations are those that peptako may be played and may in turn affect nutrient availability, energy flow, and even atmospheric chemistry through the ecosystem (Gómez-Gallego and Salminen, 2016).

To paraphrase the point, microbes are largely respon-

sible for reducing the mesmerizing movements of carbon and nitrogen cycles to a relatively complex form of phosphorus cycle. Microorganisms which inhabit the soil are the ones responsible for the mineralization of organic phosphorus compounds; these phosphate ions are subsequently crucial for plants when it comes to development. Also some microorganisms are in the process of pulling movement phosphorus by adding it to their biomass while phosphorus is temporarily locked. Further, bacterial phosphorus-solubilizing facilitates the process of accessibility of phosphorus to plants by breaking down its particles into soluble forms (Camarrota *et al.*, 2014; Hill *et al.*, 2014).

Out of this, microorganisms emerge as biochemical technicians of biogeochemical cycles, catalyzing reactions that send elements at the basis of life through various transformations and redistributions. Microbial communities are responsible for the achievement of the equilibrium of the whole ecosystem from the forests to the ocean depth, where these microorganisms contributing to the carbon, nitrogen, sulfur and phosphorus cycles that support life on Earth (Aureli *et al.*, 2011; Gómez-Gallego and Salminen, 2016).

Most Common Types Novel Microbes

Unexpected microorganisms, typically named as “microbial dark matter,” are among the most interesting areas of microorganism diversity, which has not been investigated extensively in the past. These little creatures that cannot be cultivated nor identified seem to be the reason we challenge our traditional views of microbial life and the microorganisms’ world. At the same time, the prosperous and emerging areas of biotech and nature science make us think of how much we used to forget about them. Here are some types of novel microbes and their significance: Here are some types of novel microbes and their significance:

Phylogenetic Distinctiveness:

One class of novel microbes corresponds to candidate phyla that are defined as the phylogenetically unique bacterial and archaeal lineages that were discovered via metagenomic studies but were not bacterial and archaea whose culture has not yet been established in the lab. The respective size of these microbes’ genomes is small, and their metabolism varies. Additionally, they play unidentified roles in ecosystems. Use case is Demonstrated with the discovery of candidate phylum Radiation (Fig. 1), Peregrinibacteria, and Saccha-

ribacteria. A focused study on these organisms will bring up evolutionary and diversity issues of the microbial life. The candidate phyla are unique not only in terms of their taxonomic distinctiveness but also their role in the microbial world from an evolutionary and diversity view. As they form a narrow branching of the tree of life and are hence, a substantial deviation from the well-characterized microbial groups. Hence, this singularity makes them attractive representatives and provides community stumbling blocks in order to have a broader view of the microbial diversity of Earth as well as interrelations among various microlines. Placement of candidate phyla on the tree of evolution evidences the early origin of microbial diversification and processes guiding it as well. But chance or laboratory cultivation can hardly be traced. This narrow private accessibility, however, gives rise to many impediments to their physiology, biology, ecology, and role study. The absence of culture media, which could have provided further insight into their metabolic capacities, ecosystem connections, and roles in the ecosystem processes, has proven to be a bottleneck in the process of understanding these microbes. Unraveling the hidden metabolic features of candidate phyla and the roles they play in ecosystems requires overcoming these challenges. The representative microorganisms which do not belong to any known phylum often have streamlined genomes, adapt these mainly to certain environmental niches (Gabriel and Northup, 2013; Northup and Lavoie, 2015).

