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Genetic Diversity of Soil Microbes and its Ecological Significance

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Annotation: Microbes are the main performers of all activities related to the biosphere of the Earth. Alteration in microbial dynamics of the ecosystems by any means, including but not limited to climatic change affects the biogeochemical processes of terrestral ecosystems. Therefore, soil has the largest population of microorganisms since it offers hiding places; their contact with plant roots will guarantee their survival. Unfortunately most of the microbial populations in soil are not culturable and can only be characterized by the comparison of their metagenomic 16SrRNA and other housekeeping gene sequences with reference databases IconData: http://dx.doi.org/10.17504/atts.2016.084. Therefore, large-scale cultivation independent science is on the horizon since the number of uncharacterized soil microbes to classify is growing exponentially to the growth in sequence databases. Progressively, it is recognised that functional characterisation of the soil microbiome and especially of the interactions among its members requires full-scale genetic profiling of the entire soil microbial community, especially in the changing context of climate change. A profound comprehension of the variation in terrestrial soils by these detailed studies will unmask the role of the microbial community of the soil in the efficiency and organization of the other above-ground systems. We stressed on genetic identity of the soil and what is in stored for the soil bionetwork in relation to climate change in future.

1. Introduction

In fact, microorganisms are the oldest existent life-forms on earth and they are almost omnipresent in spite of the fact that many people do not readily see them. They have the most important function to perform the key processes in the basal level of ecosystem; they for instance account for the most percentage of the mineralization of the organic matter. In natural ecosystems, the level of diversification is at the rhizosphere, which in turn is the area borders between microorganisms and plant roots especially at the epidermis of roots and in some cases it even makes its way through epidermis cells. They also operate in a dynamic manner as regards the other species as well as their aqueous and nutrient media. These rapidly changing microenvironments are controlled by microbial community genetics which in turn is dictated by the genetic variability of microorganisms present in the host. Therefore soil harbours the most complete set of bacterial phylogenetic diversities. [1][2]

Various aspects of soil-inhabiting bacteria, embracing plant pathogenic species, have been studied by various techniques and present diverse patterns of communities. In general, there are multidensities of genotypically different populations in soil microbial communities, some of which are present in significant quantity. As the sampling effort climbs the number of species does as well – a calculation of the total number of coexisting species is therefore as speculative an endeavor as can be imagined. There are also increasing indications that the total number and genotypes of microbial communities in the soil are much greater than previously anticipated, despite some issues with possible sources of bias in the examination of the populations. This paper reveals that there are numerous ways of estimating the portion of diverse population in the conservation of soil microbial community. Several types of measurements may yield divergent outcomes, which can be associated primarily with some aspects of the natural characteristics of the communities studied. Besides, it is not clear if one method is any less or more biased as the other methods, or if one method is really any more or less sensitive than any of the other methods. [3][4]

2. Importance of Soil Microbes in Ecosystems

Microorganisms in the soil are important components in agricultural as well as in natural ecosystems. Among the critical roles assigned to soil microbes is decomposition of organic matter, nitrogen mineralization of soil, and suppression of soil-borne diseases. Certain microbes either promote growth in the plants or elicit a response in the plant that helps to ward off pests. In addition, the behaviours of the interactions between the soil microorganisms regulates cycling of elements in the whole ecosystem and they are therefore directly linked with ecosystem stability and sustainability. Just over a century of basic research on the involvement of soil microbes has been the basis of microbe work. That is why having identified the fact that the density of functional and genetic diversity in soil microbes is actually high it became possible not only to focus on sophisticated relations between them and between these microbes and external prerequisites of the ecosystem which feeds them but also pay attention to the genes of soil organisms that metabolise in situ and investigate how these genes affect their functionality.

Soil microbes with high ecological value, but we can still get reasonable efficiency than conventional approaches to collect gene information to meet the need for large-scale information and concepts to analyze the gene structure of soil microbes. In addressing taxonomic questions regarding soil microorganisms, metagenomic approaches have come a long way in terms of DNA sequence pipeline technology, as have large scale, multi-national sequencing projects focusing on soil microbial communities. Therefore, a tremendous amount of DNA sequence data exists to investigate complex life forms, and there has never been so much research interest in soil microbes as in the last couple of years. Besides offering insights into the genetic community structure of soil microorganisms, advanced sequencing technologies collect data on the genes in microorganisms residing in soil and their potential for ecological studies, and the work being done on these projects also offers new directions for gene isolation and function analysis in the future. [7][8]

