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Environmental Microbial Diversity and Ecosystem Health Revealed by Metagenomics

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Abstract The continuous development of metagenomics technology, its application in the study of environmental microbial diversity is becoming increasingly widespread. This study reviews the application of metagenomics technology in the study of environmental microorganisms, focusing on the intrinsic connection between environmental microbial diversity and ecosystem health. Metagenomics technology provides a new perspective for ecological environment protection and restoration by revealing the structure and functional relationship of microbial communities. This article also looks forward to the potential and challenges of metagenomics in environmental monitoring, biological resource development, and response to global environmental challenges. This article aims to provide theoretical support and practical guidance for a deeper understanding of the relationship between microbial diversity and ecosystem health, as well as the application of metagenomics in ecological environment protection and restoration.

Keywords Metagenomics; Environmental microbial diversity; Ecosystem health; Environmental monitoring; Biological resource development

In the earth's ecosystem, environmental microbial diversity plays a vital role. They not only participate in biogeochemical cycles, but also maintain the stability and health of the ecosystem. The diversity and functional complexity of environmental microorganisms have a profound impact on ecosystems, involving many aspects from the driving of primary productivity to the decomposition of organic matter (Zhang, 2016). However, because microorganisms are tiny, diverse, and difficult to cultivate, traditional research methods often fail to fully reveal their diversity and functions.

In recent years, with the rapid development of metagenomics technology, the study of environmental microbial diversity has achieved revolutionary breakthroughs. Metagenomics, also known as metagenomics, is a research method that directly analyzes the genetic material of all microorganisms in environmental samples (Taş et al., 2021). It can comprehensively explore the genetic composition, species diversity, gene functions and interactions of microbial communities in environmental samples without the need to isolate and culture microorganisms. The development of this technology has opened up a new path for environmental microbial research and greatly promoted an in-depth understanding of the diversity and functions of environmental microorganisms (Wang et al., 2020).

This study aims to use metagenomics technology to deeply explore the intrinsic connection between environmental microbial diversity and ecosystem health. Through metagenomics analysis, it is expected to reveal the structure and function of microbial communities and their impact on ecosystem health, providing scientific basis for ecological environment protection and restoration. This research not only helps to improve the understanding of microbial ecology, but also has important practical significance and application value, and can provide theoretical support and technical support for environmental protection and sustainable development.

1 Metagenomics Technology and Its Application in Environmental Microbial Research

1.1 Principles of metagenomics technology

Metagenomics, this cutting-edge branch of biology, focuses on revealing the genetic information of all microorganisms in environmental samples, in contrast to traditional genomics, which focuses solely on a single species. Goussarov et al. (2022) focused on the principles and methods of recovering metagenomic assembled genomes from metagenomic data, emphasizing the workflow from DNA sequencing to functional annotation.

Its research begins with the collection of environmental samples, which may originate from multiple environments such as soil, water, air or inside organisms. After pretreatment such as filtration and centrifugation, cells are disrupted using physical or chemical methods to release DNA. Subsequently, the DNA is extracted and purified to remove impurities and RNA. The DNA fragments need to be further constructed into libraries and sequenced. Library construction is to connect DNA fragments to vectors to form a sequenceable DNA library. Sequencing uses second- or third-generation high-throughput sequencing technology to conduct massively parallel sequencing of DNA fragments in the library.

Garrido-Cardenas et al. (2017) describe metagenomics as a set of techniques for analyzing microbial communities that can be isolated from a specific environment without culturing. This involves large-scale sequencing, or next-generation sequencing, because of the difficulties traditional methods present when trying to transfer all the microorganisms present in a given environment into the laboratory.

Hiraoka et al. (2016) found that bioinformatics analysis makes it possible to mine huge metagenomic data sets and discover general patterns that control microbial ecosystems. Metagenomic approaches will allow us to move beyond routine analyses, broaden our understanding of microbial ecosystems, enrich reference databases, and develop more powerful biological information.

The raw data generated by sequencing is rich in genetic information and needs to be transformed into useful information through bioinformatics analysis. This includes steps such as quality control, sequence assembly, and gene annotation. Quality control ensures data accuracy and reliability and removes low-quality data. Sequence assembly splices short fragments into longer sequences to form a draft genome or transcriptome. Gene annotation determines sequence function and origin by comparing it with known gene databases (Figure 1).

