# Impact of Slash-Burning and Plant Species on Soil Microbial Community and Processes in *Jhum* Agro-Ecosystem

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**Central Agricultural University, Imphal**
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**Doctor of Philosophy**

**In**

**Soil Science and Agricultural Chemistry**

by

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# CERTIFICATE – I

Certified that **Kumari Carolyn Zothansiami** {Admission No. **CAU/CPGS/SOIL/P13/01;** Registration No. **CAU/71-A/11(PG)**} has satisfactorily prosecuted her course of research for a period of not less than four semesters and that the thesis entitled **"Impact of slash-burning and plant species on soil microbial community and processes in *Jhum* agro-ecosystem"** submitted by her to the Central Agricultural University, Imphal – 795 004 (Manipur) in partial fulfilment of the requirements for the award of the degree of **Doctor of Philosophy** in the subject of **Soil Science and Agricultural Chemistry** is the result of original research work conducted by her under my supervision and is sufficiently of high standard to warrant its presentation to the examination.

I also certify that the thesis or part thereof has not been previously submitted by her for a degree of any University.

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# CERTIFICATE- II

This is to certify that the thesis **"Impact of Slash-Burning and Plant Species on Soil Microbial Community and Processes in *Jhum* Agro-Ecosystem"** submitted by **Kumari Carolyn Zothansiami [Regn. No. CAU/71-A/11(PG)]** submitted to the Central Agricultural University, Imphal – 795 004 (Manipur) in partial fulfilment of the requirements for the award of the degree of **Doctor of Philosophy (Agriculture)** in the subject of **Soil Science and Agricultural Chemistry** has been approved by the Student's Advisory Committee after oral examination jointly with an External Examiner.

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# DECLARATION

I hereby declare that the thesis entitled **"IMPACT OF SLASH-BURNING AND PLANT SPECIES ON SOIL MICROBIAL COMMUNITY AND PROCESSES IN *JHUM* AGRO-ECOSYSTEM"** is an authentic record of the work done by me and that no part thereof has been presented for the award of any other degree, diploma, associateship, fellowship or any other similar title.

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*Dated:*

***Umiam, Meghalaya***

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# LIST OF ABBREVATION

| | |
|---|---|
| % | Per cent |
| °C | Degree celcius |
| ANOVA | Analysis of variance |
| ASA | Aryl-sulphatase activity |
| *B* | *Bacillus* |
| BC | Before christ |
| BFC | Baseline fungal community |
| bp | Basepair |
| BSA | Bovine serum albumin |
| C | Carbon |
| C | Cytosine |
| CaCl2 | Calcium chloride |
| CaCO3 | Calcium carbonate |
| CDB | Cellulose Degrading Bacteria |
| cm | Centimeter |
| CMC | Carboxymethyl Cellulose |
| $CO_2$ | Carbon dioxide |
| Conc. | Concentration |
| CPGS | College of Post Graduate Studies |
| DAS | Days After Sowing |
| DGGE | Denaturating Gradient Gel Electrophoresis |
| DHA | Dehydrogenase activity |
| DNA | Deoxyribonucleic acid |

| | |
|---|---|
| dNTPs | Deoxynucleoside triphosphate |
| DOC | Dissolved Organic Carbon |
| dw | Dry weight |
| EDTA | Ethylene diamine tetra-acetic acid |
| *et al.* | *et alia* |
| etc | *et cetera* |
| g | Gram |
| G | Guanine |
| GOI | Government of India |
| GSA | *β*- glucosidase activity |
| H | Hydrogen |
| $H_2SO4$ | Sulphuric acid |
| $H_3PO4$ | Phosphoric acid |
| ha−1 | Per hacter |
| hrs | hour |
| ICAR | Indian Council of Agricultural Research |
| ISI | Institute of Scientific Information |
| K | Potassium |
| $K_2Cr_2O7$ | Potassium dichromate |
| $K_2SO4$ | Potassium sulphate |
| KCl | Potassium chloride |
| $K_{EC}$ | |
| kg | Kilogram |
| kg $ha^{-1}$ | Kilogram per hectare |

| | |
|---|---|
| M | Molar |
| MBC | Microbial biomass carbon |
| MC | Microbial consortium |
| MC | Microbial Consortium |
| MDS | Multidimensional Scalling |
| meq | milli equivalent |
| Mg | Magnesium |
| $Mgcl_2$ | Magnesium Chloride |
| MgO | Magnesium oxide |
| min | Minute |
| mL | Millilitre |
| mm | Millimetre |
| mM | Millimole |
| MUB | Modified Universal Buffer |
| N | Nitrogen |
| $N_2$ | Di nitorgen |
| NaOH | Sodium hydroxide |
| NB | Nutrient broth |
| NE | North Eastern |
| NEH | North Eastern Hill |
| nfb | nitrogen free bromothymol |
| ng | Nanogram |
| NH4-N | Ammonium nitrogen |
| nm | nanometer |

| | |
|---|---|
| OC | Organic Carbon |
| P | Phosphorus |
| PCR | Polymerase Chain rReaction |
| PHA | Phosphomonoesterases activity |
| pMN | Potentially mineralizable nitrogen |
| pMN | Potentially mineralizable nitrogen |
| PNG | *p*-Nitrophenyl-*β*-D-glucoside |
| p-NPP | p-nitrophenyl phosphate |
| PNS | *p*-Nitrophenyl sulphate |
| POM | Particulate organic Matter |
| ppm | Parts per million |
| PSB | Phosphate Solubilising Bacteria |
| rDNA | Ribosomal Deoxyribonucleic acid |
| rpm | Rotation per minute |
| SC | Shifting Cultivation |
| SCS | Shifting Cultivation System |
| SEA | Southeast Asia |
| SMBC | Soil Microbial Biomass Carbon |
| SMBN | Soil Microbial Biomass Nitrogen |
| SMBP | Soil Microbial Biomass Phosphorus |
| SOC | Soil Organic Carbon |
| SOM | Soil Oranic Matter |
| SPSS | Statistical Package for the Social Sciences |
| TAE | Tris-acetate-EDTA |

| | |
|---|---|
| Taq-DNA | Thermus aquaticus |
| TEMED | Tetramethylethylenediamine |
| THAM | Tris (hydroxymethyl) aminomethane |
| TPF | triphenyl formazan |
| TTC | triphenly -tetrazolium chloride |
| USDA | United Sates Department of Agriculture |
| V | Volt |
| wt | weight |
| α | Alpha |
| β | Beta |
| µ | Micron |
| µg | Microgram |
| µg $g^{-1}$ | Microgram per gram |
| µL | Micro litre |
| Mm | Micro metre |
| µM | Micro-molar |

# ABSTRACT

Terrestrial ecosystem supports the above- and below-ground biota communities that interact to influence ecosystem-level processes and functions. Soil acts as the most important medium for linking the above- and below-ground communities which are very sensitive to any external disturbances. To study the effect of above- and below-ground linkages on soil microbial community composition and soil processes, the short jhum cycle can be considered as important experimental plot in farmers' field. Because the above ground plant biomass generated during fallow phase of the jhum cycle gradually rejuvenate the degraded soil system and upon burning of such biomass suddenly breakdown the linkages between above-ground and below-ground community linkages. In this study, a jhum field (approximate 1.5 ha) during fallow phase of 5 year cycle was considered from Muallungthu village, Aizawl, Mizoram and the one half part of the field was slashed and burned and the other half part of the field was kept unburnt. The bulk quantity (800 kg) of soil (0-10 cm depth) from 4 random spots (1 sqm per spot) was collected immediately next morning of burning night from the burnt field and similar way 800 kg soil from unburnt field were collected and carried to the CPGS Farm Field for setting up of mesocosm (pot) experiments under 4 conditions *viz.* burnt and unburnt soils in presence of rice crop and without rice crop. Under each of 4 conditions, 6 microbial inoculation (MI) treatments were imposed maintaining 6 replicated pots. Each pot contained 4 kg soil. Altogether 144 pots were maintained (4 conditions x 6 MI treatments x 6 replications = 144). The MI treatments were: (T1) PSB+Fungi, (T2) $N_2$-Fixer+Fungi, (T3) CDB+Fungi, (T4) PSB+$N_2$-Fixer+CDB+ Fungi, (T5) No bacteria + Fungi and (T6) No inoculation. The rice crop used was a jhum rice landrace Khawlian Buh. The crop was maintained till harvest within a plastic shade house.

The study reveals that the soil bacterial community composition altered significantly due to burning of slashed biomass on soil surface. The introduction of rice crop also altered the bacterial community composition in burnt/unburnt which shows a distinct cluster within the soil type. The Alpha proteobacterial communities of burnt and unburnt without rice crop clustered together and distinctly separated from the clusters of burnt and unburnt soil with rice crop at 45 days of rice growth and at 90 days of rice growth the impact of rice crop on composition of Alpha and beta proteobacterial community was more consicious in burnt soil then in unburnt soil. The beta proteobacterial community of burnt and unburnt soil cluster together in absence of rice crop and there cluster was distinctly separated from the cluster due to cultivation. With the progress of time (90 days of rice growth) the effect of rice crop on beta proteobacterial community was more prominent than compared to burnt unburnt factor.

Burning had significant negative effect on the activity of DHA, GSA, PHA, SOC, pMN, POM, and MBC except ASA indicating higher activity in burnt soil. Introduction of rice crop had significant positive influence on the activity of soil enzymes and soil process indicators. There was significant positive interaction on burning and cropping on soil enzymes activities soil process indicators. There was a significant difference in the activity of soil enzymes and soil process indicators among the microbial inoculants treatment soil process indicators. There was significant positive interaction between burnt and microbial inoculants or cropping and microbial inoculants.

The change in bacterial community composition due to burning and cropping factor significantly influence soil process indicator such as ASA,DHA, pMN, POM, and MBC as evident from analysis result of Multi dimensional Scale (MDS) 1 and 2. The change in alpha and beta proteobacterial community composition due to burning and cropping factor significantly influence soil process indicator like PHA, ASA, DHA, pMN, POM, SOC and MBC as evident from their significant correlation with MDS 1 and 2. Burning had significant positive influence on rice growth yield. This study indicated that introduction of crop in burn soil along with microbial inoculation may positively influenced soil processes as well as crop growth.

**Key word:** Alpha-proteobacteria; Beta-proteobacteria, DGGE fingerprint; Shifting cultivation; Soil bacterial community composition; Soil enzymes, Soil process indicator

# Chapter-1

# Introduction

Soil is heterogeneous, dynamic and complex system composed of different soil micro-organism, mineral particles and nutrients, water and air and organic matter at different stage of decomposition. It play primary role in sustaining the life of living beings on earth by providing favorable environment to soil micro-organism which in turn play a fundamental task in transformation of organic waste into an useful organic matter. Soil micro-organism determined soil health by degrading the organic compounds such as xenobiotics and naturally occurring polyphenolic compounds. Soil microbes play a leading role in biogeochemical cycles of nutrients which are essential for growth and development and even maintaining the soil structure (Dick, 1994; Tabatabai, 1994; Acosta and Tabatabai, 2000; Nannipieri *et al*., 2003; Baldrian, 2009; Haifang *et al*., 2013; Veres*et al.,* 2013; Zhao *et al.,* 2014). Soil microbes mediated about 80–90% processes that occur in the soil (Coleman & Crossley, 1996; Nannipieri & Badalucco, 2003). For which soil is often term as a living system. Its contribution towards the soil dweller is irreplaceable by none. The soil microbes are divided in to the following groups according to size: macrofauna, mesofauna, microfauna and microflora.Appropriate community structure, abundant diversity and high actions of microorganisms result in functioning of the ecosystem (Bell *et al*., 2005; Bissett *et al*., 2007; Zhang *et al*., 2013 and Zhao *et al*., 2014). Terrestrial ecosystems consist of above-ground and below-ground components that interact to influence community- and ecosystem-level processes and properties. Soil act as a system of linkages between the above-ground and below-ground components (Bradgett *et al*., 2008; Suleiman *et al*., 2013). Soils are known to house the most diverse microbial communities those are responsible for innumerable soil processes. Due to its invisibility to our naked eye and lack of knowledge on how a soil microbe helps in balancing our ecosystem indiscriminate on slaught of soil by various human activities has affected microbial community and their functions. The dynamic of soil microbial biomass, its activity, diversity, abundance and composition is affected by any disturbances that occur in their environment and their unique mechanism presence in themselves helps to response quickly in any environmental disturbances (Zhao *et al*., 2014). Decomposition of above ground litters in the soil is the main channel for soil microbes to maintain their ecosystem (Arunachalam *et al*., 1998). Organic matter deposition by leaf-litter, exudates release from roots, organic compounds deposited into the soil environment by

the above ground community results in a unique soil community's i.e below ground community (Bever *et al*., 1996; Zak *et al*., 2003). The biological input of the above-ground vegetations modulates the diversity and activity of soil biota communities. As the soil microbes have the capacity to decompose the organic matter, recycling of nutrients and stabilization of terrestrial ecosystems it regulates the soil processes as a feedback mechanism, (Wardle, 2002: Arunachalam *et al*., 1998).

At rhizospheric zone plant-microbe interactions occur which are responsible for numerous processes like carbon restoration, ecosystem services and nutrient recycling in soil. The soils influence the ability of plants to obtain nitrogen and other nutrients which is influence by the composition and quantity of microbes in the soil (Hoorman, 2011). The potential of soil for enzyme-mediated substrate catalysis is strongly affects composition of soil microbial communities in soil (Tabatabai, 1994) and large group of other enzymes was also secreted by plants in the rhizospheric zone (Baldrian, 2008; Šnajdr *et al*., 2008). For carbon and nitrogen sources soil microbial communities depend on plant root exudates, thus soil microbial community structure is thought to influence by shift in vegetation. For shaping up the microbial community plant species composition is one of the major contributing factors (Liliensiek *et al.,* 2012). Large group of soil fungi is often to ascribed for production of several polymer-degrading enzymes (Miller *et al*., 1998; de Boer *et al*., 2005; Hattenschwiler *et al*., 2005; Steffen *et al*., 2007; Baldrian, 2009) and bacterial populations. For proper flow of ecosystem properties and processes soil communities from native origin play primary roles (Wolfe and Kilrinomos, 2005). Native plant community composition and ecosystem function may greatly affected by shifts of soil microbial community composition colonized by invasive plant species (Batten *et al*., 2006).

The accumulation of microbial biomass gives knowledge regarding ecosystem functioning processes these occurs in soils which were mediated by soil microbes, catalysed and supported by chemicals bound in the biomass or secreted to the environment. The enzyme activities mediated by soil microbial community is then reflecting the current vegetation in an ecosystem (Awasthi *et al*., 2014).

The different groups of microbes produced different soil enzymes which act as the drivers of major soil biological processes (Veres *et al.,* 2013; Baldrian, 2009; Haifang *et al*., 2013). The rates of transformation of soil biopolymers into compounds that are accessible for microorganisms and plants are directly affected by the activity of hydrolytic enzymes and ligninolytic oxidases and peroxidases. Upon death the above and below ground communities released extracellular enzymes into the soil that allow them to access energy and nutrients present in complex substrates, catalyzing the

initial step of nutrient mineralization and decomposition of organic matter (Allison and Vitousek.2005; Awasthi *et al*., 2014). Soils dominated by various plant species is the functions of variation of soil microbial community (Waldrop *et al*., 2000). An external disturbance alters the soil enzymes activities. Therefore, it serves as a good indicator of the microbial community function, metabolic requirements and available nutrients. This results in comprehensive understanding the main processes linking nutrient dynamics and microbial populations (Nannipieri *et al*., 1990; Sinsabaugh and Moorhead, 1994; Hofrichter, 2002; Allison, 2006; Baldrain, 2009; Burns *et al*., 2013; Kotroczó *et al*., 2014). Bacteria and fungi play an important role in defense and cellular processes as well as acquisition of carbon (C) and nitrogen (N) (Sinsabaugh, 2010). Once in the soil environment, these enzymes mediate the biogeochemical processes of lignin degradation, carbon mineralization and sequestration, and dissolved organic C export. Stability of ecosystem functioning under variable environment is due to the presence of tolerant species which is the result of high diversity in the community (Yachi and Loreau, 1999).

The distruction of linkages between above-ground vegetations and below-ground biota by anthropogenic activities results in modifications of soil microbial communities, threatening of microbial diversity and result in losses of functions when specific structural patterns or regulation mechanisms was lost (Lavelle, 1997; da Jesus *et al*., 2009; Alguacil *et al*., 2014; Köhl *et al*., 2014).

The predominant farming practice *i.e*. *jhumming* (a common farming practice in the Northeastern Hill States of India) in the slope has been practice by the local people since time immemorial. This *jhum* farming is known for destruction of the above-ground biomass through slash and burn activities followed by cropping in forest lands result in a mass loss of above ground communities, which may lead to alteration of soil microbial communities structure and diversity who are the drivers of major ecosystem processes such as nutrient cycling (van der Heijden *et al*., 2008: Batten *et al*.,2006), bioremediation (Gilbert *et al*., 2012), plant health (Lugtenberg and Kamilova, 2009) and organic matter decomposition and formation (Veres *et al.,* 2013; Baldrian, 2009; Haifang *et al*., 2013 and Burns *et al*., 2013). Above all it leads to alteration of functional microbial groups and soil processes. Thus, the disruption of the linkages between above- and below ground biota communities may have altered the natural functioning mechanisms of soil microbial communities leading to detrimental impact on soil processes and overall ecological imbalances in soils of *jhum* agroecosystems. To date, scientific evidence is lacking on how slash and burn practices impact the functional microbial community compositions? Again, the knowledge on how the

combine interactive effects of functional microbial community and plant species can regulate/modify soil processes and functioning is grossly limited.

Keeping the above points in background the following objectives are set up in this research.

1. To examine the response of microbial functional groups in burnt and unburnt soils.
2. To determine the effect of microbial functional groups on soil processes.
3. To assess the relationship of microbial functional groups and soil processes as influence by crop plant (rice).

# Chapter-2
# Review of Literature

## 2.1 Brief overview of slash-and-burn cultivation

Slash-and-burn agriculture is a very prehistoric form of agriculture (Li *et al*., 2014) and is based on the ecological processes of forest ecosystems (Boserup, 1965; Altieri, 1999; Pedroso-Junior *et al*., 2008). Assume to originated during the Neolithic period around 7000 B.C. (Subhramanyam and Sambamurty, 2000). Mostly practices in the mountainous and hill parts of Latin America, Central Africa and Southeast Asia (SEA) (Van Vliet *et al*., 2012). This system of cultivation is also known as Swidden in South East Asia*, Milpa* in Latin America, *Tavya* in Africa, *Poddu* in Oddisha, India and *Jhum* inNorth Eastern (NE) state of India (Thakuria and Sharma, 2014). Globally known as shifting cultivation (SC). This shifting cultivation has been practiced by around 40-50 countries in world (Mertz *et al*., 2009) where as Institute of Scientific Information (ISI) Web of Science database (8 October 2013), estimated 64 developing countries practice Shifting cultivation system (SCS). It is common agricultural practice in tropical hilly areas of Southeast Asia, the Pacific, Latin America, and millennia for Caribbean and Africa (Ramakrishnan 1992; Stromgaard 1986; Lawrence and Schlesinger 2001). About 300-500 million people in the world depend on shifting cultivation for their livelihood (Brady, 1996). Shifting cultivation occupied about 30% of all arable land but provide food to only 8% of the world population which results in a wide land to man ratio (Kumar, 2008). Generally the ethnic minority groups, tribal people, hill tribes, or other indigenous peoples in South East Asia practices the shifting cultivation (Erni, 2008).

Mertz *et al*. (2009) defined shifting cultivation in Southeast Asia as “a land use system that employs a natural or improved fallow phase, which is longer than the cultivation phase of annual crops, sufficiently long to be dominated by woody vegetation, and cleared by means of fire”. They further described the shifting cultivation scenario of Southeast Asia to be a cycle of short cropping period of 1–3 years succeeds a long fallow period of about 5–20 years where clearing is done by slashing and burning and those parts of the fallow areas are often planted with useful tree crops either for subsistence or cash income. For sustaining the production of food crops fields are rotated rather than rotating the crops thus can say it is a natural resource management strategy (Garrity, 1993; Brookfield, 2001). Shifting cultivation is a multi step process which involves site selection and slash the biomass during a dry

season and sundried for about 2 months and burn it *in-situ* for nutrient management. This burning makes easy land preparation and suppress the weed growth till the onset of monsoon.To coincide with monsoon showers framers burn the dried slash biomass which is followed by mixed cropping (Ramakrishnan and Toky, 1981). In Southeast Asia and parts of humid West Africa upland rice is the most common crop. Maize and other cereal crops are more common in Latin America and sub-humid Africa, whereas bananas and tuber crops dominate in Central Africa, the Amazon and the Pacific region (Mertz *et al*., 2008). In shifting cultivation the main aim of the farmer is to sustain the family food requirement and not a commercial crop production.

