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ROLE OF CHEMOTROPHS IN AGRICULTURAL RICH SOILS

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ABSTRACT

There is relationship equilibrium among soil particles, living organisms and geo-chemicals that make agricultural ecosystem functioning. Many components and conditions play significant role for development of soil biota along with increasing soil microbial diversity and soil richness. Chemotrophic microorganisms, obtaining energy from oxidation of chemicals surrounded by them, these organisms involved in agricultural soils and playing significant role in Carbon, Nitrogen, Phosphorus, Sulphur and other elemental cycles. In recent years, de-esterification, degradation, biotransformation, bioaugmentaiton are requried steps of metabolism of certain herbicides, pesticides and other agrochemicals. For stability of these chemicals pH require maintain with acidic buffer solutions, and there are certain microorganism which possess functional groups for de-composting with these agrochemicals. Moreover, these microorganisms potential with most stable in climate conditions regardless other physic-geochemical factors of heat, salt, water holding and field capacity of soil. The organisms functioning in agro-ecosystem by degradation of chemicals and actively participating to improve soil fertility. Now it is necessary to determine all microbial community present in soil for degradation pattern of agrochemicals present in those agricultural sites. Community level study can detect with help of genetic studies that provide functional genomic information. The presence of bacteria, fungi and plant studied with genomic study profile which suggests microbial transformation and incorporation of function in ecosystem that provide effectiveness for agro-ecosystems.

KEYWORDS: ***chemotrophs, metagenomics , degradation pattern, geo-chemicals, agro-ecosystem, effective function***

INTRODUCTION

Soil possesses the most heterogeneous geochemical system in which richness of microbial diversity that plays significant role. These organisms associated with direct and indirect relationship with microbial transformation of geo-chemicals, bio-energy and nutrition. Biological, climatological and geochemical progression cooperates to model basic cycles and the formation of nutrient losses in newly formed landscapes. Loss of Nitrogen (N), Phosphorus (P) and basic cations were calculated over million year gradient from a Hawaiian mountain rainforest substrate to recognize how losses depend on changes in demand in biotic, meteorological and atmospheric condition (Hedin L.O. et al., 2003). Soil has been and represented an important system for researchers because its complex geochemical cycles, social ecosystem, soil functioning with proper management in conservation terrestrial environment.

Current molecular biological tools and techniques are rapid and advanced that bring a new science branch as metagenomics. After the DNA extraction from environmental sample, that can assessable to genome study this is called as metagenome, of all microorganisms occupying within the same environment. The information obtained from these approaches will disclose more accurate character of biodiversity and its functionality in the environment while, the previous approaches provided information from cultured organisms only. Especially, agricultural studies require more information about utilization trend among microbial communities; geochemical cycles; adaptation of community to utilize such agrochemicals through soil metagenomics (Morimoto, S., 2011).

MICROBIAL DIVERSITY AND ITS FUNCTIONAL GROUPS IN TERRESTRIAL ECOSYSTEM

Due to overuse of certain groups of chemicals, loss of plant diversity which lead to negative impact on soil organisms and their diversity; functioning and affecting their density of populations ultimately affecting to soil health and productivity. In agriculture sector, to achieve sustainable production of high quality crops and vegetables, it is essential to maintain soil fertility and overcome the soil diseases such as continuous growing diseases. For better agricultural management, study of physical and chemical properties are not enough, but also requires biological properties (Amman et al. 1995).