2.1. Nutrient Cycling and Decomposition

It is therefore expected and almost certain that genetic variation among soil microbes which are involved in decomposition of organic organic matter has an important and perhaps irreducible role to play in the complex process of nutrient recycling. This proposition has a very high importance, especially, taking into account the important roles of bacteria, fungi, actinomycetes, and Proteobacteria as basic components of the soil organic matter decay process. This process that is linked to the quality of the organic substrates explain s the effect of soil microbes on the functioning of ecosystems. To support this idea further, the following is an analysis of the consecutively planted Chinese fir trees that grow best in Mideuculture conditions under the Chinese fir-cedar type. Analyses carried out on multivariate data of diverse characteristics of soil provided interesting results as detailed below. Most significantly, the values of soil organic carbon, total carbon, recalcitrant carbon, particulate organic matter, soil light fraction organic carbon, soil microbial biomass carbon, soil basal respiration, soil microbial quotient, and soil labile carbon fractions reached their maximum rates in the soil produced by the stand that was grown under Mideuculture considerations. As remarked above, such observations appeared in contrast to the readings that were achieved when the soil was measured under mono-culture. Finally, taking a closer look to the specific interactions that contribute to the formation of such complex picture, the microbial community structure was investigated comprehensively. Along this regard the length heterogeneity polymerase chain reaction 18S ribosomal RNA gene fragments were instrumental in providing important information on the microbial diversity of the two stands. This phylogenetic approach enabled the detection of a range of and complex interactions within the microbial assemblages which gave insights into controlling parameters of nutrient cycling process. However, it is urgently necessary to highlight that edaphic microbial communities not only regulate the cycling of nutrients but also conceive stability and coping ability of ecosystems. Higher microbial diversity in the soil is useful for the ecosystem as due to the different metabolic capabilities each microbial species affects different biochemical processes. If there is a great variety of species of microorganisms, ecosystems can respond correctly to the fluctuations in the conditions of the environment and continue their activity even in conditions of extreme poverty. Besides, the genetic differences of microbes give a positive impact to the type and quality of the soil suppling plant health as well as vigor. Soil microorganisms as Mycorrhizae, in the plant ecologies attach themselves to the plant roots, and are beneficial by providing the plants with nutrients like phosphorus and nitrogen. These co-adaptive relations benefit plants together with resulting healthier vegetation growth through increased nutrient acquisition. Moreover, nutrients provided by the soil give life to microbes that subdue pathogenic organisms from affecting plants diseases and improving plant tolerance to stress. In the past decade, researchers have shown increasing attention to apply the soil microbial richness for future farming. In this paper, effective control measures will be presented as an application of the science of microbial ecology and its interaction with plants in order to decrease the extent of using chemical fertilizers and pesticides that is harmful to the environment. For example, some microbial inoculants which have been created in improving crop yields and soil nutrient availability. All these inoculants introduce plant-friendly microbes that form mutualistic partners of enhanced nutrient uptake and protection against diseases. Implementation of such microbial driven approaches in agricultural production systems increases crop productivity while at the same time decreasing on adverse effect on environment as is evident in conventional production practices. Therefore, genetic variation among soil microbes is an important determinant of the relative rates of nutrient turnover, ecosystem processes, plant health, and productive agriculture. This paper emphasizes the importance of management and conservation of soil microbes as it improves the fitness of ecosystems and supports the sustainable farming system. It was evident from the study that there is still need for more research on soil microbes and subsequent efforts put in the conservation of these riches with a view of harnessing all the enormous benefits that come with them for the enhancement of our planet [9][5][9][5][10][11][12][13]

2.2. Plant Health and Growth Promotion

There is a wide consensus that, in addition to chemical and physical characteristics, microbial content of the substrate provides protection against diseases, contributes to plants' health, and stimulates growth. That the most publicized cases of fumigants to control root pathogens that are applied before planting is because of losing this induced suppression mechanism by soil biota. The antibiosis protective mechanism was later these results revel that some of the saprophytic soil actinomycetes are common. This genotype does not produce any kind of actinomycin and is effective only on root pathogens not the crown pathogens. Thus, it probably is the case, as is believed to already happen, that chemical companies are capable of giving a much better disease protection by isolating, culturing and prosecuting disease-suppressive soil populations. This leaves one to wonder why the same actinomycetes confers seedling diseases suppression but cannot be relied on to manage diseases in natural settings [14]The observation raise question on why the same actinomycetes that could suppress seedling diseases in a controlled conditions can not be relied on to control diseases in the natural environment. The soil microorganisms work simultaneously in association with other competitors like bacteria, fungi and other actinomycetes which makes the balance not beneficial to the actinomyctes for disease control.Moreover, biotic factors such as temperature, humidity and nutrient status of the soil also depend to a very large extent on the population dynamics of the soil microorganisms and their efficacy in case of disease suppression. [15]Besides, the genetic variation within the Actinomycetes, populations may also be attributed for the variability in disease suppression in natural environment.ter discovered that the protection mechanism, antibiosis, was due to common saprophytic soil actinomycetes. This genus produces no actinomycins and is effective only against root pathogens, not crown pathogens. It may be that, as is thought to occur already, chemical companies can provide more specific protection by isolating, culturing, and using disease-suppressive soil populations. Why is it that the same actinomycetes are usually present to reduce seedling diseases but cannot maintain disease control in nature [14]One possible explanation for this discrepancy could be the complex interactions occurring within the natural ecosystem. In nature, soil microorganisms coexist with various other organisms, such as competing bacteria and fungi, which may hinder the effectiveness of the actinomycetes in maintaining disease control. Additionally, environmental factors, including temperature, moisture levels, and nutrient availability, can greatly influence the population dynamics of soil microbes and their ability to suppress diseases. [15]Furthermore, the genetic variability within the actinomycete populations might also contribute to the inconsistent disease control observed in nature. Such variation in disease suppression may be due to the differences in gene pools within the populations of systemic actinomycetes. Furthermore, these produced active metabolites can also be changed based on the DNA composition and surrounding environment of these microbes. [16] Another factor to be taken in to consideration is, parasites also live in the rhizosphere and these parasites may be antagonistic to the disease suppressive activities of the actinomycetes. These antagonist microorganisms, present in the natural environment of the soil, could be directly competing with the actinomycetes for the substrate, or release compounds that might have restraining effects on the actinomycetes activity. [17]Furthermore, the functionality of actinomycetes might diminish over time because of the dynamics of the soil ecosystems and the constant pressure exerted by biotic and abiotic factors. In due course therefore, the physical and biological environment within which these plants thrive may alter due to cultivation practices, climatic factors, or introduction of new plant species into the ecosystem etc.These alterations may distort equilibrium allowing actinomycetes to consistently suppress diseases Seedling diseases can be suppressed by actinomycetes However, the ability of actinomycetes to suppress diseases ecologically, genetically genetically and environmentally are not inversely simple.ic nature of soil systems and their constant exposure to different biotic and abiotic stresses can reduce the long-term effectiveness of actinomycetes in maintaining disease control. Over time, the soil environment may change due to factors such as agricultural practices, climate variations, or the introduction of new plant species. These alterations could disrupt the delicate balance necessary for sustained disease suppression by actinomycetes. [18]Overall, while actinomycetes have proven effective in reducing seedling diseases, their ability to consistently maintain disease control in natural environments is a complex phenomenon influenced by various ecological, genetic, and environmental factors. It may take considerable effort to get prolonged and stable disease control, and, thus, it requires improved understanding of such abiotic factors as well as the creation of new management strategies that would account for complex interactions between microbial inhabitants of the soil [19]