In shifting cultivation the farmers cultivated the land for a year or two and shift to another area for new cultivation. They abandoned the land to naturally regenerate so as recover the vegetation and soil fertility. It is a low input system where nutrient input is obtained only from the debris of plant residues and ash after burning of dried slash prior to cropping in each *jhum* cycle (Styger, 2009). The productivity and sustainability of traditional slash-and-burn agriculture relies on the short term disruption, through clearing and burning and subsequent restoration of biological processes and component through fallowing (Palm *et al.,* 1996). The fallow phase in a slash-and-burn cultivation cycle is responsible for soil fertility restoration in which over a period of several years' nutrients are taken up from the subsoil, surface soil and the atmosphere and stored in tissues of growing vegetation. The burning of the forest or fallow biomass results in the release of nutrients that can be utilized by crop plant (Nye and Greenland, 1960; Sanchez, 1976). The successful regeneration of soil productivity via fallows depends on the extent of past soil degradation, the characteristics of the fallow species and succession vegetation community, and the length of the fallow period (Uhl, 1987; Kleinman *et al*., 1996). This translates into the rate and magnitude of nutrient accumulation in plant biomass and surface soil pools. Biomass production in a fallow is a direct index of ecosystem primary productivity and nutrient cycling.

Slash-and-burn agriculture has a rich traditional ecological knowledge base and remains an important component of forested landscape in many parts of north-east India states. Indigenous shifting cultivators have a vast store of local knowledge about their particular landscape and how best to use it for survival, and have much to teach the world about the efficient use of their landscape for combined agriculture, forestry and biodiversity conservation (Yadav *et al.,* 2013). However, in any consequences there is always a negative effect which holds true in shifting cultivation as well. Shifting cultivation is known for the major causes of land degradation, deforestation and the burning result in release of green house gases

(Nye and Greenland, 1960 and Comte *et al*., 2012). Due to it's ever increase in human population there is a pressure on land for settlement, infrastructure and for cultivation. Thus, the fallow period have decrease which result in over exploitation of the resources

The primary principles of sustainable shifting cultivation are that losses of plant-available nutrients should be coordinated by new supply over the complete rotational cycle, and that all other components of soil quality (e.g., texture and organic matter content that together determine water holding capacity) should be conserved The main concern of shifting cultivation was that nutrient removal within the harvested crop as well as nutrient losses due to run-off, leaching and fire volatilisation should not exceed plant-available nutrient inputs from nitrogen fixation plus *in situ* soil biogeochemical transformations from non-available forms. (Lawrence and Schlesinger, 2001).

In tropical agricultural systems, especially slash-and-burn situations farmers do not apply fertilizer to upland rice and other crops but have traditionally relied on fallowing their land to restore soil fertility and to reduce problems from insects and weeds (Nye and Greenland, 1960). Farmers from the Yunnan province of China use to plant economic trees (*Cassia siamea, Gmelina arborea, Cajanus cajan, Alnus nepalensis, Pinus armandi,* and *Pinus yunnanensis*) during the cropping phase as a tradition and let them grow during the fallow phase of the shifting cultivation (Xu, 1991; Guo and Padoch, 1995).

The deeply rooted culture of shifting cultivation in northeast India has many intricate aspect to be understood scientifically from within. *Jhum* system remains to be a perfect institute as a in situ repository for local germplasm of paddy, cucumber, millet, bajra, maize, pumpkin, chillies, etc. having high resistence to pest and diseases. It has been a long-known practice of grown alder tree (*Alnus nepalensis*) in *jhum* lands of Nagaland to suffice the need for N (Rathore *et al*., 2010). The mix cropping pattern of this traditional agroecosystem happens to provide biochemicals within itself and maintaining a natural line of defense against invading insects and pest (Ramakrishnan, 1984).

Studies of tropical forests in Thailand and Myanmar indicated that biomass of secondary forest of 40 years after shifting cultivation was almost 95% of uncultivated forests, but species richness was far lower than that of uncultivated forests (Fukushima *et al*., 2007, 2008).

## 2.2 Impact of shifting cultivation on soil properties

The nature of shifting cultivation includes clearing of forest, sun dried the biomass for two to three months, burned the dried biomass, mixed cropping for 1-2 years. After the nutrient has depleted the *jhummias* left the land for forest regeneration which is term as a fallow phase. This fallow period is responsible for soil fertility restoration (Styger *et al.,* 2009). Shifting cultivation practice in a steep slopes (44–53%) of NEH region reported the loss of 702.9 kg of organic carbon (OC), 63.5 kg of phosphorus (P) and 5.9 kg of potassium (K) $ha^{-1}$ (Ram and Singh, 1993). Information on shifting cultivation in relation to chemical and physical soil properties with length of the fallow period, before and after burning during the first year were reported from NE India region (Ramakrishnan and Toky, 1981; Arunachalam, 2002; Saplalrinliana *et al*., 2016 and Luangmuana *et al.,* 2017).

Burning activities play a major role in nutrient lost and availability. This practices release and incorporates nutrients from burnt biomass, clears rapidly and efficiently, and reduces weeds and pests (Aguilar *et al*., 2009). The ash from the burn biomass incorporates with the soil and fertilized the soil and makes certain action nutrients Mg, Ca, available P available for plants (Sanchez *et al*., 1982; Uhl 1987; Maass 1995 and Scheuner *et al*., 2004). It is generally expected that soil pH will increase after a fire (Gil *et al*., 2010) and its increment was reported by (Tawnenga *et al*., 1996 and Arunachalam, 2002) which is due to OH-losses, oxide formation, and alkaline cations released by ashes which can enter the exchange complex and expulse protons to the soil solution (Dikici and Yilmaz, 2006).

Fernandez *et al*. (1997) reported that organic matter was almost completely removed after heating soils up to 400 °C. Post burning soil result in increase in soil organic carbon (SOC) content compare to a forest soil however it decrease during cropping season. Contribution of soil microbial biomass carbon (SMBC) to SOC increased as the duration of cultivation increased (Arunachalam, 2002).

A study conducted in Northeast Indian *jhumming* condition has shows a significant reduction in the carbon content just after burning, with most prominent in 10 and 30 year *jhum* fallow compared to 5 years old fallow. The trend for reduction in carbon continued upto a period of 90 days in l0 and 30 year *jhum* cycle sites and for a period of 30 days only in the site of 5 year cycle. After this period, carbon content in the surface soil showed an increasing trend (Ramakrishnan and Toky, 1981). The

decrement in carbon content had been attributed to the effect of dissimilar intensities of fire from unequal amount of slashed biomass of different *jhum* fallows.

Nitrogen lost by volatilization and inadequacy transfer of mineral N from the aboveground biomass to the soil after burning results in shortfall of available nitrogen for plants which is one of the limiting factor for crop production in shifting cultivation (Mertz *et al*., 2008; Pandey *et al*., 2011; Knoepp and Swank, 1993 and Tanaka *et al*., 2001) reported that mineralization after burning enhancedN supply in the *jhum* field.

Increases in the amount of available phosphorus after burning vegetation are well documented (Ramakrishnan and Toky, 1981; Andriesse, 1987; Roder *et al*., 1995; Giardina *et al*., 2000; Lawrence and Schlesinger, 2001 and Bruun *et al*., 2006).Increase in base cations was also reported by (Nye and Greenland, 1960; Brinkmann and Nascimento, 1973; Stromgaard, 1986; Juo and Manu, 1996; Frizano *et al*., 2003 and Oliveria, 2008).

Shifting cultivation practice on sloping land result in soil run-off following disappearance of the protective vegetative cover, land degradation and deterioration of surface water quality (Maass *et al*., 2002; Yadav *et al*., 2013) and disruption of soil aggregates (García-Oliva *et al*., 1999b). Severe water limitation in dry tropical ecosystems exacerbates soil degradation after forest conversion to pastures. It exposes soils to desiccation, high temperatures, and rain erosion, besides consuming soil litter, organic matter, and microbiota (García-Oliva *et al*., 1999a) that are essential for nutrient cycling (Kauffman *et al*., 1993). Percent water holding capacity increase with burning but decrease after harvesting the crops. Responded increase of bulk density to burning attributed it to the disruption of soil aggregation and loss of organic matter (Ketterings *et al*., 2000). Due to its static in nature soil texture was not effected by slash and burn activities where as slight changes in particle size distribution in the post fire soil and decrease in total number of pore volume (Are *et al*., 2009). The disruption of soil aggregates and of the processes maintaining long-term soil nutrient and water availabilities contributes to soil deterioration (García-Oliva *et al*., 1999b).

The higher amount of soil microbial biomass carbon (SMBC) soil microbial biomass nitrogen (SMBN) and soil microbial biomass phosphorus (SMBP) relatively decline in slash and burn area comparatively with forest area (Arunachalam, 2002; Maass *et al*., 2002 and Fernandez *et al*., 1997) which could be due to the abundance of diverse vegetation and vegetation cover which contributes high amount of substrate for the activities of micro organisms in the forest area. Increase in SMBC

increased as the duration of cultivation and vice versa for soil SMBN and SMBP (Arunachalam, 2002). Soil temperatures after burning; stimulate biological activity (Ojima *et al*., 1994 and Brye, 2006). Colonies of bacteria and fungi were more in number in the forest field and their population decreased after burning and then increased gradually as the duration of cultivation increased (Arunachalam, 2002). Under shifting cultivation in Papumpare district of Arunachal Pradesh, Northeast India, the bacterial (*B. clausii, B. licheniformis, B. megaterium, B. subtilis, B. thuringiensis, P. aeruginosa* and *P. stutzeri*) and actinomycetes counts were significantly higher in fired plots which signify a higher rate of recovery as compared to the fallow plots (Pandey *et al*., 2011). Study conducted on forest fire in central Colorado, revel that there was no significant difference in total microbial biomass between the unburnt and burnt soils. However, the microbial communities in the burnt sites were structurally different from the unburnt sites (Hamman *et al*., 2007). Several studies conducted some years after forest conversion to pastures have documented a decrease in soil microbial activity and nutrient losses associated with the loss of plant cover, severe erosion, and reduction in soil organic matter and microbial biomass (Maass *et al.* 2002).

## 2.3. Impact of shifting cultivation on soil microbial community

The microbial structure gets affected with a change inecosystem functions such as interaction between plants, soil and microorganisms which will influence the ecological processes (Singh *et al*., 2004)**.** Soil attributes, plant species, land management were important for maintaining the structure and functions of bacterial communities (Nusslein and Tiedje, 1999; Wieland *et al*., 2001; Steenwerth *et al*., 2002; Hartman *et al*., 2008; Lauber *et al*., 2008;Wakelin *et al.,* 2008: da Jesus *et al*.,2009 and Blasiak *et al*., 2014). With respect to soil texture there was a community structure shift among bacteria and fungi (Girvan *et al*., 2003), soil pH (Lauber *et al*., 2008) and availability of soil nitrogen (Frey *et al*., 2004). Faulty agricultural pratices and land use result in major loss of biodiversity with negative result consequences for the environment (Doran and Zeiss; 2000; Balvanera *et al*., 2006 and Navarrete *et al*., 2010). Structural shift and composition of the microbial community become strong indicators of soil quality and soil biological activity. The microbial community in soil can be effect by fire, land use and change plant species which are the main component in shifting cultivation and this component are discuss below:

### 2.3.1 Effect of Microbial Community By Land Used

Size, activity and composition of soil microbial communities gets affected by changes in the aboveground vegetation (Carson *et al*., 2010; Lemos *et al*.,

2011). Microbial communities likely to respond changes made in land use system. However, such responses are poorly characterized. Any changes in land-use can possibly cause a disturbance, which in turn might affect the soil microbial communities (Allison and Martin, 2008). Nevertheless, agricultural practices do not always deplete soil bacterial diversity. Different land uses may have a positive, negative or neutral impact to shifts in microbial diversity and structure. Although changes in soil properties due to continuous cultivation appear to be a slow process, To bridge the gap of a poorly understood on the impact of land-use changes on soil conditions and microbial communities responds studies was carried out by Lauber *et al. (*2008*)* in Calhoun experimental forest in South Carolina, USA and da Jesus *et al.* (2009) Amazonas State of Brazil at Benjamin Constant municipality. In Calhoun experimental forest in South Carolina, four different land use type (cultivated fields, pasture land, pine forest plantation, and mixed hardwood forest) was studied and the result show that Proteobacteriawas the most dominant bacteria phyla in cultivated land, Actinobacteria in pasture and Acidobacteria in Hardwood and pine forest respectively. At Benjamin Constant municipality, Amazonas State, Brazil Six (6) different land use type (crop, pasture, agroforestry, young secondaryforest (up to 5-years old), old secondary forest (5- to 30-years old) and primary forest) was studied and reveals that alteration of bacterial community was observed when crop or pasture was grown in shifting cultivation. Bacteroidetes was found to be most dominated in crop and pasture soils where as the primary forest was dominated with betaproteobacteria, firmicutes and burkholderia. In secondary old forest firmicutes and actinobacteria was present with half of alphaproteobacteria sequences were from crops land (da Jesus *et al*., 2009). This indicated thatdifferent land management system / land use alter the soil properties which thus then result in changes of soil microbial community structure. The greatest fungal taxanomic unit was reported in forest sites and arable sites with lowest fungal taxanomic unit (Lauber *et al*., 2008 and Creamer *et al*., 2015). In forest the Nitrospira genus, was statistically greater in numbers than in grassland (Suleiman *et al*., 2013). The importance of C:N ratio for phylogenetic distance shifts in fungal abundance was also reported by ( Frey *et al*., 2004; Lauber *et al*., 2008).

With a higher abundance of the genus Bradyrhizobium, shifts in bacterial community composition were also reported in slash and burn system. Betaproteobacteria was reported as most abundant bacterial group in slash and burn system (Blasiak *et al.*, 2014).

When a land use was changed from paddy to vegetables in soil bacterial diversity and soil microbial biomass was decreases despite an increase in the

abundance of culturalable microorganism (Sun *et al*., 2011). Changes in soil physical and chemical properties induced with the conversion of land use result in the transformation of soil microbial communities(Yuan *et al*., 2015).

### 2.3.2 Effect of fire to microbial community

Most critical threats to forest ecosystems is fire (Xiang *et al*., 2014). Fires likely have large direct and indirect effects on soil bacterial community composition and diversity. Fire produces a broad spectrum of effects that depend on fuel load and combustion, vegetation type, climate, topography and so on. Heat from fires can kill soil bacteria, reducing microbial biomass (Wang *et al.*, 2012) and directly impacting bacterial community composition and diversity (Hart *et al*., 2005). It results in aboveground biomass depletion, altering the physical, chemical and biological components of soil ecosystems (Certini, 2005 and Neary *et al*., 1999). Community composition and diversity of above-ground community after fire have been extensively studied. Despite the central role of bacteria in ecosystem recovery and functioning effects of fire on soil bacterial communities remain largely unexamined (Xiang *et al*., 2014). There is scanty information about the long term effects of fire on bacterial communities in soils. The sensitivity of soil microbes to fire differed bacteria tend to be more resistant to heat than fungi, and generally increase in relative abundance after a fire (Hamman *et al*., 2007 and Xiang *et al*., 2014).

Fire does not only burn out the slashed biomass but also the litter layer, and the uppermost humus layer which constitute to be the major part of the resources and habitats for soil organisms (DeBano *et al*., 1998).

Xiang *et al*. (2014) in his study on boreal forest in China reported that fire significantly result in the shift of Bacteroidetes and Betaproteobacteria with greater abundance of Alphaproteobacteria and decreased in Acidobacteria, as well as Deltaproteobacteria and Planctomycete are in low abundance and reported that Actinobacteria was not effected by fire and found no significant difference in total microbial biomass between the unburnt and burnt soils.

Hamman *et al*. (2007) reported a structurally difference among the microbial communities in the burnt sites from the unburnt sites of forest fire in central Colorado and documented that AMF abundance was high in low severity burn sites relative to the unburned no significant change.

Deka and Mishra, (1983) and Pandey *et al*. (2011) in their studies also reported fungi as the least affected group by fire, actinomycetes population get stimulation by fire and bacteria as the most affected group. Study conducted in Khasi

hills of Megahalaya, India, reported greater microbial population from the burnt plots as compared to unburnt, following two to three showers (Sharma, 1980).

A study conducted in the coast of Jalisco, México has concluded that forest conversion by means of slash-and-burn followed by cultivation results in few immediate changes in the AMF communities, which could be due to low heat conductivity of the soil and rapid combustion of plant residues (Aguilar-Fernández *et al*., 2009).

### 2.3.3. Effect of microbial community by plant

Zhang *et al.* (2013) through cluster analysis of DGGE profile showed that soil bacterial community structures under different vegetation and their restoration patterns were different. This unique characteristic association of different plant species with microbial communities was probably due to differences in amount and quality of root exudates and plant species influences on the selection of rhizophere microbes (Zhang *et al*., 2013). Ecosysytem functioning (plant productivity, soil carbon sequestration, nitrogen mineralization) was strongly effect by the coexistence of multiple plant species with particular functional traits (nitrogen-fixing legumes, C4 grasses) (Balvanera *et al*., 2006; Tilman, 1984) and may enhance the complexity of soil microorganisms by increasing the heterogeneity of organic substrates during decomposing of litter and living roots (Broughton and Gross, 2000; Stephen *et al*., 1998). The dependent of ecosystem process on the presence of plant functional types was reported by (Roldan *et al*., 2005) primary productivity (Crutsinger *et al*., 2006), nutrient cycling litter decomposition rates and ecosystem stability and resistance to disturbance. (Madritch and Hunter, 2002 and Madritch *et al*., 2006). Change in plant community composition results in changes of litter quality that alters nutrient cycling process and resultant soil conditions (Miki *et al.,* 2010). Shifts in vegetation type fungi are more sensitive to it than soil bacteria, particularly mycorrhizal fungi that form symbiotic associations with specific plant types (Heinemeyer and Fitter, 2004) or Basidiomycota which are involved in decomposing lignified plant detritus (Bardgett and Mc Alister, 1999). Shifts in carbon pools may have different effects on these two groups of microorganisms as bacteria and fungi may not mineralize the same types of carbon substrates in soil, (Six *et al*., 1999; Lauber *et al*., 2008).

## 2.4. Impact of Shifting cultivation on Soil microbial community composition

The microbial communities in soil perform a vast range of ecosystem functions. Changes in the composition and function of below-ground communities and can affect composition or species diversity of above-ground communities and vice versa (van der Heijdan *et al*., 2008). Microbial community changes respond to changes in the aboveground vegetation in soil which affect the size, activity, diversity, abundance and composition of soil microbial communities (Nusslein and Tiedji, 1999; da Jesus *et al.,* 2009 and Zhao *et al.,* 2014). These changes had an impact on the ecological services provided by soils, such as soil quality, nutrient cycling and crop productivity of terrestrial agro-ecosystems. Due to their involvement in the geochemical cycles soil organisms have a strong role to play in the cycling of nutrients. There is a significant correlation of functional genes of soil microbial communities and environmental variables. Based on whole metagenomic survey 5 yrs fallow phase have 2 time higher prokaryotic diversity than that of 20 yrs fallow phase in Nagaland (Thakuria and Sharma 2014). This might be supported by diversified aboveground plant species in early succession stages, which is closely related to the findings of Anjaneyulu *et al.,* 2011).

## 2.5. Soil Enzymes Activities as an indicator of soil processes

Terrestrial ecosystems consist of above- and below-ground components that interact to influence community- and ecosystem-level processes and properties. These above and below ground communities released extracellular enzymes into the soil upon death and lysis or for physiological reasons such as hydrolysis of polymera in oligomers or monomers to be taken up by cells (Allison and Vitousek, 2005; Awasthi *et al*., 2014). In soil these enzymes are continually synthesised, accumulated, inactivated or decomposed. The activities of these enzymes in soils undergo complex biochemical processes consisting of integrated and ecologically-connected synthetic processes, and in the immobilisation and enzyme stability.As each soil type has different amounts of organic matter content, composition and activity of its microbial communities and intensity of the biological processes thus the enzyme levels in soil systems vary in amount (Xu *et al*., 2015). As soil is interacted by different plant species the functional capacity of the microbial communities also vary depending upon plant species (Waldrop *et al*., 2000). Mineral element limitation in the ecosystem leads to high enzyme activity signals in soil (Ndakidemi, 2006). Therefore, enzymatic activities can be used as a direct expression of available

nutrients and microbial community's metabolic requirements and comprehensive understanding of nutrient dynamics microbial populations and the key processes of soil *(*Sinsabaugh and Moorhead, 1994*).* Due to the effect of external disturbance on their activity and fast to environmental changes, enzymes can serve as sensitive indicators of microbial function during invasive processes and soil quality (Nannipieri *et al*., 1990; Dick, 1994; Allison *et al*., 2006 and Baldrain, 2009). Microbial communities act as a main driver of various soil processes such as nutrient cycling (van der Heijden *et al*., 2008), bioremediation (Gilbert *et al*., 2012) and plant health (Lugtenberg and Kamilova, 2009). These microbial processes are catalysed and supported by several enzymes and other chemicals bound in the biomass or secreted in the environment (Awasthi *et al*., 2014). Enzymes are the main constituent for biological soil processes. Knowledge of soil enzyme activity also indicates the potential of soil to support some of the basic processes necessary for maintaining soil fertility (Hernandez *et al.,* 1997).The various factors of soil processes which are mediated by microbes are describe below. Furthermore, plants may also play important roles in determining soil enzymes activities, as extracellular enzymes are derived mainly from soil microorganisms, plant roots and soil animals.