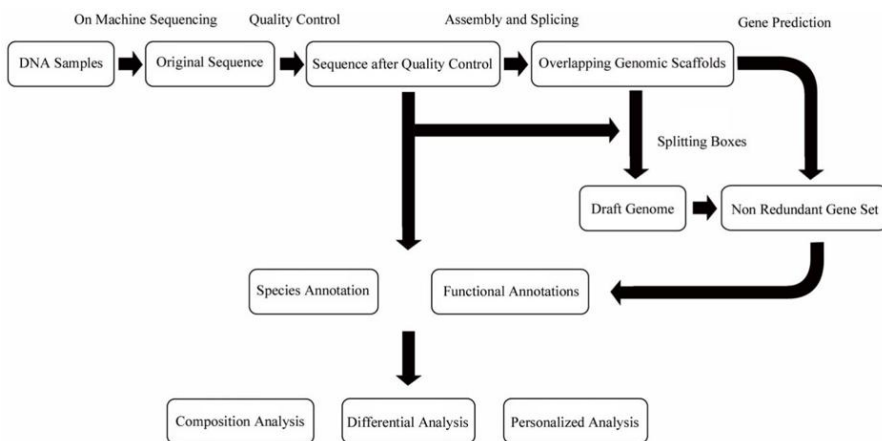


Figure 1 Common analytical processes for metagenomic sequencing analysis (Peng et al., 2022)

Metagenomics technology can reveal the species composition, gene types, functions and inter-species interactions of microbial communities in environmental samples. This information is critical to understanding the role of microorganisms in ecosystems and their interactions with environmental factors. Metagenomics provides new perspectives and methods for environmental microbial ecology research and promotes the development of this field.

1.2 Application of metagenomics in environmental microbial research

Metagenomics technology is increasingly used in the study of environmental microorganisms. It not only provides a new perspective, but also helps us gain a deeper understanding of the interaction between microbial communities and the environment.

Take the study of soil microorganisms as an example. Soil is one of the most complex and diverse ecosystems on earth, containing numerous microbial species. It is difficult to fully reveal the genetic information and functions of these microorganisms using traditional research methods. However, with the help of metagenomics technology, a comprehensive analysis of the microbial communities in soil samples can be performed.

In 2021, Liu Binbin and others from the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, used metagenomics sequencing combined with nitrogen cycle gene targeted assembly (Gene-targeted Assembly (Xander method) technology) to study the impact of long-term nitrogen fertilization (20 years) on North China. Effects of microbial communities on nitrogen cycling in plains. It was found that long-term nitrogen fertilization significantly increased the microbial abundance under most nitrogen cycle processes, but decreased the microbial abundance during nitrogen fixation. Research has confirmed that metagenomic sequencing combined with functional gene targeted assembly technology provides strong support for the realization of "finding needles in a haystack" of specific functional genes (Sun et al., 2021).

In 2023, Professor Xu Jianming's team at Zhejiang University unveiled the "veil" of soil dark matter at a global scale for the first time by analyzing global soil metagenomic big data. His research team used metagenomics technology to reveal the rich microbial diversity and genetic resource diversity of global soil microbial dark matter. This research result provides us with a new perspective in analyzing microbial communities in soil and lays a solid foundation for future mining and utilization of genetic resources (Ma et al., 2023).

1.3 Advantages and limitations of metagenomics technology in studying environmental microbial diversity

Metagenomics technology provides a new perspective for the study of environmental microbial diversity with its non-culture dependence and high-throughput sequencing capabilities. This technology breaks through the limitations of traditional culture methods, allowing researchers to more comprehensively reveal the true composition and diversity of microbial communities in environmental samples, and avoid the problem of missing microorganisms due to difficulty in cultivating them. At the same time, combined with high-throughput sequencing, metagenomics technology can acquire and analyze a large amount of genetic information in a short time, accelerate the research process, and deepen the understanding of the structure and function of microbial communities. Through in-depth analysis of the species composition, gene types and interaction relationships of microbial communities, metagenomics technology provides important support for understanding the role of microorganisms in ecosystems and their interactions with environmental factors (Staley and Sadowsky, 2016).

