

Research Progress of Soil Microbial Species Diversity in China

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Abstract

Microorganisms are the most widely distributed life forms, which are distributed to almost all habitats on earth. They can use a variety of organic compounds and inorganic salts as energy to live in cold polar regions, hot springs up to 100 °C or extreme environments with high salinity and alkalinity under aerobic or anaerobic conditions. Microorganisms are the second largest group of organisms on the earth after insects, and their species resources are extremely rich. The study of microbial diversity is the main component of the whole biodiversity study. Microbial diversity mainly studies the population, abundance, distribution uniformity, structural changes and functional diversity of microbial communities in the environment. Microbial diversity can be divided into genetic diversity, functional diversity, structural diversity and species diversity, among which species diversity is the most basic content in soil microbial diversity research. The study included all the bacteria, archaea and fungi in the soil.

Keywords

Microbes; Microbial diversity; Soil microbes.

1. Introduction

Microorganisms are the most abundant, widely distributed and earliest biological group on earth [1]. They exist in a variety of habitats, such as soil, lakes and oceans, among which soil contains the highest microbial community richness [2]. Microbial communities play a key role in terrestrial ecosystems by participating in carbon and nitrogen cycles [3], decomposing plant organic matter [4], and mediating soil mineralization. Accurate measurement of soil microbial species richness is not only an important basis and prerequisite for correctly revealing its spatial distribution pattern, community formation mechanism and functional characteristics [5], but also an important reference information for risk assessment of endangered species and sustainable environmental development [6]. Bacteria and fungi are the two main parts of soil microorganisms, which contribute to the diversity of soil microorganisms. At present, there are few studies on the estimation of OTU richness of these two microbial groups, and the estimation results of these studies vary greatly [7]. The soil samples were taken from different ecosystems, including forests, oceans, grasslands and farmland ecosystems, but the differences in the habitats themselves were not large enough to produce such large differences in the estimates.

China is one of the countries with the richest biodiversity in the world, with a vast territory spanning from the tropics to the cold temperate zone, diverse climatic conditions, complex geographical environment and ecosystem types. The diverse habitats contain rich microbial diversity. Especially in recent years the study of microbial diversity from the traditional training methods, turning to the points of cultivating child biology technology is given priority to, such as DNA fingerprint, molecular hybridization, clone library sequencing, high-throughput sequencing (pyrosequencing), stability, isotope detection (stable isotope probing, SIP), gene chip (gene chip) and transcriptome

study technology. Using advanced molecular biology technology, Chinese scholars have greatly improved the research level of microbial diversity in China.

According to in situ, uncultured microbial phylogeny studies, 95% to 99% of microbial populations in nature have not been isolated, cultured or described, thus estimating that there are 100,000 to 500,000 species of bacteria on earth alone^[8]. Studies have also calculated that the known species of viruses, bacteria and fungi account for approximately the estimated species, 5% and 10% respectively^[9].

