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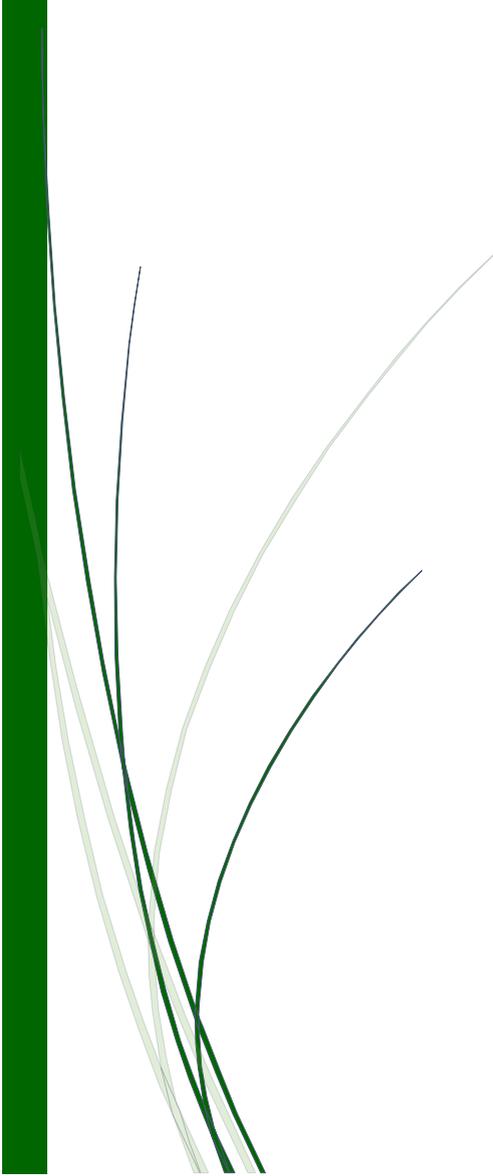
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Utilization of Plant Probiotic Microorganisms for the Improvement of Agriculture

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ABSTRACT

Pesticides and fertilizers are in intensive use due to agricultural push of needs in high productivity. This ruthless practice of chemical fertilizers negatively on humans' animals along with the natural properties as water soil etc. to reduce these environmental problems scientist studying on plant probiotic microorganisms in short PPM which are also known as bio-control Bio-protectants, Bio-stimulants and Bio-fertilizers that can by the microorganism to the plant and reduce environmental stress. The PPM mostly is engaged with a harmonious free-living relationship with the plant or they can work diversely in an unexpected way, now and again with explicit capacities to accomplish acceptable plant advancement. The study is about the PPM introduction, portrayal and several function and various ways of function with the application. A huge group that is named as plant growth promoting group or in short PGP. The group contains some bacterial and fungal species that stimulate plant growth and they can stimulate the growth through various mechanism. Many of the biogeochemical process are maintained by the soil borne microflora. Soil chemical fertilizers are needed to replace by an alternative. Scientist are studying on PPM to have it as the alternative as they don't provide with any environmental problems, they directly improve the nutrient supply. The species are truly organic. They have high role in biodegradation of pollutants. They also can decrease the chances of antibiotic-resistant bacteria and disease. The principle approaches are explained includes, the way of life subordinate methodology for the microorganisms contained in the plant material are additionally disengaged by refined and are distinguished by a blend of phenotypic and sub-atomic techniques and the refined free temperature microorganisms are recognized without developing them.

Key words: Cultivating, Microorganisms, Biodegradation, Decrease, PGP

It is said that the plants are never alone like human. They are always accompanied by microorganism known as plant probiotic microorganism with which they are involved with a symbiotic or symbiotic association. Humans and animals are strongly dependent upon the plant Kingdom activities for their survival. From the plant Kingdom activities agriculture and forestry are important for human survival throughout the whole history [1]. The high yield maintenance is now a problem for over countries due to population increase climate exchange soil degradation environmental contamination so we need high yield group that can feed the whole population [2-3].

