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THE HIDDEN UNIVERSE BENEATH OUR FEET:

HOW METAGENOMICS UNVEILS THE SECRETS OF NATURAL FARMING

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Soil is not merely a medium for anchoring plant roots, it is a vibrant ecosystem inhabited by billions of microorganisms. These microorganisms influence nutrient availability, the decomposition of organic matter, plant health, and the resilience of the ecosystem. The goal of natural farming is to promote sustainable agricultural production by harnessing ecological processes and locally available resources. However, a significant portion of the microbial world, which underpins these processes, remains invisible to the naked eye. Metagenomics, an advanced DNA-based technique, offers an opportunity to explore this hidden world by analyzing genetic material obtained directly from environmental samples. By uncovering the diversity and functionality of soil microbial communities, metagenomics can help researchers understand how natural farming practices affect soil health, as well as the interactions between plants and microorganisms. This paves the way for evidence-based and sustainable agricultural management (Badiyal et al., 2024; Gajjar et al., 2026a).

Discovering the Invisible Workforce Beneath Our Feet

A single handful of soil can contain an incredibly diverse community of bacteria, fungi, archaea, and other microorganisms. These organisms interact with plant roots, organic matter, and each other, facilitating biological processes that sustain agricultural ecosystems. Some microorganisms participate in nitrogen fixation, the solubilization of phosphorus, the decomposition of organic matter, and the cycling of essential nutrients. Others can help plants withstand environmental stress or suppress certain soil-borne pathogens. However, their abundance and activities vary depending on soil properties, climate, crop varieties, and farming practices. Through metagenomics, scientists can study microbial communities without needing to cultivate each organism individually in a laboratory. This expands our understanding of soil biodiversity and its ecological significance (Clagnan et al., 2024).

Metagenomics: Reading the Genetic Language of Soil

Traditional microbiological methods have provided valuable information about soil microorganisms. However, many of these organisms are difficult to cultivate under standard laboratory conditions. Metagenomics overcomes this limitation by analyzing DNA extracted directly from soil, the rhizosphere, compost, and other environmental samples. In shotgun metagenomic sequencing, DNA fragments from various organisms are sequenced and analyzed using bioinformatics tools to identify microbial communities and investigate genes associated with specific biological functions. Such analyses can reveal the genetic potential related to nutrient cycling, carbohydrate decomposition, stress responses, and interactions between plants and microorganisms. Importantly, the detection of a gene indicates potential functionality, but it does not prove that the corresponding process is actually occurring under field conditions. Integrating metagenomic findings with soil measurements, microbial activity assays, and field experiments provides a more comprehensive understanding of the soil ecosystem (Clagnan et al., 2024; Jagadesh et al., 2024).

Natural Farming: An Exploration of Microbial Foundations

Natural farming methods often emphasize biological processes, locally available resources, crop diversity, mulching (covering the soil), and the recycling of organic matter. These practices can influence soil moisture, the availability of organic matter, the

environment surrounding plant roots, and the resources accessible to microorganisms. Metagenomics provides a means to compare microbial communities across natural and conventional farming systems, helping researchers determine whether specific agricultural practices induce changes in microbial diversity and functionality.

In India, natural farming inputs such as beejamrut, jeevamrut, ghanjeevamrut, and panchagavya offer opportunities to investigate microbial characteristics and evaluate their effects scientifically. Under the Network Research Program on Bharatiya Prakritik Krishi Paddhati (Natural Farming) through Biotechnology Interventions, supported by the Gujarat State Biotechnology Mission, Department of Science and Technology, Government of Gujarat, metagenomics and microbial studies have been identified as key tools for investigating the interactions between natural farming inputs and soil microorganisms (https://btm.gujarat.gov.in/Natural-Farming.htm). Nevertheless, establishing the efficacy of different formulations and practices requires appropriate experimental controls, standardized protocols, and crop-specific field validation (Gajjar et al., 2025; Jain et al., 2026).

Unlocking Nutrient Cycling and Soil Fertility

Healthy soil resources are tested for their potential use as components in bio-fertilizers or microbial consortia (groups of microorganisms). However, the mere presence of functional genes does not determine the rate at which nutrients will be released, nor the total quantity of nutrients that will ultimately become available to crops. Chemical soil analysis, enzymatic assays, and field measurements remain essential for translating genetic information into practical recommendations (Clagnan et al., 2024).

Strengthening Plant Health through Beneficial Microbes

Plants and microorganisms maintain complex relationships in and around their roots. The narrow zone of soil influenced by root exudates, known as the rhizosphere, provides a dynamic environment where microorganisms compete, cooperate, and interact with plants. Certain bacteria and fungi can promote plant growth, enhance nutrient uptake, produce biologically active compounds, or contribute to protection against specific pathogens. Metagenomics can assist researchers in identifying the microbial groups and genes associated with these functions, while comparative studies can reveal how agricultural practices influence plant-associated microbial communities. Such findings can facilitate the development of locally adapted microbial inoculants and biologically informed crop management strategies. However, these beneficial effects are often strain-specific and depend on interactions with the plant genotype, soil conditions, climate, and existing microbial communities. Therefore, potential organisms identified through metagenomics should be isolated or otherwise characterized and their safety, efficacy, and field performance must be evaluated before they are put to practical use (Jagadesh et al., 2024).