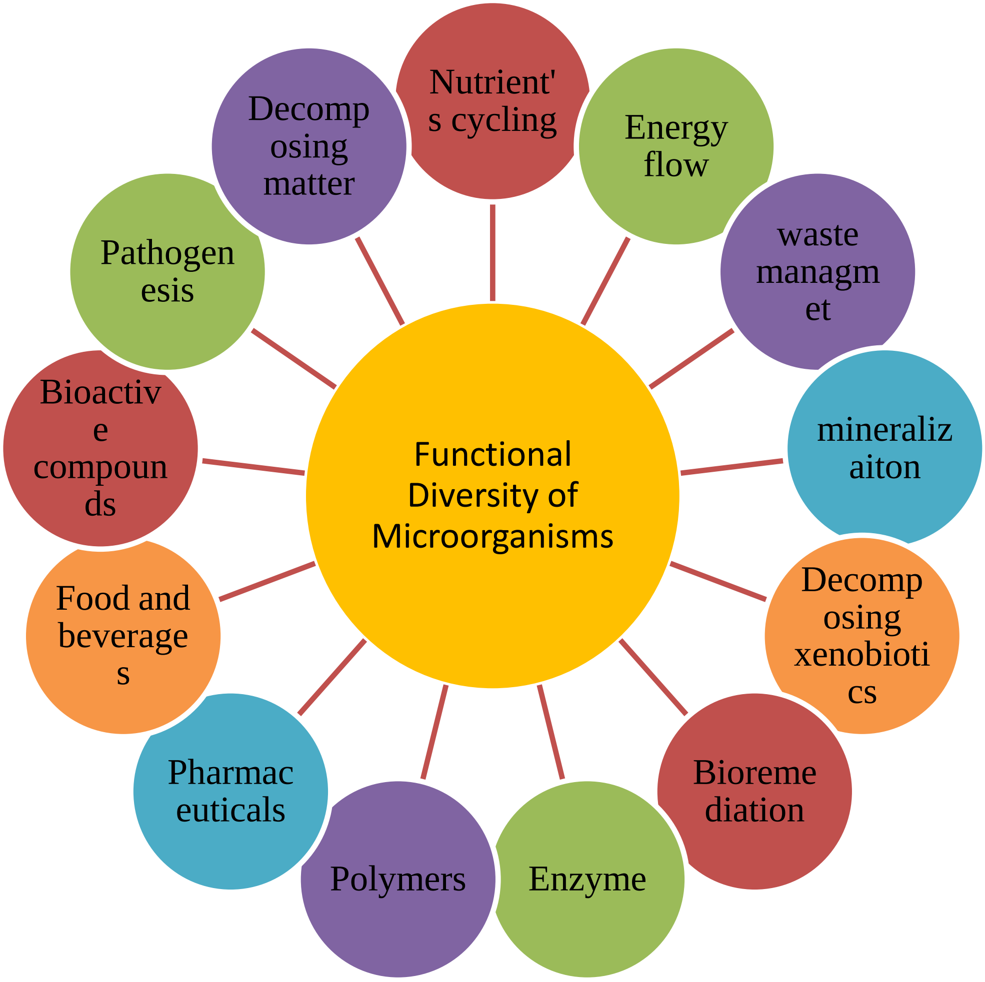

Fig.1: Functional Diversity of Microorganisms

In recent era, role of microorganisms and their functional groups requires detail study at gene level for soil geochemical functionality and ecosystem development (Fig.1). Soil microorganisms require micronutrients and macronutrients for their metabolisms which furthermore involved in geochemical cycles. Although such functional groups like diazotrophs involved nitrogen fixation process with legumes, this group are important for plant richness (Cleveland et al., 1999; Reed et al., 2011). Apart of these microbial groups such other groups viz., nematodes, rotifers and protozoans belonging this group too, act as nutrients recyclers, regulating the bacterial and fungus populations. The preferences for soil biodiversity, distribute them in different groups or categories having decomposers, predators so they associate to each other and create a food chain.

As microbes are the primary pollutant degradation in contaminated habitats (including agriculture ecosystem), through biotransformation, metabolic process and geochemical cycles. To understanding microbial processes in essential for predicting the best strategy for geochemical processes where microbial communities play vital role (Bergey, D.H.; Holt, John G., 1994). Among these all communities chemotrophs involved in most bioprocesses, with optimal strategy for remediation of ecosystem.

The several complex agrochemical compounds are accepted by the soil. These processes of percolation and capillary movement of chemicals produced inhibitory impact on growth and activities of beneficial microorganisms. More than 95% of the applied herbicides and 98% of insecticides reach on microbial flora instead of reaching target pest. Spraying method of pesticides are proportionately across the entire field, irrespective to affected area lead to impact on potentiality of microorganisms. Hence, total quantity of applied pesticides, about 0.1% reaches to target organisms while remaining quantity pollutes the agricultural soil and environment (Aktar,W et al.,2009). These agrochemicals accumulate in soil and alter the effectiveness of macro and micronutrients which are most important for crop production.

These microorganisms are primarily decomposers of organic matter and also perform other functions such as providing N,P,K and other minerals to plants and other geochemical cycles through fixation and mineralization. They are not only helping plant growth promotion but also detoxify harmful chemicals, suppress disease-causing organisms, and produce substances that may stimulate plant growth. Soil microbes also mineralized plant nutrients which are essential to improve crop productivity, encourage growth and active stress responses, e.g. Rhizobia, Bradyrhizobia (Broughton, W.J. et al, 2003).