Ford these problems as population increase we do

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need high yield of edible crops so application of input such as pesticides fertilizers and become very compulsory in days to provide that yield. The chemical composts and pesticides have been negative impact on dirt (soil) contamination and water contamination and whole food chain is getting suffered for this. Scientist had also tried to reduce pesticide by selecting cultivars resistant to specific disease but in that case the resistance can cause dumping of crown rot root rot and many more diseases [4]. Therefore, the use of products based on PPM known as by a protected by chemicals by fertilizers by stimulated is a promising solution to overall the environment quietly and ecosystem that can maintain the equilibrium and reduce the excess cause of chemical fertilizers. The article is focusing upon the recent advantage of PPM. Plant culture improvement was also studied. Improvement stains are also studied in the study.

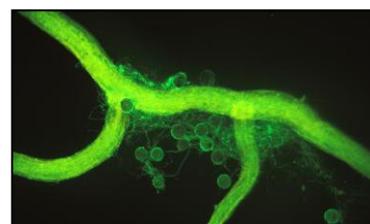


Fig 1 Microbes in soil

MATERIALS AND METHODS

PPM

Now a day what population is gradually increasing and some other problems are being faced by the humankind. The problems could be soil degradation environmental contamination climate change agriculture Hollister degrees which have critical for human activities and animal survival. So, the PPM is studied as the base product of alternative to Bio-fertilizers, Bio-pesticides or Phytoremediation. PPM is beneficial organism that can be found with plants in either symbiotic or free-living relationship. Primarily the association occurs in soil. Microalgae associate bacteria are also included to the types of PPM. There is a higher microbial presence of soil environments in the root system due to rhizodeposits and root exudates. Some of these germs can support their host which stimulates plant growth, reduces pathogen infection, increases yield, and reduces the pressure of biotic or abiotic plants as salt pressure. PPM are plant growth promoting microorganisms are consistent in soil microbial population plant disease suppressing bacteria fungi nitrogen fixing cyanobacteria as active member cities add toilet accident degrading microbes are also present in soil microflora. *Bacillus megaterium* or also a plant that causes the mutation of abscisic acid deficiency inhibition in the growth of mutant plants. *Bacillus* and *Pseudomonas* are the most predominant genera for the important PPM groups as plant growth promoting bacteria in short PGPB present in the soil. It is been believed that soil is the only source of PGP but some studies have shown that the bacteria are also associated with microalgae that stimulates the *Bacillus okhensis* case of growth. Aamantrit probiotic producing

bacteria are also considered as biocontrol for their activity against pathogenic microorganisms they can be lactic acid producing bacteria are generally recognized as safe GRAS status which is included in the FDA regulations in title 21 for code of federal regulations (21CFR). Another study to PPM the fungi is highly studied with important functions. For example, the endophytic fungi like *Exophiala* sp. Secrets the phytohormone that can improve the plant growth. *Trichoderma* strains have also studied for the identification of molecular mechanism of activation during in vitro interaction with tomatoes and *Trichoderma alongibrachiatum* MK1. The PPM interactions are influenced by crop rotation type and degree of fertilization toys of cultivation PPM performance and fields satisfactory etc.

PGP

Plant growth promoters are microorganisms such as bacteria and fungi that stimulate plant growth through different mechanisms. Some direct PGP action mechanisms include nitrogen amelioration phosphorus or iron fixation and plant hormone production. Biomolecules as varied as antibiotics, enzymes and antimicrobial and pathogen inhibiting volatile compounds which can lower plant ethylene levels and induce systematic resistance are produced by PGP indirectly. PGP abilities can be presented by both Rhizosperic and endophytic soil bacteria. Rhizospere microbes are mainly found in the root inhibitors and endophytic bacteria are found with tissues of the plant itself or are free living. Food production systems are containing great importance to PGP as they are responsible for increasing the productivity.