### 2.5.1 Arylsulphates (E C 3.1.6.1)

Plant uptake sulphur in the form of inorganic sulphate. However, certain portion of sulphur is bound into organic compounds and become unavailable for the plant uptake. Thus, accessibility to the plants depend on the extracellular hydrolysis of these aromatic sulphate esters or intra cellular oxidation of soluble organic matter absorbed by the micro-organisms to yield energy and carbon skeletons for biosynthesis by which some inorganic sulphate are released as a by-product to the external environment as a response to sulphur limitation (McGill and Colle, 1981 and Dodgson *et al*., 1982). These mineraliation and immobilization and dependent on arylsuphatases enzymes (Strickland and Fitzgerald, 1984 and Fitzgerald and Strickland, 1987). It is known to play a role in sulphur cycling. Its occurrence in different soil systems is often correlated with microbial biomass and rate of S immobilisation (Klose and Tabatabai, 1999; Vong *et al*., 2003). The environmental factor that effect the conversion of soluble sulphur to insoluble sulphur is reported by Burns, 1982, heavy metal pollution (Tyler, 1981); changes of soilpH in the soil solution (Acosta-Martinez and Tabatabai, 2000); organic matter content and its type (Tabatabai andBremner, 1970; Ladd, 1978; Sarathchandra and Perrott,1981; Dalal, 1982); the concentration of organic sulphateesters (Dodgson and Rose, 1976). The difference

caused by burning could be a reason for change in ASA activity and similar result was also reported by (Vong *et al*., 2003).

### 2.5.2 β-Glucosidase (E C 3.2.1.21)

The β-glucosidase is the most predominant glycosidase activity in soil one among the glycosidases which plays a vital role in the large-scale C cycle, as well as small scale processes of releasing a labile carbon energy source for microorganisms (Acosta *et al*., 2007). Various organisms i.e. plants, animals, fungi and bacteria produce this enzymes (Esen, 1993). Fungi have been suggested as the predominant source of β-D-glucosidase (Hayano and Katami, 1977; Hayano and Tubaki,1985) activity in soils. Zygomycetes are identified as sucrose and cellulose degraders (sugar fungi), while some Basidiomycetes are recognized as lignin degraders (Hanson *et al*., 2008; Xiong *et al*., 2014). Thisβ - glucosidasebreaks down labile cellulose and related carbohydrates with 1–4 glucosidic bonds, degrading plant cell walls and thus contributing to the first phases of plant cell tissues decomposition, which then facilitate the activities of other enzymes such as proteases and phosphatases. Its final product is glucose, an important C energy source of life to microbes in the soil. (Esen, 1993). Its sensitivity to soil management is reported by (Dick *et al.,* 1996; Bergstrom *et al*., 1998; Bandick and Dick, 1999; Bandick and Dick, 1999; Ndiaye *et al*., 2000), soil pH (Bergstrom *et al*., 1998; Bandick and Dick, 1999 and Acosta-Martinez and Tabatabai, 2000) and may give a reflection of past biological activity. A good indicator as an advanced change in organic carbon was reported by (Dick, 1994 and Wick *et al*., 1998). Thus it served as a good biochemical indicator for measuring ecological changes.

As the plant invasion accelerates nutrient uptake and nutrient cycling in soil higher soil enzymes phosphatase and β- glucosidase activities in association with faster water and nutrient cycles, lower concentrations of some nutrients in the soil and with higher levels of nutrients in stand biomasses and faster growth. Microbes adjust their extracellular release of soil enzymes to maximize the mobilization of substrates rich in their limiting element (Burns *et al*., 2013). Since β-glucosidase is involved in cellulose catabolism, more abundant and extended litter production in invaded stands may also explain the higher activity of this enzyme in this type of forest (Burns *et al*., 2013).

### 2.5.3 DEHYDROGENASE (E C 1.1.1.X)

The dehydrogenase exist in soils as integral parts of intact cells (Taylor *et al*., 2002) its gives correlative information on microbial populations in soil and soil

biological activity (Wolinska and Stepniewska 2012). At the time of the test it gives immediate metabolic activities of soil microorganism. It is an oxidative degradation process .i.e., dehydrogenation of organic matter by transferring hydrogen and electrons from substrate to acceptors (Makoi and Ndakidemi 2008). Many specific dehydrogenases act as to transfer the nicotinamide adenine dinucleotide or nicotinamide adenine dinucleotide phosphate. Through these co-enzymes the H atoms take part in the reductive processes of biosynthesis. These processes are part of respiration pathways of soil micro-organisms (enzymes of the respiratory metabolism, the citrate cycle and N metabolism) and are closely related to the type of soil and soil air-water conditions (Kandeler *et al*., 1996). Thus serves as an indicator of the microbiological redox systems and may be considered as a good measure of microbial oxidative activities in soil (Kumar *et al*., 2013). Several environmental factors, including oxidation reduction potential, soil pH, soil moisture, oxygen availability, organic matter content, temperature, depth of the soil profile, season of the year, soil fertilization, heavy metal contamination or pesticide use can affect significantly DHA in the soil environment (Baruah and Mishra 1984; Dkhar and Mishra 1983; Sinsabaugh *et al*., 2008; Wolinska and Stepniewska, 2012; Kumar *et al*., 2013 and Veres *et al*., 2013). Additionally, dehydrogenase enzyme is often used as a measure of any disruption caused by pesticides, trace elements or management practices to the soil as well as a direct measure of soil microbial activity (Skujins, 1978; Trevors, 1984; McCarthy *et al*., 1994 and Garcia and Hernandez, 1997). It can also indicate the type and significance of pollution in soils. For example, dehydrogenase enzyme is high in soils polluted with pulp and paper mill effluents but low in soils polluted with fly ash (Pitchel and Hayes, 1990). Similarly, higher activities of dehydrogenases have been reported at low doses of pesticides, and, lower activities of the enzyme at higher doses of pesticides (Baruah and Mishra, 1986). Dehydrogenase is an enzyme that exists only in viable microbial cells. It is often used as an indicator of microbial activity (Skujins, 1976; Nannipieri *et al*., 1990; Dick, 1994.). Dehydrogenase activity was originally used as a test for measuring respiration of soil micro-organisms in situ (Casida *et al*., 1964).

### 2.5.4 Acid Phosphatases (E C 3.1.3.2)

Phosphatase enzymes play an important role in phosphorus cycling (Speir and Ross, 1978; Zhang *et al*., 2013). It is capable of catalysing hydrolysis of esters and anhydrides of phosphoric acid (Schmidt and Lawoski 1961). An excellent indicator of the organic phosphorus mineralization potential and biological activity of soils (Dick and Tabatabai, 1993). Apart from being good indicators of soil fertility, phosphatase enzymes exercise key roles in the soil system (Dick and Tabatai, 1992;

Eivazi and Tabatabai, 1977). Environmental conditions affected this activity but also reflects and feeds back on community composition (Sinsabaugh *et al*., 2002). This enzyme is produced by many organisms in the soil. Bacteria and fungi that break down insoluble nutrient sources in the soil produce extracellular enzymes. These are proteins that are produced inside the cell and exported out into the soil solution. Its purpose is to remove the phosphate molecule from organic compounds such as phospholipids and nucleic acids. Once the phosphate is cleaved it becomes soluble and can be taken up by the cell. Land plants have evolved many morphological and enzymatic adaptations to tolerate low phosphate availability. Scientist in their studies reported that phosphatases activity was correlated with organic matter in various studies (Guan 1989; Jordan and Kremer, 1994; Aon and Colaneri, 2001), soil pH (Eivazi and Tabatabai, 1977; Tabatabai, 1994; Acosta- Martínez and Tabatabai, 2000; Makoi *et al*., 2008), soil and vegetation conditions (Herbien and Neal, 1990), responds to changes in management, and seasonal changes in soil temperature and moisture. Many organisms, including soil fungi, release phosphatases into their environment. These phosphatases are introduced into the soil by active exudation, leakage or cell lyses. P deficiency often enhances extracellular phosphatase activity from plant roots, fungi and other microorganisms (Li *et al*., 1997). There is no doubt that the presence of plants has an effect on enzyme activities, including phosphatase (Kiss *et al*., 1975 and Juma and Tabatabai 1977). The effect of plants can be direct when the roots secrete acid phosphatase and indirect when related to changes in soil organic matter content and microbial populations (rhizosphere effect). Enzyme activity was higher in rhizosphere soils than in before planting and non – rhizosphere soils. Increase phosphatase activity with an increase in P deficiency caused by increased root density and decreased soluble inorganic P levels was reported by Sarapatka 2002**.** The positive correlation between phosphatases and C and N is in good agreement with the results of (Šarapatka and Kršková 1997) the correlation between acid phosphatase and pH is similar to the observations of (Herbien and Neal, 1990). Fire decreases the acid phosphatase activity and serve as an indicator of overall microbial activity, (Eivasi and Bayan, 1996; Boerner *et al*., 2000).

Some enzyme functions are associated with the microbes themselves, such as dehydrogenase activity of which the main localization is the plasma membrane of bacteria or in mitochondrial membranes of fungi. Other enzymes are synthesized and secreted extracellularly by bacteria or fungi (e.g. phosphatases, urease, cellulases, pectinases). Microbially-secreted enzymes may take part of the soil matrix as extracellular enzymes, also called abiontic (Dick, 1994; Sinsabaugh, 1994).

Activities of b-glucosidase and phosphatase have been shown to increase in a tall-grass prairie following fire (Ajwa, 1999), and to decrease or be unchanged in oak-hickory forests (Boerner *et al*., 2000; Boerner and Brinkman, 2003; Eivazi and Bayan, 1996). Greater soil phosphatase activity has been reported in forests that were burned and thinned compared to unburned or burned only treatments, although these differences were only apparent a growing season later (Boerner *et al*., 2005). In contrast, when the activities of various soil enzymes were examined in eight North American forest ecosystems being restored by the use of prescribed fire and mechanical thinning, fire lowered phenol oxidase activity but did not affect phosphatase or chitinase activity (Boerner *et al*., 2008). However, when the effects on forests in the eastern United States were pooled together, phosphatase activity was lower in areas that were both burned and thinned (Boerner *et al*., 2008). Changes in soil enzyme activity in the years following a fire have also been shown in grasslands, with wildfires decreasing overall activity by 10-20% in the first year, 25-50% the following year, and enzyme activities returning to pre-fire levels after three years (Gutknecht *et al*., 2010). Overall, the effects of fire on soil microbial enzyme activity are variable and may depend on both ecosystem type and past site history, as well as time since fire event (Fritze *et al*., 1994). Microbial enzyme activity has been linked to rates of decomposition (Sinsabaugh *et al*., 1991, 1994), suggesting that fire-induced changes in enzyme activity could affect organic matter decomposition rates. β-glucosidase may be regulated primarily by substrate availability, whereas phosphatase and NAGase are regulated by the soil microclimate and chemical factors (Sinsabaugh *et al*., 1992,). Therefore, any changes in β-glucosidase activity could indicate substrate lteration by fire, while changes in phosphatase may indicate physicochemical alteration.Long-term N fertilization significantly increased activities of β-glucosidase and acid phosphatase but decreased urease activity (Ajwa *et al*., 1999). By examining organically cultivated soils of different ages, Monokrousos *et al*. (2006) found that acid phosphatase activity increased from newest to oldest organic systems whereas the activities of amidohydrolase and alkaline phosphatase were highest in the middle-aged ones.

## 2.6. Soil Biochemical Activities In Jhum Agro Ecosystem

Burning plays an important role in *jhum* agro-ecosystem. During burning nutrients are released from parent material and biomass and become available for crop uptake, escape via volatilization, leaching or surface runoff, or remain bound in recalcitrant ash complexes (Ramakrishnan, 1992). Researchers have the view that within a shifting cultivation schedule, burning of the forest or fallow biomass results in

the release of nutrients that can be utilized by crops planted after the burning process is over (Sanchez, 1976). Incorporation of cations from nutrient-rich ash into the cation exchange pool result in short-term increment of soil fertility (Nye and Greenland, 1960). Several soil biochemical activities (Soil Organic Carbon, Dissolve Organic Carbon, Particulate Organic Matter, Microbial Biomass Carbon, Potentially Mineralizable Nitrogen) were taken into consideration and describe below

The past studies have widely describe the decrease in SOC content after burning (Nye and Greenland, 1960; Fernandez *et al*., 1997; Saplalrinliana *et al*., 2016; Lungmuana *et al*., 2017). Topsoil temperature (242°C±10°C) during burning alters the SOC content, burning of forest floor litters leads to limited incorporation of litter materials in burnt plots (Tinker *et al.,* 1996). Findings indicated that the content of SOC increased with the increase in the length of fallow phase and the differences in SOC contents among fallow phases were significant. The single most important indicator of soil productivity was soil organic matter (Haynes, 2005). As its role for maintaining soil fertility and soil structure, soil organic matter reflects the productivity of shifting agricultural systems.

Significant reduction ($P = < 0.05$) of carbon content just after burning in Northeast Indian *jhumming* condition and the phenomenon was more prominent in 10 and 30 year *jhum* fallow compared to 5 years old fallow. Upto a period of 90 days in reduction of carbon continued in l0 and 30 year *jhum* cycle sites and 30 days for 5 year cycle. Carbon content in the surface soil showed an increasing trend after this period (Ramakrishnan and Toky, 1981). A study conducted in Beforona, the central eastern Madagascar has shown that slash-and-burn of a 5-year-old fallow resulted in a decrease of the topsoil carbon concentration by approximately 20% which indicates that fire affected the organic matter in the first few centimetres of topsoil (Brand and Pfund, 1998).

Soil microbial biomass reflects to soil organic pool which is responsible fororganic matter decomposition affecting soil nutrient content and primary productivity in most biogeochemical processes in terrestrial ecosystems (Franzluebbers *et al*., 1999; Gregorich *et al*., 2000; Haney *et al*., 2001; Sharma *et al*., 2004). Microbes are the primary decomposers of plant material due to the diversity of the enzymes produced and their unique ability to produce enzymes to break down both simple molecules such as cellulose and more complex plant derived compounds such as lignin. While the microbial (bacterial and fungal) community are commonly associated with transformations of SOC in soils (Tardy *et al*., 2015) it has also been shown that the interaction between microbes and soil fauna (including mites, earthworms,

collembolans, enchytraeids and nematodes) aid this process and typically simulate decomposition thus affecting carbon cycling. Soil microbial biomass and fungi plays a key role for carbon sequestration in soil (Clemmensen *et al*., 2013). Inclusion of soil microbial biomass, respiration and fungal richness have been found to be key indicators of carbon cycling and potential storage of soil organic carbon. (Creamer *et al*., 2015).

Burning results in reduction of MBC and MBN (Prietro-Fernández *et al*., 1998; Ajwa *et al.,* 1999 and Liu *et al*., 2010). Past findings indicated that many of the soil decomposer community would get reduced or totally die because of the burning effect (DeBano *et al.,* 1998; Malmström, 2012). The remaining species that may have survived would also be suppressed because of the sudden change in the environment like change in pH, temperature and the low soil moisture content which are outcome of the burning activities. Reduction in microbial activity may also be attributed to the loss of SOC and N after burning operations (Choromanska and DeLuca, 2002).

Dissolved organic carbon (DOC) is the primary form of C that is transported from forest floor to mineral soils (Yano *et al*., 2000). Itis produced by soil enzyme-catalyzed depolymerization of organic matter and is comprised of low molecular weight chemicals that are often water soluble and thus moreaccessible to microbial assimilation as energy, carbon and nutrient sources. Microbial utilization of these soluble compounds leads to microbial immobilization as well as soil C and N mineralization. Heterotrophic microbes in soils play important roles in N dynamics, and that their metabolism is often restrained by the availability of C in the soil (Starr and William, 1993). Due to differences in chemical compositions of soil organic matter and plant litters dissolved organic matter, soil enzyme activity, and soil C decomposition relationship seem to be inconsistent across various ecosystems. (DeForest *et al*., 2004 and Waldrop and Zak, 2006). Increase in the concentration of dissolve organic carbon in forest soil was recorded after the application of synthetic N fertilizer where as the oxidative enzymes activities decline (Sinsabaugh *et al*., 2005).

Relationships among dissolved organic matter, soil enzyme activity, and soil C decomposition has been studied on forest and grassland ecosystems (Carreiro *et al*., 2000; Saiya-Cork *et al*., 2002; Waldrop *et al*., 2000; Sinsabaugh *et al*., 2005; Zeglin *et al*., 2007).

Particulate organic matter (POM) is mainly derived from plant material, and only to a limited extent derived from soil macro-fauna. A study conducted in slopy upland in Thailand shows a greatest proportion of in the tilled wetland rice soil followed

by the relatively undisturbed forest soils and with the lowest content in the recently afforested soils. The highest in wetland rice field cultivation could be due to actual breaking and turning of the soil matrix. Topsoil profiles of C and particulate organic matter were affected by land use but unaffected by slope position in landscape, indicating minor effects of erosion Aumtong *et al*., 2009.

The aboveground biomass and dissolved oganic carbon increase with increasing N input across various ecosystems (Liu and Greaver, 2010; Liu *et al*., 2014). Soil microbial biomass and respiration reduces under N enrichment condition (Treseder, 2008; Liu and Greaver, 2010; Liu *et al*., 2010). Low levels of N inputs stimulate soil microbial biomass C, N, and soil microbial respiration (Treseder and Holden, 2013; Liu *et al*., 2010).

Potentially Mineralizable Nitrogen (pMN) can be defined as the fraction of organic nitrogen converted to plant available (or mineral) forms under specific conditions of temperature, moisture, aeration, and time. Determination of pMN levels can provide an estimate of available N in the soil. pMN originates mainly from microbial biomass and plant and animal tissues—the main source of the organic nitrogen pool. It represents the fraction of nitrogen easily decomposable by soil microorganisms and is considered an indirect measure of nitrogen availability during the crop growing season (if measured during that period). While anaerobic N mineralization potential may be a good indicator of the potential for soil to deliver N, it does not necessarily reflect microbial biomass N levels. It was suggested that the ratio of N mineralized to total organic nitrogen N could serve as a sensitive indicator of differences in soil organic matter (SOM). As a readily available fraction of total N, pMN is an important potential source of N for crop growth and yield, especially in synthetic N-fertilizer-free agricultural operations (eg. organic farming). pMN can be a source of available N for microorganisms and indirectly enhances microbial growth and activities, including C and N cycling. In well drained soils, PMN is made available to plants and microorganisms, mostly in the form of nitrate, through aerobic mineralization. In poorly drained soils (such as rice fields), pMN is made available, in the form of ammonium, through anaerobic mineralization.

At temperatures above 300°C, soil organic N is lost during the thermal oxidation of organic matter in the form of oxidized N gases and $N_2$ (Raison, 1979). The content of $NO_3$-N has a declining trend after burning (Ramakrishnan and Toky, 1981). Loss of nitrogen at temperature as high as 100°C was reported by DeBano *et al*. (1979), which in the case of conventional *jhumming* usually exceed this threshold temperature.

## 2.7 Denaturing gradient gel electrophoresis (DGGE) fingerprinting

In principle, DGGE fingerprinting method is the separation of a mixture of about equal size 16S rDNA fragments based on sequence variation by electrophoresis in a polyacrylamide gel containing linearly increasing gradient of denaturants (Muyzer *et al*., 1993). Unlike most commonly used electrophoresis methods that separate nucleic acid fragments by size, DGGE separates DNA strands by their sequence composition (Hovig *et al*., 1991). Differential migration of equal size fragments occurs because more denaturant is needed to separate sequences with higher guanine (G) + cytosine (C) content due to differences in the number of H bonds between complementary nucleotides holding DNA strands together. There are three H bonds between guanine and cytosine, and only two between adenine and thymine. As DNA strands separate, their migration becomes retarded in the gel. To produce sharp bands, fragment migration is stabilized by adding a high GC sequence (GC clamp) to the end of one PCR primer, thereby preventing complete strand separation (Sheffield *et al*., 1989). If a mixture of PCR products with different sequences is amplified from a sample, then this type of gel will separate them during electrophoresis. The resulting genetic profiles or fingerprints represent the community structure, an approximation of the numbers of populations (represented by each band) and their relative abundance (represented by band intensity) within the amplified community. Because PCR is the first step in DGGE, the fingerprint profiles are representative of the proportion of PCR products, which may not directly correlate to the proportion of that population within the community (Chandler *et al*., 1997).

Although there are many advantages to using PCR-DGGE for microbial community analysis, method limitations must be recognized for interpretation of result. The greatest challenge in performing DGGE and attaining reproducible results is minimizing variation between gel gradients. It is very difficult to exactly reproduce gel gradients; this must be kept in mind when performing between-gel comparisons. Another limitation of DGGE is that the number of bands observes in a profile cannot be interpreted to be the exact numbers of populations in a community. In some cases investigators have found that a single laboratory isolate can produce multiple bands by DGGE (Satokari *et al.,* 2001), and conversely a single band may represent multiples populations (Yang and Crowley, 2000). Combining DGGE profiling with other techniques, such as sequencing of bands or hybridization with probes can reduce the ambiguity of band identification (Stephen *et al.,* 1998). Nevertheless, the method can estimate of richness that enables researches to determined subsequent analyses that

can be conducted and a means of choosing samples representing unique or representative communities.