High concentration of pesticides and other agrochemicals influence to the soil nutrition and have direct effect on soil microbiota, which are biological indicator of soil fertility and influencing plant growth promotion. Many researchers also reported about impact of pesticides on soil enzyme indices viz., hydorlyzes; nitrate reductase; nitrogenase; urease; dehydrogenase, etc. Interruption in these enzyme activities affects soil nutritional status and transformation rate. The consequence effect of this, reduced soil microbial biomass (MCB), functional diversity and microbial population. Hence, geochemical cycles affected that finally make remarkable changes in soil food chain and web (Onder,M. 2011).

MICROBIAL METABOLIC DIVERSTY AND DISTRIBUTION PATTERNS

All ecological factors significantly influenced on microbial activity and play role in temporal dynamic as well spatial diversity of microorganisms in natural environments. Microbial metabolic properties and their distribution depend on their evolutionary relationships. One of the classification method of microorganism, is metabolic capacity at using carbon and energy resources. Depending upon the source of energy microorganisms are called as phototrophs (using light as a source of energy) or chemotrophs (using chemicals as a source of energy). Similarly microorganisms can be either autotrophs (using inorganic chemicals as a source of energy) or heterotrophs (using organic chemicals as a source of energy). Microorganisms have different mode to interact with each-other as well associate with plants and animals. The diversity of microbial metabolisms extends far beyond the typical animal and plant metabolic capacities. The adaptation and genetic modification make microorganism capable to survive in extreme conditions resulting in metabolic variation. For example, the nitrate-reducing chemolithoautothroph *Pyrolobus fumarii* can grow at temperatures of up to 113^{0}C (Bloachl et al., 1997).

The complex microbial communities of soil cultivated in laboratory and also visualized microscopically under traditional cultivation conditions. Cultivated strains further studied with metabolism and behaviour of microorganism from agricultural soil, but the composition of microbial communities can be determined more rapidly and through extracted nucleic acids without cultivation. The classical approach to study microbial activity and its associated diversity derived from cultured microorganism altered with recent advanced approach of genetic tools (Cole et al. 2009).