Microorganism	Function
<i>Alcaligenesfaecalis</i> strain	Salt tolerance increase in <i>Arabidopsis thaliana</i>
<i>Bacillus subtilis</i>	Alleviates the adverse effects of soil salinity on wheat growth
<i>Arthrobacter</i> sp.	Promotes early plant growth
<i>Bacillus megaterium</i>	Increases plant biomass and the salt tolerance of rice
<i>Bacillus okhensis</i>	Inhibits abscisic acid (ABA) deficient mutant plants
<i>Fusarium culmorum</i> FcRed1	Promotes growth of a gibberellins (GAs)-deficient mutant cultivar and normal GAs biosynthesis cultivar rice seedlings
<i>Bacillus subtilis</i> GB03	Promotes early plant growth in <i>Sorghum bicolor</i> (L.) Moench
<i>Exophiala</i> sp.	Down-regulates expression of the high-affinity K ⁺ transporter (HKT1)
<i>Halomonas</i> sp.	Increases plant biomass and the salt tolerance of rice
<i>Lactobacillus plantarum</i> BY	Promotes early plant growth
<i>Novosphingobium</i> sp.	Reduces soft rot disease severity
<i>Penicillium minioluteum</i>	Metabolizes ABA in vitro
<i>Phomglomerata</i>	Mitigates the adverse effects of salinity stress in various plants
<i>Penicillium</i> sp. LWL2	Promotes the growth of GAs-deficient dwarf mutant Waito-C and Dongjin-beyo rice
<i>Pseudomonas fluorescens</i>	Can help with the enrichment of proteins related to energy metabolism and cell division
<i>Sinorhizobium meliloti</i>	Produces Indole-3-acetic acid (IAA)
<i>Trichoderma longibrachiatum</i>	Promotes growth and/or increased biotic and abiotic tolerance to stresses

Stress tolerance property

More than 30% of worldwide losses in crop production are due to the environmental stresses as soil salinization, soil solidification, and draught flooding soil pH UV light heavy metals environmental temperature abiotic stress. Primary signal such as change in ionic level so what are clauses and others and secondary signals as phytohormones as secondary metabolites releases are involved in the stressful conditions plant cascade which is responsible for such situations. Turgor pressure and mass production is affected by draught while the plants regulation cosmetic pressure ionic stress, oxidative stress. PGPR

interactions with other microorganisms and have effect on plant physiology [5]. Aminocyclopropane-1-carboxylic acid (ACC) deaminase is an enzyme present in the PGPR. Role of this enzyme is to regulate the hormone in plants. ACC deaminase is regulating ethylene, which is known as the stress hormone. The plant productions of these hormones are responsible for the roots acceleration that's response of abiotic and biotic process. The normal plant development, leaf abscission, senescence, follower wilting, chlorosis and low yield are inhibited by the high concentration of ACC deaminase. ACC deaminase containing bacteria inoculated plants have the increase in root height and biomass. This

happens for reduction in ethylene levels. Thus, they are beneficial for the plants in sense of stress tolerance.

Bioremediation

Due to the increase in industrial growth the environmental pollution are growing at a higher speed. Scientists are continuously trying to recover the contaminated soil. Due to the high cost and danger of the process of chemical cleanup for conventional hazards the study is becoming hard. Halogenated compounds like perchloroethylene, trichloroethylene, Pesticides like atrazine and bentazon, petroleum hydrocarbons, polycyclic aeromantic hydrocarbons, polychlorinated terphenyls are the main contaminants of soil. Primary inorganic contaminants are heavy metals (cadmium, chromium, lead, copper, zinc, nickel, mercury). For the remediation of polluted soil, the eco-friendly and cheaper ways are still being found. Phytoremediation is thought to be one of them as it includes plants that can accumulate heavy metals and recover the land. Another factor for the technique is to ensure the ability of microbe to tolerate heavy amount of contaminants. For the potential for metal bioaccumulation in polluted environment that is enhancing metal uptake and promote the plant growth the bio-fertilizers containing metal tolerant microorganisms (PGPR) is being studied. Soil decontamination and plant development is contributing the bioremediation which follows the mechanism of microbe plant interactions. Recently researchers have used PGPR availability to minimize arsenic toxicity on Malbec grape

seedlings. *M. luteus*, one of three tested species (*Micrococcus luteus*, *Bacillus lincheniformis* and *Pseudomonas fluorescens*) show high decrease in the arsenic toxicity and improving the biomass [6]. For another studies it was found that *Bacillus thuringiensis* improved metal accumulation and growth in the species *Alnus firma* in mine trailing soil. Inoculation of the microbe helped in root length increase, shoot height increase, plant biomass increase and heavy metal accumulation in inoculated plants of *Bacillus thuringiensis*.