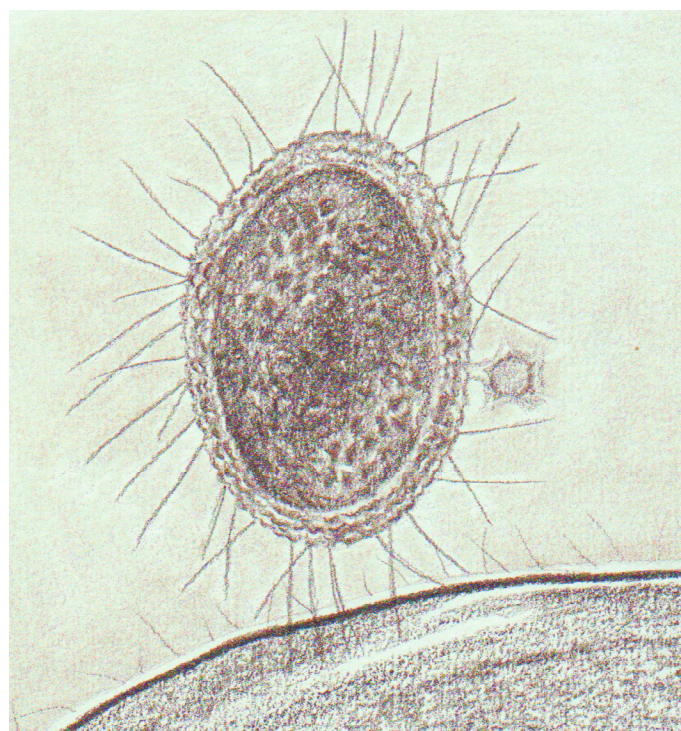


Figure 1: Candidate phylum radiation.

Uncultured Microorganisms

The uncultured microorganisms which comprises almost all of the microbial diversity that has largely unique to us due to the difficulty of culturing those microbes in the laboratory setting. Microbes are ubiquitous in various sites, including soils, sediments, and the oceans, and from deep seawater vents. This pictures however, has posed their biology, physiology, and ecological functions as mostly unknown due to its inability to cultivate them. Lack of culturing these microorganisms to own scales, we're just limited by our lack of understanding of the related requirements to its growth, nutritional, and environments. Thus, these unrefined microorganisms stayed unidentified for an extended period of time and represent a notable gap in our comprehension of the microbial life on our planet. The evolution of culture-independent techniques, such as single-cell genomics and metagenomics, is currently a game-changer that enhances our capacity in dealing with the genetic diversity and ecological importance of these microorganisms and also ven They help scientists to get even into genomes of single cells or whole microbiological community in environmental samples using the next generation sequencing technologies that are not dependent on laboratory culturization. Through NGS and sequencing of DNA or RNA from the samples retrieved culture-independent approaches provide an opportunity to identify and reconstruct the genomes of uncultured microorganisms, recognize their metabolic capabilities and infer their ecological niche in natural ecosystems. In consequence, culture-independent techniques assist to unmask those hidden and fascinating worlds of uncultured microorganisms and discover untapped treasures behind their Through the use of these innovative methods researchers are capable of solving mysteries related to the microbial components of dark matter, discovering unexplored microbial diversity, and extending the frontiers of microbiology into previously unknown territories. Cultural independency methods that go newer and newer seem to be able to provide opportunities for the whole pool of bio-diversity extremely rich in genetics and metabolism used by society and environment (Sun *et al.*, 2020; Lewis *et al.*, 2021).

Cryptic microbes

Cryptic microbes, a subset of microbial life, are incredibly fascinating and usually barely get quantified with conventional methods due to their miserly abun-

dance or cunning lives in habitats that are natural to them. These tenacious microbes can inhabit regions as diverse as soil and sediment, or as distant as the deep ocean where, hidden from our view, they create their own niches and embody the ecological relationships around them at a quieter level. Although their detection and exigency are difficult, spontaneous microbes can exert significant role in the ecosystem, having different metabolism capability or exchanging symbiotic requirements with other organisms (Newman *et al.*, 2016).