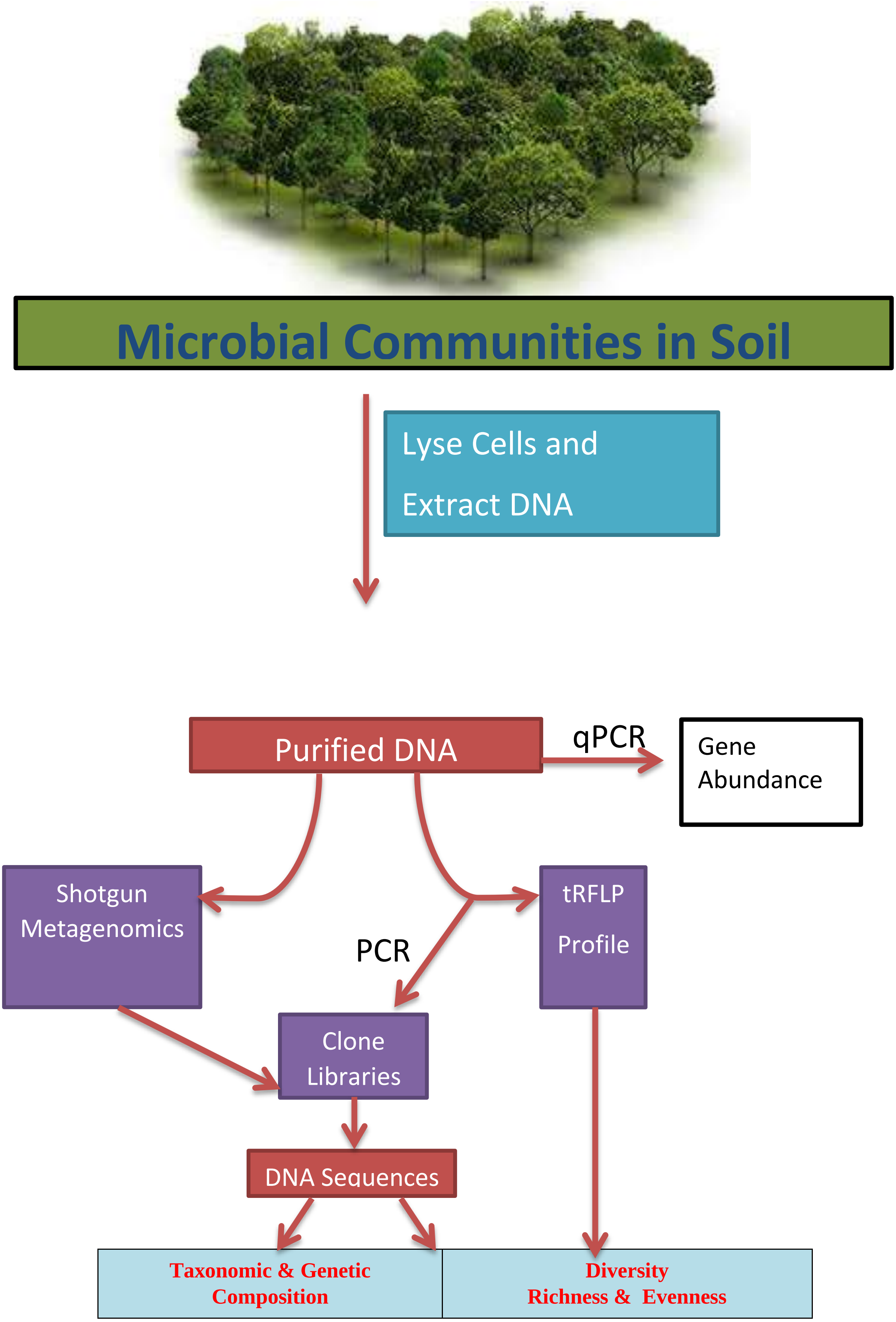

Fig.2: An overview of molecular approaches use to detect composition and diversity of microbial communities.

The key to comparing these complex microbial communities is obtaining DNA sequencing which are encoded for function of the gene (Fig.2). Over the time changes accumulated, so organisms can be grouped with the closest relatives having fewest differences. To provide enough material for sequencing, the target gene in an environmental sample must be amplified from each microbe, through the process of Polymerase Chain Reaction (PCR). Further it product used for comparative analysis of the gene encoding the small subunit ribosomal RNA (Cole et al. 2009). Amplified 16S genes can cloned into plasmid vectors, sequencing directly with massively parallel next-generation sequencing. This gene study provides a taxonomic description of microbial community and also offers insight into the metabolic potentials of communities. Advanced method of molecular technique applicable and useful in many environmental and agricultural issues, viz., detection of microbial community, soil heterogeneous structural matrix, plant genomic study.

IMPACTS OF AGROCHEMICALS ON AGROBIOLOGY

There is a significance impact of agricultural chemicals in soil ecosystem and studies shown their harmful effect also documented. The beginning of fast and reliable systematic techniques has covered the way for larger sympathetic of the long-term effects of agrochemicals and related health and environmental issues. The command for agriculture development is to feed and provide satisfactory nutrition and excess to mounting human population without compromising on ecology and environment of the biosphere. Agricultural chemicals and their use are considered as magic bullets in developing nations. Agricultural chemicals cause serious hazards to soil environment and human health because a lot of chemicals and their derivatives remain in the soil system for considerable period.

The root exudates of the through chemicals soil environment interact either positively or negatively with living organism that inhibit in soil. Microorganism such as Bacillus, Micrococcus, Variovarax, Flavobacterium, Psudomonas etc., are scarcely observed on root endophytic bacteria affected. Such other organisms which are incorporated in nitrogen fixation and geochemical cycle, Rhizobium, Bradyrhisobium, Mycorrhizia also affected to their nodule number, biomass, and colonization cultivations (Tilak, et al, 2005).

CHEMOTROPHIC MICROORGANISMS

Bacteria and fungi contributed as the most common type of chemotrophic organisms, where carbon act as the most essential molecule for their existence and reproduction. The major characterization of the chemotrophs , capacity to produce own organic or carbon containing molecules. The organisms are further classified as – chemoautotrophs and chemoheterotrophs (Kelly, D. P.; Wood, A. P., 2006).

Chemoautotrophs are able to synthesize their own organic molecules from the fixation of carbon dioxide. These organisms are able to produce their own source of food, or energy. The energy required for this process comes from the oxidation of inorganic molecules such as iron, sulfur or magnesium. Chemoautotrophs are able to thrive in very harsh environments, such as deep sea vents, due to their lack of dependence on outside sources of carbon other than carbon dioxide, flow of this electrons managed from Chemoautotrophs to chemolithotrophs (Fig.2). Chemoautotrophs include nitrogen fixing bacteria located in the soil, iron oxidizing bacteria located in the lava beds, and sulfur oxidizing bacteria located in deep sea thermal vents (Dobrinski, K.P.,2005).