Plant nutrition improvement

Plant growth production is favoured by different methods of soil fertilization such as chemical fertilization, organic fertilization and microorganism use for the macro and micro nutrients, mainly nitrogen and phosphorus. Bio-fertilization is having a definition as microbial usage for increase the supply of primary plant nutrition. Direct effects on nutrient availability, root growth enhancement, root pathogen antagonists, and soil detritus decomposition are included in nutrient improvement mechanism. Bacteria and fungi are among the microorganisms that can promote plant growth and have been identified as plant growth promoting *Rhizobacteria* as *Acinetobacter*, *Alcaligenes*, *Arthrobacter*, *Azospirillum*, *Azotobacter*, *Bacillus*, *Beijerinckia*, *Burkholderia*, *Enterobacter*, *Erwinia*, *Flavobacterium*, *Pseudomonas*, *Rhizobium*, *Serratia*, and *Arbuscularmycorrhizal* fungi [7-9].

PGP	Effect
<i>Trichoderma</i> spp.	Secondary metabolites produced by <i>Trichoderma</i> spp. affected the growth of tomato (<i>Lycopersicon esculentum</i>) and canola (<i>Brassica napus</i>) seedlings.
<i>Trichoderma harzianum</i>	<i>T. harzianum</i> caused effects on maize plant growth but only in combination with mineral fertilization and with disinfected soil as growth substrate.
<i>Pseudomonas</i> , <i>Ralstonia</i> , <i>Enterobacter</i> and <i>Pantoea</i>	Plant growth promotion was evaluated by screening for indoleacetic acid (IAA) production and mineral phosphate solubilisation in vitro.
<i>Bacillus velezensis</i>	Increased the growth of some tested plants (including beet, carrot, cucumber, pepper, potato, radish, squash, tomato, and turnip) at various levels in different plant parts.
<i>Azospirillum lipoferum</i>	Decreased plant water stress in maize (<i>Zea mays</i> L.) with abscisic acid (ABA) and gibberellins (GAs) production by <i>Azospirillum lipoferum</i> .
Endophytic bacteria (217) and fungi (17) from coffee tissues.	Strains were evaluated for their potential to control coffee leaf rust (<i>Hemileia vastatrix</i>) and to promote coffee seedling growth. Bacterial strains named 85G (<i>Escherichia fergusonii</i>), 161G, 163G, 160G, 150G (<i>Acinetobacter calcoaceticus</i>), and 109G (<i>Salmonella enterica</i>) increased plant growth. 64R, 137G, 3F (<i>Brevibacillus choshinensis</i>), 14F (<i>S. enterica</i>), 36F (<i>Pectobacterium carotovorum</i>), 109G (<i>Bacillus megaterium</i>), 115G (<i>Microbacterium testaceum</i>), 116G, and 119G (<i>Cedecea davisae</i>) significantly reduced disease severity.

Plant growth promoting *Rhizobacteria* (PGPR)

PGPR has the greater contribution in enhancement of plant growth and yield because they are part of the rhizosphere biota that in association with plants, stimulates the host growth. PGPR are providing a large adaptability in a wide variety to the environment, enhances growth rate and biochemical versatility that allows them to metabolise a very wide range of natural and xenobiotic compounds. PGPR can be classified as rhizospheric and extracellular or and intracellular endophytic, according to the association between PGPR and the plant host. Extracellular PGPR in short e-PGPR are those PGPR that exists in the rhizosphere on the rhizoplane in the space between root cortex cells and intercellularly (i-PGPR) inside of the root cells mainly in nodular structure. Some examples of ePGPR are *Agrobacterium*, *Arthrobacter*, *Azotobacter*, *Azospirillum*, *Bacillus*, *Burkholderia*, *Caulobacter*, *Chromobacterium*,

Erwinia, *Flavobacterium*, *Micrococcus*, *Pseudomonas* and *Serratia* families. The examples of iPGPR are *Allorhizobium*, *Azorhizobium*, *Bradyrhizobium*, *Mesorhizobium*, and *Rhizobium* in rhizobiaceae family. The rhizobacteria are mostly belonging to the group are mainly Gram-negative rods. Sometimes they can be the gram-positive rods and sometimes may be cocci or pleomorphic. Intercellular PGPR or iPGPR are the bacteria that are colonizing in special root nodular structure and include bacteria that can fix atmospheric N₂ [10-13].