However, metagenomics technology also faces some limitations. Data analysis is one of the biggest challenges. The huge amount of data requires high-performance computers and professional bioinformatics tools to process, increasing research costs and requirements for researcher skills. In addition, uncertainty in gene annotation is also a problem, and similarities between microbial genomes may lead to misjudgments or omissions. Newly discovered microbial species and genes may not match known databases, making annotation results incomplete. The complexity of environmental samples also makes accurate analysis difficult, requiring more careful and precise data interpretation.

Zhang et al. (2021) and Techtmann and Hazen (2016) discuss the evolution from short-gun sequencing to next-generation sequencing (NGS) and third-generation sequencing (TGS), which allow rapid detection of pathogenic microorganisms and better An overview of the classification of microbial species. However, they also acknowledged limitations, such as challenges in metagenomic assembly and annotation due to the complexity of environmental samples.

New and Brito (2020) discussed the advantages and limitations of metagenomics, emphasizing its ability to provide higher resolution and functional content among species and strains. However, they noted significant challenges in data analysis, including the need to provide an extensive database of environmental bacteria.

Metagenomics technology has significant advantages in studying environmental microbial diversity, but it also has limitations. With the continuous development and optimization of technology, these challenges are expected to be solved, and metagenomics technology will play a greater role in the study of environmental microbial diversity.

2 The Relationship between Environmental Microbial Diversity and Ecosystem Health

2.1 The impact of environmental microbial diversity on ecosystem health

Environmental microbial diversity has a profound and complex impact on ecosystem health. It is like an invisible web that maintains the balance and stability of the ecosystem. Microbial diversity contributes to nutrient cycling and energy flow in ecosystems. Microorganisms decompose organic matter and release carbon dioxide, water, inorganic salts, etc., which in turn become important sources of nutrients for plant growth. At the same time, microorganisms also play a key role in the energy transfer process, converting energy in organic matter into a form that can be used by plants and other organisms (Sun et al., 2021).

Microbial diversity is critical to the health of soil ecosystems. Research by Delgado-Baquerizo et al. (2016) showed that soil microbial diversity is positively related to the multifunctionality of terrestrial ecosystems, and any loss of microbial diversity may reduce climate regulation, soil fertility, and food and fiber production. Soil is the home of microorganisms, inhabited by a large number of bacteria, fungi, actinomycetes, etc. These microorganisms have a profound impact on the structure, fertility and productivity of the soil by decomposing organic residues, fixing nitrogen, and promoting plants to absorb water and nutrients. When microbial diversity is rich, the soil ecosystem is better able to cope with environmental stresses such as drought and salinity, thereby maintaining soil health.

In addition, microbial diversity can enhance ecosystem resistance and resilience. When the ecosystem faces threats such as alien invasion and environmental pollution, rich microbial diversity means that more species can adapt to environmental changes and inhibit the expansion of harmful species through competition, predation, and other methods. At the same time, microorganisms also play an important role in the degradation of pollutants and the adsorption of heavy metals. They help reduce environmental pollution and promote the self-repair of ecosystems. Environmental microbial diversity has a comprehensive impact on ecosystem health. It is not only related to the balance and stability of the ecosystem, but also affects soil health, nutrient cycling, energy flow and other aspects. Maron et al. (2018) found that the reduction of microbial diversity affected the decomposition of autotrophic and heterotrophic carbon sources, thereby reducing global CO₂ emissions. This finding indicates the changes in microbial diversity caused by the soil carbon cycle. More sensitive than previously expected.

2.2 Impact of ecosystem health on environmental microbial diversity

The relationship between ecosystem health and environmental microbial diversity is close and complex. A healthy ecosystem has a stable internal environment, abundant resources, and low pollution pressure, providing ideal living conditions for microorganisms (Luo et al., 2018). In such an environment, there are abundant microbial species, which coexist harmoniously and jointly maintain the balance of the ecosystem.

A healthy ecosystem means adequate nutritional resources and low environmental stress, which provides a good environment for microorganisms to grow and reproduce. Microorganisms can better perform their ecological functions under such conditions, such as decomposing organic matter and promoting nutrient recycling, thereby supporting the normal operation of the ecosystem.