Instance of microbiobome crypto is rare soilbomics, which reside in deep soil ecosystem and do vital jobs of nutrient cycle and soil dynamic. Such microbiome could develop unique adaptations while fostering healthy functioning of soil, providing system's stability and allowing ecosystems to grow. Just as the archaea flourishing at the oceans' depths live in conditions of extreme pressure, there are special organisms that perform biogeochemical processes like carbon cycling and methane metabolism deeply beneath the surface. These micro-organisms might have developed their own specific metabolic pathways, which enable them to cope with the high pressure, small temperature and scarce nutrients levels found in deep-sea environments (Oliynyk *et al.*, 2007)

So too are microscopic microbes capable forging fateful symbiotic connections to other cohabitators, thereby, increasing difficulty in discerning them. Mutualistic microbes may be housed within or even within the cells of hosts instead of being extracellular, and they may serve as nutrient providers, protect against pathogens or boost the host metabolism. Examples of such are bacterium that is in combination with the root of plant that has been responsible for the absorption of the nutrients and paves the way for the growth of the plant. Additionally, such microbes that are symbiotic with the guts of animals are responsible for the digestion of solids and immune functions (Liu *et al.*, 2014).

The challenging ecosystems of the hidden micro-organisms provide the opportunity to reveal the unknown phenomena of concealed microbial diversity and ecological interactions that create the work of ecosystems. Through the use of modern molecular technology paired with collaborative methods, researchers can explore the roles of unknown microbial communities in biogeochemical cycling, community interactions, and ecosystem resilience (Baral *et al.*,

2018).

Methods for Identifying Novel Microbes

Successfully isolating and characterizing novel microbes, especially those that have been largely undetectable, using the current cultivation methods warrant the application of molecular technologies that leverage the new developments gathered in biology, genomics and bioinformatics. Here are some key methods used for identifying novel microbes: Here are some key methods used for identifying novel microbes:

Metagenomics

Metagenomics is a technology involved in the sequencing and analysis of genetic materials acquired directly from an environmental sample through the process of “taking without raising in the laboratory”. This way a possibility of seeing the genome hodgepodge of the microbe population present in a certain ecosystem gets opened, it also the researcher gives a chance of distinguishing these microbe communities, and describing the novel taxa and functional genes. Metagenomic analysis has brought about truly a new Frame in microbial ecology which looks at the microbial diversity and the roles of the microbes in different environments, such as soil, water and even the human microbiome (Chiu *et al.*, 2019)

Single-Cell Genomics

Genomic characterization of a single cell from a microbe now became possible thanks to single-cell genomics on which it became clear how the genetic diversity of the uncultured microorganism is and what metabolic activities can be attributed to it on the basis of a single cell. They do this by recovering, sequestering, and genetically manipulating DNA molecules separated from single microbial cells from the environment. Single-cell genomics as the most important tool in revealing mysterious microbial lineages, metabolic pathways, and genetic adaptations, those were not possible to find by cultivation-based approaches (Paolillo *et al.*, 2019)

Metatranscriptomics

Metatranscriptomics refers to the whole RNA sequencing and analysis process which are extracted from microbial communities, which in this way, uncover gene expressions and metabolic activities going on in-situ. When sequencing the active micro-

bial genes and pathways within the environmental samples, the metatranscriptomics can spot out the dynamics the functional communities of microbes, which also reveal the novel genes (Bashiardes *et al.*, 2016).

Culturomics

With culturomics, high-speed and modern genome-centric microbiological methods and techniques are used to enumerate and characterize microorganisms that have not yet been cultured. It is a technique which involves improving the culture conditions, efficiently targeting media and also using high throughput screening approaches to isolate different microbial strains from various environmental samples. The rising of culturomics has been responsible for the discovery of new microbial taxa and genetic indicators which, together with culture-independent methods, have offered effective identification of microorganisms in ecosystems (Ladle *et al.*, 2016).