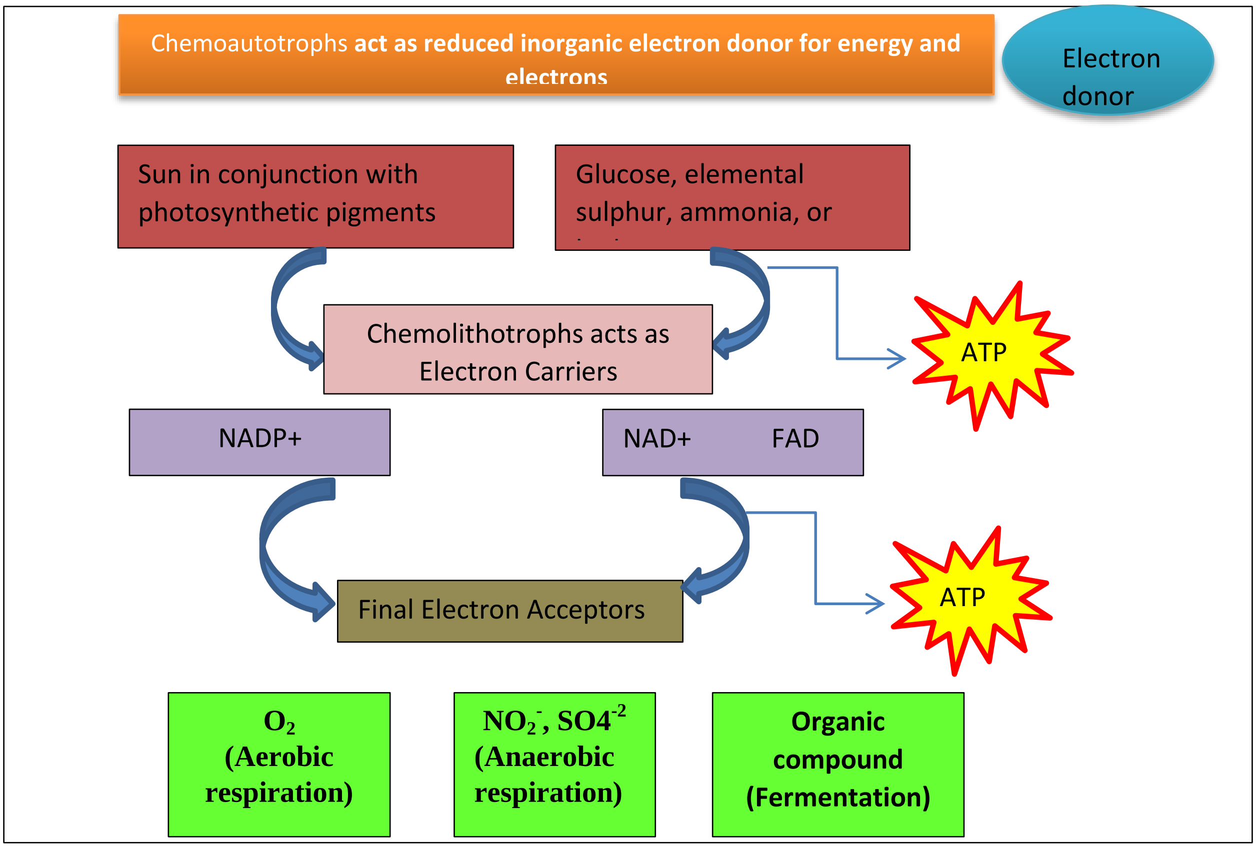

Fig.2: Flow of electron managed by Chemorganotrophs and Chemolithotrophs

Chemoheterotrophs, unlike chemoautotrophs, are unable to synthesize their own organic molecules. Instead, these organisms must ingest preformed carbon molecules, such as carbohydrates and lipids, synthesized by other organisms. They do, however, still obtain energy from the oxidation of inorganic molecules like the chemoautotrophs.

Chemoheterotrophs are only able to thrive in environments that are capable of sustaining other forms of life due to their dependence on these organisms for carbon sources. Chemoheterotrophs are the most abundant type of chemotrophic organisms and include most bacteria, fungi and protozoa.

FUNCTIONALITY OF CHEMOTROPHS IN AGRICULTURAL ECOSYSTEM

Soil microbial biomass and activities also detected by pattern of substrate utilization which is also consider as functional diversity. Because of flexibility, short generation time, ability to exchange genes over deep phylogenetic barriers and ability of adaption, prokaryotes are dominating on the earth. Important to know contributions of microorganisms, requires to understand their complex ecosystem functioning to identify primary diverse microbial diversity and their community structures (Woese, 1987; Woese and Fox,1977).