However, when ecosystems are disrupted or face environmental stress, microbial diversity is often severely affected. Excessive agricultural activities, industrial pollution, etc. can lead to soil and water pollution and cause

direct harm to microorganisms. Climate change, land degradation, etc. will also destroy the living environment of microorganisms, leading to the reduction or extinction of microbial populations.

Hernandez et al. (2021) proposed that by assessing the diversity and structural changes of the soil microbiome along 40 stress gradients (altitude/moisture availability gradients), it was shown that natural microbiomes exhibit network properties of unstable communities under sustained stress.

Chen et al. (2019) showed that the loss of soil microbial diversity exacerbates the spread of antibiotic resistance. This study demonstrated that high microbial diversity can serve as a biological barrier to prevent the spread of antibiotic resistance.

Reduced microbial diversity can have serious negative impacts on ecosystem health. Microorganisms play a key role in ecological processes such as nutrient cycling and energy flow. When microbial diversity decreases, these ecological processes may be disrupted, leading to a decrease in ecosystem stability and productivity. This will not only affect the overall health of the ecosystem, but may also have a negative impact on human society and economic development. Maintaining ecosystem health is an important prerequisite for protecting microbial diversity. By reducing pollution, protecting the ecological environment, and promoting sustainable development, we can provide better living conditions for microorganisms and thereby maintain the stability and prosperity of the ecosystem.

2.3 Microbial community structure and functional relationships revealed by metagenomics

As a cutting-edge technology, metagenomics reveals to us the complex and delicate structural and functional relationships within microbial communities (Figure 2). With the help of high-throughput sequencing technology, metagenomics can capture the genetic information of all microorganisms in environmental samples, and then analyze the composition, relative abundance, and interactions of each species in the community.

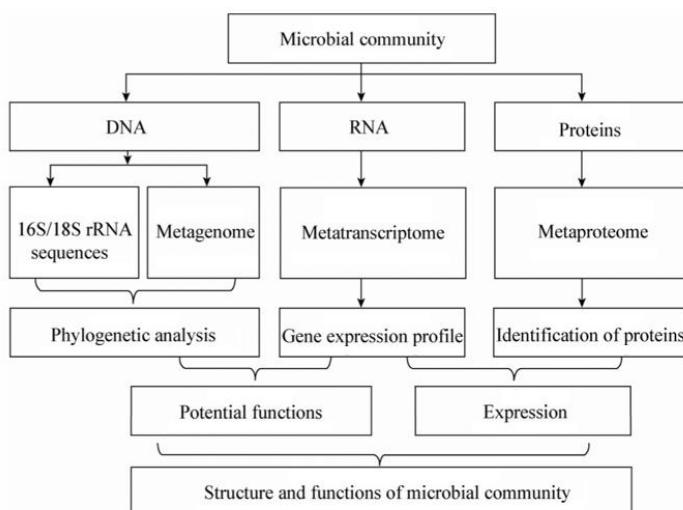


Figure 2 Meta-omics to study the structure and function of microbial community (Ma et al., 2015)

Kour et al. (2021) conducted metagenomic-based taxonomic, strain-level, functional and phylogenetic analyzes of microbial communities using bioBakery 3, a comprehensive set of improved methods, revealing new disease-microbiome interactions. connect.

Metagenomics provides us with unprecedented detail when it comes to microbial community structure. Even in the same type of environment, the microbial community structure will be different due to differences in geographical location, climatic conditions, human interference and other factors. This difference is not only reflected in the diversity of species composition, but also in the interactions between species. For example, there

may be a competitive relationship between some species, in which they compete for nutrients, space and other resources to maintain their growth; while other species may have a symbiotic relationship, in which they cooperate with each other to achieve common survival. Ofaim et al. (2017) introduced a metabolic network-based framework for metagenomic interpretation that converts environment-specific gene catalogs into metabolic network representations to predict dominant taxa for the entire community by establishing functional-taxonomic links. Performance impact.

In terms of microbial community function, metagenomics can infer the functional characteristics of each species in the community through the analysis of gene sequences in the microbial community. These functional characteristics include metabolic pathways, enzyme activities, signal transduction, etc., which together constitute the functional system of the microbial community. This functional system has an important impact on the stability and productivity of ecosystems. For example, some microorganisms may break down organic matter to release nutrients and promote plant growth, while others may slow the effects of climate change by fixing carbon dioxide.