2.3. Climate Change Mitigation

On a global scale, there are generally two types of soil organic carbon storage: for years because of the cold climate and the rest …..physical, chemical, biological and ecological. Thus, members of the SMF play a key role in the cycling of soil carbon both as a storage and as potential decomposition. Enhancement of microbial carbon-oxidizing enzymes stimulate the carbon degradation; further, increased SM bio mass could enhance the microbial degradation of soil carbon. The microbial dynamics in switch regimes shifted from fungal-dominant to bacterial-dominant, and altered the soil aggregates structure by decreasing the level of degradation. It is important to establish that the warming process will augment the process of oxidation of carbon to low molecular weight compounds carbon dioxide and methane which also provides feedback between warming of soil and the old carbon. [20][21][22]

Microorganisms play an important role in determining the soil carbon balance because through the stimulation of short term enhancement, microorganisms are able to rapidly translate the carbon stored on soil into the atmosphere through respiration. However, the nitrification and denitrifications processes which are activities of the microorganisms also sequesters greenhouse gases like nitrous oxide and methane at the surface of the soil which is also undesirable in combating climate change. Prokogenic photosynthetic bacteria as oxygenic phototrophic prokaryotic organisms possess a certain potential to perform carbon dioxide fixation. Information on containing a certain quantity of carbon and storing carbon temporarily in regions with high carbon content but low nitrogen also seem to have some positive impacts towards climate change. Thus, research on the occurrence and potential role of photosynthetic bacteria and other soil microbiota associated with carbon assimilation contribute to broadening use of constructed wetlands as tools for climate change adaptation. [23][24]

3. Genetic Diversity of Soil Microbes

Most authors have defined genetic diversity as the variation existing in resources of genetic stocks, the makeup of these stocks, or the forming of biological variety. Northern Evaluate the significance of genetic variation of microorganisms in relation to their relative habitat, the terrestrial ecosystems? In my opinion, one can only guess what the answer is at best. Transfer of microflora from sterile soil to non-sterile soil proved that even the aboveground ecosystem carbon and N including, litter decomposition, straw decomposition and root exudate mineralization cumulatively was the overall total microbial genetic status up to 40% of that present in natural soil, along with the heterotrophic bacterial, ATP synthase activity level and community level PME. Such effects as reduction in soil bacterial numbers due to abiotic or biotic factors, including the effects of acid rain or chemical pollution were observed. Some of the microbial populations specific to low pH are no longer detected while instead, the microbial population capable of producing extracellular pH buffers are prominent. [11][25]

For instance, grasslands receiving acid depositions affect the triggering group of pH sensitive ammonia-oxidizing bacterial group to be promptly displaced by the acidophillic one. The native faecal population comprises of microfungi that are resistant to acids has a much higher genetic variation than the filamentous population. In addition, the microbial genetic diversity of specialized populations in different functional sites with different ecological significance is unequal: for example microbial communities in the rhizospheric soil are dissimilar than those of bulk soil; the gene sources of fungal samples also vary in the n and n+1 layers in coniferous and broadleaved forests. Similar genetic variation in the functional population indicated the fertility level and nutrient requirement of the soil in the cycle progress phase. Shifting focus to an important group of bacteria, rhizobium permanent nitrogen fixation the process of converting nitrogen in the atmosphere to a form nitrogen necessary for plant growth. High genetic diversity in chemical symmetry: only in nature, due to physical, chemical and ecological factors genetic variation in microbial populations is generated. These may be mutual interactions between microorganisms, or due to physiological interactions with other microorganisms due to of ecological processes like competition, predation, parasitism or symbiosis with other organisms, or physical and chemical change, or human interfiance[15][26]

3.1. DNA Sequencing Technologies

“DNA sequencing” is a group of technologies that enables the generation of large amounts of information in the form of the nucleotide sequences of DNA molecules. To investigate microorganisms in soil at an organismic level, three generations of DNA sequencing have been used for large scale community profiling. These generations include Sanger sequencing in 1977 because the capillary electrophoresis provides very long sequence reads. Nevertheless, Sanger technology is not effective for microbiome research anymore because of low throughput and high cost. A technology currently commonly referred to as next-generation sequencing or high-throughput sequencing reached explosive growth around 2005 after the introduction of various platforms. NGS improved a consensus throughput figure of 0.1-12 Gb per run from Sanger platforms by orders of magnitude. More recently a third generation of sequencing technologies has been identified. In contrast to the first two generations of sequence by synthesis platforms, single-molecule real-time (SMRT) sequencing platforms target the direct reading of single DNA molecules without needing to amplify or ligate the DNA sequence. Similarly, other versions work with a single molecule of the DNA strand. These new platforms also provide higher read length and fewer sources of bias in amplicon sequencing that make them highly desirable options for exploring the genetic variation of microbes in the soil [27][28][29][30]