Agricultural soils containing chemical fertilizers, biological fertilizers, pesticides, herbicides and other PGRs those accumulated in soils and microorganism through different adaptations mechanisms as well gene transfer start to utilize them. This consider as functional diversity of microorganisms and community may succeed in survive with climaxity of agricultural ecosystem.

Unutilized agrochemicals lead to affect soil healthy conditions and furthermore agricultural crop production. Long term fertilization dramatically supressed N fixation rates and the relative abundance of keystone and phylogenetically clustered N fixers, during fundamental N fixation process and its associated microbial communities, will become more and more supressed as terrestrial fertilization continues to increase (Fan et al.,2019).

Microorganisms from heavy metal contaminated agricultural soils possess various functional pathways, to involved by soil change with microbial structure variation, many of which are related to the heavy metal tolerance of the soil microbes (Feng et al., 2018). With historical agricultural studies and evidences, soil microbial communities directly influenced on soil health (Buyer et al., 2010), changes in crop species, crop rotations sequence (Xuan et al., 2012), and cultivation (Zhang et al., 2014) will effect below-ground physical and biological properties.

METAGENOMICS AND EMERGING TOOLS

Agricultural genomics or metagenomics , the applications of genomics in agricultural biology which is leading future in agriculture. In recent era, unprecedented population growth, urbanization and climate change require to increase complex and dynamic agricultural landscape area. Farmers motivated to advance productivity along with effectiveness to provide world's food supply demand and improving plant breeding challenges.

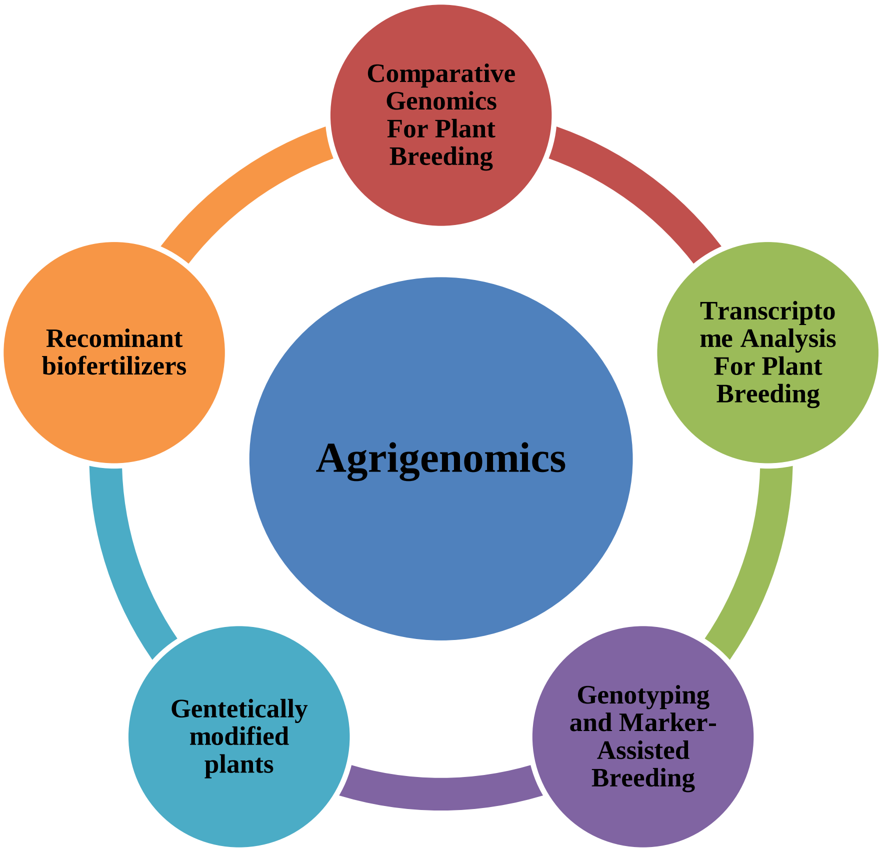

Fig.3: Ability of Agriculture Genomics to serve agricultural ecosystem

Current research in molecular science, metagenomics or advance genomic studies provide understanding of responsible gene for adaptaion, mutation, and recombination segments in both plants as well agricultural soil microbial communities (Fig.3). It also helps to improve microevalution, natural selection theory, biotransformation pathways of microorganism as well interactions among microbial community and/with agriculturally important plants (Torvik,V., 2002).