Arbuscularmycorrhizal fungi

Arbuscularmycorrhizal fungi or AMF can be enhancing solubility and availability of nutrients, including phosphorus and micronutrients, which are absorbed by the plant itself under many other different conditions. Phosphorus and nitrogen nutrition of *Medicago sativa* are

affected by AMF as well as carbon assimilation and water loss through modification of stomatal behaviour. The majority of plant roots are symbiotically associated with AMF. The AMF are *Glomeromycota*, family *Acaulosporaceae*, *Gigasporaceae* and *Glomaceae*. The interaction between AMF and bacteria may result in benefice impacts on plants. Fungal colonization in roots, interaction positivity influenced nitrogen and phosphorus enhancement was improved by PGPR. In improvement of availability of carbon and phosphorus compounds are improved by PHB (phosphate solubilizing bacteria) and AMF. AMF has important potential as Reforestation enhancement. Since the tropical forest are destroying at a high rate the investigation of AMF community in root structure and rhizospere soils of *Aquiliary crassna Pierre* ex lec and *Tectonsgrandis* lini. f. The field work was done on understanding weather the AMF vary to host plants. It was revealed that AMF community composition in *A. creassna*

and *T. grandis* were similar by the terminal restrictions fragment length polymorphism, complemented with clone libraries. Total 38 distinct terminal restriction fragments were found. 31 of them were share between *A. creassna* and *T. grandis*. Authors reported that TRF were attributed to *Claroideoglomeraceae*, *Divrrsisoraceae*, *Gigasporaceae*, and *Glomaceae*. The production of seedlings with high probability of survival required by Regengarating strands of valuable tropical hardwood tree species for sustainable harvest. Four families are being represented by the AME communities *Glomeraceae* (49%), *Acaulosporaceae* (24.9%), *Claroideoglomeraceae* (29.8%), and *Gigasporaceae* (4.8%). Which species were incubated in in vitro and colonized by all the study of a m f. in the results we find that the a.m. inoculated plants or taller than normal curated plants that suggest a high possibility of a MF symbiosis with both re forestation and important tree species productions in greenhouse studies [14-16].