3.2. Metagenomics and Metatranscriptomics

Metagenomics or characterisation of the entire population of genes from environmental samples represents a global snapshot of the metabolic capabilities of organisms within the sample. This makes it possible to sequence endogenously all of the DNA pulled from an environmental community, affording a spatial and temporal portrait of the sampled microbiota. Specifically, metagenomics has effectively been proved in numerous scenarios ranging from microbiota of the human body to extremophiles, that is organisms thriving in extreme conditions on our planet. It has already been easier to study the potential of specific functional groups in various environmental samples but these advancements imply the necessity for dealing with large volumes of data. Thanks to improved methods in sequencing and the development of novel tools in bioinformatics together with attempts to establish an ideal procedure for extracting environmental eDNA, numerous metagenomes have been analyzed in detail. [31][32]

Integrated community transcriptional analysis is the characterization of microbial RNA extracted without prior culturing of the sample. The primary strength of applying this tool on top of metagenomics is that not only is the potential metabolic function of the microbial community revealed, but also the potential expression of those functions. This is in contrast to metagenomic approaches which widely identify what the community is competent of doing but not what the microbial community is doing at the time of sampling. In addition, the results of metatranscriptomics, which are derived from gene expression profiles, can include information about populations and interactions of certain populations with the environment and other microbes: including changes in microbial community composition in response to the conditions of the niche in which organisms find themselves, changes in actively functioning communities over time, and while metagenomic and metatranscriptomic sequencing are, overall, comparable in most studies[33][34]

3.3. Biogeography of Soil Microbes

In this paper, the nature of soil is considered as a heterogeneous environment, therefore, it is supposed that characteristics of investigated soil could predetermine density of microbial population and antecedent populations of some microorganisms. Hence the result of geographical history and features of geographical areas right from the surface of the earth up to the deep down, the climate and vegetation characteristics, land use, coverage and farming modes make those samples. The relations between the change of the use of soil and the coverage of ground and the dynamics of soil microorganisms vary according to the size of the territory and the selection of microorganisms. The above factors result in variation in the populations of microbes in the soil thus affecting variations in other soil ecological process and the resultant ecosystem benefits. [35][36]

Although many researchers have attempted to analyze the connection of the above factors with the amount of diversity of soil microbial population, very few of them are available on the comparison of microbial communities residing in the soil for different land use/land coverage category or cities across the world, not to mention for a comparatively larger depth. However, as the field of microbiome advances, culture and, therefore, the bioinformatics tools are still conducive to enhance taxonomically and functionally the database. Some level of variation in microbial populations are seen when comparing different samples of the same site as well as microbial composition between different sites. Alterations to function of similarity in microorganisms compose the soils’ biogeography. To date, there is little information of the biogeographic distribution of SM [soil microorganisms]. Therefore, the further development of the field of view and the goal of understanding the factors affecting biogeography should involve the scale of impact of the different functional SMF on the soil and ecosystem services, and the other SM communities should also do the same ecological research. The capacity of the science of study of Biogeography. [37][38]

4. Factors Influencing Soil Microbial Diversity

They are the most diverse community in the biosphere with a key function in many aspects of the trophic structure of terrestrial ecosystems. Soil microbes genetic structure can have many characteristics, pattern and factors with regards to genetic structure. Among the environmental factors, the SPVs showed that the physicochemical properties of the soil, the types of vegetation, and spatial scales of sample points explained variations in the genetic diversity of soil microbes to certain level. Microorganisms can actively participate in many types of substance change processes, including organic pollutants, migrating elements, and energy use of the soil ecological system. Also, the use of microorganism is again very helpful as a bioindicator for the assessment of soil ecosystems. Hence, it becomes necessary to choose correct soil characteristics with a view to assess the genetic variability of the SSMs and their relationship with SFS with reasonable degree of precision[39][40]

4.1. Soil Type and pH

The impacts of MAT on SM characteristics are also well understood, particularly the variation in SMD associated with soil type. Samples were collected from grassland, forest and agricultural area across the globe and the content of bacterial fungi was compared in the soil of these regions. However, such large scale study includes the soil information of few large areas only and therefore does not present the second order effects related to these broad categories of soil habitats. There was a clear variation in microbial [richness and composition] between the various soil types for fungi. Soil pH is another major determinant of the distribution of different groups of soil microorganisms. These works indicated that, of the two factors, soil pH and substrate organics are consistently the dominant factors controlling the composition of soil microbes. [2][41]

The chemical nature of the soil from the pH of the soil matches with the soil type and vegetation type. The study was carried out on the largest sample size known to date. In addition to phyla, the more refined such divisions as the ecotypes and ASVs were analyzed concerning the pH and classes. The result showed that both ecotypes and ASVs had the highest or the fewest corals at relatively low pH from 4.5 to 7, and most of these soil pH-corals organisms belong to different lineages . In additionally, various soil pH had shown opposite effective method for the numerous and few microbes. A varied number of Acidobacterial and Actinobacterial populations, for example, were labelled generalists in terms of habitat by harboring genes associated with central Syntrophy metabolic processes. At the same time, rare Actinobacteria from lower pH, the most abundant Chytridiomyceta fungi and moderately abundant d7 and d6I group bacteria from higher pH exhibit generalised transporters.