However, among all traditional methods Effective Microbial Consortium is most common technology to exploit as biofertilizers. The recombination of several microbial species, as per their nature of utilization of agrochemicals available/accumulated in soil can serve high performance of agricultural crop production and management.

Still our knowledge on the soil microbial/biological properties not enough to overcome the agricultural crop management, molecular methodology of study the microbial ecology make possible functionality of their microbial community in agricultural soils. Identification of soil microbial community available in agricultural soil studied with metagenomics (Vogel et al.,2009) , while functionality of community studied with metaproteomics (Qian and Hettich, 2017). When these two approaches utilized to the same target soil microta it create linkage between various microbial community composition and ecological processes (Zampieri et al., 2016).

Ribosomes play a vital role in the functioning of all living organisms that ribonucleoprotein machinery in which protein synthesis. Prokaryotic ribosomes are 50S and 30S subunits which composed of 23S rRNA, a 5S rRNA, and over 03 proteins while the small subunits contains 16S rRNA and 20 proteins. Functional restraints located which area of an rRNA sequence must remain conserved and which may be variable without altering integral structural components.

Current molecular combination- omics technique (Fig.4) viz., 16S rRNA sequencing, culturomics and meta proteomics that helps to study microbial community functions, geochemical transformations, linkages of microbial population and their pattern of biotransformations (Martinez-Alonso et al, 2019).

One of molecular method, denaturing gradient gel electrophoresis (DGGE) of polymerase chain reaction (PCR)-amplified genes from environmental samples is important tool in field of environmental microbiology and microbial ecology. The PCR-DGGE, targeting appropriate sequence to study microbial community structure within ecosystem (Muyzer,1999).

Metagenomic approach using in PCR-DGGE is rapid, cheep along with convenient to compare total diversity of microbial community structure and functions from agricultural soils. On the other hand, metagenome-sequencing provide complete information about biodiversity present in agricultural soil sample and triggering gene code for viz., chemical pollutant tolerant, biocatalysts for biosynthetic or biodegradation process, biotransformation, fertility factors, antibiotic production, antagonistic chemicals. To screen such informative genes, metagenomic library already constructed since 2000, these works for better management in agricultural field (Elsas et al.,2008).

Culture dependent study in last few decades completed with gene sequence studies, their DNA fragments almost characterised and adoptated for metagenome studies. The application of metagenomics provide appropriate for representing the complex patterns of interactions among microbial communities in soil and in plant rhizosphere.

