Roles of Microbial Community in Soil for Disease Prevention

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Description

Soil microbial ecology and its impact on plant ecosystem function, dynamics, and production is a hot topic in science right now. Components ranging from research scientists to home gardeners have wished for the development of quick and thorough approaches to study soil microbial communities in terms of composition, diversity, biomass, and possible influence on plant productivity. The biological components that live in soil are made up of a diverse and complex population, making the creation of a single, self-contained test difficult. When the right questions are asked, terminology are defined, and the limitations of each methodology are understood, the right methodologies may be used to accurately characterise the structure and function of soil [1].

Phenotypic parameters have been used extensively in the past to define the composition and diversity of microbial communities in soils. Because phenotypic approaches are limited to species that can be isolated or cultivated, such an approach has resulted in an insufficient evaluation of microbial diversity in soil ecosystems. The proportion of the microbial community residing in environmental samples capable of being cultivated on laboratory media is minuscule relative to that present, resulting in a vast underestimation of both the population size and diversity of soil-inhabiting microorganisms, as has been well documented and repeatedly articulated [2].

Although some phenotypic methods may be useful in determining relative differences between soil microbial communities, depending on the method used, such an approach may be ineffective in determining the abundance or identity of specific microorganisms in a population, or it may be completely inappropriate due to the organism's nonculturable state. Recently, molecular analytical technologies have been used to define the biology of soil ecosystems, revealing a wealth of new information on the variety of microbial species present in these environments. These researches have shown that using molecular approaches to recover new species from soil habitats is more likely than not to be successful [3].

As a result, using such methods to the study of soil microbial ecology and soil borne plant diseases has the potential to reveal a wealth of information on the function of microorganisms in soil ecosystems, as well as their interactions with one another and the plants they colonise. Molecular methods, on the other hand, have their own set of constraints. Typically, such tests use the polymerase chain reaction, which can be skewed by primer design or specificity, or fail to detect people in a group due to low copy numbers of the target DNA. Although evolutionary links can be observed in the case of microbiological classifications resulting from the application of such approaches, the identifications achieved are only as good as the data available.

Similarly, providing no additional discrimination of populations beyond

that provided by methods such as denaturing gradient gel electrophoresis or terminal restriction fragment length polymorphism analysis does not provide significant insight into the composition of these populations beyond a comparative or descriptive level. Although genomic investigations of soil microbiology and ecology have provided a wealth of descriptive data, there have been few attempts to relate these studies to the function of microbial communities and their impact on plant development and health. As a result, these early investigations have just begun to broaden our understanding of the functional nature of microbial populations beyond what was known prior to the development or use of molecular methods [4].

Instead of establishing what these microorganisms are doing and what variables regulate the dynamics of microbial communities in soil, the focus has been on better defining the makeup of microbial communities. The cataloguing of soil microorganisms has value and continues to warrant research effort because this information, when combined with a management practise or a specific observation about plant growth or disease development, can lead to the discovery of a disease causal or suppressive agent or complex. Knowledge of the dynamics of soil microbial community structure has the potential to be extremely useful in developing strategies for manipulating such populations in order to improve plant health.

The biological definition of a disease-suppressive soil is a frequently asked issue. Determining this concept has taken a lot of time and effort, and in some cases, many careers have been spent figuring out the biological processes at work in a single system. The use of molecular biology technologies in research on the function and structure of soil microbial communities, as well as the impact of these biological characteristics on the development of soilborne plant diseases, offers a lot of potential. These methods have shown tremendous promise in terms of defining and characterising the biological nature of disease-suppressive soils more quickly [5].

The processes of suppressive soils, both produced and naturally occurring, were studied. This review focuses on the molecular techniques that may be used to monitor and analyse soil microbial communities, as well as studies that have used these technologies to see how management practises affect the makeup of these populations and their influence on plant health. Due to the constant development of new derivative approaches, the discussion will be confined to a few regularly used procedures.

Conflict of Interest

None.

References

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How to cite this article: Pozo, Marquina. "Roles of Microbial Community in Soil for Disease Prevention." J Biodivers Biopros Dev 8 (2022):9.