Bioinformatics and Comparative Genomics

Two basic bioinformatics tools and comparative genomics analysis techniques are employed for exploration and identification of new microbes by comparison of sequenced genomes with reference genomes and phylogenetic trees respectively. By using metagenomic data from newly sequenced microbial isolates or a ecdysed sample, researchers are able to pinpoint novel genetic markers, taxonomic indication and functional annotation related to newly discovered microbial lineages. Moreover the machine learning algorithms and predictive models can play an important role in the microbial classification stage by means of genomic features characteristic and evolutionary relationships (Glaeser *et al.*, 2017).

Functional Screening and Phenotypic Assays

Functional screening involves screening the physiological and biochemical properties of microbial isolates to detect the excellent bio-mechanical features, enzymatic activity and biotechnological traits. These tests will usually be growth assays performed on varying substrates, enzyme activity assays, or bioassays intended for examination of specific activities of interest. Genotypic screening and genomic analysis simultaneously can provide a rich and well-informed knowledge of the genetic basis of native microorganisms and the strategies they use to acclimate to ecosystem variations and dynamics (Vincent *et al.*, 2015).

In extreme, it can be suggested that a combination of independent culture techniques, highly-efficient sequencing technologies approach, bioinformatics analysis and functional methods can stay the cornerstone for revealing of the new microbes and their ecological footprint, metabolic roles and biotechnological potential. These approaches which are interdisciplinary enables the microbiologist to broadly study the microbes concealed diversity and the hidden revolutionary innovations that are responsible for the evolution of microbial life on earth (Minter *et al.*, 2016).

Novel Microbes and Carbon Cycling

Unique microorganisms, especially culturing-resistant ones, play an important role in the carbon cycle of the biomes. The Carbon Cycle is a set of convoluted biochemical reactions through which carbon circulates between the atmosphere, oceans, land, and organisms. Microbes that have first appeared in the history of evolution also participate to carbon cycling through its assimilation, organics decomposing and gas emission in the greenhouse effect. Here's how they impact carbon cycling: Here's how they impact carbon cycling:

Carbon Fixation

Autotrophic photo synthesizing micro-organisms including some genera of cyanobacteria and algae remain among the most important micro-organisms in the global carbon cycle because evolutionarily they adapted to fix atmospheric carbon dioxide (CO₂) biologically into organic compounds by photosynthesis. Such microbes are known as photosynthetic kind which take up the available light energy and process pyruvate before discharging carbon dioxide and oxygen in addition to additional organic matter. In marine areas, small unicellular algae are the main players in primary production and carbon sequestration that be a stakeholder of global carbon budget and climate regulation (Gong *et al.*, 2018).

Organic Matter Decomposition

Not only bacteria, but also other microbes work in the process of decomposition, releasing CO₂ by breathing it out into the environment as well. Decomposer microorganisms such as bacteria and fungi work to break down the complicated organic compounds. Components like the dead plants, animals, and soil organic make these compounds. CO₂ is released in the process of breaking down this complex organic

compound. This is the initial stage in the carbon cycle. Microbes here act as the primary degrading component that releases the organic carbon back into atmosphere and soil (Wang *et al.*, 2019).

Methanogenesis

Wetlands (such as ricepaddies) are synonymous to the anaerobic environments where anaerobic methanogenic archaea – a group of novel microbes – thrive and produce methane (CH₄) as a byproduct of their metabolism. Methanogenesis is a significant carbon cycle pathway, as the greenhouse gas methane is also one of the strongest anthropogenic warming contributors that are of high climate change importance. Nontrivial methanogenic microbes participate in methane emissions, due to natural and anthropogenic sources, whose methane concentration in atmosphere affects Earth's Earth's radiative imbalance (Akinyemi *et al.*, 2018).