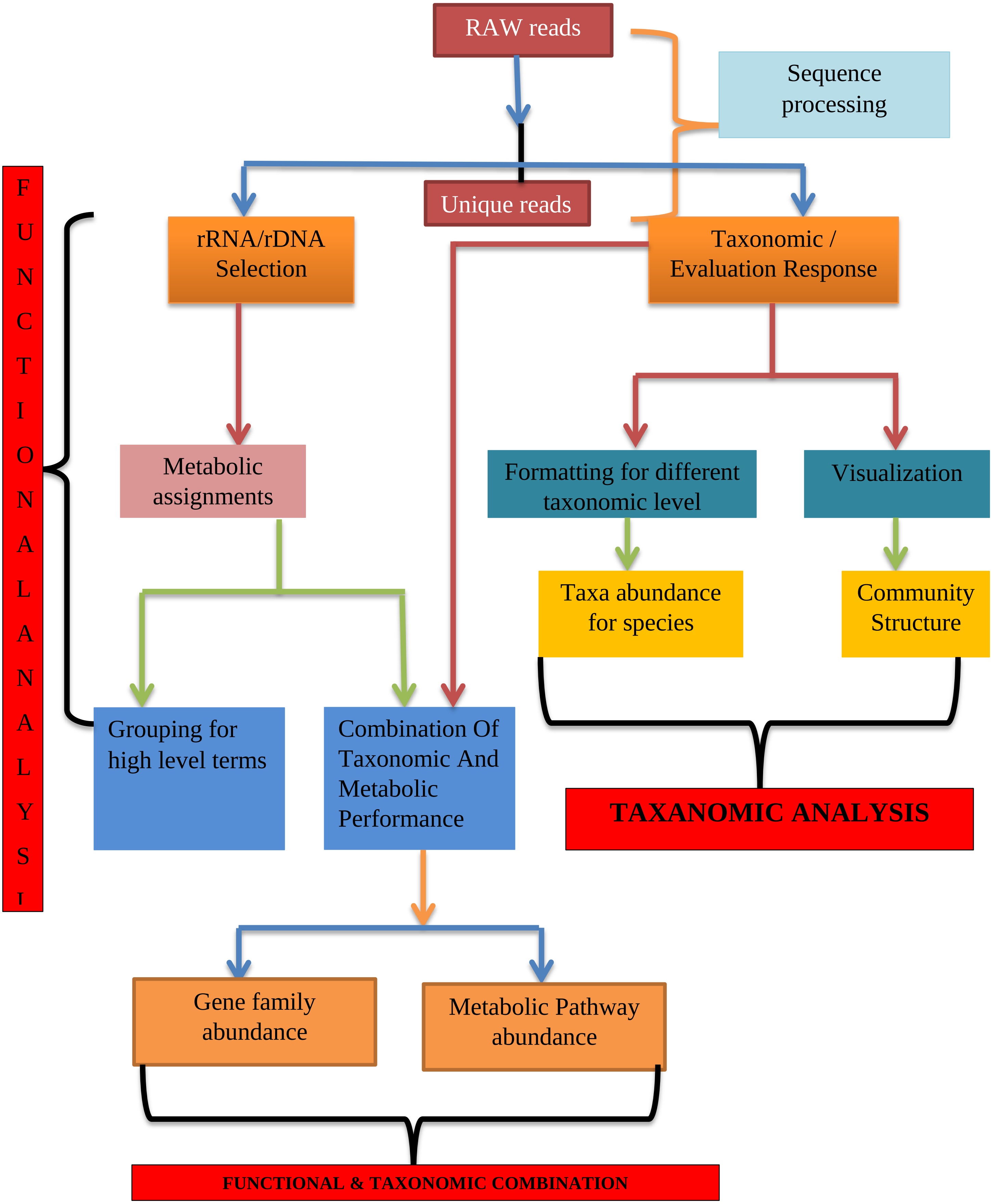

Fig. 4. Work flow of Metagenomics in Agricultural Ecosystem

In morden era, Metaprotemics is combination of various omics methods viz., metametabolomics, metatrasncriptomics along with classical methods of genetics, molecular biology and biochemistry. These approaches interpret ecosystem functionality and integrate ecosystem biodiversity, their role and interaction. This approach of microbial community study with complex consortium helps to identify functionality of uncultivated microorganisms in ecosystem functions. In future, improved approach of current molecular techniques help to access the protein expression from individual cell within ecosystem and it's functional contribution. Therefore, combinations of metagenomics tools lead to understand ecosystem and also helpful to exploit their functions in agricultural ecosystem in new era (AP.Florence et al, 2015).

However, advances in genomic technologies-the development of genome arrays and the advent of next generation sequences of chemotrophic organisms associated in agricultural soil beneficial in selection of agriculture remediation. Genomic Selection (GS) is based on principal that from a large number of markers can used to estimate specific gene and its functionality, precise behave and focusing on target group subset marking. With the application of GS in agrogenomics values the score potential plant growth and bioremediation in affected agro-soils.

CONCLUSION

Now a days, due to increasing salinity of soil and changes in water table, farmers are facing issues of unutilized agrochemicals in field. It is recent development in field of molecular biology, where with the help of whole community study and available genomes present in agricultural field known as metagenomics .

Chemotrophic microorganisms are using available chemicals in ecosystem for their constitutive or induced metabolic pathways. In single individual approaches, complexity and functionality of specific microbial cells requires more detail study viz., resistance, metabolism, enzyme production and structural changes. The description of molecular component in communities of same ecosystem, aims to understand evolutionary process or adaptation mechanism that influence genetic variability. Benefit of nucleic acid sequencing in all majority data analysis of metabolism, approaches for metabolic and structural adaptation, improving productivity in agricultural field. The key role play by microbes in agriculture in fitness of plant, soil geochemical properties, quality and quantity of crop production. However, microbes community like chemotrophs which includes both chemolithotrophs and chemoorganotrophs are the biggest carbon reservoirs on the earth.

Usefulness of chemotrophs from agricultural soils in empowered the generation of more accurate and continuous to maintain fertility of soils, crop productivity and adequate use of agrochemicals. Current chemicals used in agricultural field require to study their degradation pattern and utilization pathways by chemotrophic bacteria, metagenomics helps to total study of community composition, geochemical transformation, degradation pattern and ecosystem function.

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