## 2.8. Research gaps:

Literature review revealed that scientific evidence is lacking on how slash and burn practices impact the functional microbial community compositions. Scanty of research data on how interactive effects of functional microbial community and plant species can regulate/modify the soil processes and thereby soil functioning as well as to what extent such combined effects are altered due to slash and burn practices in *jhum* agroecosystem are not known. The knowledge on the relationship among microbial functional groups and plant species under the influence of slash and burn practices is grossly limited.

# Chapter-3

# Materials and Methods

## 3.1 Description of the sampling site

Mizoram is one among the North Eastern states where we can find that shifting cultivation is practices extensively. Due to the increase in population the area for agricultural land has decrease and thus lead to a pressure on land which results in reduces of *jhum* cycle into 3-5 years from 10-20 years in many areas. Keeping this in view five (5) years *jhum* cycles from Muallungthu village Aizawl district Mizoram was selected as a study area which lies between $23^0$36.279' N latitude and $92^0$42.909' E Longitude at altitude of 841-857 m. As shifting cultivation is part of the Mizo culture till date it is impossible for the people to completely change their type of cultivation.

## 3.2 Climate and soil

Aizawl district of Mizoram experiences warm humid tropical climate. Muallungthu falls on the southern part of Aizawl district which experiences hot-humid weather during the summer months with an average temperature of 25°C during May to August. Winter months usually remains cold with moderate summer months. Maximum and minimum temperature in Muallungthu ranges from 20.8°C to 31.6°C and 7.1°C to 20.2°C, respectively. Out of total annual rainfall (2115 mm), about 81 % occurs during May to August and relative humidity ranges between 60.7 to 80.9% during most of the periods.

Soils of Aizawl district falls under red soil group and the dominant soil order is Inceptisols followed by entisols and ultisols. Soils are mostly light to medium texture (sandy loam and clay loam) with depth ranging from deep to very deep.

## 3.3 Soil sampling and processing for microcosm experiment

From the identified 5 years *jhum* cycle before slashing the biomass soils sample at a depth of 0 to 15 cm of about 5 quintals were collected. Then, next day after burning the biomass before sowing of seeds soil samples at a depth of 0 to 15 cm of about 5 quintals were again collected. The soil samples which were collected before slashing the biomass will represent as unburnt soils as well the soil samples which were collected after burning will represent as burnt soils. The collected bulk soils both burnt and unburnt soils were carried to research farm at College of Post Graduate Studies, Central Agricultural University, Umiam, Meghalaya for microcosm

experiments. The collected soils from burnt and unburnt situations were allowed to passed through 2 mm sieve separately and removed all visible fine roots and other organic debris and keep it ready for the microcosm experiment.

## 3.4 Location of the Microcosm experiment

To study the Impact of slash-burning and plant species on soil microbial community and processes in *Jhum* agro-ecosystem microcosm experiment was carried out set under poly house at the Experimental Farm of the College of Post Graduate Studies, Umiam, Meghalaya. The study area is located at 91°54.643″ E, 25°40.929″ N latitude and 950 m above mean sea level. The maximum and minimum temperature in the study site ranges from 20.9°C to 28.3°C and 4.4°C to 19.1°C, respectively. Out of total annual rainfall (2190 mm), about 76% occurs during May to September. The relative humidity ranges between 50.91 to 83.87% during most of the periods.

## 3.5 Microcosm experiment

The sieved soil mentioned in 3.3 was used for microcosm experiment. A series of pots were arranged in 4 groups as depicted in figure 1.In two groups i.e burnt and unburnt soil *jhum* rice was grown where in the other 2 groups no crop was grown. The pot filled with 4.0 kg sieved soil and 2 kg sieved soil. The bulk density of the pot soil was adjusted based on weight by volume basis to mimic the bulk density in field situations. Only after the pot soil mimic bulk density of the field situation functional microbial groups were inoculated. Only after functional microbial inoculation rice seed was sown in the pot. The pot which was filled only by 4.0 kg sieved soil was used for growing rice crop and no crop was grown in the pot which was filled by only 2 kg sieved soil. Soil moisture in the pot was maintained at field capacity throughout the experimental period. Just before inoculating the functional microbial groups a soil sample of approximately 100gm was collected from each groups and store the soil sample at $4^0$C for further analysis.

### 3.5.1 Treatment details

Each group of pot experiment was treated with different bacterial functional groups and a synthetic fungal community. Factoral Complete Randomized Design was used as an experimental design in these studies. Three functional bacterial groups are: (1) $N_2$- fixers, (2) Phosphate Solubilising Bacteria (PSB), and (3) Cellulose Degrading Bacteria (CDB). All together six (6) treatment combinations was imposed viz. T1: 5 strains PSB + 5 strains synthetic fungal community, T2: 5 strains

$N_2$-fixers+ 5 strains synthetic fungal community, T3: 5 strains CDB + 5 strains synthetic fungal community, T4: 5 strains each of PSB + $N_2$-fixers + CDB +5 strains synthetic fungal community, T5: No bacteria + 5 strains synthetic fungal community and T6: No inoculation.

Upland rice variety khawlian buh was used as a test crop. In each pot rice seeds (3 seeds per pot) was sown where rice is to be grown and no seeds were sown where only 2 kg of soil were kept in the pot.

## 3.6 Background of the native functional microbial groups (bacteria)

A repository of 300 bacterial cultures was maintained in the Microbial Ecology Laboratory, College of Post Graduates Studies, CAU, Umiam, Meghalaya. These bacteria was isolated from the roots and rhizosphere of wild and cultivated rice species of North East India under a research programme funded by the department of Biotechnology, GOI, New Delhi. These isolates were preliminarily screened for their ability to produce ammonia in nitrogen free bromothymol (nfb) semi solid agar, solubilization zone in CMC amended minimal agar, tri calcium amended Pikovskaya's agar. Based on their behavior in three media isolates were tentaviley categorized into 3 groups: cellulose decomposing bacteria (C-group), nitrogen fixing bacteria (N-group) and phosphorus solubilising bacteria (P-group) and on the basis of their screening result 5 efficient isolates were considered and farther used for investigating their role on soil processes. The pure culture isolates hereafter referred as C1,C2,C3,C4,C5 for C group; N1,N2,N3,N4,N5 for N group and P1,P2,P3,P4,P5 for P group.

## 3.7 Isolation of Fungi

Rose Bengal agar medium (pH 4.5) supplemented with streptomycin sulphate was use to grow the fungal colonies (Subba Rao, 1999). Fresh soil sample (10 g) was added to a conical flask containing 100 ml of sterile distilled water. The suspension was vortex at maximum speed for 5 minute to get a uniform soil suspension. An aliquot (100 μl) was spread over the rose Bengal agar medium using a sterile L speader and the plate was incubated at 30 $^0$C constant temperature for 5-7 days. For each soil sample, 3 replicates plates were used. After incubation, distinct colonies (colonies were distinguished in terms of colony size, shape, colour, vigour and days to appear) were recorded for each soil sample. Then, a binary matrix based on presence or absence of fungal colonies was generated for all the soil samples for analysis of culturable fungal diversity.

## 3.8 Production of microbial consortium

Well decomposed compost collected from CPGS farm was used as a carrier material. The compost was air dried, grinded and sieved through 1mm sieve to obtain an uniform and homogenous powdered forms for easy handling and utilization. These carriers was then packed in an auto-clavable plastic bags, air-tighten with a rubber band and performed tyndallisation process of sterilization in order to avoid contamination from unwanted microbes. The bags are than labeled and stored in a clean chamber at room temperature until mixing with the microbial formulation.

Five efficient functional bacteria from each 3 groups were grown as a pure culture in 5 ml of nutrient broth (NB) and were incubated ($30^0$c±0.5 at 160 rpm) for 22 hrs till attainment of maximum viable cells. One milliliter of mother culture from each bacterial groups was transferred aseptically in a series of 150 ml NB and incubated in an environmental shaker cum incubator at $30^0$c±0.5 at 160 rpm for 22 hrs.

After incubation 150 ml broth of each functional microbial groups (150 ml X 5=750 ml in 1000g of compost for each group i.e. C, N and P) was mixed uniformly using aseptically sterilized gloves, trays and beakers. The carrier and inocuatant mix were checked properly in order to obtain uniformly mixed. The mixing should not be too dry or too wet. The microbial consortium (MC) was then packed in a sterilized plastic bags and labeled properly.

Five efficient synthetic fungal community was grown as a pure culture in 100 ml of Rose Bengal Agar Media and were incubated ($30^0$c±0.5) for 5 days till attainment of maximum viable cells. The full grown spores was grind by using autoclaved mortal and pestal. After grinding the synthetic fungal community aseptically it was mixed with 1000 gm sterile soil uniformly using sterilized glove, trays and beaker.

## 3.9 Application of microbial consortium

As per the microcosm experiment lay out in fig1 10 gm of different microbial consortium 5 strains $N_2$- fixers, 5 strains PSB, 5 strains CDB and 10 gm of 5 strains synthetic fungal community were used as soil inoculants before sowing of seeds. The consortium and the pot soils were mixed uniformly.

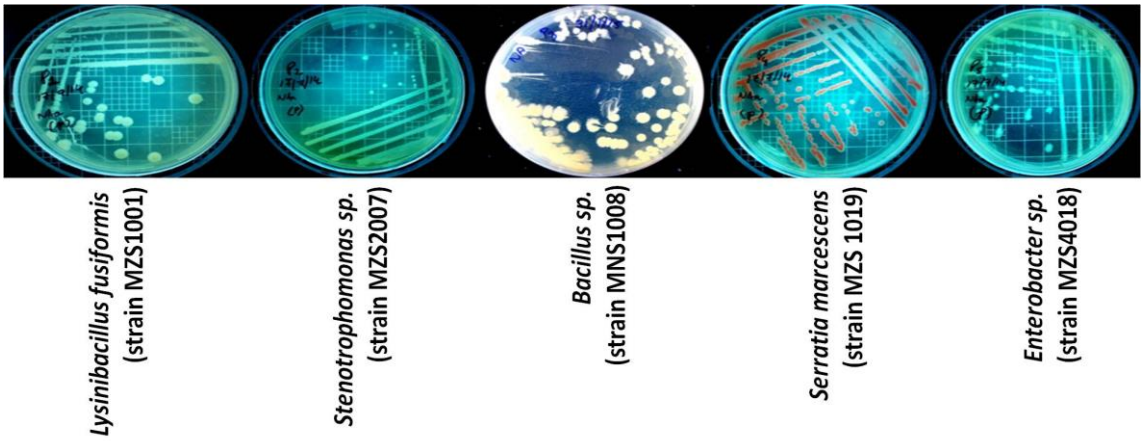


**Plate No. 3.1:Synthetic PSB community used as an inoculants**

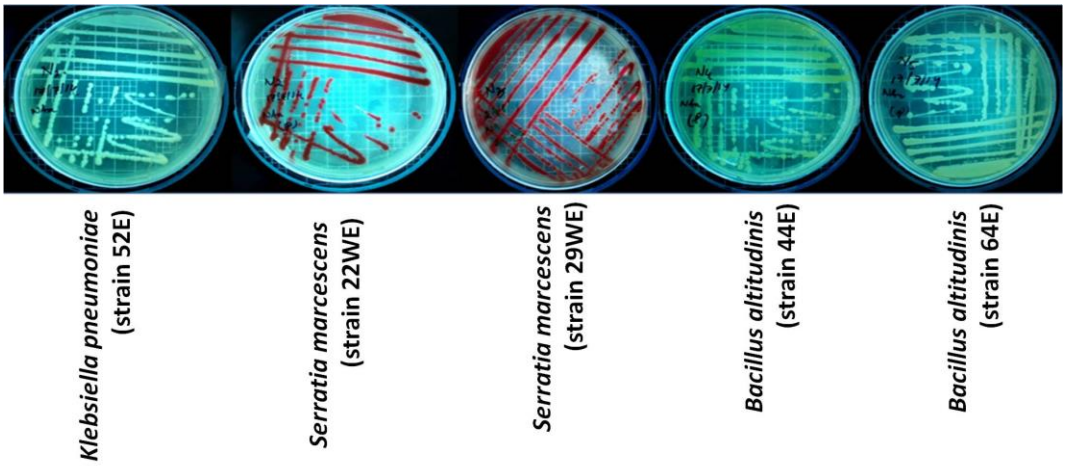


**Plate no. 3.2. Synthetic di-nitrogen fixer community used as aninoculants**

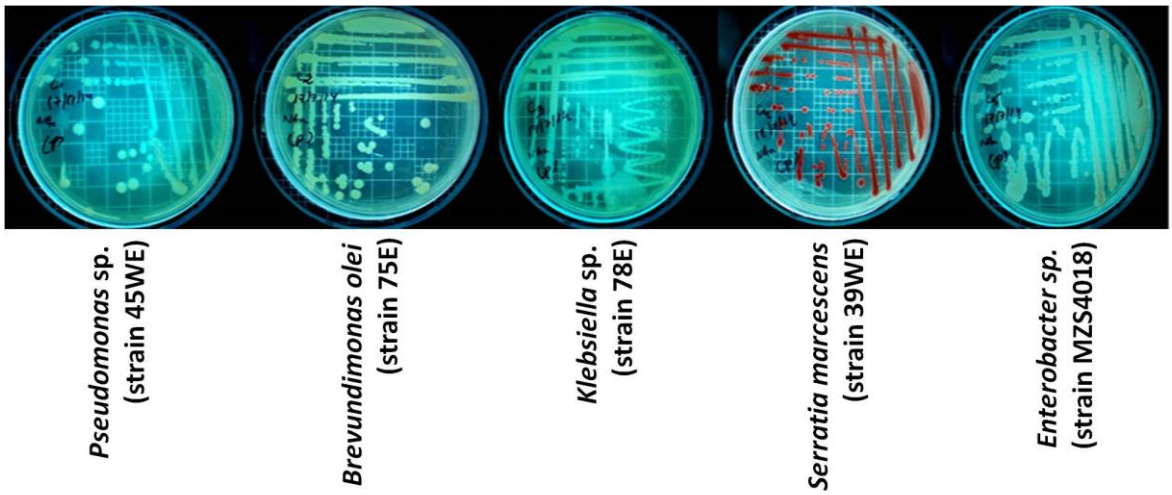


**Plate no 3.3. Cellulase Degarding bacterial community used as an inoculants**

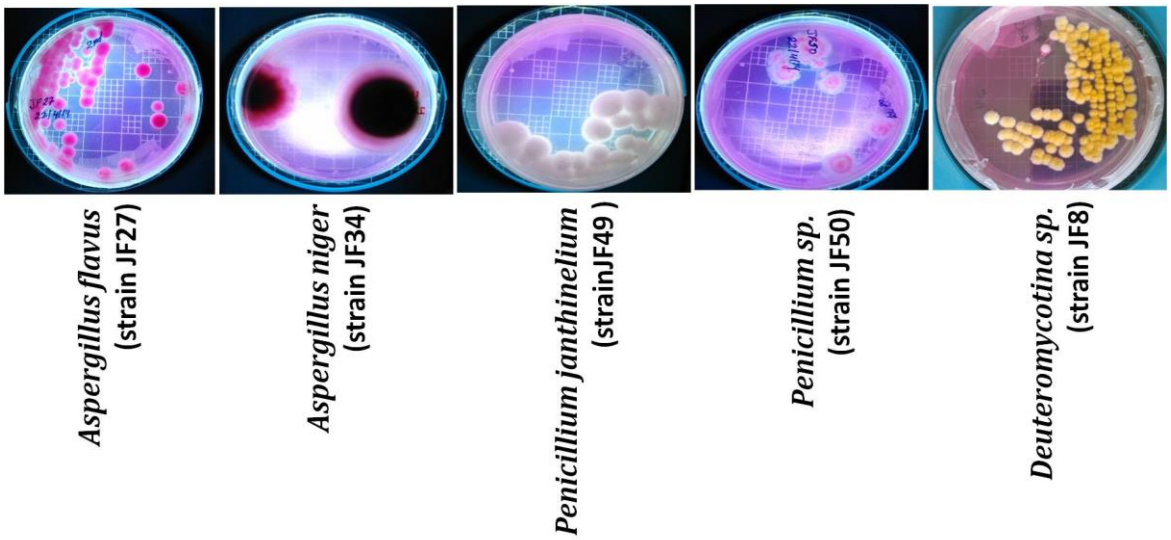


**Plate no. 3.4. Synthetic fungal community used as an inoculant**

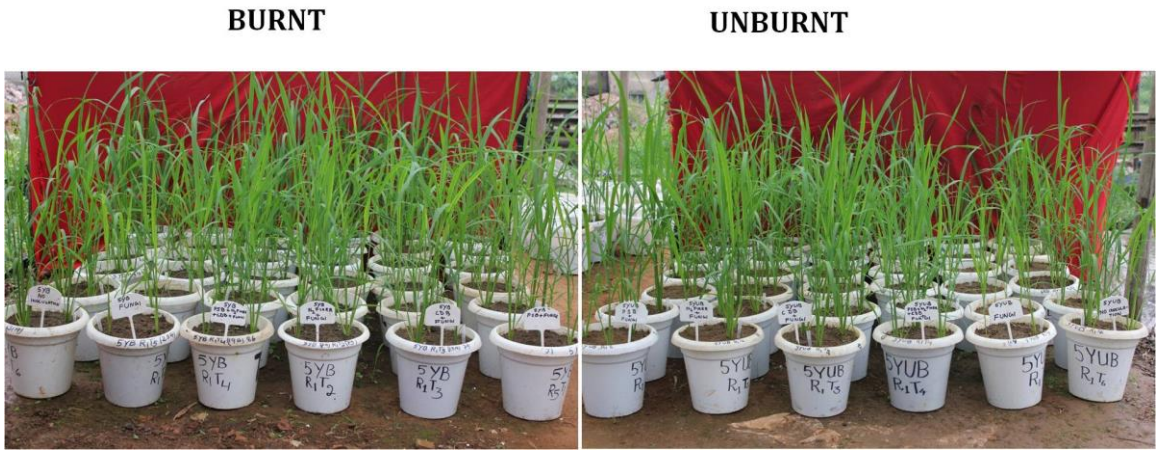


**Plate no. 3.5 Plant growth at 45 days**

## 3.10 Sampling

Soil cores (0 to 10 cm depth) were collected from each pot using a core sampler of 2.5 cm diameter at 0,10.45 90 and 120 days after sowing (DAS) of *jhum* rice and packed in sterile polythene bags. Each soils were stored at 4°C for analysis of their biological and biochemical properties.

## 3.11 Soil chemical and bio-chemical properties

### 3.11.1 Soil physico-chemical properties

#### 3.11.1.1. Bulk density (BD)

Bulk density of the soil was determined by Keen (Rackzowski) box method as described by Baruah and Barthakur (1997).

#### 3.11.1.2. pH

Soil samples were analyzed for pH (1:2.5 soil/water suspension) using a standard pH meter (Mettler Toledo, Switzerland).

#### 3.11.1.3. Electrical conductivity (EC)

Soil samples were analyzed for electrical conductivity (1:5 soil/water suspension) using a standard conductivity meter (Mettler Toledo, Switzerland).

#### 3.11.1.4. Soil Available Nitrogen (Avl N)

Fresh soil (0.5 g) sieved through 1 mm sieve was used for determination of available nitrogen by alkaline permanganate oxidation method as described by Subbiah and Asija (1956). Soil sample was taken in a distillation tube and to this 40 mL of 0.32% $KMnO_4$ and 40 mL of 2.5% NaOH were added and distilled for 6 min in an automated distillation chamber (Classic DX, Pelican Equipment, Chennai). Ammonia generated during distillation was collected in 2% boric acid containing few drops of mixed indicator (Composition of mixed indicator: 0.1 g bromocresol green with 0.07 g of Methyl red and dissolved this mixture in 100 mL ethanol) in a conical flask and finally amount of boric acid used for absorption of ammonia was determined by titrating with standard 0.02 N $H_2SO_4$. Available nitrogen was expressed in kg $ha^{-1}$.

### 3.11.1.5. Soil Available Phosphorus (Avl P)

Available phosphorus in soil was determined by following the stannous chloride blue colour method (Bray and Kurtz, 1945; Page *et al.,* 1982). Finely grinded air dried soil (0.5 g) was extracted with 50 mL of 0.03N $NH_4F$ in 0.025N HCl for 5 min in a reciprocating shaker. After shaking, the soil suspension was filtered through Whatmann No. 42. A 5 mL volume of filtrate was taken for developing blue colour by adding 5 mL of Dickman Bray's reagent and 1 mL stannous chloride. Finally, intensity of blue colour was measured at 660 nm using microtiter plate reader (Multiskan, Thermo Scientific, USA) and concentration of P was obtained from the standard curve. Available phosphorus was expressed as kg $ha^{-1}$.

### 3.11.1.6. Soil Available Potassium (Avl K)

Soil available potassium was determined by following the ammonium acetate method described by Hanway and Heidel, (1952). An aliquot (25 mL) of neutral normal ammonium acetate was added to 5 g finely grinded air dried soil sample and shook for 5 min in a shaker. After shaking, the soil suspension was filtered through Whatman No.1 and the concentration was measured using a flame photometer.

