

Application of Metagenomics Technology in the Management of Middle and Low Yield Fields

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Abstract

Food security is an important guarantee for world peace and development, an important foundation for building a community with a shared future for mankind, and bears on the sustainable development, future and destiny of mankind. With the growth of population and the acceleration of urbanization, cultivated land resources are increasingly strained, and as an important part of cultivated land resources, the problems of unstable output and low utilization rate of medium and low yield land have gradually become prominent, which has become an important factor restricting the sustainable development of agriculture. In recent years, metagenomics technology, as a powerful research tool, has enhanced people's understanding of the composition, distribution and diversity of microorganisms in different environments, and has been widely applied in the field of farmland soil microorganisms. In this paper, the concept and technical process of metagenomics are reviewed, and the application and development prospect of metagenomics in soil microbial research in middle-low yield field management are reviewed.

Keywords

Metagenomics Technology; The Middle and Low Yield Fields; Apply.

1. Current Situation of Medium and Low Yield Fields

With the 2020 Central Economic Work Conference taking "Solving the problem of seeds and cultivated land" as one of the eight key tasks in 2021, the utilization and protection of cultivated land resources has been mentioned to an unprecedented height. However, the quality of China's cultivated land resources is suffering from serious limitations and shortcomings. The results of the "2019 National Cultivated Land Quality Grade Bulletin" show that the national cultivated land quality grade is divided into 1 to 10 grades from high to low, and the average grade is 4.76[1]. In recent years, China's agricultural production has maintained the mode of high input and high yield, cultivated land has been used for a long time with high intensity and overload, and cultivated land quality has shown a trend of "three" and "three low"[2]. The "three" are the large proportion of medium and low yield farmland, the large area of cultivated land quality degradation and the large area of polluted farmland, and the "three low" are low organic matter content, low grade of supplementary cultivated land and low basic land capacity[3]. On the whole, the average contribution rate of farmland basic land capacity in China is about 50%, which is about 20 percentage points lower than that of developed countries in Europe and the United States. The main reason for the decline of cultivated land quality in China is the shallow

tilling layer, the deterioration of soil physical properties, the reduction of soil organic matter and the decline of fertility caused by frequent shallow tillage operations for a long time, resulting in a wider distribution of medium and low yield grain fields in cultivated land. Therefore, it is urgent to improve the low-and medium-yield fields and increase grain production.

2. An Introduction to Metagenomics Techniques

With the unprecedented development of sequencing technology in recent years, macroomics with metagenomics, macrotranscriptomics and macroproteomics as its main contents has been formed [4]. Metagenomics focuses on the study of microbial diversity[5], and single-cell sequencing technology in metagenomics can better cope with the genetic heterogeneity among individuals[6]. Metagenomic sequencing can not only obtain the overall species composition of the community, but also conduct in-depth studies at the gene and functional levels[7-8], which is the most widely used in the field of microbial sequencing. Metagenome refers to the sum of the genomes of all microorganisms in the environment[9]. At present, the microorganisms that can be cultured in the laboratory only account for 0.1%-1% of the total microbial quantity in the environment, and the vast majority of microorganisms are still in the stage of undiscovered and unstudied[10]. In addition, because microorganisms will enter a state of "survival but unculturable" under the pressure of environmental changes, the limitations of traditional culture methods in the development of microbial research have been further amplified. The advantage of metagenomics technology is that it can overcome the process of microbial isolation and pure culture, reveal the genetic composition and community function of all microorganisms in the soil, and establish the relationship between soil microbial species and the environment[11]. Metagenomics itself provides genetic information on potential novel biocatalysts or enzymes, genomic links between function and phylogeny of uncultured organisms, and an evolutionary profile of community function and structure. Therefore, it is widely used to detect the genomes of microbiomes in various environments, and to study the functional diversity, genetic diversity, species diversity, community structure and metabolic status of environmental microorganisms [12].

There have been many studies using metagenomic techniques to study the community structure and function of soil microorganisms to further reveal the soil microbial processes in the system[13]. However, compared with amplicon sequencing technology, there are relatively few reports on the use of metagenomic technology to study soil microbial communities and functions in middle and low yield fields. With the development of sequencing technology and the decline in price, metagenomic technology will be more widely used.

3. Application of Metagenomics Technology in Middle and Low Yield Fields

Metagenomic sequencing technology was applied to conduct an in-depth study of soil microbial community, gene function and metabolic network in middle and low yielding fields, and elucidated the causes and mechanisms of low fertility in middle and low yielding fields from the perspective of molecular biology, providing an important basis for the mining of microbial community and functional genes in middle and low yielding fields, and providing theoretical support for the management of middle and low yielding fields.

Acknowledgments

This research was funded by Shaanxi Provincial Land Engineering Construction Group (DJNY-YB-2023-25).

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