3 Application Prospects of Metagenomics in Ecological Environment Protection and Restoration

3.1 Application of metagenomics in environmental monitoring and assessment

Metagenomics technology is increasingly used in environmental monitoring and assessment. With its unique perspective and methods, it provides us with a new way to examine and assess environmental health.

Datta et al. (2020) studied microbial diversity, bioremediation, pollution monitoring, enzyme and drug discovery through metagenomics technology, demonstrating the great potential of this technology in identifying and monitoring unculturable microbial communities.

In marine pollution monitoring, metagenomics also shows its unique value. By conducting metagenomics analysis of microbial communities in polluted sea areas, researchers have discovered some special microorganisms that can break down plastic waste. The existence of these microorganisms provides the possibility to develop new biodegradable materials and provides new ideas for solving the problem of marine plastic pollution (Techtmann and Hazen, 2016).

Additionally, metagenomics plays an important role in assessing ecosystem health. Taking a certain forest ecosystem as an example, through several years of metagenomics monitoring, scientists found that the diversity and functional characteristics of the microbial community were declining year by year, which is related to the loss of biodiversity and the degradation of ecosystem functions in the forest ecosystem. closely related. This discovery provides a scientific basis for us to take timely ecological restoration measures.

In 2022, a group of research teams in Singapore, Karrie et al., proposed a strategic vision to "establish a new global monitoring system based on full transparency from all parties, using the most advanced digital tools to connect information centers around the world, including Animal and Environmental Health Monitoring". Monitoring methods based on metagenomics provide opportunities for this ambitious idea. and explored the potential of metagenomics-based monitoring to accelerate and change the global environment and detect human health risks (Ko et al., 2022).

3.2 Tapping the potential of metagenomics in the development and utilization of biological resources

Metagenomics technology has opened up new paths for the development and utilization of biological resources, and its potential has been demonstrated in many aspects. In the development of biological resources, metagenomics provides us with the means to directly obtain and utilize genetic resources from the natural environment. Through metagenomics analysis, researchers can screen out microorganisms with special functions from environmental samples, such as microorganisms that produce special enzymes, have specific metabolic pathways, or have high degradation capabilities for specific substrates. These microorganisms have broad

application prospects in agriculture, industry, medicine and other fields. For example, certain microorganisms can synthesize metabolites with unique biological activities. These metabolites can be used as candidate substances for the development of new drugs, providing new resources for the pharmaceutical industry.

Madhavan et al. (2017) described how metagenomic analysis has become a powerful tool for mining new biocatalytically active enzymes from environmental samples, reflecting the application prospects of metagenomics in the development of biological resources.

Kodzius and Gojobori (2015) outline the use of marine metagenomics as a source of biological resource development, particularly its potential to explore novel genes, pathways and genomes in uncultured samples.

Metagenomics technology also helps us to deeply explore and utilize new functional genes in microbial communities. By sequencing and analyzing the metagenomes of microbial communities in environmental samples, we can discover a large number of genes with unknown functions that may have potential application value. Through gene cloning and expression analysis, we can further verify the functions of these genes and apply them to fields such as biocatalysis and biosynthesis. For example, some microorganisms have efficient degradation capabilities. Through metagenomics analysis, we can discover relevant degradation genes and apply them to environmental remediation and pollution control.

Metagenomics technology can also promote the sustainable utilization of microbial resources. Traditional microbial resource development often relies on the isolation and cultivation of specific microorganisms, while metagenomics technology allows us to obtain and utilize microbial genetic resources directly from environmental samples without the need for cumbersome isolation and cultivation processes (Prayogo et al., 2020), This not only improves the efficiency of resource development, but also helps protect the diversity and sustainability of microbial resources.

3.3 The strategic position of metagenomics in addressing global environmental challenges

As global environmental challenges become increasingly severe, the strategic position of metagenomics technology has become increasingly prominent. As an advanced technology that can comprehensively analyze the structure and function of environmental microbial communities, metagenomics plays an indispensable role in addressing global issues such as climate change, biodiversity conservation, and soil remediation.

Laudadio et al. (2019) assessed how metagenomics can improve our knowledge of microbial community composition in samples ranging from environmental to human samples, highlighting the widespread impact of this technology on environmental science, ecology, and public health on a global scale.