### 3.11.1.7. Soil Organic Carbon (SOC)

Finely grinded (< 0.1 mm) air dried soil was used to determine SOC by following the potassium dichromate wet oxidation method described by Walkley (1947). Soil sample (0.5 g) was mixed with 10 mL of 1N $K_2Cr_2O_7$ and 20 ml of conc. $H_2SO_4$ in a 500 mL conical flask and kept for 30 minutes. After oxidation, 200 mL distilled water and 5 mL $H_3PO_4$ was added to the flask. The residual $K_2Cr_2O_7$ was titrated with freshly prepared 0.5 N ferrous ammonium sulphate in presence of diphenylamine indicator. SOC content in soil was expressed in g $100g^{-1}$ soil (%).

#### 3.11.1.8. Microbial Biomass Carbon (MBC)

Freshly collected soil samples were used for MBC determination by the procedure chloroform-fumigation-extraction method (Brookes and Joergensen, 2006). First the root debris and all the visible organic residues were removed from the sample. Each soil sample was divided into two sub samples (each sub sample weight was 25 g). Each sub sample was taken in 50 mL beaker. One sub-sample was fumigated for 24 h with chloroform vapour in a desiccator and the other sub-sample kept in a desiccator as check without fumigation for 24 h. After incubation for 24 h, the residual chloroform in the fumigated sample was removed by releasing the pressure maintaining valve. To each sub-sample 100 mL 0.5 M $K_2SO4$ (1:4 ratio) was added

and the samples were shaked for 30 min at 200 rpm in an orbital shaker (Rotek LES, Pelican Equipment, Chennai). Then, soil suspensions were filtered through a Whatman No. 42 filter paper and 10 mL of the supernatants were used for determination of C by wet oxidation method similar to that described for determination of SOC in the section 3.4.4. The difference in C content between fumigated and non-fumigated sub-samples was determined and then, MBC was calculated using a conversion factor, $K_{EC}$ = 0.38 (Vance *et al*., 1987; Wu *et al*., 1990; Dilly and Munch, 1998). MBC content was expressed in µg $g^{-1}$ (dw) soil.

#### 3.11.1.9. Potentially mineralizable nitrogen (pMN)

Static anaerobic incubation procedure was used to determine pMN in freshly collected soil samples. Each soil sample was divided in to 2 sub-samples. From one sub-sample, 16 g portion of soil was taken in test tube and 40 mL distilled water was added. Trapped air was removed by lightly tapping the tubes and then, the mouth is closed using screw caps. Soils were incubated at 40˚C for 7 days. The other sub sample is added with same amount of distilled water but is kept as such without incubation. The inorganic $NH_4$-N produced during 7 days incubation under anaerobic situation was extracted using 40 mL of 4M KCl solution by shaking the sample for 1 h and then filtered through Whatman No. 42 filter paper. 10 mL of the aliquot taken in digestion tube and 0.5 g of freshly ignited MgO is added into the tube. Mineralized N content was determined in the samples by following the regular Kjeldahl method The mineralisable N during 7 days incubation was calculated by the difference between incubated and non-incubated samples (Page *et al*., 1982; Franzluebbers *et al*., 2000; Tirol-Padre *et al*., 2007). pMN is expressed in µg $g^{-1}$ (dw) soil.

#### 3.11.1.10. Dissolve Organic Carbon (DOC)

Extraction of DOC in the field moist was done by using 1M KCl solution at a ratio of 5:1 (v/w). In 10 g of field moist soil 50 ml of 1M KCl solution was added and shake it for 30 minutes at 160 rpm. Soil suspension was filtered through 0.45 µm membrane filter (Zsolnay, 1996). 10 ml of the filtered solution was for determination of carbon by wet oxidation methods. DOC content is express in µg $g^{-1}$ (dw) soil.

#### 3.11.1.11. Particulate Organic Matter (POM)

Physically uncomplexed organic matter is composed of particles of organic matter that are not bound to soil mineral particles and can be isolated from soil by density or size fractionation. Uncomplexed organic matter isolated by sieve is usually referred to as ‘particulate organic matter’ (Cambardella and Elliott 1992) but has also referred as ‘sand size organic matter’ or ‘macro-organic matter (Gregorich

and Ellert 1995). It is isolated by dispersing the soil and collecting the sand fraction on a sieve. The soils are first pass through a 2mm sieve. The POM recovered on a 53µm sieve can be defined as ranging in size from 53 to 2000 µm in diameter and such represent a quantifiable component of thw whole soil organic matter.The field moist soil was allowed to pass through 2mm sieve and air dry it. 25 gm of air dried soil was placed in a bottle having a lid and mixed with 100 ml of sodium hexametaphosphate solution and shake it for 16 hrs. The suspension was poured to a 53µm sieve and rinse with a little amount of water. By this a sillt+clay sized fraction which includes minerals and fine organic matter was washed and the aggregates were gently crush with a rubber policeman. The POM (sand+large particles of organic matter) was retained in the sieve. The particles which retained in sieve was transferred to a moisture cane box and oven dried it at $60^0$c for overnight. By using a mortar and pestle the dried samples was grinded uniformly and was sieved it using a 250 µm

**3.11.1.12Arylsulphatase Activity (ASA)**

Arylsulphatase was measured following the principle described by Tabatabai and Bremner, (1970) which was based on determination of *p*-nitrophenol released after incubation of soil with *p*-nitrophenyl sulphate (PNS). Moist sieved (1 mm) soil was added with 0.25 mL toluene, 4 mL 0.5 M acetate buffer (pH 5.8) solution, 25 mM 1 mL *p*-nitrophenyl sulphate and incubated at 37°C for 1 h. After incubation, 1 mL of 0.5 M $CaCl_2$ and 4 mL 0.5 M NaOH were added to the soil suspension and filtered using Whatman No. 42 filter paper. Intensity of yellow colour was measured in the filtrate at 400 nm using microtiter plate reader (Multiskan, Thermo Scientific, USA). The concentration of *p*-nitrophenol in the filtrate was determined against a standard curve prepared by using *p*-nitrophenol standard solution. Arylsulphatase enzyme activity was expressed as µg (PNP) $g^{-1}$ (dw) soil $h^{-1}$.

**3.11.1.13. *β*-glucosidase Activity (GSA)**

*β*-glucosidase was determined following the assay outlined by Tabatabai (1982) and Eivazi and Tabatabai (1988). Moist sieved (1 mm) soil was added with 0.25 mL toluene, 4 mL MUB (Modified Universal Buffer, pH 6.0) solution, 1 mL *p*-nitrophenyl-*β*-D-glucoside (PNG) and incubated at 37°C for 1 h. After incubation, 1 mL of 0.5 M $CaCl_2$ and 4 mL 0.1M THAM buffer, pH 12.0 were added to the soil suspension and filtered using Whatman No. 2v folded paper. Intensity of yellow colour was measured in the filtrate at 400 nm using microtiter plate reader (Multiskan, Thermo Scientific, USA). The concentration of *p*-nitrophenol in the filtrate was

determined against a standard curve prepared by using *p*-nitrophenol standard solution. *β*-glucosidase enzyme activity was expressed as µg (PNP) $g^{-1}$ (dw) soil $h^{-1.}$

#### 3.11.1.14. Dehydrogenase Activity (DHA)

Dehydrogenase was determined in air dried soil samples as per the method described by Casida *et al*. (1964). Soil sample (10 g) was mixed with 0.1g $CaCO_3$ and then, the mixture was divided into three parts (each part weighed 3 g) and transferred to three screw cap test tubes. To each test tube 0.5 mL of 1% 2,3,5-triphenly-tetrazolium chloride (TTC) and 1.25 mL of distilled water were added and mixed thoroughly by gentle tapering and incubated it at 37°C for 24 h. After 24 h incubation, the soil suspension was filtered through glass funnel fitted with absorbent cotton. Methanol was added to extract the soil suspension until the cotton plug's colour became white and the final volume was made up to 50 mL. Intensity of reddish colour was measured by using microtiter plate reader at a wavelength of 485 nm (Multiskan, Thermo Scientific, USA). The concentration of triphenyl formazan (TPF) in the supernatant was determined against a standard graph prepared using known concentrations of TPF. DHA was expressed as µg (TPF) g-1 (dw) soil $h^{-1}$.

#### 3.11.1.15. Phosphomonoesterase Activity (PHA)

Fresh sieved (1 mm) soil samples were used for phosphomonoestarase determination following the protocol described by Tabatabai and Bremner (1969). Soil sample (1 g) was taken in an Erlenmeyer flask and to this 4 mL of MUB (Modified Universal Buffer, pH 6.5), 0.25 mL of toluene and 1 mL of *p*-NPP (*p*-nitrophenyl phosphate) were added and incubate at 37°C for 1 h. After incubation, 1 mL of 0.5 M $CaCl_2$ and 4 mL 0.5M NaOH were added to the soil suspension and filtered using funnel fitted with cotton plug. Intensity of yellow colour was measured in the filtrate at 400 nm using microtiter plate reader (Multiskan, Thermo Scientific, USA). The concentration of *p*-nitrophenol in the filtrate was determined against a standard curve prepared by using *p*-nitrophenol standard solution. phosphomonoestarase enzyme activity was expressed as µg (PNP) $g^{-1}$ (dw) soil $h^{-1.}$sieve openings. Then the carbon content was analysed by wet oxidation methods.

## 3.12 Soil Biological Analysis

### 3.12.1 Extraction of soil DNA

Soil DNA was extracted based on the principle of *in-situ* lysis DNA extraction method. An amount (0.25 g) of fresh soil was used for extraction of soil DNA using the Power Soil™ DNA isolation kit (MoBio Laboratories Inc., Carlsbad, USA)

according to the manufacturer's protocol, with the following modification to improve DNA yield. The Power Bead tube with soil sample was incubated at $60^0$C for 15 min in a Thermomixer compact (Eppendorf Make, Germany) at 60ºC for 15 min and at 300 rpm. After incubation, rest steps were followed as per manufacturer's instruction. DNA was eluted in 50 µl elution buffer and stored at $-20^0$C.

### 3.12.2 Agarose gel electrophoresis

Quality in terms of molecular size of extracted soil DNA was determined by electrophoresis of 5 µl of DNA aliquot in an agarose gel (0.8% w $v^{-1}$ containing Gel-Red fluorochrom stain with a working strength of 0.06X, Biotium, USA) using a mini gel electrophoresis assembly (HU10, Sci-plas, Hongkong). Gels were visualized and images captured using gel documentation system (BioRad, CA, USA). EcoRI/*Hind*III-cut bacteriophage lambda DNA molecular size marker (250 ng; Invitrogen, UK)was included on gels as standard and the amount of DNA in samples was determined by comparing the fluorescence of genomic DNA bands to that of ladder and was expressed as µg $g^{-1}$ dry wt of soil (Zhou *et al*., 1996).

### 3.12.3Spectrophotometry

The absorption spectrum of DNA extracts (230-280nm) was determined using a Nano-drop® 2000 spectrophotometer (Thermo Scientific, USA) according to the manufacturer' s instructions. DNA was quantified based on the absorption at 260 nm and expressed as µg $g^{-1}$ (dw) soil. A decrease in absorption ratio at 260/230 and 260/280 nm was used as indicator of humic acid, polysaccharide and protein impurities (Krsek and Wellington, 1999; Stach *et al*., 2001; Thakuria *et al.,* 2008).

## 3.13. Polymerase Chain Reaction (PCR)

### 3.13.1. PCR amplification of bacterial 16S rRNA genes from soil DNA

Extracted soil DNA was amplified in a Gradient Master Cycler 5331 (Eppendorf Make, Germany) with primer pair (27f and 1492r) specific to bacterial domain (Lane *et al*., 1991). This primer pair is specific to 16S rRNA genes of the bacterial domain and yields amplified product size of approximate 1465 bp. The amplification reactions were carried out in a 25µl volume containing 25 ng soil DNA as template, 100 nM of each oligonucleotide primers [27f (5'-AGAGTTTGATCCTGGCTCAG-3') and 1492r (5'-GGTTACCTTGTTACGA CTT-3')], 12.5 µl of Go-Taq DNA polymerase (Promega, USA) along with bovine serum albumin (BSA concentration 0.1 µg $µl^{-1}$; New England Biolabs, UK) and the required quantity of PCR grade water (HiMedia, India). The PCR reaction condition included an initial 3

min denaturation at 94ºC, and was followed by 30 thermal cycles of 1 min at 94ºC, 1min at 62ºC and 2 min at 72ºC. Amplification was completed with the final extension step at 72ºC for 7 min. All PCR products were examined by electrophoresed in an agarose gel (1% w $v^{-1}$) using a 100 bp DNA ladder (New England Biolabs, UK.

### 3.13.2. PCR amplification for α-proteobacteria

The extracted DNA was amplified in thermo scientific thermocycler using a primer pair of 203fα and 1494 r (203fα: 5'-CCGCATACGCCCT ACGGGGGAAAGATTTAT and 1494r: 5'-CTACGGTCTAGCCTTGTTACGAC). The PCR reaction consist of 1X buffer with1.5 mM $Mgcl_2$ 100µM dNTPs 100mM of each 203f and 1494r primers, 5.0 µl BSA (concentration 0.1 µg $µl^{-1}$), 1U of Taq-DNA polymerase and 1-2 µl DNA template. PCR reaction conditions consisted of an initial denaturation step (94ºC for 3min) followed by 30 cycles of 45 second of denaturation at 94ºC, 45 second at 62ºC for primer annealing, and 1 min at 72ºC for primer extension, followed by final step at 72ºC for 7 min and hold at 10ºC. Products were first analyzed by electrophoresis in an agarose gel (1% w $v^{-1}$) using a 100bp DNA ladder (New England Biolabs, UK). The amplified template was re-amplified using a primer pairs of 984fgc and 1378r (984fgc: 5'-CGCCCGGGGCGCGCCCCGGGCGGGGC GGGGGCACGGGGGGAACGCGAAGAACCTTAC and 1378r 5'-GCGGTGTGTACAA GGCCCGGGAACG). Amplification was carried out in the same manner as discussed in section 3.13.3.

Table: 3.1 Different Primers used for studying soil bacteria community

| Sl. no. | Specificity | Primer pair | Annealing temperature | Reference |
|---|---|---|---|---|
| 1. | α-proteobacteria | 203fα:(5'-CCGCATACGCCCTACGGGGGAAAGATTTAT)<br>1494r: (5'-CTACGGTCTAGCCTTGTTACGAC)<br><br>984fgc:5'-(CGCCCGGGGCGCGCCCCGGGCGGGGCGGGGGCACGGGGGGAACGCGAAGAACCTTAC)<br>1378r (5'-GCGGTGTGTACAAGGCCCGGGAACG) | 62ºC<br><br>62.2 ºC | Heuer and Smalla. 1999. |
| 2. | β-proteobacteria | F948βgc: (5'-CGCCCGGGGGGCGCCCCGGGCGGGGCGGGGGCACGGGGGCCGCACACGCGGTGGATGA)<br>1494r: (5'-CTACGGTCTAGCCTTGTTACGAC). | 63.1 ºC | Gomes *et al*. (2001). |
| 3. | Soil Bacterial DNA | 27f (5'-AGAGTTTGATCCTGGCTCAG-3')<br>1492r (5'-GGTTACCTTGTTACGACTT-3') | 62 ºC | Weisburg *et al*., 1991 and Heuer, 2007. |

### 3.13.3. PCR amplification for β-proteobacteria

The extracted DNA was amplified in Thermo scientific thermocycler using a primer pair of F948βgc and 1494 r (F948βgc: 5'-CGCCCGGGGGGCGCCCCGGGCGGGGCGGGGGCACGGGGGCCGCACACGCGG TGGATGA and 1494r: 5'-CTACGGTCTAGCCTTGTTACGAC). The PCR reaction consist of 1X buffer with1.5 mM $Mgcl_2$ 100µM dNTPs 100mM of each F948βgc and 1494r primers, 5.0 µl BSA (concentration 0.1 µg $µl^{-1}$), 1U of Taq-DNA polymerase and 1-2 µl DNA template. PCR reaction conditions consisted of an initial denaturation step (94ºC for 3min) followed by 30 cycles of 45 second of denaturation at 94ºC, 45 second at 63.1ºC for primer annealing, and 1 min at 72ºC for primer extension, followed by final step at 72ºC for 7 min and hold at 10ºC. The PCR reaction mixture and electrophoresis in an agarose gel analysed was similar as with the amplification of bacterial 16S rDNA products mention in 3.13.1.

### 3.13.4. Denaturing gradient gel electrophoresis (DGGE) fingerprinting of bacterial community composition

Denaturing gradient gel electrophoresis (DGGE) was performed using Ingeny PhorU2 system (Ingeny International BV, The Netherlands). The PCR products (amplified with DGGE primer: mention in table 3.1) were loaded on to 8% (w $v^{-1}$) polyacrylamide gel with a denaturing gradient of 40% and 60% (100% denaturant tends for 7M urea plus 40% formamide in 1 X TAE buffer). Approximate 500 ng of PCR product was loaded into each well and electrophoresis was carried out for 18h at constant 90V in presence of 1X TAE buffer (242 g Trizma, 57.1 ml glacial acetic acid and 100 ml 0.5M EDTA and volume made up to 1 l; pH adjusted to 8.0) at a constant temperature of $60^0$C. After electrophoresis the gel was stained with Gel-Red fluorescent nucleic acid dye (working concentration 0.6X; Biotium, USA) for 30 min. The stained gel was visualized and image was captured using gel documentation system (BioRad, CA, USA).

From the image of each DGGE fingerprint a reference DGGE profile was created that contained all maximum possible bands of DGGE profiles. Then, DGGE profiles were scored visually for presence or absence of bands comparing to the reference profile. Thus, a binary presence-absence matrix was developed for each DGGE fingerprint (Kropf *et al*., 2004). These binary matrices were exported to Excel worksheet 4.0 (Microsoft Office Excel, 2003) and arranged in a single sheet according to band numbers. This combined binary matrix was finally exported to PRIMER v6.1.9

software (Primer-E Ltd, Plymouth, UK) and dataset was standardised by total method (Magurran, 1988). This standardised dataset finally used for all multivariate analyses.

## 3.14. STATISTICAL ANALYSIS

### 3.14.1 Univariate statistics

All univariate statistical analyses were performed using SPSS v12.0 (Statistical Packages for Social Science Inc., Chicago, IL, USA). Each physico-chemical parameter i.e. sand content, silt content, clay content, moisture content, pH, total organic carbon, total nitrogen, cation exchange capacity analysed for different seasons or within a parameter i.e. DNA yield, DNA quality, Margalef's richness and Shannon's diversity irrespective of sites and seasons were normally distributed as determined using the Kolmogorov-Smirnov test and wherever, normality was not observed the data were subjected to mild transformation (square root transformation). Paired t-test was performed to determine for any significant differences between seasons within a site. For determination of any significant differences within a parameter irrespective of sites and seasons was performed by one way analysis of variance (ANOVA) [incorporating the Levene Statistic to test for the equality of group variances, and the Tukey's Honestly Significance Difference (HSD) test at $P<0.05$ for pairwise comparisons].

### 3.14.2 Multivariate statistics

All multivariate analyses results presented in this study were computed using PRIMER v6.1.9 software (Primer-E Ltd, Plymouth, UK).

### 3.14.3. Non-metric multidimensional scaling ordination (NMDS) of community data:

A Bray-Curtis resemblance matrix was generated using the square-root transformed standardised presence-absence binary matrix (Bray and Curtis, 1957; Clarke, 1993). The resemblance matrix was plotted in 2-dimensions by NMDS ordination (50 restarts, 0.001 minimum stress, Kruskall fit scheme 1 and Shephard step-wise function) (Kruskal and Wish, 1978). Dendrograms were constructed by hierarchical cluster analysis (group-average linking) using the Bray-Curtis resemblance matrix (Clarke, 1999). Clusters were superimposed on the NMDS plot to form ellipses at arbitrary resemblance levels of slices drawn through the dendrograms. One-way analysis of similarity (ANOSIM) was performed on Bray-Curtis resemblance matrix (incorporating 999 permutations for Global R statistics) to determine the significance of differences between microbial community structure with respect to rice filed sites.

### 3.14.4. Relationship study of community data and environmental parameters using principal component analysis

The environmental parameter data matrix (soils attributes as rows and the different sampling sites as columns) was normalized to eliminate the effects of different units and then square-root transformed while performing principal component analysis (PCA). The square root transformed normalized data matrix was ordinated in 2 dimensions based on the scores of the variables (environmental parameters) in the first two principal components and the euclidean distance was used as a measure of dissimilarity between sites.

To know how DGGE /or RISA bands relate to the status of a physicochemical parameter in different rice fields, the binary data matrix of DGGE /or RISA bands were superimposed on the PCA plot. Then individual environmental parameter was selected to display their plot values as bubbles (higher value corresponded to large bubble area) in the PCA plot and the DGGE / or RISA bands were highlighted as vector lines based on their correlation (Pearson correlation) with principal axes. By following bubble plot technique, relationships between DGGE /or RISA bands and individual soil physicochemical parameter were determined.

# Chapter-4

# Result

There were 3 objectives in this investigation and the objective-wise results are presented in this chapter.