Carbon Storage

Sometimes the carbon stocked in the soils and slide rocks is due to a group of earlier identified microorganisms that are involved in the formations of stable organics and mineral complexes. Here is an illustration. Some bacteria and fungi produce extracellular polymeric substances (EPS) that bind soil particles and organic matter together, and thus creating concentrated empty space between soil particles that improve the structure of soil and aid in carbon sequestration. On the other hand, new and unique microbial communities found within deep-sea sediments are also engaged with the continuum of the matter, contributing to long-term carbon storage and the regulation of the CO₂ content in the atmosphere during geologic times (Kumar *et al.*, 2018).

Microbial Interactions

Certain microbes that emerge as novel make partners with symbiotic relationships, competition, and predation involving other organisms within a microbial community, and thus influence the carbon cycling. Another such case is the symbiosis relationship between nitrogen-fixing bacteria and plants and the latter converts carbon dioxide into organic matter through increased production of plants and deposit organic matter into soils. On the other side, microbial linkages as an example microbial loop in marine ecosystems transfer carbon through microbial food-webs, and they have an effect on the cycling of carbon and on the dynamics of ecosystems (Ahrens *et al.*, 2015).

To cut the long story short, novel microbes carry out these tasks in three terrestrial, aquatic, and the aerial systems. Their versatile metabolic functions, negative impacts on other species, and community's ability to adjust to different habitats make them an essential component of the Earth in maintaining the carbon flow through ecosystems. It is also crucial to authenticate the part played by the newly discovered bacteria in carbon cycling. Such knowledge will help in forecasting the impact of environmental change on the ecosystem and facilitate measures to mitigate climate effects while also creating sustainability pertaining to carbon stocks for proper resource use (tang *et al.*, 2015).

Novel Microbes and Nitrogen Cycling

Specific microbes, for instance those which have not been tractable to many conventional cultivation methods, are the essential cycles for the nitrogen within ecosystems. A key biogeochemical process that occurs in nature is the nitrogen cycle which involve the shifting and recycling of nitrogen between different reservoirs which include the atmosphere, soil, bodies of water and living organisms. New microbes act as wide a range of nitrogen cycling functions as such as nitrogen fixation, nitrification, denitrification and ammonification. Here's how they impact nitrogen cycling: Here's how they impact nitrogen cycling:

Nitrogen Fixation

Nitrogen-fixing microorganisms are the integral part of nitrogen cycle, giving the atmospheric nitrogen gas (N₂) the preferred forms that can be usefully taken up by plants and other organisms. Bacterial groups like *Rhizobium* & *Azotobacter* and Archaea like methanogens are some of the known Nitrogen fixers. These microorganisms are always rich in nitrogenase enzymes that can catalyze reduction of nitrogen to ammonium under either anaerobic or microaerophilic environment. The *Zobneria* isolate that proved to be effective in converting atmospheric nitrogen to biologically available nitrogen is a source of input of nitrogen to ecosystem supporting plant growth and productivity (Burns *et al.*, 2012).

Nitrification

Nitrifying microorganisms which play the nitrification role that evolves ammonia to nitrite (NO₂-), and nitrate (NO₃-) are the nitrifying microbes. This step in the nitrogen cycle is carried out by two groups of

microbes: ammonia oxidizing bacteria (AOB) and ammonia oxidizing archaea (AOA), which carry out the oxidation of ammonia to nitrite, and nitrite oxidizing bacteria (NOB) which further oxidize nitrite to nitrate. In these nitrifying categories; the novel microbes belonging to them, has been found to be at the diverse environments, such as soils, sediments and aquatic systems, where they contribute to the ammonia oxidation and nitrate production, a form of nitrogen that readily uptaken by plants (Daims *et al.*, 2015).