2. Bacteria

Bacteria, as a "dynamic" component of the ecosystem, give life to the soil, are the link between aboveground vegetation and underground ecological processes, and play a central role in the maintenance of the biosphere. For example, it participates in the recycling and transformation of carbon, nitrogen, phosphorus and other elements in soil, and maintains the balanced flow of soil elements through their metabolic pathways, such as nitrogen fixation, nitrification and denitrification. At the same time, it participates in the decomposition of soil organic matter and the formation of humus, and plays an active role in the formation of soil fertility, such as the decomposition of cellulose. Microbial community in soil is also closely related to soil structure formation, water and fertilizer retention ability. Soil microorganisms are also sensitive biological indicators in the environment. Community structure changes reflect changes in soil physical, chemical and biological characteristics, and can be used as indicators to predict soil changes. At the same time, soil microorganisms are rich in species resources, important genetic resources and metabolic product resources such as enzymes and antibiotics^[10], but only some species of actinomycetes, bacteroides, cyanobacteria, proteobacteria and firmicutes can produce bioactive substances. Microorganisms are also widely used in the degradation of heavy metals, such as bacillus subtilis, enterobacteria, rhizopus, pseudomonas and other microorganisms^[10, 11]. Widden's study found that 1g of soil generally contained about 1.0×10^8 bacteria, but only about 1 percent were isolated and cultured in the lab, and less than 5 percent of microbiological species were identified and named. Currently, microflora commonly found in soil include: Flavobacterium, Pseudomonas, Mycobacterium, Xanthomonas, Acinetobacter, agrobacterium, Alcaligenes, Arthrobacter, rhizoma There are more than 20 genera including Rhizobium, Bacillus, rhizobacterium, Azotobacter, Caulobacter, Cellulomonas, Corynebacterium and Staphylococcus, among which there are different species in each genus. Liu yingliang et al. studied the composition of soil microflora of pinus masonicus and identified 9 genera of bacteria, including the dominant genera bacillus (43.28%), Beijerinckia (35.82%), Clostridium (5.97%) and nitrogen fixers (2.99%).

3. Fungi

There are a large number of fungi in the soil. The fungi mainly exist in a free state and can also form mycorrhizal relationship with plant roots. The fungi mainly exist at 0 ~ 10cm in the soil surface layer. Fungi are important components of soil microorganisms. Fungi have good compression resistance and fungal performance. This has also been confirmed in recent studies. As a result, fungi in the arid region of the harsh ring. Environmental conditions can still be widely distributed^[12] and have important ecological functions. Soil fungi are the unicellular or multicellular heterotrophic microorganisms living in the soil in the form of hyphae, the number of which is second only to bacteria in the soil. The diversity of soil fungi and their community structure composition have a profound impact on the ecosystem and play an important role in the balance of the ecosystem^[13]. The Tsujit study estimated that there are about 1.4 million species of true fungi in the world, and only 5% ~ 10% have been officially identified and described so far, while the vast majority of fungal species are unknown^[14]. The most common fungi in soil are semi-knowns, such as Penicillium, Geotrichum, Aspergillus and Trichoderma, but large Numbers of cistomycetes and basidiomycetes can also be found. Indigenous yeasts in the soil are mainly semi-knowledge bacteria, such as Cryptococcus and can-dida. Candida and cryptomyces can only be isolated from soil, indicating that soil is their natural

environment. Previous studies on the composition of soil microbial flora of masson's pine have identified 6 fungal genera: penicillium (83.89%), Mucor (5.37%) and trichoderma (4.03%) as the dominant genera, with penicillium as the dominant genera. Most soil fungi are widespread, but some species have optimum habitats. The distribution of penicillium and trichoderma was more in the north than in the south, while the distribution of fusarium, rhizopus, isopsis, jieji and aspergillus was more in the south than in the north. The species and quantity of soil fungi were the most in the topsoil and subtopsoil, which gradually decreased with the deepening of the soil, but some species of penicillium, aspergillus, trichoderma, diosporium and trichoderma were common deep soil distribution bacteria. The general formula for the growth and decline of soil fungi is as follows: sugar fungi → hemicellulose decomposing bacteria and pectin decomposing bacteria → cellulose decomposing bacteria → chitin decomposing bacteria. Penicillium, aspergillus, trichoderma, trichoderma, fusarium, streptosporum and cladosprium are the dominant glycosomes. Some species of penicillium, aspergillus, rhizopus, fusarium, boespora and spore are relatively common hemicellulose decomposing bacteria and pectin-decomposing bacteria. Trichoderma, fusarium, trichoderma, penicillium, aspergillus, sapropelomyces, trichoderma, trichoderma, trichoderma, trichoderma, trichoderma, trichoderma, trichoderma, trichoderma, trichoderma and certain species of trichoderma have strong cellulosic activity. Some species of the genera of psoriasis, pneumocystis and rhizopus have strong activity in decomposing keratin. Some species of the genera galatospira, penicillium, cladomyces monospora, and coleospora have decomposition activities for pseudoides such as vanillin and p-hydroxybenzaldehyde under laboratory conditions, while some species of penicillium, bramospora, and astragalus may be associated with humus decomposition. The ebb and flow of rhizosphere fungi order vary with the crop plant age, such as oat rhizosphere fungi in the plant's first with sporanox and don't know of white mycelium infertility as dominant fungi, age stage in the plant of spherical shell with drafting for dominant fungi, bacteria in the aging stages of plants with sickle, do not know of the dark as the dominant fungi hyphae and infertility ascomycetes. The number of soil fungi varies according to the season, and the number of fermentative fungi (soil fungi that become active when available substrates are available) is the highest in autumn. The number of native fungi is highest in summer.