4.2. Climate and Temperature

Many studies mentioned above have revealed that climate zones, temperature gradients or seasonal fluctuations might affect changes in the genetic structures of soil bacteria and archaea. Overall, soil bacterial and archaeal genetic diversities in warmer and lower latitudes were significantly lower than those in colder and higher latitudes. Likewise, genetic variations of temperate zone soil fungi were superior to that of Boreal zones and these were followed by desert, tropical zone, and the genetic variations of cold temperate zone soil actinobacteria were superior to tropical zone. Temperature is known to exert a large geographical scale control on the genetic diversity of various communities of microbes in the soil because of the role that it plays in shaping the structure of communities of soil microbes. The changes that have been observed might be attributed to the effect that temperature has on biosynthesis and development, fecundity of microorganisms in the soil and their ability to survive in certain climates. Iobal temperatures can in general reduce the degree of genetic variation in the members of soil microorganisms. For instance, the number of species of the soil fungal populations of Glacial field samples was smaller than that of Non glacial field samples since fewer of them can survive such stress from exceedingly low temperatures of the glacier soils. The organisms capable of provoking bacterial cold shock responses have been isolated under these conditions. Hence, these results demonstrated that cold shock protein genes exist within members of the bacterial community in Arctic permafrost and the number of different species that contain these genes are relatively few [44][45][46][47][48]

4.3. Land Use and Management Practices

The role of management and history of utilization of the ecosystems are the other factors that influenceShapes of the soil microbial species. It has been found that relatively, other ecosystems including natural soils tend to host a rich microbial population. Change occurred when natural grasslands were converted to intensive agricultural lands leading to the increase of Proteobacteria as well as of the Gemmatimonadetes groups. The restoration of agroecosystems: bacterial and archaeal communities and fungi showed that the reversion of the agroecosystems back to the natural system laid a great impact far from the microbial taxonomic community. These changes in the fungal and bacterial communities were considered from the decreased pesticide application, the increased grassland codiversities, and the improved soil structure. Furthermore, afforestation alters the microbial richness and diversity and increased the relative abundance of Acidobacteria and Verrucomicrobia. As shown in forest Acidobacteria subgroup community analysis, the type of biomes can also change the community composition. [49][50]

This research established that the land use and management practices in agroecosystems influence the microbial alpha diversity levels. Organic farming as one of the strategies in agroecosystem management may result in, or enhance the levels of enzymatic gene abundance, microbial diversities and microflora community in the soils respectively. A research with applying the conversion of conventional farming to organic farming in different European countries is shown that; conversion of conventional farming to that of organic farming increases the diversity of bacteria, fungi and ammonia oxidizing bacteria but not the archaea and ammonia oxidizing archaea. [51]

5. Methods for Studying Soil Microbial Diversity

Soil microbial diversity has been revealed in great detail over the last decade especially for bacteria. While there has been a huge amount of work done on phylogenetic diversity, a vast majority of this has been on the topic of species diversity. The rationale for presenting some detail of the nature of microbial genetic diversity and the recent advances in ecological inference is to explain why accurate estimation of microbial population characteristics has become critical. We will also assess species and genetic data for bacteria, mycorrhizal fungi and nematodes and compare it with existing and widely known general ecological principles. At the end of this chapter, we shall outline our ideas on how this book should best be used to introduce an ecological approach to the contemplation of microbial diversity – the overarching narrative being the character of the soil business and its biology, chemistry, and part in planetary processes. In fact, the strategies for understanding the spatial distribution and activity of soil microbial communities are virtually limitless. All have their respective purposes and aims; but the implementation of molecular methodologies in ecological inference, particularly in species-limited habitats, often involves the analysis of primitively an imposing number of ecological attributes, for which joint quantification of these parameters is invariably necessary. These would be Total: total species: All culturable forms; Molecular groups: identification of the specific molecular groups determined to be present and active at the greatest taxonomic resolution; Ribotypes and ecological clusters: number and distribution of ribotypes and ECOLOGIC units; Linear genetic diversity by marker genes and genomes; Multiple gene distribution of genes involved in high priority nutrient cycling. Although there are a number of such strategies in currently use, no one has yet put forward the sort of assay or complementary suite of assays that would provide a complete set of information needed when addressing major questions involving biotic interactions and the function, dynamics and management of nutrient cycling, retention, sequestration, decontamination, and global biogeochemical cycles. Interestingly, this objective is not considered as needing the hardest of feats; what is required – is not doable by the slow, incremental advances those investigators who believe in the power of their favorite best practice think can be achieved [52][53][54][55]

5.1. Culture-Dependent Techniques

Earlier methods of identification of microbial communities including soil microbes have relied on culture-dependent approach. However, there are a number of reasons to believe that such techniques underestimate seriously the true richness of the intricate microbial communities. Of course, a significant number of soil microbes have not been cultured and, in turn, documented. This problem is because of the bias in isolation methods and kinds of culture media that so many microbes did not get cultured, and because of the inadequate ways that are used now to characterize organisms. Molecular techniques such as cultivation and cultivation-independent analysis have shown that over 99% of the soil microbial species have not been isolated or cultured. The exponential increase in the number of sequences from highly predominant soil clones indicates that this approach would easily saturate limits by the vast numbers of such soil microbes. [7] [56]

A clear predominance of the soil microbes at least in terms of the sensitivity of amplification followed by cloning and sequencing belong to the category of the so-called ‘Uncultivated Vast Majority’ that likely comprise representatives from almost all the major groups of soil microbes in which bacteria and their interactions with physical, chemical and adaptive processes could be described. While it is now technically feasible to enrich, at least by using grossly biased PCR primers, close to all the DNA in a given soil which can be targeted for analysis, there are still many unknowns about the absolute and relative abundance and distribution of microbial taxa in any given soil, including questions of spatial variability. When ‘amplifying’ all the microbial taxa within a sample by targeting specific functional gene sequences, these involve assumptions may include possible bias from the amplification process, the presumption that experimental methods can estimate total abundance of microbial taxa in soil, and the countless tasks in procedure and analysis that are required in order to generate sequences. [56][57]

