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SOIL METAGENOMICS

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In terms of the microbial community, soil is arguably the most difficult of all natural environments for microbiologists. According to Paul *et* al. (1989), cultivated soil and grasslands have 2×10^9 prokaryotic cells per gram, and forest soil is thought to hold 4 x 10^7 bacterial cells per gram (Richter *et* al., 1995). Analyses may not have included genomes from rare and unrecovered species. These figures may be understated (Torsvik *et* al., 2002).It is considered that the high degree of spatial heterogeneity, multiphase nature and intricate chemical and biological features of soil habitats are responsible for the diversity of microorganisms found in soil samples.

Soil as a Microbial Habitat

The soil biota, organic molecules in varying states of decomposition and mineral particles with a range of forms, sizes and chemical properties make up soil. Prokaryotes are the most prevalent organisms in soil and can make up the majority of the biomass in soil (Hassink *et* al., 1993). Sand grains and clay-organic matter complexes are two examples of soil components where soil microorganisms frequently adhere or adsorb heavily. The surfaces of soil aggregates and the intricate pore spaces between and inside the aggregates are microhabitats for soil microorganisms (Foster *et* al., 1988). Due to size limits, some pore spaces are inaccessible to microorganisms. The makeup of soil microbial populations changes as a result. The availability of water and nutrients has a significant impact on the metabolism and viability of soil microorganisms.

Prokaryotes are a crucial part of the system that breaks down soil, which is a significant organic carbon storage area. Only small amounts of organic carbon are readily accessible to microbes, despite the high levels of organic matter found in most soil types. Through a mix of microbiological and abiotic processes, the majority of the organic matter

derived from plants, animals, and microorganisms is converted into humus during this phase. The half-life of these stable organic matter complexes with respect to biological degradation is roughly 2,000 years. Humic compounds are stable and resistant to microbial decomposition processes. The scope of soil surveys must be broad in order to adequately document the microbiological diversity and the corresponding gene pool.

Why Metagenomics?

- Discovery of
  - ✓novel natural products
  - ✓new antibiotica
  - ✓new molecules with new functions
  - ✓new enzymes and bioactive molecules
  - ✓diversity of life
  - ✓interplay between human and microbes
  - ✓how do microbial communities work and how stable are they
  - ✓holistic view on biology

Soil Meta-genomics

Methods that depend on culture restrict analysis to microorganisms that can grow in a laboratory setting. Most people agree that only 0.1–1% (depending on by using a laboratory, microorganisms can be cultivated (depending on the environmental sample). Agricultural practises that underexploit 99% or more of the microbial diversity. Furthermore, bacteria can enter a state known as "viable" under environmental stress but unculturable," which further restricts these bacteria's exposure to conventional cultivation technique. As a result, microbial identification that depends on culturing risks underestimating microbial diversity. In order to analyse genomes that are similar but not identical in the environment, the term "metagenomics," which refers to the direct extraction of genetic material from the environment, was developed. Metagenomics may be used to describe the functions of environmental DNA through direct cloning for heterologous expression in a surrogate host organism or to target the structure of the metagenome through cloning and sequencing technologies. No sequence homology to previously defined genes or other a prior sequence information is necessary for the functional metagenomics method because it relies on the cloned ambient DNA's capacity to provide a phenotypic function to the host. Accordingly, functional metagenomics can be seen as a genuine discovery technique for locating and

describing novel gene families, metabolic characteristics, bioactive substances or pathways from uncultured soil bacteria.

Metagenomics as a Tool for Sustainable Agriculture

The soil-dwelling micro-flora and micro-fauna are an essential component of soil biodiversity systems (SBS) and integrated nutrient management (INM) and they play a significant impact in plant growth and overall development. Chemical fertilisers and pesticides can have harmful impacts on the health of the soil and plants, which can have a negative impact on the ecosystem. A critical option for establishing sustainable agriculture output is beneficial microbial riches of agricultural value. Metagenomics improves in the prediction of microbial community structure and, as a result, can address and handle major scientific issues pertaining to microorganisms used in agriculture. By focusing on nif, this strategy has been effectively tested for the evaluation of the diazotrophs found in the rhizosphere of native red kidney beans (RKB) of the Western Indian Himalaya. This metagenomic study investigated the diversity and community structure of N_2-fxing bacteria in a Himalayan RKB rhizosphere, which can be investigated to serve as the foundation for additional research.To better understand community development, interspecies coordination and competition for vital nutrients, and the distribution of metabolic activities among community members, metagenome information for a rhizosphere is starting to reveal detailed information about associated community structure, dynamics, and functional activities. Also known as "rhizosphere engineering," functional metagenomics can be investigated to change the makeup of the rhizospheric microbial community and to readdress microbial activity.

Conclusions

Although, it is commonly recognised that microorganisms play a crucial role in the establishment and maintenance of plant ecosystems, the vast majority of the rhizosphere's population remains uncharacterised and unknown. The evaluation of community structure and function using a combination of conventional and cutting-edge metagenomic approaches will open up new perspectives on the microbial life in the soil. Identifying the signals, exudates, and important components of the rhizosphere's microbial community will also yield chemical and microbial markers that can be used to explain how plants attract and promote beneficial microbes. Additionally, soil metagenomics has the potential to increase agricultural output and unearth numerous as-yet-undiscovered soil microbes, their roles, and genes for a variety of applications. The most diverse microbial communities can be found on Earth in

soil habitats. The genomic, metabolic, and phylogenetic diversity that is stored in the soil metagenome has so far only been partially explored by metagenomic techniques. The development of techniques that capture the heterogeneity and dynamism of complex soil microbial communities, both over time and space, represents one of the main difficulties for soil metagenomics. Although there has been significant progress in the characterisation of microbial communities by random sequencing, it is still necessary to enhance sequencing technology, lower the cost of sequencing, and develop bioinformatics tools for analysing the massive amount of data collected.

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