Microorganism	Plant	Purpose	Bio-inoculation effects
<i>Rhizobial</i> strains		ACC deaminase production	ACC deaminase-producing organisms decrease plant ethylene levels that lead to plant growth inhibition or even death
<i>Staphylococcus</i> sp., <i>Bacillus</i> sp., <i>Curtobacterium</i> sp. M84, <i>Arthrobacter oxidans</i> BB1	<i>Arabidopsis thaliana</i>	To investigate pathogen resistance and salt stress tolerance	Strains BB1 and M84 showed the best performance under pathogen stress, and BB1 and L81 were better under salt tolerance
<i>Pseudomonas</i> spp.	<i>Zea mays</i> (maize)	To evaluate the potential of five <i>Pseudomonas</i> spp. in alleviating drought stress in maize	Bioinoculation with <i>Pseudomonas</i> spp. improved maize development under drought stress
<i>Agrobacterium tumefaciens</i> , <i>Zhinguelliella</i> , <i>Brachybacterium saurashtrense</i> , <i>Vibrio</i> , <i>Brevibacterium casei</i> , <i>Haererohalobacter</i>	<i>Arachis hypogaea</i>	To investigate the influence of these PRPGs in response of salinity	<i>A. hypogaea</i> development decreased in the control treatment under salt conditions. On the other hand, the presence of PGPR promoted plant growth and salt tolerance.
<i>Pseudomonas</i> GGRJ21	<i>Vignaradiata</i> (Mung bean)	To evaluate how the bacteria promote plant growth and alleviate drought stress.	The alleviation of drought stress in Mung beans by <i>Pseudomonas</i> is related to the production of antioxidant enzymes, cell osmolytes, hormones, and upregulation of stress-responsive genes in the host plant.
<i>Bacillus cereus</i> Pb25	<i>Vigna radiate</i> (Mung bean)	To evaluate the influence of bio-inoculation in Mung bean development under salt stress	<i>B. cereus</i> Pb25 showed an important role in mung bean plant protection due to increased production of its plant growth-promoting activity
<i>Bacillus amyloliquefaciens</i> RWL-1	<i>Oryza sativa</i> (Rice)	To investigate if the abscisic acid producer bacteria is able to protect rice crop from salinity stress	<i>B. amyloliquefaciens</i> was able to grow in different salt concentrations without affecting abscisic acid production and produced increased plant height, biomass, and total chlorophyll content.
PGPR isolated from <i>Hordeum secalinum</i> and <i>Plantago winteri</i>	<i>Hordeum vulgare</i> (Barley)	To isolate rhizobacteria associated with barley and <i>P. winteri</i> and evaluate the effect of bioinoculation on barley development under salt stress	The isolate E110 identified as <i>C. flaccumfaciens</i> was the most effective growth promoter and stress alleviator
<i>Azotobacter chroococcum</i> W5, <i>Mesorhizobium ciceri</i> F75, <i>Pseudomonas striata</i> P27, <i>Serratia marcescens</i> L11 and <i>Anabaena torulosa</i>	Wheat seeds	To evaluate the influence of phototroph heterotroph biofilm on wheat development	Soil treatment with biofilm led to an increase in soil chlorophyll, high concentrations of acetylene reduction activity using <i>Anabaena Serratia</i> biofilm, and <i>Anabaena-Pseudomonas</i> increased P-uptake
<i>Acetobacter</i> spp., <i>Azotobacter</i> spp., <i>Rhizobium</i> spp.,	<i>Camellia sinensis</i>	Soil recovery from excessive use of chemical	Lower chemical fertilization with biofilm improved soil microbiota and quality,

<i>Bradyrhizobium</i> spp., <i>Colletotrichum</i> spp. <i>Pseudomonas mendocina</i>	(Tea) <i>Lactuca sativa</i> (Lettuce)	fertilizers. To investigate the effect of interaction between PGPR and AMF in lettuce under salt stress.	favoring plant growth and Rhizoremediation <i>P. mendocina</i> was able to increase plant biomass under high salt level, while AMF were less effective in alleviating salt stress. Co-inoculation did not show an additive effect on plant growth
<i>Pseudomonas alcaligenes</i> , <i>Bacillus polymyxa</i> , <i>Mycobacterium phlei</i>	<i>Zea mays</i> (Maize)	To investigate the effects of Bio-inoculants on maize development in two types of soil.	The bio-inoculant stimulated the plant development and assimilation of N, P, and K in a low nutrient and saline soil.

Improvement of soil

Now days it is found that the increase in sustainable agriculture lead the necessity of new technological development for the reduction of environmentally harmful chemicals and fertilizers pesticides that are used by the agricultural people. Many other studies have put in light the plant probiotics as the alternative of soil fertilizers and their use as fertilizers in agriculture. Many of the studies have shown that they are used in agriculture improve the supply of management of nutrients in adverse conditions. They also took role in biochemical processes of plants with some specific effective natural substances and soil contaminated Bio-composts and antibiotic pressure tolerance [17].

Methods to study the microbial ecology of plants

It is important to study the plant associated microorganisms not only to understand the role in ecology and plant interactions also for the biochemical applications for those microorganisms in the management of the crops for high yield. Two different approaches are done upon the general knowledge of microbial community structure of different plants. Those two are culture dependent approach and culture independent approach. In culture dependent approach the isolated microorganism from plant material is cultivated and identified by a combination of molecular method and phenotype method from which their morphology and role can be studied. While in the other hand the culture independent approaches containing microorganism detected without cultivation based on extraction and DNA analysis through which their genetics can be easily studied. From there genetic library could be easily identified [18].