Behzad et al. (2015) discussed the current progress of airborne metagenomics, especially the challenges and opportunities of conducting such research, pointing out that airborne microorganisms may have important impacts on atmospheric events, global climate, and human health.

In response to climate change, metagenomics technology provides us with in-depth understanding of the mechanisms of microbial community responses to climate change. Through metagenomics analysis, we can reveal how microbial communities adapt and respond to environmental changes such as global warming and extreme climate, as well as their role in key biogeochemical cycles such as the global carbon cycle and nitrogen cycle. These understandings help us develop effective response strategies to mitigate the effects of climate change (Nowrotek et al., 2019).

In terms of biodiversity conservation, metagenomics technology provides us with new means to assess ecosystem health and biodiversity. Through metagenomics analysis, we can understand the distribution and diversity of microbial communities in different ecosystems and evaluate the impact of biodiversity loss on ecosystem functions. This information is of great significance for formulating biodiversity protection policies and

implementing ecological restoration projects.

In terms of soil remediation, metagenomics technology provides us with new ways to discover and utilize microbial remediation mechanisms. Through metagenomics analysis, we can discover microbial species or genes with special degradation capabilities and reveal their mechanism of action in soil pollution remediation. These findings help us develop efficient and environmentally friendly soil remediation technologies and promote the sustainable use of land resources (Yadav and Kapley, 2021).

Metagenomics plays an important and strategic role in addressing global environmental challenges. By comprehensively analyzing the structure and functional relationships of environmental microbial communities, metagenomics technology provides us with a powerful tool to deeply understand environmental problems, formulate response strategies, and promote sustainable development. As technology continues to develop and improve, the role of metagenomics in addressing global environmental challenges will become more prominent.

4 Summary and Outlook

4.1 Summary of results of metagenomics in the study of environmental microbial diversity

As a revolutionary research method, metagenomics has achieved remarkable results in the exploration of environmental microbial diversity. It not only greatly deepens our understanding of the microbial world, but also brings unprecedented opportunities to the fields of environmental science and ecological protection.

Through high-throughput sequencing technology, metagenomics can comprehensively analyze the genetic information of all microorganisms in environmental samples, thereby providing a comprehensive view of the composition, structure, and functional diversity of microbial communities. This technology not only allows us to glimpse the richness and complexity of environmental microbial communities, but also reveals the interactions between microorganisms and environmental factors at the species and genetic levels (Staley and Sadowsky, 2016).

In the study of environmental microbial diversity, metagenomics has provided us with a large amount of data on microbial species diversity and genetic diversity. By comparing metagenomes in different environmental samples, we can find significant differences in the composition of microbial communities in different ecosystems, which reflects the adaptability of microbial communities to environmental changes. At the same time, metagenomics also reveals the genetic diversity within microbial communities, which is of great significance for understanding the niche differentiation, speciation, and evolutionary mechanisms of microorganisms.

Datta et al. (2020) gave an overview of the applications of metagenomics technology in the fields of microbial diversity, bioremediation, pollution monitoring, enzyme and drug discovery, etc., emphasizing the important role of this technology in identifying and monitoring unculturable microbial communities.

Metagenomics also provides us with rich information on the functional diversity of microorganisms. By annotating and analyzing gene sequences in metagenomes, we can understand the function and expression of various genes in microbial communities, and thus infer the functions and roles of microbial communities in the ecosystem. These functional information include material cycles, energy flows, biogeochemical cycles, etc., which provide important clues for us to understand the stability and sustainability of ecosystems.

The results of genomics in the study of environmental microbial diversity are impressive. It not only provides us with comprehensive microbial community information, but also helps us gain a deep understanding of the interaction between microbial communities and environmental factors. These results not only enhance our understanding of the microbial world, but also provide important theoretical foundation and technical support for ecological environment protection and restoration.

4.2 In-depth understanding of the relationship between microbial diversity and ecosystem health

The importance of microbial diversity as a core component of ecosystem health has received increasing attention.

Through advanced technologies such as metagenomics, we have a deeper understanding of the relationship between microbial diversity and ecosystem health.