Decoding Natural Farming Inputs through DNA Sequencing

Traditional natural farming practices involve mixtures of organic substances, the microbial composition of which can vary depending on the ingredients used, preparation methods, storage conditions, and the local environment. Metagenomics offers an opportunity to study the microbial diversity within these preparations and investigate their potential biological functions. Comparing preparations made using different ingredients or fermentation conditions can help researchers identify consistent microbial patterns and understand how preparation processes influence microbial communities. For instance, studies on Jeevamrut, Ghanjeevamrut, and other locally used preparations can reveal the presence of microorganisms involved in nutrient cycling or the promotion of plant growth (Gajjar et al., 2026b). Such research can also assist in identifying undesirable microorganisms and improving quality control procedures. Nevertheless, the identification of a potentially beneficial microorganism does not automatically confirm the efficacy of a preparation. Factors such as microbial viability, metabolic output, safety, reproducibility, and performance under field conditions must also be evaluated.

Bioinformatics and Artificial Intelligence: Turning DNA Data into Agricultural Insights

Metagenomic sequencing generates vast amounts of DNA sequence data, which require specialized computational approaches for meaningful analysis. Bioinformatics pipelines assist researchers in assessing sequence quality, classifying microorganisms, assembling DNA fragments, predicting genes, and comparing functional profiles within soil samples. Public databases and reference genomes are instrumental in identifying microbial communities and annotating genes associated with key biological processes. Machine learning can complement these approaches by uncovering relationships between microbial profiles, soil characteristics, agricultural practices, and crop performance. Given sufficiently large, representative,

and well-validated datasets, predictive models could eventually help identify microbial indicators of soil health or distinguish between management systems based on their microbial signatures. However, computational predictions are contingent upon data quality and rigorous validation. Artificial intelligence cannot compensate for poorly designed experiments, nor can it serve as a substitute for field-based evidence (Kumar et al., 2026).

Building Climate-Resilient and Sustainable Farming Systems

Climate change exposes agricultural systems to mounting challenges, including drought, salinity, heat, and erratic rainfall. Soil microorganisms can contribute to ecosystem resilience through processes such as nutrient transformation, the decomposition of organic matter, plant-microbe interactions, and other ecological functions. Metagenomics can help researchers understand how microbial communities respond to these stressors and identify specific genes or organisms that warrant further evaluation for their potential role in plant adaptation. Comparing agricultural systems across diverse agro-climatic zones may also reveal whether certain microbial characteristics are consistently associated with healthy soil or more resilient crops. Such insights could inform the development of site-specific management strategies that integrate biological resources with soil testing and agronomic knowledge. While microbiome-based approaches hold significant promise, their benefits must be demonstrated through long-term, multi-location trials before they can be recommended for widespread adoption (Gajjar et al., 2026a).

Challenges and the Road Ahead

Despite its potential, metagenomics faces several scientific and practical challenges. Microbial communities in soil are highly diverse, and their composition varies according to location, season, crop variety, and soil depth. Processes for DNA extraction, sequencing technologies, reference databases, and bioinformatics pipelines can also influence the results. Furthermore, DNA-based analyses may detect genetic material from inactive or dead organisms. Moreover, the abundance of a gene does not necessarily indicate that it is active or performing a biological function. Factors such as the cost of sequencing, the need for computational expertise, and the limited availability of reference data specific to a given region can also hinder the adoption of these techniques. Integrating metagenomics with metatranscriptomics, metabolomics, microbial cultivation, soil health assessments, and carefully designed field experiments can help bridge the gap between genetic potential and the actual functioning of an ecosystem. Collaboration among microbiologists, bioinformaticians, agricultural experts, and farmers will be crucial for translating microbial discoveries into reliable and locally applicable agricultural solutions (Gajjar et al., 2026b).

Conclusion

Metagenomics is unveiling a new world, a hidden biological realm that sustains agricultural soils. By shedding light on microbial diversity and the genetic potential of soil- and plant-associated communities, this technology can deepen our understanding of nutrient cycling, plant health, and the ecological processes influenced by natural farming practices. Applying metagenomics to natural farming inputs and soil ecosystems can assist researchers in identifying promising microorganisms, developing improved assessment methods, and formulating evidence-based approaches for soil management. When integrated with bioinformatics, artificial intelligence, conventional soil testing, and field validation, metagenomics can contribute to a more comprehensive understanding of sustainable agriculture. Its ultimate potential lies not merely in the discovery of more microorganisms, but in understanding how microbial communities function within actual agricultural systems, and how this knowledge can support productive, resilient, and environmentally responsible agriculture.

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