



## Application Of Metagenomics In Agriculture

Shovana Pal<sup>1</sup>, Keshab Ghosh<sup>2</sup>, Dr. Aritri Laha<sup>3\*</sup>

<sup>1</sup>Student of M.Sc., Department of Microbiology, School of Life Sciences, Swami Vivekananda University, Barrackpore, 700012, West Bengal, India.

<sup>2</sup>Student of M.Sc., Department of Microbiology, School of Life Sciences, Swami Vivekananda University, Barrackpore, 700012, West Bengal, India.

<sup>3\*</sup>Assistant Professor, Department of Microbiology, School of Life Sciences, Swami Vivekananda University, Barrackpore, 700012, West Bengal, India.

**\*Corresponding Author.: Dr. Aritri Laha**  
E-mail: aritril@svu.ac.in

<i>Article History</i>	<i>Abstract</i>
Received: 30/09/2023 Revised: 05/10/2023 Accepted: 03/11/2023	Metagenomics is the evaluation of the structure and function of entire nucleotide sequences isolated and analysed from a bulk sample. In comparison to conventional methodologies, metagenomics contains a larger amount of genetic data. It is crucial to understand and increase crop yields in both rural and urban agriculture because the microbial community associated with plant roots is crucial for plant growth and development. Metagenomic approaches can be utilised to identify the microorganisms and their functional genetic features even if some of these microbes are currently not culturable in the lab. Improved plant development and sustained crop production in soil and soilless agriculture should result thorough understanding of these species and their interaction procedure. The goal of this review is to shed light on metagenomic approaches used to investigate the microbial ecology and related microbiota of plant roots. Metagenomics is enabling an understanding of these microbes and their biotechnological potentials, which may then be leveraged to create novel, useful, and eco-friendly bio-fertilizers and bio-pesticides.
CC License CC-BY-NC-SA 4.0	<b>Keywords – Metagenomics, microbial ecology, sustainable agriculture, pollution control</b>

### Introduction:

The rate of increment of global population is expected that by 2050, will cross about 10 billion. To manage the food requirement of these huge population more advancements in sustainable agriculture are needed which is influenced by various factors such as biodiversity conversion, plant and animal health, pollution management, green technology, economy, political stability and urban agriculture (Levy and Lubell, 2018). The utilisation of chemical fertilizers is never healthy and ecofriendly agricultural practices that can be replaced by the utilisation of microorganisms which able to increase the crop production by 50-60% and agricultural output by 10-50% by reducing the dependency of synthetic fertilizers (Singh et al., 2019). Metagenomics is the study of direct genetic analysis of the whole genomic material of any microorganisms, collected from soil, water, air.

Understanding the soil microbial community, creating therapeutic chemicals, making biotechnological advances, and promoting sustainable agriculture may all be aided by metagenomics. Halobionts, a collection of several microbial species, promote essential physiological processes and the integrity of ecosystems by interacting intimately with plants. This review explains the significance of metagenomics in prospect of agriculture and soil health.

### **Approaches of Omics Tools in Sustainable Agriculture:**

In sustainable agriculture soil microbiology has a great contribution because soil bacteria are important producers of natural compounds and are referred to as the "metagenome" (Garrido-Oter et al., 2018). Omics strives to characterise of biological molecules that are relevant to an organism's or a group of organism's structure, function and dynamics (Bevivino and Dalmastrì, 2017). To research microbial communities, metagenomics employs sequence-based and functional methodologies that result in gaining new insights because to improvements in DNA sequencing technology and falling costs, including the discovery of novel genes, proteins, and secondary metabolites. Research activities are going on numerous bacterial phyla, including as Proteobacteria, Bacteroidetes, Actinobacteria, and Firmicutes, have been discovered in the rhizosphere through studies (Sabale et al., 2019). The sample DNA are fragmented and evaluated by loading on agarose gel that helps in differentiation and distribution by the use of suitable marker (Farouk et al., 2020).

### **Soil Health: Plant-Microorganisms Interaction:**

Soil agroecosystems are crucial for biodiversity and environmental adaptation in the development of sustainable agriculture. They introduce plant and microbial communities, influencing soil structure and composition. Rhizosphere soil is sensitive to climate changes, land use, and management, and can self-heal after disturbance. Metagenomic approaches have revealed many functions not important for life sustenance. However, agricultural practices like agrochemicals, excessive fertilizers, erosion, and multiple cropping contribute to soil degradation, leading to challenges in sustainable agriculture. To sustain soil health and improve soil characteristics, it is essential to improve soil characteristics for the agricultural ecosystem and human survival. By metagenomic approaches such microorganisms can be able to apply in agricultural fields that have the capacity to remove or detoxify pollutant, created through agricultural activities (Guerra et al., 2018; Ma et al., 2020; Ruiz et al., 2021).

### **Sequencing:**

In metagenomics technique two methods are applied, those are Sanger sequencing and other next-generation sequencing techniques. However, they are constrained by issues including high sequencing costs, the inability to sequence several samples at once, and the requirement for additional DNA. Illumina/Solexa and 454/Roche are two common technologies (Zhang et al., 2021). Plant roots and organic materials from bioponic systems were sequenced using Illumina MiSeq, showing several microbial species. Urban agricultural projects like rooftop farming have a substantial influence on the diversity and composition of microbial communities, demanding experimental or real-world investigations specific to rooftop farming (Babalola et al., 2020).