5.2. Culture-Independent Techniques

Five culture-independent approaches each with more specific improvement has been used recently for the isolation of physiological information of uncultured microorganisms in soil systems, biodiversity assessment, microbial community and population dynamics. Terminal-restriction fragment length polymorphism and denaturing gradient gel electrophoresis PCR are two techniques that produce only quantitative profiles of bacterial 16S rRNA genes in environment. These techniques can be used employing the total environmental DNA or else after cloning and PCR products. This method also gives information on the relative sequence heterogeneity of the natural populations. Bias inherent in this method originates from PCR amplification, subsequent primer annealing, stability of DNA during extraction process and preferential enrichment of identified bacterial DNA during extraction. [58]

454 FLX pyrosequencing, one of the advanced generation of sequencing technologies allows for the sequencing of a large number of DNA samples, as well as microbial analysis sampling, which include the diversity of microbial population from various substrates. This method is positively influenced by large genome gaps, the lack of small sequence reads, however, it offers extraordinary fragment coverage together with simultaneous high sequencing throughput. Functional gene probe arrays are also available for investigation of biogeochemical processes for the soil ecosystems. These arrays allow the identification of several target genes within several samples derived from different environments. When used in parallel, methods for the identification of functional genes and phylogenetic markers offer a feasible approach to the evaluation of bacterial genetic potential and ecological roles in situ. Despite significant progress in the application of these methods, they were found to have various technical issues and, therefore, have some limitations. Hence, subsequent progress of these methods should be not only how they enhance their application and worth but also how they might be eradicating these drawbacks [59][60]

5.3. Bioinformatics and Computational Tools

However, biochemical or computational methods are mandatory for an integrative assessment of soil microorganisms. These are employed at the first input sequence data relating to 16S rRNA gene or the predicted protein sequences from microbial genomes. However, the vast majority of the publications used the two most popular softwares to analyze microbial sequencing data, namely QIIME and Mothur. A free web server can accommodate, process, and disseminate the metagenome sequence data at a very high speed. As for the tools of soil microbial ecology, more have been created in the last few years. A prediction metagenome service can utilize the 16S rRNA marker gene which can target the functional aspects of 16S rRNA sequence data. Software can extend and merge biomolecular interactions in the context of merging huge LS-S samples of organisms in cells. [61]

The investigation of metabolic functions in relation to community distributions of environmental factors through the FBA model of in silico predictive ecology is critically important for the analysis of metabolic regulation. Some of the tools of data mining of microbial resources are Genome databases; Genomics; Metagenomics; Transcriptomics; Proteomics; Mouse data; Ribosome databases and the whole lot others are relatively popular and are a section of bioinformatics analysis. Some web servers have been created that provide information on physical and chemical properties of proteins. However, there are other features added which can be used to convert some data suitable algorithms.The above forms also include some distinct features which can be used for data conversion. The availability of these bioinformatic tools for all researchers will promote the improvement in our knowledge of soil microbial diversity. However, the increasing data must be analyzed with getting to extreme care because improper statistical approach would lead to confusing the inference and make the interpretation of the analysis data doubtful[61][62]

6. Applications of Soil Microbial Diversity Research

Soil microbial diversity research interpretation shall increase the knowledge of soil ecosystem roles and explore the stability of community and circulation material process of ecosystem functioning mechanisms. This knowledge will enable us make rational utilisation of the soil functions and services; and in turn enhance sustainable utilisation of soil resources. To some extent, understanding the patterns of soil microbial communities will contribute to elucidating the rules effective at higher levels of the ecological hierarchies in order to support the theoretical background for the integration and progression of the ecological environment and human society. The sheer size, complexity, and number of today’s environmental issues demand the explication and protection of biological integrity. This is true especially in soil science where there is lesser focus given to the roles of soil life than they give to their roles and also the fast and dynamic change of ecosystem by human interventions, entropy has become important in diversity studies. There is considerable diversity of microorganisms in the soil. They are involved in many transformations, substance and energy, and the biological part creates a dense and intricate regulatory system in the soil, a great contribution to the multiple and stable work of the soil. Hence, microbial diversity is of significance to be investigated, and theoretical and practical proofs to support the soil service function and regulation of sustainable usage of the soil resource should be offered. Since soil is utilized as the spatial context in analyzing microorganisms, a host of techniques needs to be chosen deliberately to this end. The existing state of microbial diversity on land (with emphasis on bacterial) and research techniques are all discussed in this paper The contents of the study are separeted into six categories with the development of molecular biology technology in recent years and the research directions [39][2][63]

6.1. Agriculture and Crop Improvement

Agronomic yield depends on among other things seed quality, nutrient inputs, plant diseases due to insects and diseases organisms. Microbial communities in plant ecosystem promote the growth of plants and therefore provide valuable information concerning the role of plant microbiomes in enhancing stress tolerance in plants. The fact that microbiome function enhances the rate of genetic improvement is also postulated. Furthermore, since crops constantly communicate with microbes throughout their life span, the development of a new generation of plants from biologically active seeds based on these interactions is relevant for agriculture. [64]