Methods that depends upon the culture

Mostly the methods that are depending upon the culture are used in determining the microbial ecology of plants. Most diverse plant systems have their diversity in microorganism too. Some diverse cleanser banana, strawberry, rice, potato, eucalyptus in wheat which has diverse variety of microorganisms. The method is based on growing after microbial cultures on agar plates or other nutrient plates and then characterizing and identifying them through various steps. Main lead identification is done by phenotype related identifications. Phenotype dependant identifications maybe morphological physiological or metabolic. Changes in growth condition and natural mutation can be changing these characters. So in this case such procedures may be insufficient for correct and reliable identification of the microorganisms that are cultured. In the other hand the procedure is time consuming and hard in laboratories. Recent recently many scientists have developed molecular method that can study microbial ecology and

overcome many limitations as we discussed in the field of understanding plant system microorganism diversity [19].

For the characterizing of plant growth promoting microorganism in short PGPR the sequence conservation regions of microbial DNA has been taken as a higher step. Generally, for investigation of bacterial community the 16 s rRNA gene is triggered for PCR amplification but 26 s and 18 s r RNA gene is normally targeted in eukaryotic commit investigation that is the major difference in investigation of community of eukaryotic and prokaryotic. Many other polyphasic approaches applied to identify and many endophytic bacteria isolated from maize and other crops. Biochemical applications were performed as growth in carbon sources intrinsic tolerance of antibiotics and biochemical test for catalase nitrate reductase and urease. Several genetic identifications are also performed as box PCR and sequencing of 16 s rRNA. Identifications revealed the presence of bacteria belonging to the genera *Pantoea*, *Bacillus*, *Burkholderia* and *Klebsiella*.

Further identification of groups and differentiation of microbial species in plant materials several methods applied such as BOX-PCR, REP-PCR, RAPD, RFLP, AFLP, ARDRA and PCR fingerprinting. The theory that the DNA varieties in microbial state that can be used for classification is proposed by all those methods we have done. It is hard to choose between many of the methods as a particular from the available literature as there are many other methods described in the literature. There are two main points depending on which the method or choosing one of them is microbial culture grouping priors to sequencing. And the other is microbial strain characterization within a species. In a study REP-PCR technique using the (GTG)⁵ primer was employed for the bacterial endophytes isolation from strawberry fruits. In that particular study a cluster was found that was a total of 45 (GTG)⁵ – REP-PCR cluster with the help of 16s rRNA sequencing of some microorganisms. Some of the microorganisms are *Bacillus subtilis*, *Bacillus* sp., *Enterobacter* sp., *Enterobacter ludwigii*, *Lactobacillus plantarum*, *Pseudomonas* sp, and *Pantoea* sp. It was evident that REP PCR techniques are a promising technique as a potential genotype tool for rapid and relatable detection of bacterial endophytes. Some other genetic tools are also finding successful for plaster plant microbial culture as ADRA-PCR in rice roots, BOX-PCR in maize and AFLP in banana roots [20-23].

Method that or not depending on culture

The method that are not dependent upon culture are extremely useful for understanding and isolating microorganisms but the microorganism cannot be cultivated because in this study physiological requirements not previously known so the microbial community composition