## 4.1 Objective 1

### 4.1.1 Physico-chemical properties of soil

Physico-chemical properties (BD, pH, EC, SOC, Avl N, Avl P and Avl K) of soils under burnt and unburnt conditions is presented in Table 1. Values of BD, pH, EC, Avl P and Avl K in burnt soil were significantly higher relative to their values in unburnt soil under 5 year jhum cycle. On the other hand the contents of SOC and Avl N under burnt soil were significantly lower relative to their values in unburnt soil.

**Table 4.1.** Influence ofburning on physico-chemical attributes of *jhum* soils

| 5 year Jhum cycle | BD (Mg $m^{-3}$) | pH 1:2.5 (soil: water) | EC (µS $s^{-1}$) | SOC (%) | Avl N (kg $ha^{-1}$) | Avl P (kg $ha^{-1}$) | Avl K (kg $ha^{-1}$) |
|---|---|---|---|---|---|---|---|
| **Unburnt soil** | 1.52±0.07a | 4.70±0.12a | 24.8±2.7a | 1.44±0.04b | 273±23b | 6.18±1.6a | 220±10a |
| **Burnt soil** | 1.65±0.08a | 5.08±0.16b | 33.7±3.4b | 1.18±0.06a | 212±18a | 9.56±1.7b | 258±14b |

The response of soil bacterial community to application of culture of microbial species mixture (PSB community, $N_2$-fixer community, CDB community and fungal community) in presence or absence of rice crop under both burnt and unburnt soils of 5 year *jhum* cycle was studied in mesocosm experiment. The changes in soil bacterial community (using domain specific primer set 27 f and 1492 r) was studied at 10 days of rice seedling growth and the phylum level (alpha-proteobacteria and beta-proteobacteria) community composition at 45 and 90 days of rice plant growth. The PCR-DGGE fingerprint technique was used to decipher the bacterial community composition.

### 4.1.2 Effect of burning, cropping and microbial inoculation on soil bacterial community

#### 4.1.2.1. Soil bacterial community at 10 days of rice growth

The PCR-DGGE fingerprint of the bacterial community composition in burnt and unburnt soils in presence or absence of rice crops at 10 days of rice plant growth is presented in (Fig.4.1). The number and the relative intensity of bands are clearly visible in the PCR-DGGE fingerprint. The MDS plot developed on binary matrix of PCR-DGGE fingerprint showed distinct clustering between burnt and unburnt soils (Fig 4.2). The bacterial community of burnt soil or unburnt soil clustered separately according to the absence and presence of rice crop at 80% similarity level and the separation among clusters were positively differ from each other as confirmed by Hierarchical cluster analysis (incorporating SIMPROF test at 95% confidence limit) (Fig 4.3). Interestingly, the clusters representing bacterial communities of burnt soil distinctly separated out from the clusters of unburnt soil irrespective of rice crop present or absent (Fig. 4.2). Within burnt or unburnt soil conditions, the two distinct clusters were represented by the bacterial communities in presence or absence of rice crop. Though there were variations in bacterial community compositions among the treatments, these treatment induced variations couldn't mask the effect of burning and cropping. The stronger factor of variability in shaping the soil bacterial community composition was found to be in the order burning > cropping > microbial inoculation treatment (Fig.4.1, Fig.4.2 and Fig.4.3).

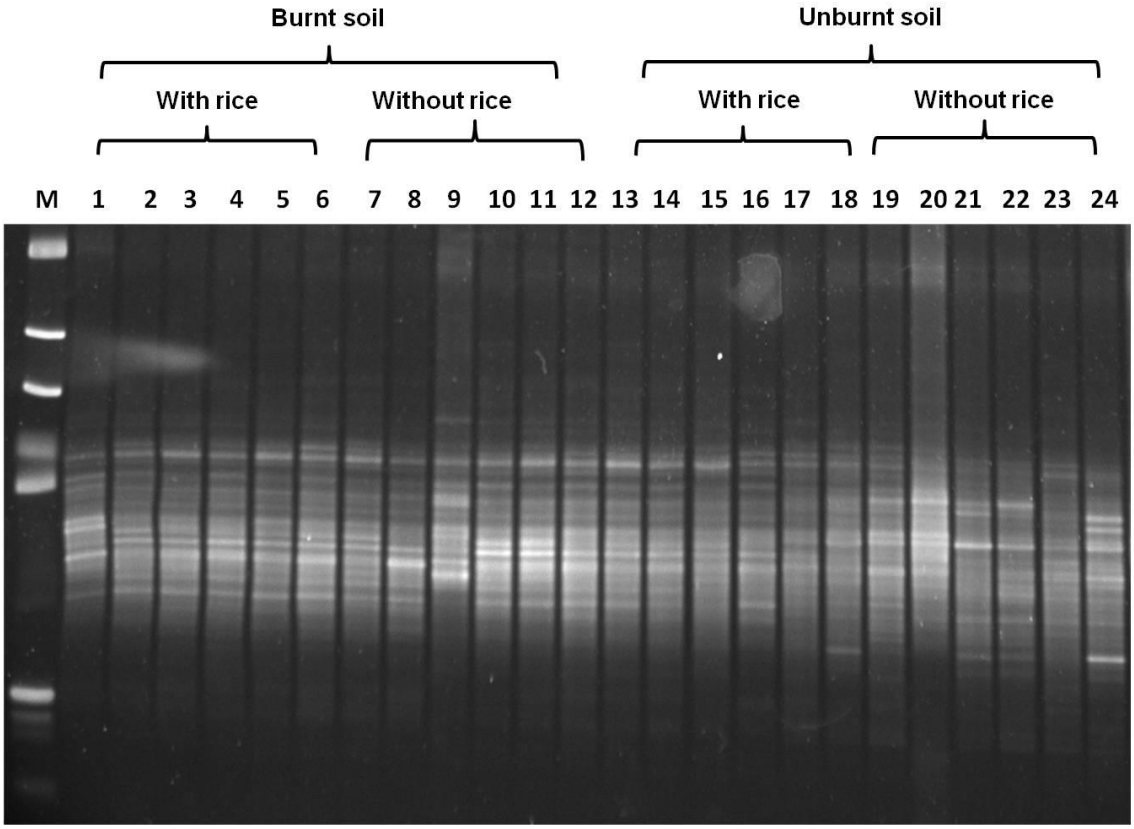


Fig.4.1: Soil bacterial community at 10 days growth of rice plant

The DGGE fingerprint depicting soil bacterial community at 10 days in *jhum* rice rhizosphere and bulk soils under burnt and unburnt situations of 5 years *jhum* cycle as influenced by application of microbial community composed of $N_2$-fixers (NF), phosphate solubilizing bacteria (PSB), cellulose degrading bacteria (CDB), NF+PSB+CDB, fungi, and control (no inoculants).

M – 100 bp marker, lane 1 -PSB+Fungi, lane 2 -$N_2$-fixers+Fungi, lane 3 -CDB+Fungi, lane 4 -NF+PSB+CDB +Fungi, lane 5 -Fungi, lane 6 -Control(no inoculation) lane 7 -PSB+Fungi, lane 8 -$N_2$-fixers+Fungi, lane 9 -CDB+Fungi, lane 10 -NF+PSB+CDB +Fungi, lane 11 -Fungi, lane 12 -Control (no inoculation) lane – 13 PSB+Fungi, lane 14 -$N_2$-fixers+Fungi, lane 15 -CDB+Fungi, lane 16 - NF+PSB+CDB +fungi, lane 17- Fungi, lane 18 -Control (no inoculation), lane 19 -PSB+Fungi, lane 20 -$N_2$-fixers+Fungi, lane 21 - CDB+Fungi, lane -22 NF+PSB+CDB +Fungi, lane 23 -Fungi, lane 24 - Control(no inoculation)

Lane 1-6 Burnt with rice, Lane 7-12 Burnt without rice, Lane 13-18 Unburnt with rice, Lane 19-24 Unburnt without rice

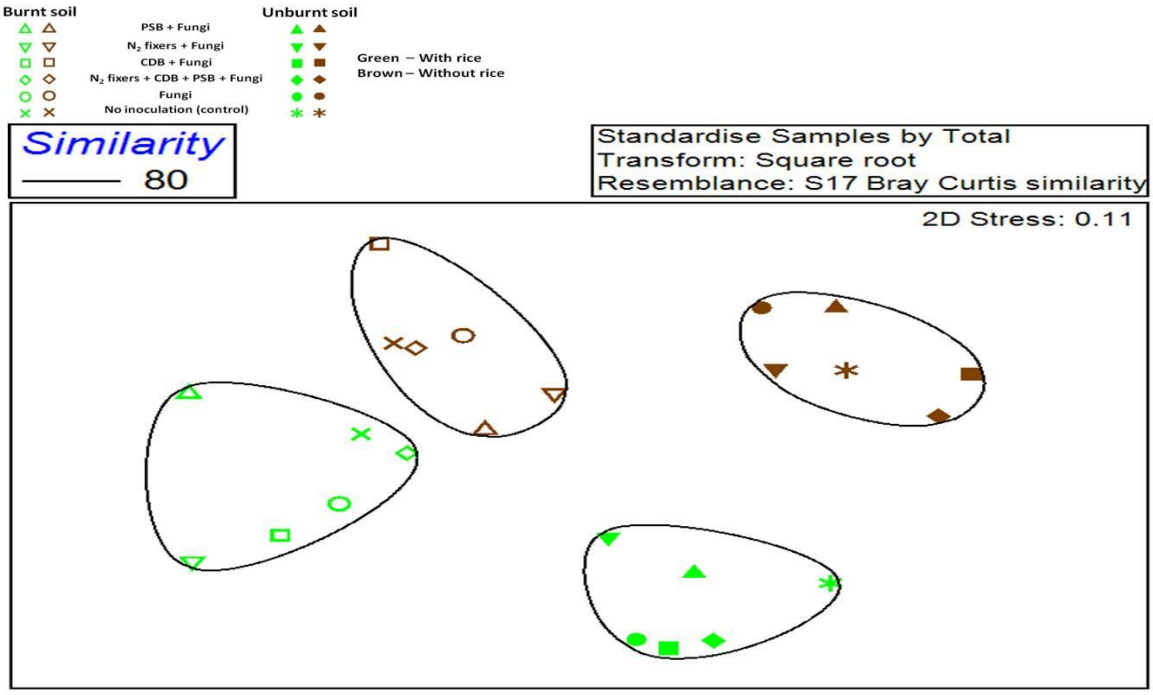


Fig.4.2: MDS Clustering of bacterial Community at 10 days of rice growth in response to burning, cropping and microbial inoculants in soils of 5 years *Jhum* Cycle.

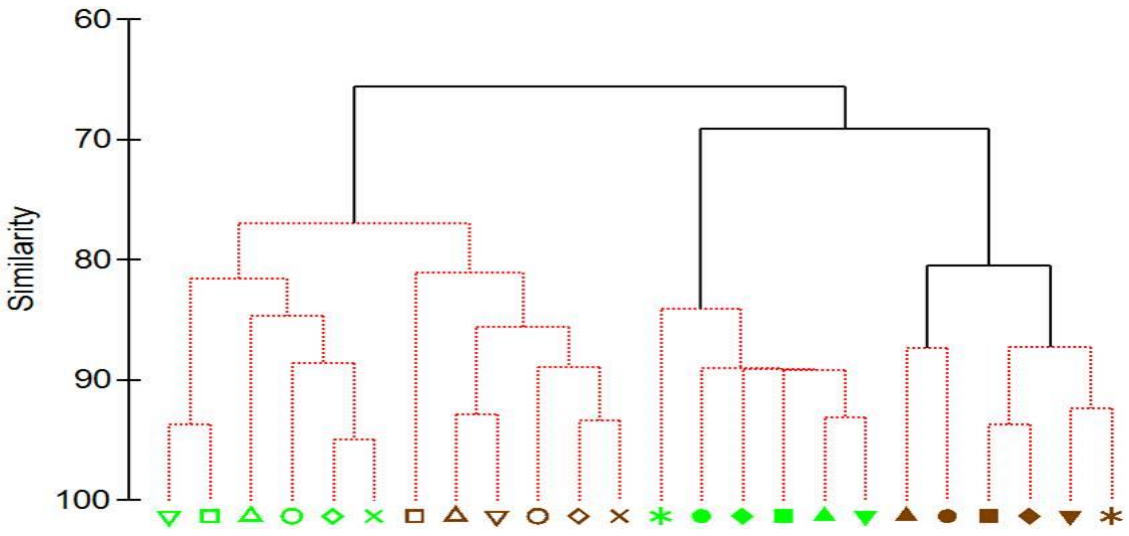


Fig.4.3: Hierarchical Clustering of bacterial Community at 10 days of rice growth in response to burning, cropping and microbial inoculants in soils of 5 years *Jhum* Cycle

### 4.1.2.2 Soil bacterial (alpha-proteobacteria) community at 45 days of rice growth

The changes in alpha-proteobacteria (using domain specific primer set 203fα:5' and 1494r: 5' nested with 984fgc:5' and 1378r 5'.) was studied at 45 days of rice plant growth in burnt and unburnt soils with presence or absence of rice crop. The PCR-DGGE fingerprint revealing the alpha-proteobacteria community composition at 45 days of rice plant growth is depicted in (Fig. 4.4.). The number and the relative intensity of bands are clearly visible in the PCR-DGGE fingerprint. The MDS plot developed on binary matrix of PCR-DGGE fingerprint showed distinct clustering between burnt and unburnt soils (Fig. 4.5.). The bacterial community of burnt soil or unburnt soil clustered separately according to the presence and absence of rice crop at 72% similarity level and the separation among clusters were significantly different from each other as confirmed by Hierarchical cluster analysis (incorporating SIMPROF test at 95% confidence limit) (Fig.4.6.). Interestingly, the clusters representing bacterial communities of burnt soil distinctly separated out from the clusters of unburnt soil according to the present or absent of rice crop (Fig. 4.5.). Within burnt or unburnt soil conditions, the two distinct clusters were represented by the bacterial communities in presence or absence of rice crop. Though there were variations in bacterial community compositions among the treatments, these treatment induced variations couldn't mask the effect of burning and cropping. The stronger factor of variability in shaping the soil alpha-proteobacterial community composition was found to be in the order burning > cropping > microbial inoculation treatment (Fig.4.4, Fig. 4.5. and Fig. 4.6).

### 4.1.2.3. Soil bacterial (alpha-proteobacteria) community at 90 days of rice growth

The changes in alpha-proteobacterial (using domain specific primer set 203fα:5' and 1494r: 5' nested with 984fgc:5' and 1378r 5'.) was studied at 45 days of rice plant growth in burnt and unburnt soils with presence or absence of rice crop. The PCR-DGGE fingerprint revealing the alpha-proteobacteria community composition at 90 days of rice plant growth is depicted in (Fig.4.7). The number and the relative intensity of bands are clearly visible in the PCR-DGGE fingerprint. The MDS plot developed on binary matrix of PCR-DGGE fingerprint showed distinct clustering between burnt and unburnt soils (Fig. 4.8.). The bacterial community of burnt soil or unburnt soil clustered separately according to the presence or absence of rice crop at 58% similarity level and the separation among clusters were significantly different from each other as confirmed by Hierarchical cluster analysis (incorporating SIMPROF test at 95% confidence limit).

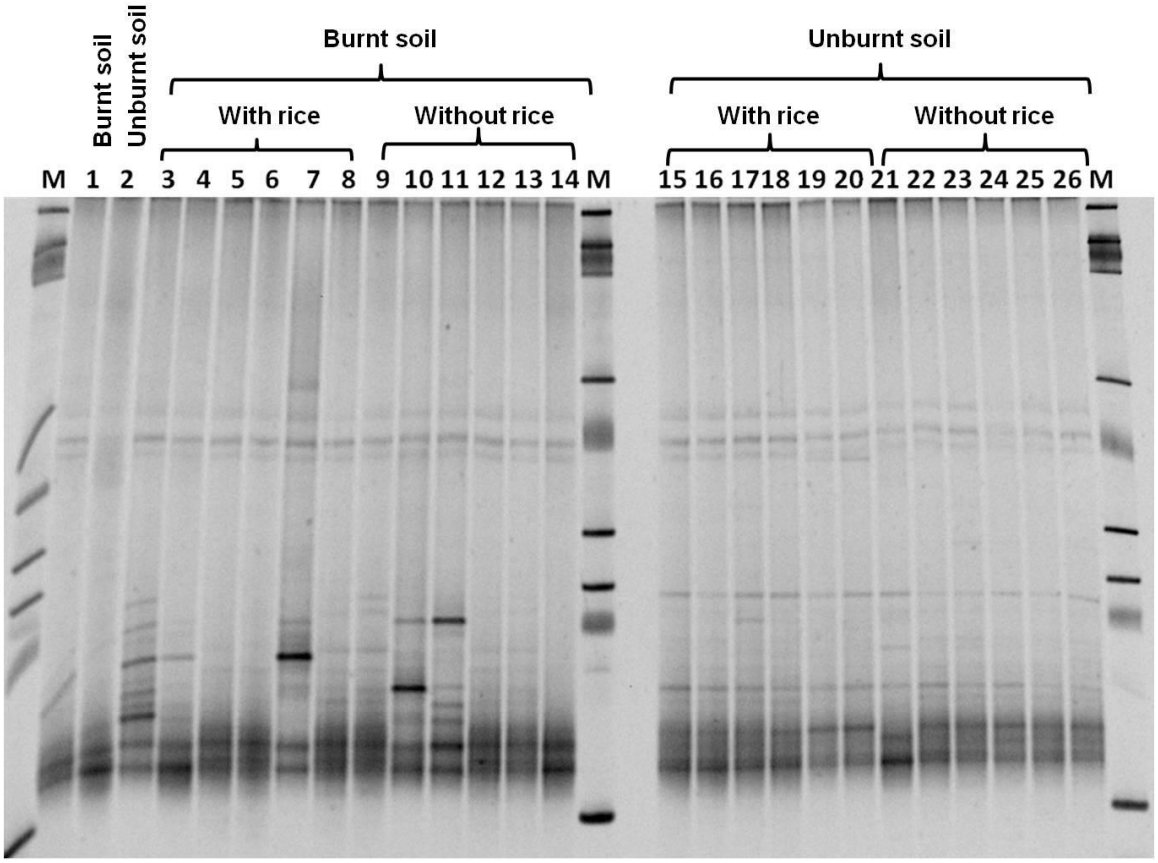


Fig.4.4: PCR DGGE of Alpha-proteobacterial group at 45 days growth of rice plant

The DGGE fingerprint depicting alpha-proetobacterial community at 45 days in *jhum* rice rhizosphere and bulk soils under burnt and unburnt situations of 5 years *jhum* cycle as influenced by application of microbial community composed of $N_2$-fixers (NF), phosphate solubilizing bacteria (PSB), cellulose degrading bacteria (CDB), NF+PSB+CDB, fungi, and control (no inoculants).

M – 100 bp marker, lane 1 –Burnt at 0 days, lane 2 -unburnt at 0 days, lane 3 -PSB+Fungi, lane 4 -$N_2$-fixers+Fungi, lane 5 -CDB+Fungi, lane 6 -NF+PSB+CDB +Fungi, lane 7 -Fungi, lane 8 -Control(no inoculation) lane 9 -PSB+Fungi, lane 10 -$N_2$-fixers+Fungi, lane 11 -CDB+Fungi, lane 12 -NF+PSB+CDB +Fungi, lane 13 -Fungi, lane 14 -Control (no inoculation) lane 15 -PSB+Fungi, lane 16 -$N_2$-fixers+Fungi, lane 17 -CDB+Fungi, lane 18 -NF+PSB+CDB +fungi, lane 19 -Fungi, lane 20 -Control (no inoculation), lane 21 -PSB+Fungi, lane 22 -$N_2$-fixers+Fungi, lane 23 -CDB+Fungi, lane 24 -NF+PSB+CDB +Fungi, lane 25- Fungi, lane 26 -Control(no inoculation)

Lane 3-8 Burnt with rice, Lane 9-14 Burnt without rice, Lane 15-20 Unburnt with rice, Lane 21-26 Unburnt without rice

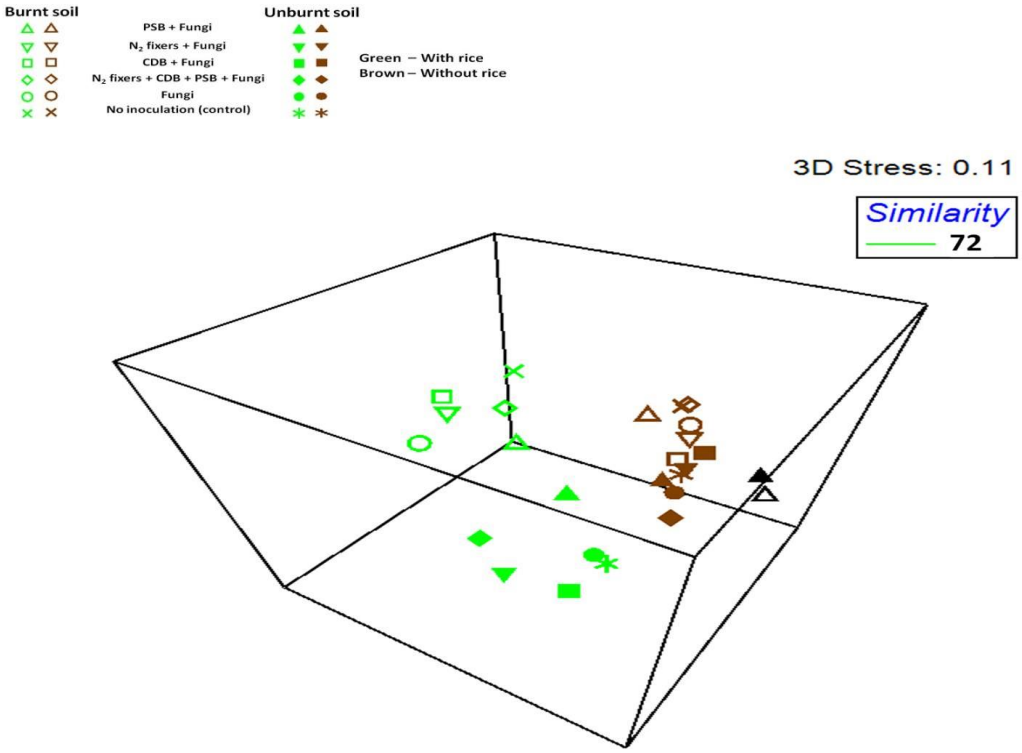


Fig.4.5: MDS Clustering of alpha-proteobacterial Community at 45 days of rice growth in response to burning, cropping and microbial inoculants in soils of 5 years *Jhum* Cycle.