As the most complex and diverse component of the ecosystem, microbial communities play a vital role in maintaining ecosystem balance and stability. Microorganisms provide basic support for the normal operation of ecosystems by decomposing organic matter and participating in processes such as material circulation and energy flow. At the same time, the diversity in the microbial community also provides the ecosystem with strong resistance and resilience, allowing it to cope with external environmental pressures and disturbances (Shi et al., 2021).

Delgado-Baquerizo et al. (2016) studied two independent large-scale databases and found that soil microbial diversity is positively related to the multifunctionality of terrestrial ecosystems, even when considering multiple multifunctional driving factors (climate, soil non-organisms) at the same time. biotic factors and spatial predictors), the direct positive effect of microbial diversity was also maintained.

Microbial diversity affects ecosystem health at multiple levels. First, microbial diversity is directly related to the biological diversity and functional diversity of the ecosystem. The richness and complexity of microbial communities directly affect the stability and productivity of ecosystems, and the interactions and symbiotic relationships between microorganisms form an important basis for ecosystem functions. Secondly, microbial diversity has an important impact on the nutrient cycle and energy flow of ecosystems. Microorganisms promote the recycling and reuse of nutrients and maintain the energy flow and ecological balance of the ecosystem through processes such as decomposing organic matter and fixing carbon sources. In addition, microbial diversity also directly affects key elements of the ecosystem such as soil quality and water quality, and has an important impact on the overall health of the ecosystem.

Through technologies such as metagenomics, we can gain a deeper understanding of the relationship between microbial diversity and ecosystem health. However, there is also a need to recognize the complexity and dynamics of this relationship. The response and adaptation of microbial communities to environmental changes is a complex process involving the interaction and regulation of multiple factors (Luo et al., 2018). Therefore, in future research, we need to comprehensively consider more environmental factors and biological factors to comprehensively understand the relationship between microbial diversity and ecosystem health, and provide more scientific basis and guidance for ecological environment protection and restoration.

4.3 Analysis of the prospects and challenges of metagenomics in ecological environment protection and restoration

With its unique perspective and powerful technology, metagenomics has shown great potential and broad application prospects in ecological environment protection and restoration. In the future, with the continuous development and improvement of technology, metagenomics is expected to bring revolutionary changes to ecological environment protection and restoration.

Metagenomics will play a more important role in environmental monitoring and assessment. Through metagenomics analysis, we can quickly and accurately obtain the structural and functional information of microbial communities in environmental samples, so as to promptly discover environmental problems and assess environmental risks. This will help us formulate environmental protection policies more scientifically and provide strong technical support for ecological and environmental protection.

Metagenomics will play an important role in ecological restoration and pollution control. Through metagenomics analysis, we can discover and mine microbial resources with special degradation capabilities, providing new ideas and methods for pollution control. At the same time, metagenomics also helps us understand key species and key processes in the ecosystem, providing precise targets and strategies for ecological restoration (Kour et al., 2021).

Offiong et al. (2023) reviewed the application of metagenomics in environmental chemistry, especially the characterization of chemical contaminants in contaminated sites and its application in bioremediation research, emphasizing the potential of metagenomics technology in improving remediation efficiency.

However, metagenomics also faces some challenges in ecological environment protection and restoration. First, parsing and interpreting metagenomics data remains a huge challenge. Metagenomic data are large and complex, requiring advanced bioinformatics methods and computational technologies for analysis and interpretation. This requires strengthening interdisciplinary cooperation and improving data processing and analysis capabilities.

The application of metagenomics technology also needs to consider issues such as cost, efficiency and feasibility. At present, the cost of metagenomics technology is relatively high, which limits its promotion and application in practical applications. Therefore, it is necessary to continuously optimize the technical process, reduce costs, and improve the practicality and feasibility of metagenomics technology.

In addition, metagenomics technology needs to be combined with other technologies in practical applications to form a comprehensive solution. For example, combining metagenomics with remote sensing technology, geographic information systems, etc. can provide a more comprehensive understanding of ecological environment conditions and problems, and provide more scientific and effective support for ecological environment protection and restoration (Ofaim et al., 2017).

Metagenomics has broad application prospects and huge potential in ecological environment protection and restoration. In the future, we need to continue to overcome technical challenges, strengthen interdisciplinary cooperation, promote technological innovation and application, and provide more scientific and effective technical support and solutions for ecological environment protection and restoration.

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