Denitrification

The difference between denitrifying microbes and nitrifying microbes is that the former helps in the reduction of nitrate and nitrite to nitrogen gas (N₂) or nitrous oxide (N₂O), a process called denitrification, while the latter help in the production of nitrous oxide (N₂O) from nitrite. Nitrification proceeds under anaerobic conditions, which are performed by a diverse range of bacteria and archaea. The process is often carried out by facultative anaerobes like *Pseudomonas* and *Paracoccus* bacteria species. The denitrifying bacteria actually have a pivotal role in nitrogen belching. This role helps to alleviate nitrogen pollution as well as the greenhouse gas emissions. The use of novel denitrifiers is important in many environments including the soil, wetlands, and aquatic systems to keep their nitrogen level stable as well as control nitrogen availability in ecosystems thereby reducing nitrogen loss in the environments (Lichtfouse *et al.*, 2024).

Ammonification

The microorganisms producing ammonia-type micro-cultures are called ammonifying organisms and they convert organic nitrogenous components into ammonia or ammonium ions (the process of ammonification or mineralization). Microbes in the soil breakdown organic matters such as dead plants, dead animals, or carbon-rich soil materials releasing N as ammonia. Both bacteria and fungi major in the process of NH₃ creation, among them proteolytic and cellulolytic producers. The new ammonifying microbes are a part of the process of nitrogen recycle and nutrient circulation in the ecosystems where they improve the soil with the nitrogen they release coming from organic sources (Hochroth *et al.*, 2024).

Nitrogen Assimilation and Mineralization

An example of the detrimental microbes are those which participate in nitrogen fixation and mineraliza-

tion. In these processes monoammonium and nitrate are incorporated into biomass and nitrogen is set free from organic nitrogen compounds respectively. Such microbe-based processes play nitrogen out, become available for uptake by plants, microorganisms as well as other organisms in various ecosystems. The cyclic flow of nitrogen could be achieved through microbes that are able to capture nitrogen within the biomass or organic nitrogen compounds, which would then be subject to mineralization and subsequently to increase in ecosystem productivity (Seyfried *et al.*, 2024).

The exotic microbes with novel metabolism, ecosystem interaction and adaptive strategies facilitate nitrogen reformation, relocation as well as usage. Comprehending the tasks of new microorganisms in nitrogen cycling is fundamental for providing newmers with the nitrogen inputs and outputs in environmental rocks, dispelling nitrogen pollution, and supporting the sustainable nitrogen utilization in agronomy and environmental prudence.

Implications for Biogeochemical Cycling Models

Microbial discovery and characterization for the purpose of biogeochemical cycling assessments are highly significant as these models are used to predict and simulate the major element cycling in ecosystems. Using annotation ability of novel microbes into these models will add to our knowledge regarding microbial processes, ecosystem dynamics and the responses of biogeochemical cycles to the changes in the atmospheric environment. Here are some key implications for biogeochemical cycling models: Here are some key implications for biogeochemical cycling models:

Improved Representation of Microbial Diversity

Traditional biogeochemical cycle models usually simplify microbial communities by combining the activity of multiple microbial taxa into generic compartments. As such, the occurrence of microbial processes is overseen, and the diversity and functional redundancy of microbial taxa are minimized. Through the consideration of new microbes in the models, scientists may amplify the microbial diversity, particularly for rare species, uncultivated lines and cryptic microorganisms. Thus, the increased microbial resolution on this fine scale can improve the validity and the realism of models of biogeochemical cycling, hence, creating predictions of the biosystems dynamics that are more

accurate (Sardans *et al.*, 2023).

Refinement of Microbial Processes

Novel microorganisms play a critical role in biogeochemical cycling because of their selection of novel metabolic pathways, species competitions, and various adaptations to ecosystem specific conditions. Using such new information, it is possible to transform biogeochemical cycling models to accommodate description of the actions and make-up of the novel microbes such as carbon fixation, nitrogen fixation, nitrification, denitrification, and organic matter decomposition. Through portrayal of the diversity in microbial functioning, the model would better recreate biogeochemical processes of recycling and transformation of specific compounds within an ecosystem (Huang *et al.*, 2024).