### **Assembly:**

Contigs made up of metagenome sequence reads are assembled, and the size and consistency of data gaps affect how well the sequence data is covered. Short read assembly is used to create large contigs to recover the genomic sequence of uncultured organisms. Assembly is urgently required for the analysis of lengthy and complicated genomic characteristics and repetition classes. Mainly two fundamental methods are used for assembly, those are de novo and reference-based methods. For metagenomic datasets with genomes from closely related groups, reference-based assembly is employed. De novo assembly based on more calculations and calls for additional equipment. Read length and annotation needs are two factors that affect metagenomic assembly. In the absence of reference metagenome sequence for alignment, innovative de novo assemblers like Meta-IDBA, metaSPAdes, Genovo, Ray Meta, and Contig Extender are applied to sequence novel microbial genomes (Young and Gillung, 2020).

## **Environmental Microorganisms Important to Sustainable Agriculture: Phylogenomic Analysis:**

A popular computational technique for analysing sequenced metagenomic data is phylogenomics, however it has the same constraints as the species tree. Phylogenomic or phylogenetic analysis helps in the identification and discovery of new organisms and also establishing evolutionary connections, predicting gene function, and tracking lateral gene transfer are all part of it (Emms and Kelly, 2019). This procedure, however, could result in skewed sampling, imbalanced data sets, and incorrect phylogenetic conclusions. It is also difficult to distinguish between the impacts of mutation and genetic backgrounds that are uniform.

### **Stable Isotope Probing:**

Stable Isotope Probing (SIP) is a method that maps environmental functions to microbial communities. It involves feeding a labelled substrate to the population and characterizing the higher concentration of communal DNA. This helps identify microbes involved in processes like phenol degradation and glucose metabolism. SIP and metagenomics have increased the potential to study microbes' functions and diversity, enabling the detection of labelled nucleic acids. SIP involves incubating an environmental sample with a substrate labelled with a stable isotope, such as C-labeled substrates or N and varying types of labelled water. In doing so, the target substrate can be taken up by and integrated into the genomes of the active microorganisms. DNA is taken from the sample and filtered through SIP to look for potential "hits" in metagenomic libraries. This focused metagenomic strategy directly links substrate collection to functional communities while condensing complexity to a small number of well-known species (We et al., 2018b).

### **Meta transcriptomics:**

A recent advancement in meta-omics called metatranscriptomics concentrates on investigating the transcripts of microbial populations that have been isolated from settings where the population has been disturbed or altered. This method can aid in the discovery of new genes and allows for the taxonomy of microbial groups. Compared to metagenomics, metatranscriptomics takes less sequencing data and can offer information on functional information and patterns of gene expression. To illustrate the active production of antibacterial resistance genes and their potential for environmental danger, 65.8% of identified antibiotic resistance genes (ARGs) are transcribed in activated sludge (Salem et al., 2020).

### **Metaproteomics:**

The study of the protein profiles of microbial communities, known as metaproteomics, focuses on the function of various bacteria. It was developed for acid mine drainage (AMD) microbial communities and depends on accurate metagenomic data. Metaproteomics detected and quantified over 2000 proteins, allowing 30–40% of the microbial community to be examined but only picking up populations of less than 1%. Future proteomics research that target low-abundant taxa in particular will benefit greatly from this information (Gupta et al., 2018).

## **Application of Metagenomics in Sustainable Agriculture:**

A technique for reshaping and addressing microbial activity in soil, functional metagenomics, or rhizosphere engineering, is particularly helpful in agriculture. It aids in understanding how the rhizosphere, soil environment, and plant tissues interact. For industrial uses, metagenomics provides crucial enzyme molecules that enhance soil fertility, crop development, and yield (Goel et al., 2017; Louca et al., 2018).

In order to produce bioethanol and break down lignocellulosic materials, novel halotolerant enzymes from the soil have been discovered using metagenomic applications (Salem et al., 2020). These enzymes, which come from fungus, yeast, and bacteria, improve soil and guarantee crop output. Additionally, they have the potential to be converted into feed for animals and sustainable biofuels.

Combining shotgun and MS-based proteomics with *nifH* genes and genome sequences led to the identification of a novel protein cytochrome that is crucial for iron oxidation and acid mine drainage (Bevivino and Dalmastri, 2017).

**Conclusion:**

With the use of metagenomic techniques, the rhizosphere microbiome may be fully understood, and novel microbes for urban agriculture and environmental remediation can be found. Numerous rhizosphere microorganisms have been discovered by researchers to be advantageous for plant development and sustainable agriculture, including *Proteobacteria*, *Acidobacteria*, Bacteroidetes, BRCI, *Chloroflexi*, *Actinobacteria*, *Firmicutes*, *Cyanobacteria*, *Planctomycetes*, *Chlorobi*, and *Nitrospira* (Ghosh et al., 2018). Through the discovery of underutilised soil microorganisms, increased crop yield, and increased phytopathogen resistance, metagenomics supports sustainable agricultural growth. Data interpretation and diversity analysis are aided by shotgun metagenomics and bioinformatics technologies. As a result, metagenomics application is a very effective technology for sustainable agriculture.

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