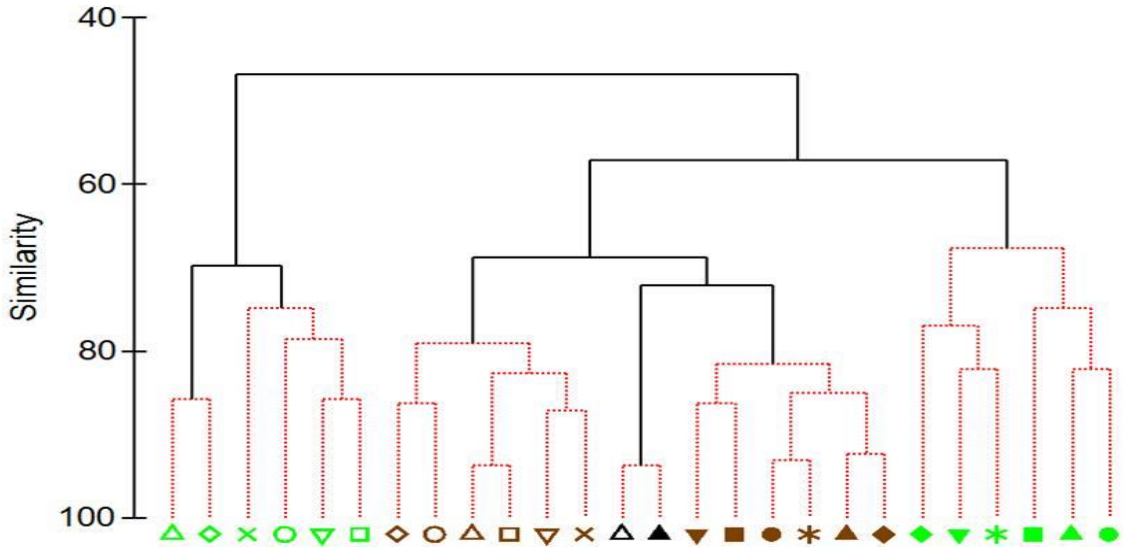


Fig.4.6: Hierarchical Clustering alpha-proteobacterial Community at 45 days of rice growth in response to burning, cropping and microbial inoculants in soils of 5 years *Jhum* Cycle.

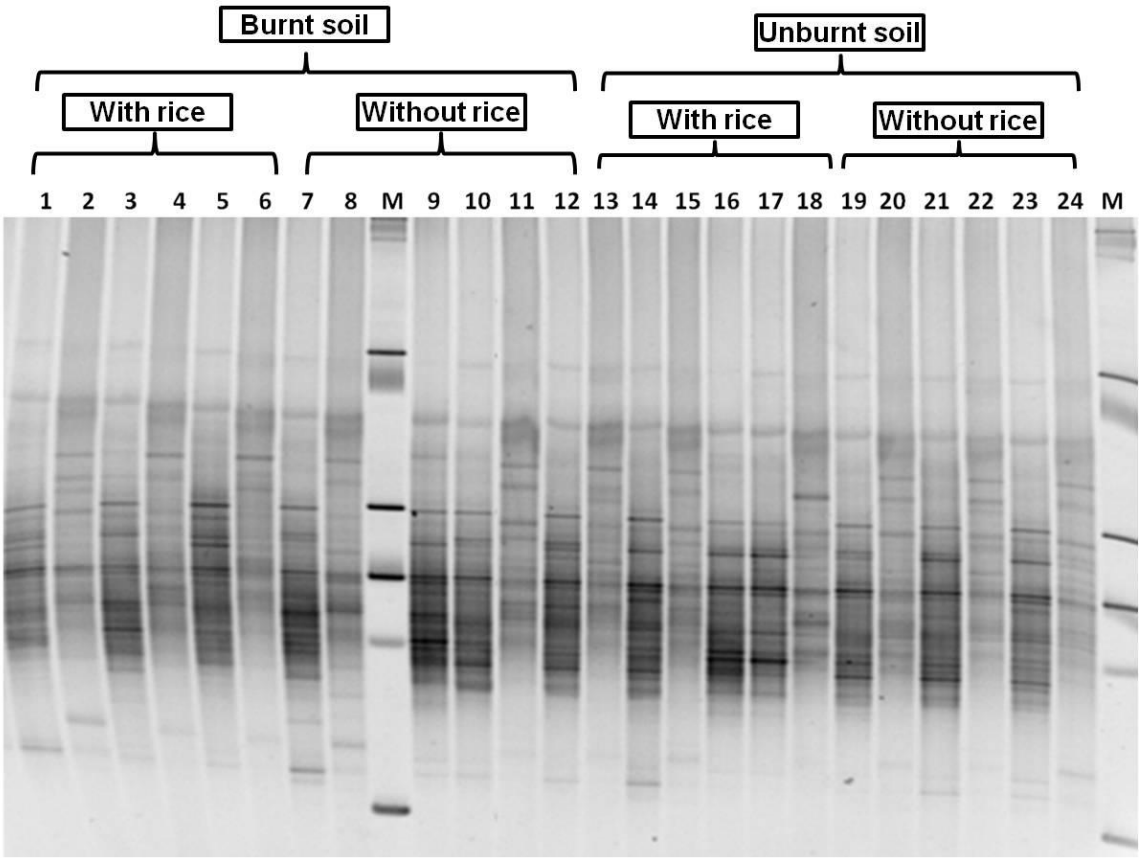


Fig.4.7: The PCR-DGGE OF Alpha-proteobacterial at 90 days of rice plant growth

The DGGE fingerprint depicting alpha-proetobacterial community at 90 days in *jhum* rice rhizosphere and bulk soils under burnt and unburnt situations of 5 years *jhum* cycle as influenced by application of microbial community composed of $N_2$-fixers (NF), phosphate solubilizing bacteria (PSB), cellulose degrading bacteria (CDB), NF+PSB+CDB, fungi, and control (no inoculants).

M – 100 bp marker, lane 1 -PSB+Fungi, lane 2 -$N_2$-fixers+Fungi, lane 3 -CDB+Fungi, lane 4 -NF+PSB+CDB +Fungi, lane 5 -Fungi, lane 6 -Control(no inoculation) lane 7 -PSB+Fungi, lane 8 -$N_2$-fixers+Fungi, lane 9 -CDB+Fungi, lane 10 -NF+PSB+CDB +Fungi, lane 11 -Fungi, lane 12 -Control (no inoculation) lane – 13 PSB+Fungi, lane 14 -$N_2$-fixers+Fungi, lane 15 -CDB+Fungi, lane 16 - NF+PSB+CDB +fungi, lane 17- Fungi, lane 18 -Control (no inoculation), lane 19 -PSB+Fungi, lane 20 -$N_2$-fixers+Fungi, lane 21 - CDB+Fungi, lane -22 NF+PSB+CDB +Fungi, lane 23 -Fungi, lane 24 - Control(no inoculation)

Lane 1-6 Burnt with rice, Lane 7-12 Burnt without rice, Lane 13-18 Unburnt with rice, Lane 19-24 Unburnt without rice.

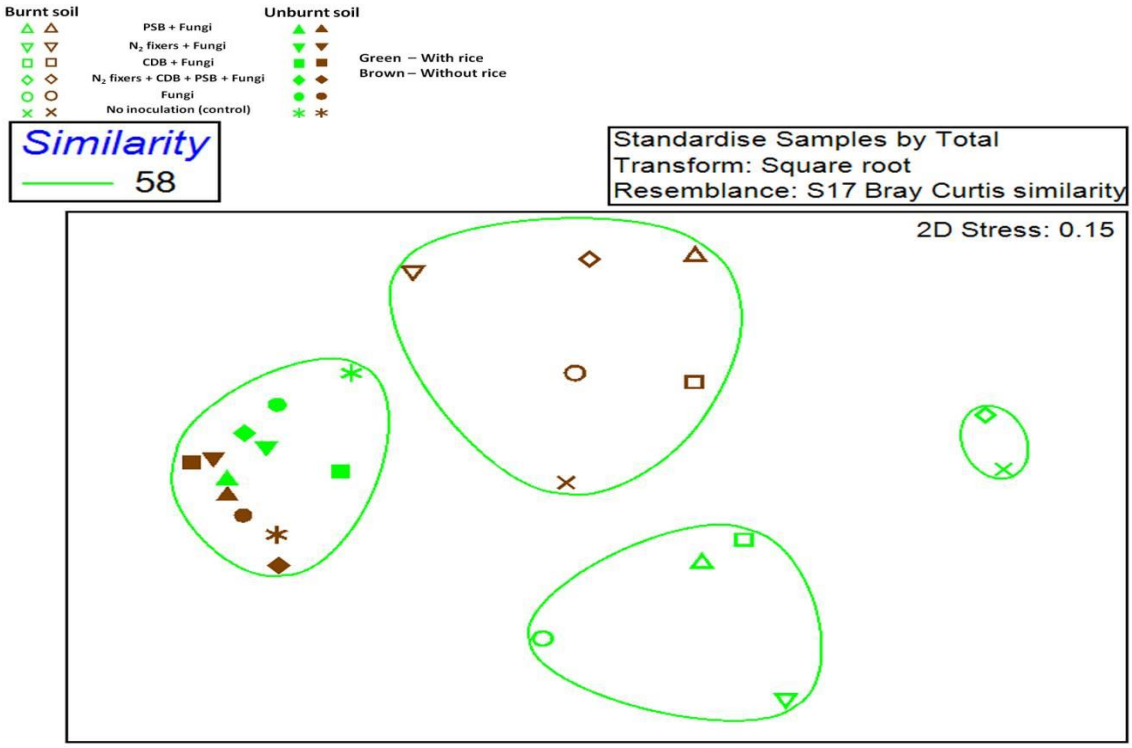


Fig.4.8: MDS Clustering of alpha-proetobacterial Community at 90 days of rice growth in response to burning, cropping and microbial inoculants in soils of 5 years *Jhum* Cycle**.**

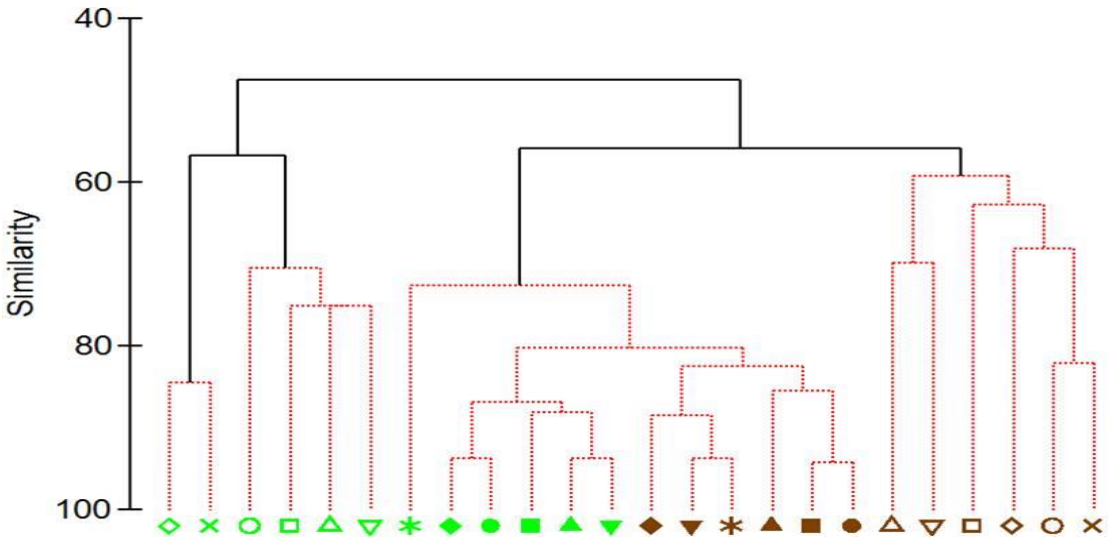


Fig.4.9: Hierarchical Clustering alpha-proetobacterial Community at 90 days of rice growth in response to burning, cropping and microbial inoculants in soils of 5 years *Jhum* Cycle

(Fig. 4.9.). Interestingly, the clusters representing bacterial communities of burnt soil distinctly separated out from the clusters of unburnt soil according to the present or absent of rice crop (Fig. 4.8.). Within burnt or unburnt soil conditions, the two distinct clusters were represented by the bacterial communities in presence or absence of rice crop. Though there were variations in bacterial community compositions among the treatments, these treatment induced variations couldn't mask the effect of burning and cropping. The stronger factor of variability in shaping the soil alpha-proteobacterial community composition at 90 days was found to be in the order burning > cropping > microbial inoculation treatment (Fig.4.7, Fig.4.8 and Fig.4.9).

### 4.1.2.4. Soil bacterial (beta-proteobacterial) community at 45 days of rice growth

The changes in beta-proteobacteria (using domain specific primer set F948βgc: 5' and 1494r: 5'.) was studied at 45 days of rice plant growth in burnt and unburnt soils with presence or absence of rice crop. The PCR-DGGE fingerprint showed the beta-proteobacteria community composition at 45 days of rice plant growth is depicted in (Fig.4.10). The number and the relative intensity of bands are clearly visible in the PCR-DGGE fingerprint. The MDS plot developed on binary matrix of PCR-DGGE fingerprint showed distinct clustering between burnt and unburnt soils (Fig. 4.11). The bacterial community of burnt soil or unburnt soil clustered separately according to the presence or absence of rice crop at 75% similarity level and the separation among clusters were significantly different from each other as confirmed by Hierarchical cluster analysis (incorporating SIMPROF test at 95% confidence limit) (Fig. 4.12.). Interestingly, the clusters representing bacterial communities of burnt soil distinctly separated out from the clusters of unburnt soil according to the present or absent of rice crop (Fig. 4.11.). Within burnt or unburnt soil conditions, the two distinct clusters were represented by the bacterial communities in presence or absence of rice crop. Though there were variations in bacterial community compositions among the treatments, these treatment induced variations couldn't mask the effect of burning and cropping. The stronger factor of variability in shaping the beta-proteobacterial community composition was found to be in the order cropping > burning > microbial inoculation treatment (Fig.4.10, Fig.4.11. and Fig.4.12.).

### 4.1.2.5. Soil bacterial (beta-proteobacterial) community at 90 days of rice growth

The changes in beta-proteobacterial (using domain specific primer set F948βgc: 5' and 1494r: 5'.) was studied at 90 days of rice plant growth in burnt and unburnt soils with presence or absence of rice crop. The PCR-DGGE fingerprint revealing the beta-proteobacteria community composition at 90 days of rice plant growth is depicted in (Fig.4.13). The number and the relative intensity of bands are clearly visible in the PCR-DGGE fingerprint. The MDS plot developed on binary matrix of PCR-DGGE fingerprint showed distinct clustering between burnt and unburnt soils (Fig. 4.14.). The bacterial community of burnt soil or unburnt soil clustered separately according to the presence or absence of rice crop at 80% similarity level and the separation among clusters were significantly different from each other as confirmed by Hierarchical cluster analysis (incorporating SIMPROF test at 95% confidence limit) (Fig.4.15). Interestingly, the clusters representing bacterial communities of burnt soil distinctly separated out from the clusters of unburnt soil according to the present or absent of rice crop (Fig. 4.14.). Within burnt or unburnt soil conditions, the two distinct clusters were represented by the bacterial communities in presence or absence of rice crop. Though there were variations in bacterial community compositions among the treatments, these treatment induced variations couldn't mask the effect of burning and cropping. The stronger factor of variability in shaping the beta-proteobacterial community composition was found to be in the order cropping> burning > microbial inoculation treatment (Fig.4.13, Fig.4.14 and Fig.4.15).

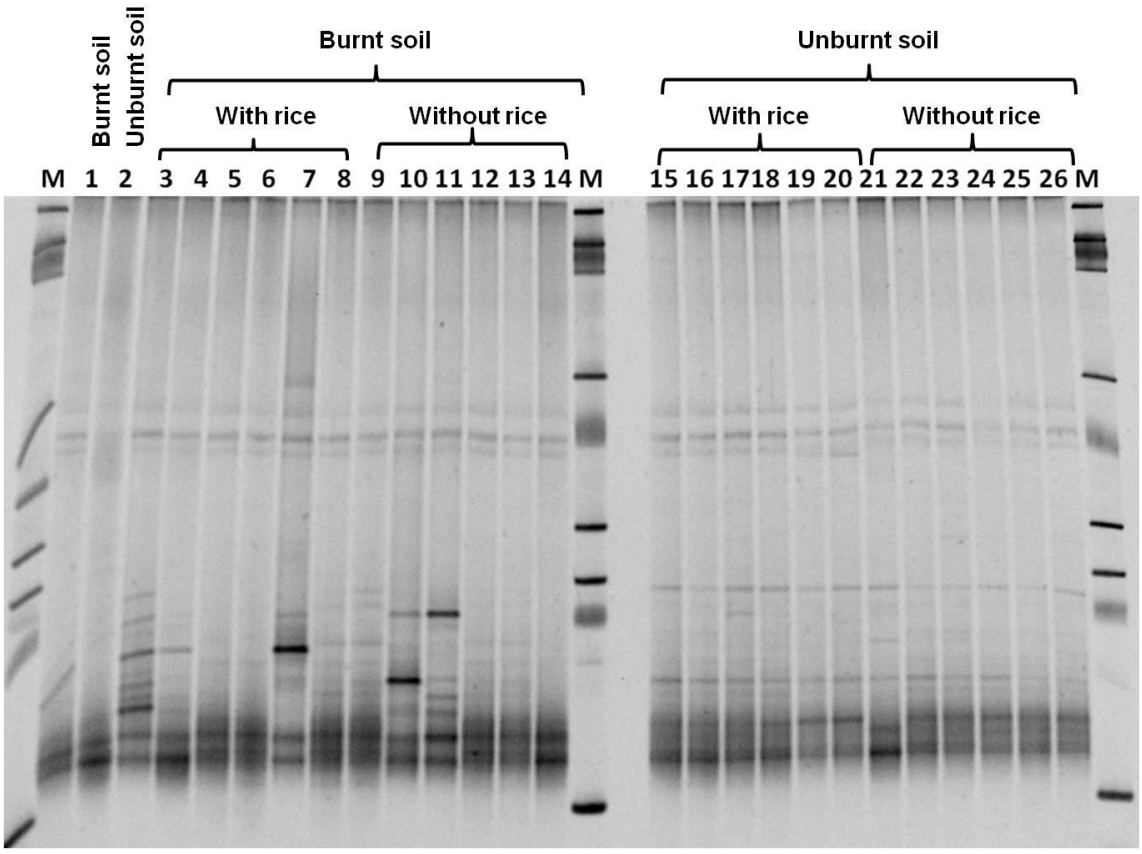


Fig.4.10: The PCR-DGGE of Beta-proteobacterial at 45 days of rice plant growth

The DGGE fingerprint depicting Beta-proetobacterial community at 45 days in *jhum* rice rhizosphere and bulk soils under burnt and unburnt situations of 5 years *jhum* cycle as influenced by application of microbial community composed of $N_2$-fixers (NF), phosphate solubilizing bacteria (PSB), cellulose degrading bacteria (CDB), NF+PSB+CDB, fungi, and control (no inoculants).

M – 100 bp marker, lane 1 –Burnt at 0 days, lane 2 -unburnt at 0 days, lane 3 -PSB+Fungi, lane 4 -$N_2$-fixers+Fungi, lane 5 -CDB+Fungi, lane 6 -NF+PSB+CDB +Fungi, lane 7 -Fungi, lane 8 -Control(no inoculation) lane 9 -PSB+Fungi, lane 10 -$N_2$-fixers+Fungi, lane 11 -CDB+Fungi, lane 12 -NF+PSB+CDB +Fungi, lane 13 -Fungi, lane 14 -Control (no inoculation) lane 15 -PSB+Fungi, lane 16 -$N_2$-fixers+Fungi, lane 17 -CDB+Fungi, lane 18 -NF+PSB+CDB +fungi, lane 19 -Fungi, lane 20 -Control (no inoculation), lane 21-PSB+Fungi, lane 22 -$N_2$-fixers+Fungi, lane 23 -CDB+Fungi, lane 24 -NF+PSB+CDB +Fungi, lane 25 -Fungi, lane 26 -Control(no inoculation)

Lane 3-8 Burnt with rice, Lane 9-14 Burnt without rice, Lane 15-20 Unburnt with rice, Lane 21-26 Unburnt without rice.