4. Actinomycetes

Actinomycetes in soil refer to unicellular microorganisms which are transitional between bacteria and fungi. It has branching hyphae with a diameter of 0.5-0.8 μ M. Typical actinomycetes belong to Streptomyces and Micromonospora. All of them are aerobic heterotrophic type, which can widely use carbon and nitrogen compounds such as cellulose, hemicellulose, protein, lignin, etc. The optimum pH is 6.8-7.5, and the optimum temperature is 25-30 °C. Streptomyces is the main Actinomycete in farmland soil. At present, the number of actinomycetes is very large, among which Streptomyces and Nocardia account for the largest proportion, followed by actinomycetes (Actinomyces), micromonas and other actinomycetes, all of which belong to soil of indigenous microorganisms. Actinomycetes can survive in the arid desert soil, and they are resistant to dry conditions; they are more suitable to grow in alkaline or neutral conditions, and sensitive to acid conditions.

5. Expectation

According to hawks worth's estimation, there are about 1.5 million species of fungi (eukaryotes) in the world, and about 97861 species^[15] are known, accounting for only 6.5% of the estimated species. At present, 14700 species of bacteria have been found in China, and about 30000 species of vascular plants have been known in China. If the estimation method of hawks worth (1991) is used (number of vascular plants: number of bacteria = 1:6), the estimated number of bacterial species in China is about 180000, and the number of known species accounts for about 8.2% of the estimated number. In addition, according to incomplete statistics of mora et al.^[16], there are about 11010 kinds of culturable bacteria and 503 kinds of Archaea reported in the world at present, while the total number

of culturable species reported in China accounts for about 10% of that reported in the world, which shows that the research of microbial diversity resources in China still has a long way to go. With the development of science and technology, the research of microbial diversity has gradually shifted from the traditional morphology and culture methods to the molecular biology technology to avoid culture. In particular, the combination of high-throughput sequencing of macro genomic DNA and DNA barcode technology will reveal a large number of undiscovered micro biological groups in the environment, and the application of stable isotope detection, gene chip and transcriptome technology will be extremely important Improve the research level of microbial functional diversity.

With the deepening of the research on soil microbial diversity, the future research work will focus on the following four aspects: alleviating human crisis in food, energy, resources and environment; promoting the development of soil microbial ecology; examining the relationship between microbial system development and functional diversity from a new perspective; designing and exploring more accurate, simple, visible or readable And strengthen the connection between different methods of molecular biology and the organic combination with traditional research methods.

In a word, the research of soil microbial diversity in the future should focus on the soil biological process, ecological service function and the relationship between them, and focus on the establishment and improvement of the research index and method system of soil microbial diversity, so as to clarify the soil biological process that human production activities affect soil microbial diversity and its ecological service function [36]. It can also artificially introduce some beneficial microorganisms to inhibit the development of harmful pathogens, improve soil ecological fertility, enhance the absorption and purification capacity of soil ecosystem for waste, promote the benign cycle of the whole terrestrial ecosystem, improve the living environment of human beings, and realize the harmonious and sustainable development of human beings and nature.

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