

# Metagenomic Approach for Studying Soil Microbiome

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## Keywords

Metagenomics, Microbial diversity, Microorganisms, Sequencing, Soil microbiome

### *How to cite this article:*

Upadhayay, V. K. 2023. Metagenomic Approach for Studying Soil Microbiome. *Vigyan Varta* 4(5): 83-85.

## ABSTRACT

The soil microbiome represents a soil microbial community associated with many functional activities of the terrestrial system. The culturable techniques are not sufficient to give a holistic picture of the soil microbiome, therefore, than non-culturable techniques, the metagenomic approach gives better insight into the detection of microbial diversity, community structure and functional potential, and moreover overcomes the limitations of traditional culturable Approach. This article covers the basics from sample collection, sequencing and data analysis to deciphering applications, challenges and future directions in soil microbiome research.

## INTRODUCTION

The soil microbiome, a vast and complex ecosystem, consists of a vast community of soil-dwelling microorganisms that play a crucial role in the functioning of terrestrial ecosystems. This complicated system is composed of up of thousands of different microbial species that interact with one another and their surroundings. Soil microorganisms are intimately engaged in a variety of essential processes, including nutrient cycling, carbon sequestration, and plant growth promotion, and their activities have substantial effects on soil health, plant productivity, and global biogeochemical cycles. The majority of soil

microorganisms were challenging to cultivate in a laboratory setting, which limited our understanding of their characteristics and limited the exploration of the soil microbiome.

With extraordinary advances in sequencing technology, however, metagenomic approaches have emerged as a potent method for studying the soil microbiome. Metagenomics enables the direct examination of microbial communities from environmental samples, thereby eliminating the need for cultivation. This method has provided a unique perspective on the microbial diversity, community structure, and functional potential of the soil microbiome, and has the potential to

revolutionize our understanding of the role microorganisms play in terrestrial ecosystems.

This article discusses the use of metagenomic technology in soil microbiome research, including sample collection, sequencing, and data analysis, as well as the applications, challenges, and prospective directions of metagenomics in soil microbiome research.

### **Metagenomics:**

As an advanced tool, the metagenomic approach is essentially required to study the microbial communities directly from environmental samples such as soil, water, etc. It involves the extraction of DNA from appropriate environmental samples, followed by high-throughput sequencing and bioinformatics analysis. The resulting data can then be used to identify and quantify the microbial taxa present in the sample and to decipher their functional potential.

### **Sample Collection and Preparation:**

Collecting and preparing soil samples is the initial phase of a metagenomic analysis. To accurately represent the immense diversity of the soil microbiome, soil samples should be collected from multiple locations and depths. It is imperative that specimens are stored or frozen as soon as possible to avoid DNA deterioration. Samples are homogenized in the laboratory and DNA is extracted using either a commercial reagent/kit or a standardized method.

### **Sequencing and Data Analysis:**

The collected DNA is then sequenced utilising high-throughput sequencing systems like Illumina, etc. The resultant readings are then processed with bioinformatic techniques to eliminate reads of poor quality and assemble the reads into contigs. After that, the contigs can be annotated and compared to various reference databases in order to determine the microbial species that are present in the sample as well as their possible functional applications. These studies can reveal information about the composition, diversity, and potential utility of the soil microbiome.

### **Applications of Metagenomics in Soil Microbiome Studies:**

Metagenomics has multiple applications in soil microbiome research. It can be employed to identify microbial taxa involved in particular functions, such as nitrogen fixation or carbon sequestration. In addition, it may be utilized to reveal prospective microbial indicators of soil health or to track shifts in the soil microbiome as a consequence of environmental factors such as shifts in land use or climate change. In addition, metagenomics can be used to identify new microbial species or genomes with potential biotechnology applications.

### **Challenges and Limitations:**

Despite its numerous benefits, metagenomics presents a number of obstacles and limitations. A major hurdle is the soil microbiome's high complexity, which can lead to low sequencing coverage and hardship in assigning functions to microbial taxa. The possibility of contamination during sample collection, DNA extraction, or sequencing can also lead to false-positive results. In addition, metagenomics can be costly and computationally intensive, necessitating specialized resources and infrastructure.

### **CONCLUSION**

Cultivable approaches reveal the limited microbial species in a given system, but a metagenomic approach is required to examine the entire microbial taxa present. Metagenomics shows the potential to transform the understanding of the functional properties of microorganisms in terrestrial ecosystems. This approach also faces some obstacles and limitations, but continued advances in sequencing technology and bioinformatics tools are likely to increase the effectiveness of metagenomics in soil microbiome research.

### **REFERENCES**

- Jansson, J. K., & Hofmockel, K. S. (2018). The soil microbiome—from metagenomics to metaphenomics. *Current opinion in microbiology*, 43, 162-168.

Kaviya, N., Upadhayay, V. K., Singh, J., Khan, A., Panwar, M., & Singh, A. V. (2019). Role of microorganisms in soil genesis and functions. Mycorrhizosphere and pedogenesis, 25-52.

Leite, M. F., van den Broek, S. W., & Kuramae, E. E. (2022). Current Challenges and Pitfalls in Soil Metagenomics. *Microorganisms*, 10(10), 1900.