Prediction of Microbial Responses to Environmental Changes

Newly emerging microbes could possess particular behaviour that results in the organisms being sensitive to ecological shifts or even isolated to specific environments, such as climate change, land-use change and pollution. Being the model that harnesses the description of the microbial physiological features and its ecology makes them able to establish the likelihood of the community functioning in an environment under perturbation conditions (Martiny *et al.*, 2023).

Integration of Omics Data

Omic technologies are of the utmost importance including metagenomics, metatranscriptomics, and metaproteomics which supply extremely important information on the micro-biome within the ecosystem i.e. its structure, functionality, and activity. The Omics datapoint used with the biogeochemical cycling models of researchers helps in the parameterization of model parameters, validation of model prediction and restricting the model uncertainties. Interdisciplinary approaches that integrate empirical data with model-based assessments bring facets emerging behind the operational mechanism of microbes and reveal details of the role of microbial population in ecosystem functioning (Sathyanarayanan *et al.*, 2023).

Assessment of Biotechnological Potential

Microbes newly found are likely to contain a big number of genes encoding enzymes that can demonstrate the hidden value for biotechnology, biomedicine,

and environmental cleaning. Biogeochemical cycling models could be employed to foresee the biotechnological potential of the new microbial species with respect to their metabolic functions, substrate effects and ecological interactions. Established methodological models, in turn, can be used to define candidates for potential biotechnological applications. Afterwards, experiments on novel enzymes, biosynthetic pathways, and bioactive compounds with a broad industrial and medical spectrum may be carried out (Fanelli *et al.*, 2023).

Using information about new bacteria within biogeochemical cycles models increase the possibility of our prediction and simulation of what the biogeochemical cycle dynamics look like inside an ecosystem. The models are of interest in their ability to mimic the diversity, functions and responses that occur in microbial communities, and thus, provide an in-depth knowledge about ecosystem functioning, environmental change and biotechnological potential of novel microbes. These further developments, such as integration of the data coming from microbial processes and the modeling approaches, could bring us closer to understanding the mysteries of the biogeochemical cycling and its big picture implications for global environmental change (Srivastava *et al.*, 2023).

Conclusion

In conclusion, the investigation of brand new micro-organisms stands out as being a frontier in microbial ecology giving a more intricate knowledge of their functions of cycling biogeochemicals inside ecosystems. As our research journey unfolds, we take you through the importance of these hidden community of microscopic organisms, discovering their critical roles in both carbon and nitrogen cycling systems which are the key drivers for the operations of the terrestrial, aquatic, and atmospheric ones.

We began our microbial ecology journey at the introduction and went through all the way to the ramifications of microenvironment and metagenomics and saw how diverse the microbes are and at what extent they can impact the organism's life. Our research has proved the necessity of modeling biogeochemistry in a way that includes information about extant microorganisms, eventually leading to a more accurate perspective on ecosystem processes and offering predictions related to environmental changes.

Through explaining the functional roles of this novel microbes in organic matter decomposition, carbon fixation, nitrogen fixation, nitrification, denitrification and ammonification, we have hence demonstrated their significance in driving a majority of life-supporting biogeochemical processes on Earth. Also, we have stressed the role of novel microbes in seeming biogeochemical cycling by combining experimentation along with modelling to develop models that will improve our understanding of how microbial communities influence ecosystem functioning.

With our microbial space still largely unexplored, expect more information to emerge from all areas of their ecological relationships to old biotechnological potential- in the future. Through promoting multidisciplinary steps and taking advantage of recent innovations, we can undo the puzzles behind microbial dark matter and utilize their potential to combat the biosphere and environment, as well as take care of human health.

The pathway of discovering new microorganisms and their participation in biogeochemical cycle is both intriguing and significant. This not only enriches us with more knowledge in bacterial diversity and abiotic weathering reactivity but also points the direction for resolving critical environmental issues while emerging biotechnological novelty is just around the corner.

Author's Contribution

All authors contributed equally in the manuscript.

Conflict of interest

The authors have declared no conflict of interest.

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