At the moment, microbial seed treatment products are in demand by growers, producing both organic and traditional crops, as well as greenhouse growers because of the shared overall health of plants, earlier and more effective physiological development, the company’s cost-effectiveness, as well as the possibility of increasing yield when managing problems associated with plant pathogens. In addition, the microbial inoculum on the seed or as a seed treatment might be a best agricultural practice. Besides, it has been known for approximately one hundred years that Rhizobia fix atmospheric nitrogen when they are associated with special organs of the legumes. For these reasons, extensive efforts have been made to study the molecular mechanisms controlling root–stem nodule interaction, and more than one hundred root nodule formative genes have been discovered so far. [65]

6.2. Bioremediation and Pollution Control.

The soil microbes in the natural environment are diverse and are used in different practical issues for example, bioremediation of the soil, environmental pollution, reclamation of wastes, and management. This principle is closely related to four basic ecological functions of soil microbes, and these practical issues suggest that disturbing the genetic diversity of soil microbes will have severe consequences in this respect. However, some techniques have enabled us to conduct research on the activity of the soil organisms at gene level which has given a new perspective into soil microbial ecology. [26]

Among all the bioremediation parties, the microorganisms are perhaps the most important parties. At present, it is generally believed that they have a two-stage function, which includes the following steps: the organisms chemosynthetically disassembling and reminearlizing the chemicals in the waste; the microorganisms build adhesion films on the surface of the wastes which in turn provide proper environmental requirements for the succession of some plants to settle. The metabolic activities of the microorganisms are one of the reasons for the constraints on the bioremediation process. The spotting of microorganism resources is considered an important parameter of the bioprocess [66]

6.3. Pharmaceutical and Biotechnological Innovations

Comprehensive utilization of beneficial microorganisms at the present time, excluding allergenic and pathogenic properties, paves ways to the formation of a number of innovative drugs and preparations with antibiotic and symbiotic properties. In the battle against inflammation particularly tick borne or neonatal encephalitis there have already been endeavour to employ microorganisms by bacterial instillation in the organs of the affected mice using Lactobacillus casei H-strain, L. bulgaricus, L. acidophilus, or Bifidobacterium longum. During this experiment, the survival of the mice was less, the toxin concentration in the blood was decreased, and it was confirmed that the possibility exists that the virus concentration descends below the limiting detectability by the polymerase chain reaction technique.

That new prebiiotic preparations using gastrointestinal bacteria decrease IL-6 and TNF-alpha production in the liver and also reduce PoII-2 levels in the blood of rats during the development of hepatocarcinoma caused by azooxymethane is no general secret. In the future, the introduced niche of soil actinomycetes, filamentous fungi, or plasmodial slime molds will be applied. The determination of the action spectra of the extracts of pure benzoic, hippuric, and cinnamic acids, or their esters may be considered a boundary stage from the point of view of identifying which of them occurs most frequently in the limited context of the organism’s narrow environment. In fact, there can be no doubt that these drugs will become more harmless and optimal with regard to concentration in combination with the soil carriers. Moreover, the potential will turn into the real for numerous people moving by in electronics hands, who each time can buy these preparations containing prebiotics in cashboxes for the prevention of gastrointestinal diseases. [69][70]

7. Challenges and Future Directions

The chemical element cycle and the environment adaptation in ecosystem belong primarily to the soil microbes. Microbial diversity is the foundation of ecosystem function and stability and its manifestation, correlation, and effects mechanism are the frontier research areas in ecology and environment. It is found that topographic factors, climate, vegetation, type of land use, and physical/chemical properties of soil are the major factors influencing the genetic variability of the SSMs. On this basis, the research results showed that soil physicochemical properties are more critical for determining soil microbial distribution. However, the methods used to quantify SM bio-diversity are still more or less related to assessment of microbial biomass, activity and genetic diversity. Every present method has its lots of disadvantages. [71][72]

Soil microbial diversity metagenomics has greatly enhance the investigation of soil microbes. In addition to the usual biases associated with rDNA it offers the chance of how rare species, functions, and non-equilibrium interactions may be identified. It offers more information than the conventional techniques to investigate the first order processes determining microbial genetic variability with regard to their functional roles in global climate change and feedback mechanisms in ecosystems. But it must be understood that genome assembly in the soil remains a critical bottleneck because soil is filled with heavily duplicate, horizon DNA of the host, associated invertebrate zoology of animals. Thus, although some 150 bacterial and archaeal genomes have been reconstructed from the largely extracted soil metagenome, with 96% success, the detailed methods as to how best to separate plant and soil microbe genome sequencing reads remain a mystery and must be created. Moreover, getting a soil genome that is complete in the genomes of the soil microbial community is more difficult in comparison with the simple microbial community of a soil area, but in the heterogeneous soil space. For these limitations, the methods include five sampling farms in the study, and the employment of synthetic metagenomics in offering broad evaluations of the bioinformatics procedure, bioassembly of full genomes and a final analysis of results. The outcomes of these exercises will offer methods for subsequent investigations that enhance plant and soil microbe genome assembly and also valuable perceptions into the technical issues that demand synchronisation and temporary structure among the investigation teams of upstream and downstream procedures in soil multi-omics. [73][74][75][76]

7.1. Standardization of Methods

Several requirements are required, and some technical issues have to be harmonised in order to obtain a genuine comparative repository of microbial community level beta-diversity. To some, it may come as shocking that in the current world, there lacks a convergence on a number of fundamental issues including what DNA needs to be investigated, and which marker gene needs to be sequenced. The first issue is in many ways a question of scope. Interestingly there is no universally accepted unit or analysis in microbial ecology. That is, the choice… macrobiologists may consider a species or a population, while microbiologists will pay attention to individuals. The definition of genotypic difference is quite straightforward for all the scale of organisms, but the meaning of what genotypic difference implies is quite different at different scales. [77]