could be known but could not be cultivated in this process. It is started that plants grow in ecological niche and nutrient rich ecosystem. So, it is heart for selective media and culture conditions to full feel the requirements of reproduction of the ecological niche and relationships behind bacteria plant and bacteria interactions as there is a vast difference are known to us. The main principle of the method independent of culture based on amplification of PCR of the microorganism's RNA gene [24]. This technique is a valuable technique itself. Through this technique we can easily get instant info about the microorganisms specially the structure. The microorganisms who have in habitat in nutrient rich ecosystems whose growth conditions are very difficult to simulate can be easily identified through this technique. Potential to study the microphone quickly. That thing was just as equal to mi stone in this field. That has another impact economically and it lacks the time taking process. Sometimes the methods are done by denaturing gradient gel electrophoresis in short DGGE [25]. Through this method we can easily and directly profile the specific ecosystems microbial population through separating PCR products that have originated with universal primers. Mainly the Primus is based on the melting domain of specific DNA molecules. In the study of different plant species endophytic bacteria, the PCR-DGGE contains a greater potential as aiding [26]. It is confirmed by several authors that there is a difference between the naturally occurring species of plant growth promoting bacteria and the isolated bacteria. the indigenous bacterial flora diversity associated with potato plants essays to buy the use of both plating and PCR-DGGE. The results were very shocking to show that the PCR-DGGE analyzed sequences (*Telluria mixita*, *Caulobacter* sp., *Agromyces cerinus*, *Afipiageno* sp. and *Pseudomonas agarici*) did not matched from the isolated sequences. Get clearly suggest us about uncultivable or not yet cultural in the organisms that are detected in the DGGE analysis [27].

That clearly shows the importance of using both the culture dependent and culture independent methods for the understanding of ecological role of endophytic bacteria as well as its biochemical applications in agriculture. There are several techniques of culture independent methods as cloning and sequencing the whole communities rRNA sequence to explore the natural ecosystem microbial diversity [28]. Sequence of those RNA gene helps to let free the tools for gaining a more precise image of a given ecosystem diversity of species. Microbial diversity of plants is mainly discovered by the help of those liberates. Some scientist has reported the versatile and wild range of bacteria in the roots of rice [28-29]. The liberates are 16s rDNA which contains subclasses as alpha, beta, Gama, delta and epsilon subclasses of *Proteobacteria*, *Cytophaga*, *Flexibacteria*, bacteroids phyla, low G+C Gram positive bacteria, *Deinococcus thermus*, *Acidobacteria* and *Archaea*.

Scientist has found citrus grove bacterial community 16s rDNA Library. A total of 2062 clones were classified in to seven phyla, which are *Bacteroidetes*, *Dictyoglomi*, *proteobacteria*, *Actinobacteria*, *firmricutes*, *chlamydiae*, *verrucomicrobia*. Recently, for rare species detection and greater depth providing is done by some massive parallel sequencing platform as NGS (next gen sequencing). The NGC platform includes technology from 454 life sciences and solexa1G instruments. Another contender which is considered as serious, the name is ABI's solid platform. These techniques perform tens of thousands or more sequence reaction in single test tube. The new sequencing techs are highly impacting microbial study. In potato roots 454 pyrosequencing was examined. Scientist has detected several bacterial operational taxonomic units apparently 477 strains. The units are belonging to a total 238 genera of 15 phyla within banana roots [30-31]. Five of the endophytic potato plant microorganism's genera are *Rheinheimaea*, *Dyadobacter*, *Devosita*, *Pedobacter* and *Pseudoxanthomonas*. Other scientists have used 16 s rRNA illumina sequencing to access endophytic bacteria in Alovera. With a predominate of proteobacteria, Actinobacteria, firmricutes, Chlamydiae, found in the analysis. NGS technologies have power to capture microbial diversity in plant tissue [32]. This can easily improve the understanding between microbe's plant interactions. NGS platform use can quickly identify microbial candidates that can influence plant production and growth.

CONCLUSION

From this study we could easily conclude that plant probiotic microorganisms in short PPM are very beneficial microorganisms which are associated with the plant to improve their growth. There is a high chance of the use of PPM as bio-fertilizer and bio-pesticides. In several studies it is also found that they can prevent several microbial diseases by secreting some molecules dangerous to other pathogens. There is a group in plant probiotic microorganisms which is called the plant growth promoters who can stimulate the plant growth through different mechanisms. The mechanisms can be nitrogen fixation Phosphorus fixation iron fixation production of plant hormones which can helps the growth and immunity of the plant. Bio-molecules antibody enzymes antimicrobial and pathogen inhabiting volatile compounds could be secreted by plant growth promoters or plant probiotic microorganisms. It is very important to molecular characterization and identifies plant associated microorganisms not only for the understanding of people logical role and plant interactions but also to enable the biochemical application of the cultures and to optimize the agricultural productivity.

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