The second problem is associated with another matter of resolution. Most scholars have not agreed about the intensity and diversity of DNA that can be used as a unit. Chen and colleague pointed out that when a marker gene is employed as a surrogate DNA we have to realize that the marker gene is not representative of all the genetic and functional potentials of the microorganisms in the soil. The choice of a molecular marker for assessment of microbial community distributional data in soil at the extended spatial and temporal scale is critical. The future molecular strategies must also examine the coarseness of taxonomic distinctions, the speed of sequence variation, similarity between related taxa, and essential characteristics such as gene multiplicity after replication, sensitivity to distinguish significant microbial divisions, signal-to-noise ratios, and the presence of universal primers. [78][79]

7.2. Integration of Multi-Omics Approaches

The stated-above genomics, transcriptomics, proteomics and other biological omics technologies, which can reflect the real biological status of soil microbes, can more deliver the soil microbial ecology and the evolution of the latter. Here, using soil microbiomes as an example, we focus on the significance of crucial multi-omics life cycle data in ecological research. Multi-omics integration technology means calling a single set of biological data and performing the genetic regulatory network analysis to show genuine biological events or other properties. However, many people focus on the individual key technology approaches of Multi-omics analysis on each To generate the biological information for a specific type of biological process or biological response to a single omics. [80][81]

General conclusions can be made even though the number of investigations concerning the soil microbiome is becoming larger and larger at the present time. The performance of a squeaky clean and effective integrated system of multiple omics approaches can contribute to better biological and ecological results and conclusions. By these integrated multi-omics, one can identify multiple biomolecule response or process profiles and regulation across gene, protein, metabolite levels, as well as their network level integrative communication. This also provides wider opportunities to understand a variety of molecular and metabolic connections of soil microbiome’s diversities and functions. Therefore, they can provide more accurate and reasonable hypothesis based on various association relationships and interacting models between variable statistical learning and network inference biological networks. The above specified combination of data sets seems to be perhaps the most common or recognized set according to different goals or technical background. In addition, most frequent matches used in research practices are very basic and there are plenty of exciting and promising research questions suggested in a wide range of these matches. [82][83]

7.3. Predictive Modeling and Machine Learning

Machine learning concerns the use of algorithms in one of two classifications as supervised or unsupervised learning to determine patterns in data. It has been used to attack a wide range of problems that occur in various field of study. It has also been increasingly applied in the microbial ecology field because of technology improvements including cheaper and faster sequencing. These methodologies have enabled researchers to obtain taxonomical, functional and/or beneficial potential using either rRNA or shotgun sequencing. However, methodologically, the application of high-throughput sequencing has facilitated functionally-establishable datasets, for which machine learning-based approaches contribute advanced statistical and computational techniques to functionally interpret. When including the ‘omics’ as well as the biogeochemical data in its utilization, this method has been used to analyze various ecosystems as well as their components’ interconnection. Application of an ML approach to microbial ecology has also led to a development of numerous tools and databases for accelerating analysis pipelines and detecting new patterns of ecological and biotic significance. For instance, for ultimately using prediction models for microbiota dysbiosis at different time points, a pipeline for microbial ecology was designed. Likewise, a machine learning pipeline was learned to predict the pH of the soil samples from sequences derived from the bacteria there underlying it and this model accounted for 46% of variability. An innovative pipeline was established to identify the taxon composition in rRNA gene amplicon data of second-generation sequencing using machine learning algorithms and no conventional and time-consuming quality filtering of sequences is required. Similarly an expert knowledge approach based machine learning tool was suggested for the fast and thorough human microbiome characterization. Input data assessment and models, with an explication of the produced forecast were based on a software package of the model. Multiple regression models were built and tested for establishing the relationship between the prokaryotic taxa and the selected soil properties with the models for the prediction of the different properties in soil settings. In another study, a random forest approach was followed for probing into the ability of the non-sampling factors to forecast the microbial function in regard to genus-level lineages as well as for the metagenomic complete proteins dataset. [84][85][86][87]

8. Conclusion

Distribution of soil microorganisms is affected by different factors and exhibits a clear spatoon territory pattern. It links very well to both the structure and the functions of terrestrial ecosystems. Some of the negative management practices include; irrational use of fertilizers, chemicals, and tillage, which reduce the overall population and density of the soil microorganisms. Individual genetic richness, functionality, composition, and proportion are the key measures of soil microbial richness; nevertheless, high-throughput sequencing has possible sources of prejudice that must be considered to quantify soil bacterial richness.

The soil is the habitat and breeder of Terrestrial organisms and the provider of feedstock that release to the Earth's environment. Alterations in the distribution of soil microbes by species and biomass in soils will impact the flow and cycling of matter, energy, and the roles played by soil biotic communities. It is necessary to comprehend the soil microbial genetic diversities and its driving focus and ecological significance to study the maintenance mechanism of the soil ecosystem diversities, stabilities, and formation in depth. Here, genetic variety of the substratiferous microorganisms is both a part of the general biochemical diversity of the environment as well as the primary and crucial constituent of the groundep_BLK Pertaining to microbial genetic variation it has been emphasized that the continuance of such variation is central to the sustenance of terrestrial biome. The recognition of the processes regulating ecological threads, and the management of microbial genetic diversities of soil core, is considered of great importance to maintain the efficiency, compounds, and stability of the terrestrial ecosystem. Therefore, microbial gene resources should be enriched and preserved because they help maintain people's health and the sustainable development of society.

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