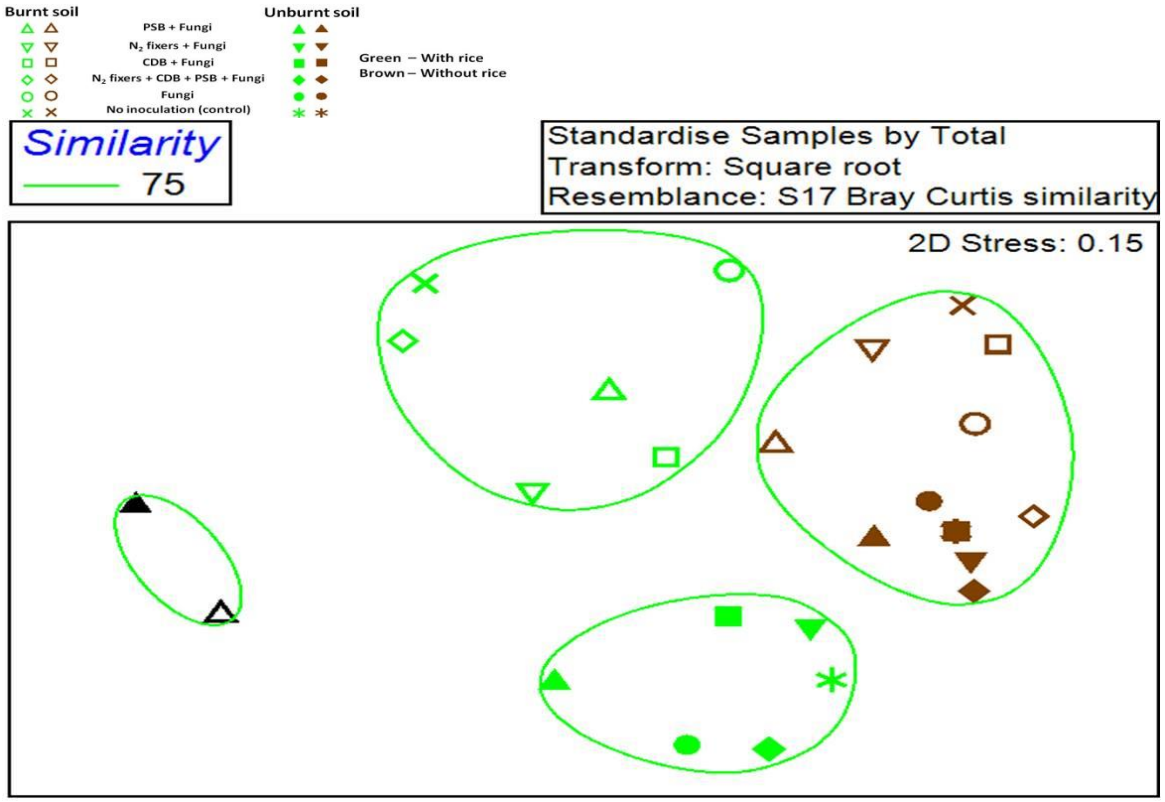


Fig.4.11: MDS Clustering of beta-proetobacterial Community at 45 days of rice growth in response to burning, cropping and microbial inoculants in soils of 5 years *Jhum* Cycle.

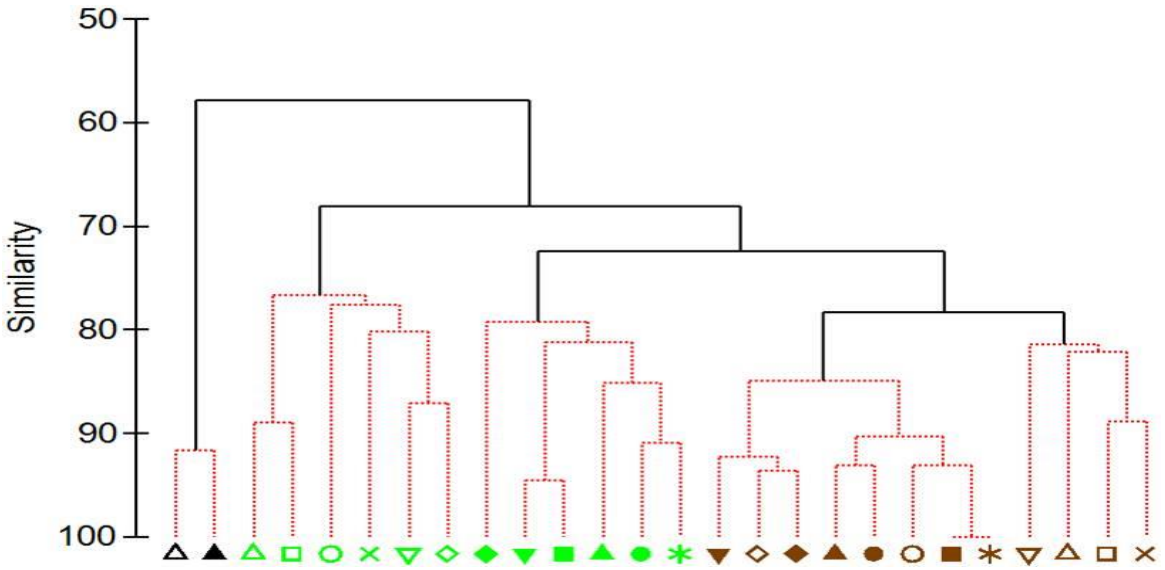


Fig.4. 12: Hierarchical Clustering beta-proetobacterial Community at 45 days of rice growth in response to burning, cropping and microbial inoculants in soils of 5 years *Jhum* Cycle

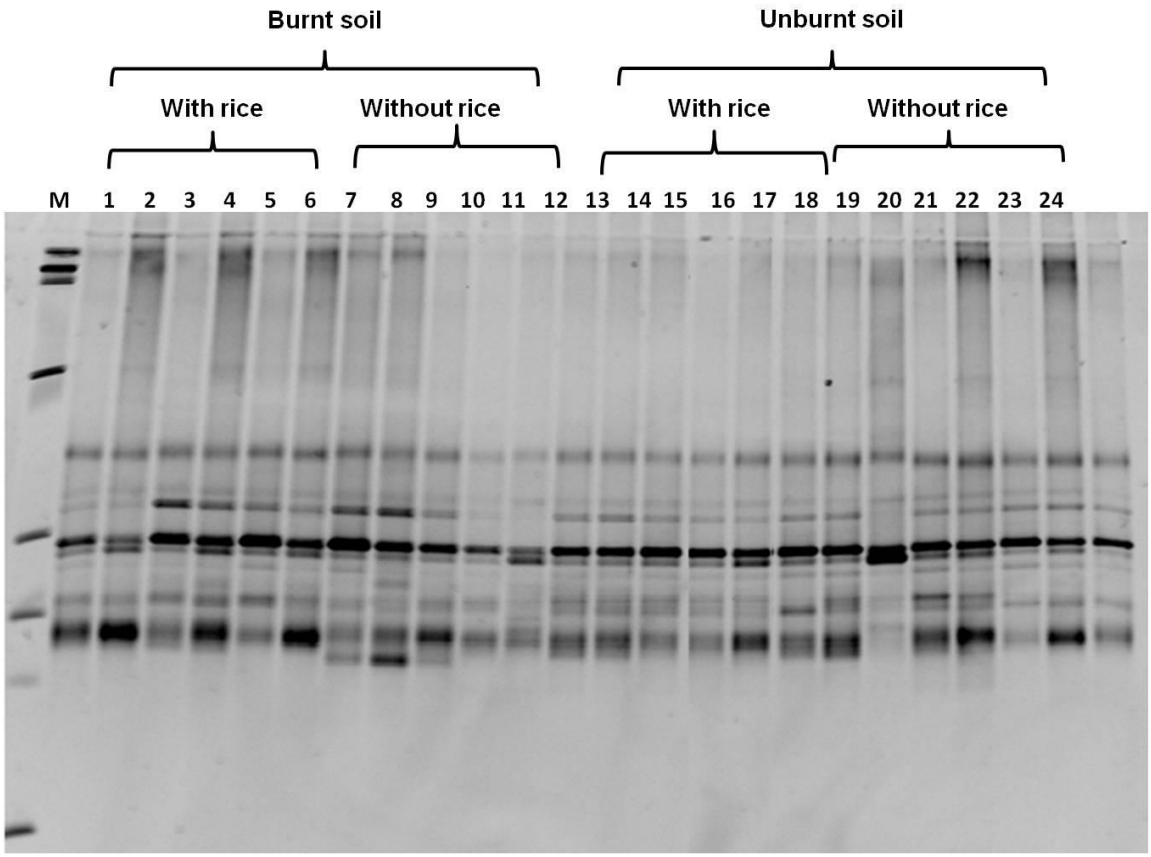


Fig.4.13: The PCR-DGGE of Beta-proteobacterial at 90 days of rice plant growth

The DGGE fingerprint depicting Beta-proetobacterial community at 90 days in *jhum* rice rhizosphere and bulk soils under burnt and unburnt situations of 5 years *jhum* cycle as influenced by application of microbial community composed of $N_2$-fixers (NF), phosphate solubilizing bacteria (PSB), cellulose degrading bacteria (CDB), NF+PSB+CDB, fungi, and control (no inoculants).

M – 100 bp marker, lane 1 -PSB+Fungi, lane 2 -$N_2$-fixers+Fungi, lane 3 -CDB+Fungi, lane 4 -NF+PSB+CDB +Fungi, lane 5 -Fungi, lane 6 -Control(no inoculation) lane 7 -PSB+Fungi, lane 8 -$N_2$-fixers+Fungi, lane 9 -CDB+Fungi, lane 10 -NF+PSB+CDB +Fungi, lane 11 -Fungi, lane 12 -Control (no inoculation) lane – 13 PSB+Fungi, lane 14 -$N_2$-fixers+Fungi, lane 15 -CDB+Fungi, lane 16 - NF+PSB+CDB +fungi, lane 17- Fungi, lane 18 -Control (no inoculation), lane 19 - PSB+Fungi, lane 20 -$N_2$-fixers+Fungi, lane 21 - CDB+Fungi, lane -22 NF+PSB+CDB +Fungi, lane 23 - Fungi, lane 24 - Control(no inoculation)

Lane 1-6 Burnt with rice, Lane 7-12 Burnt without rice, Lane 13-18 Unburnt with rice, Lane 19-24 Unburnt without rice

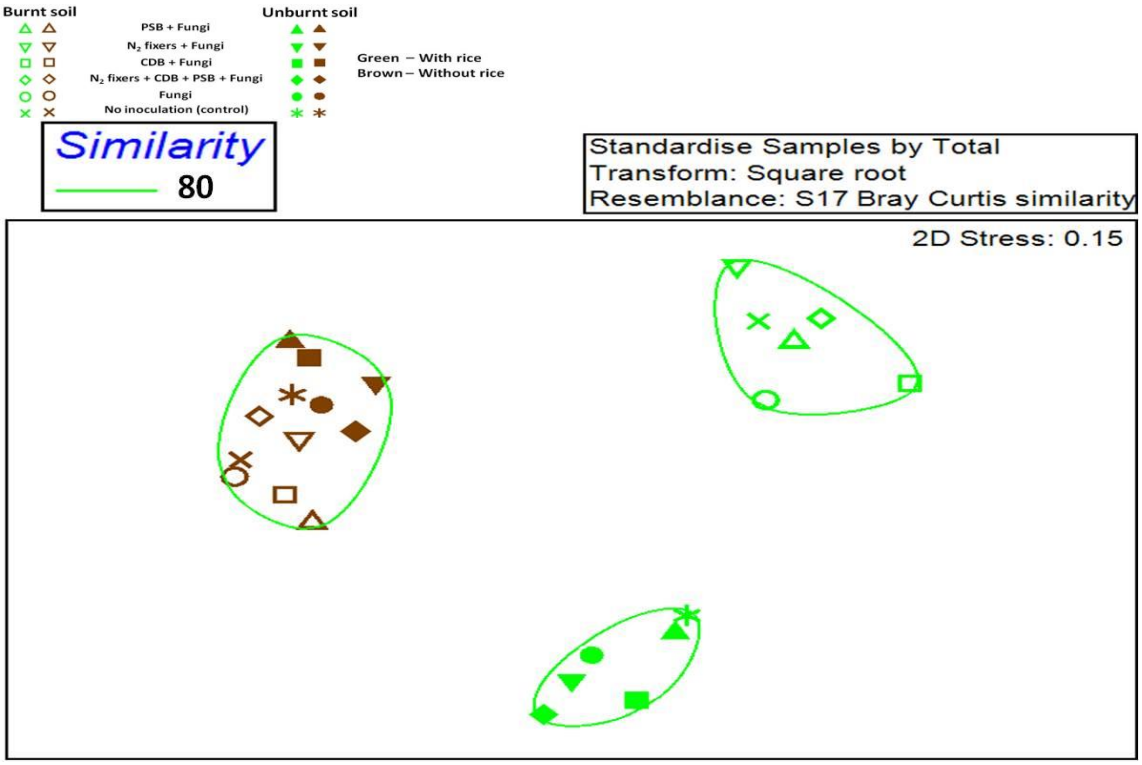


Fig.4.14: MDS Clustering of beta-proetobacterial Community at 90 days of rice growth in response to burning, cropping and microbial inoculants in soils of 5 years *Jhum* Cycle.

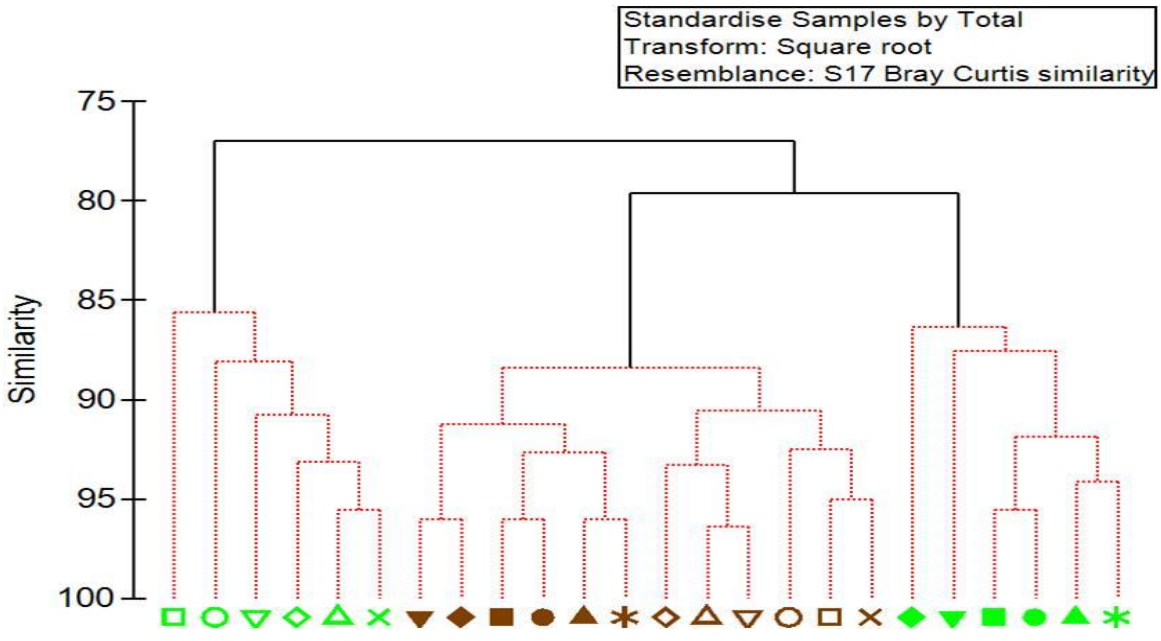


Fig.4.15: Hierarchical Clustering beta-proetobacterial Community at 90 days of rice growth in response to burning, cropping and microbial inoculants in soils of 5 years *Jhum* Cycle.

## 4.2 Objective - 2

The response of soil bacterial community to application of microbial community (PSB community, $N_2$-fixer community, CDB community and fungal community) in presence or absence of rice crop under both burnt and unburnt soils of 5 year *jhum* cycle was studied in mesocosm experiment. The change in soil enzymes and biochemical properties was studied at 10, 45, 90 and 120 days of rice plant growth.

### 4.2.1 Effect of burning, cropping and microbial inoculation on soil enzymes activity as an indicator of soil processes

#### 4.2.1.1 Soil enzymes activities at 10 days of rice plant growth

The soil enzymes such as DHA, GSA, ASA and PHA were strongly influence by the burning, cropping and microbial inoculation (Table 4.2 and annexure 4.1, 4.2, 4.3, 4.4.). The activities of DHA, GSA, and PHA were decrease in burnt soil where as a slight increase in the activity of ASA was found in burnt soil.

Cropping had a great influence to soil enzymes which shows the enzymes activity increase in presence of rice crop than the bulk soils.

Each of the microbial inoculation responds was differ to each enzymes activity. The inoculation of synthetic $N_2$ fixer had a greater impact to soil DHA, CDB had greater impact to GSA, PSB inoculants affect the PHA and fungi inoculation greater impact at ASA at 10 days of rice plant growth.

The interaction between jhumming* cropping; jhumming * microbial innoculation; cropping * microbial inoculation and jhumming * cropping * microbial inoculation were significance at a level $P \leq 0.01$.

#### 4.2.1.2 Soil enzymes activities at 45 days of rice plant growth

The soil enzymes such as DHA, GSA, ASA and PHA were strongly influence by the burning, cropping and microbial inoculation (Table 4.3 and annexure 4.5., 4.6., 4.7., 4.8.). The activities of DHA, GSA, and PHA were decrease in burnt soil where as a slight increase in the activity of ASA was found in burnt soil.

Cropping had a great influence to soil enzymes which shows the enzymes activity increase in presence of rice crop than the bulk soils.

Table 4.2: Interaction effect of burning, cropping and microbial communities on soil enzyme activities in 5 years *Jhum* cycle at 10 days growth of rice plant

| **Treatments** | DHA | GSA | PHA | ASA |
|---|---|---|---|---|
| | µg TPF $g^{-1}$ (dry) soil $h^{-1}$ | µg PNP $g^{-1}$ (dry) soil $h^{-1}$ | | |
| **Jhumming (J)** | | | | |
| Burnt | 0.51b | 365.8b | 560.4b | 74.06b |
| Unburnt | 1.39a | 383.4a | 612.1a | 104.4a |
| **Cropping ( C )** | | | | |
| With rice | 0.90b | 340.9b | 571.9b | 90.71a |
| Without rice | 0.99a | 408.2a | 600.6a | 87.80b |
| **Microbial Inoculation (MI)** | | | | |
| PSB + Fungi | 1.1b | 428.1b | 646.0b | 94.40b |
| $N_2$ fixer + Fungi | 1.2a | 384.6c | 626.7c | 85.15c |
| CDB + Fungi | 1.0c | 452.4a | 705.4a | 86.07c |
| PSB + $N_2$ fixer + CDB + Fungi | 0.8d | 319.3e | 529.7e | 83.69c |
| Fungi | 0.7e | 342.7d | 547.0d | 101.3a |
| No inoculation (control) | 0.6f | 320.3d | 462.7f | 84.88c |
| **Interactions** | | | | |
| J * C | ** | ** | ** | ** |
| J * MI | ** | ** | ** | ** |
| C * MI | ** | ** | ** | ** |
| J * C * MI | ** | ** | ** | ** |

DHA – Dehydrogenase activity; GSA – beta-glucosidase activity; PHA – acid phosphomonoesterase activity; ASA – aryl sulphatase activity. *,** are levels of significance at the probability $P \leq 0.05$ and 0.01, respectively.
Within a parameter he values followed by different letters are significant different at ≥0.05 within a factor (J, C, MI)

Table 4.3: Interaction effect of burning, cropping and microbial communities on soil enzyme activities in 5 years *Jhum* cycle at 45 days growth stage of rice plant

| **Treatments** | DHA | GSA | PHA | ASA |
|---|---|---|---|---|
| | µg TPF $g^{-1}$ (dry) soil $h^{-1}$ | µg PNP $g^{-1}$ (dry) soil $h^{-1}$ | | |
| **Jhumming (J)** | | | | |
| Burnt | 08.30b | 321.6a | 524.8a | 110.8b |
| Unburnt | 16.10a | 306.1b | 502.2b | 118.3a |
| **Cropping ( C )** | | | | |
| With rice | 14.48a | 296.7b | 520.6a | 131.2a |
| Without rice | 09.92b | 330.9a | 506.5b | 98.09b |
| **Microbial Inoculation (MI)** | | | | |
| PSB + Fungi | 12.5c | 298.3d | 559.a | 116.4bc |
| $N_2$ fixer + Fungi | 14.1b | 260.1e | 511.3d | 109.7c |
| CDB + Fungi | 15.7a | 433.3a | 543.4a | 130.1a |
| PSB + $N_2$ fixer + CDB + Fungi | 10.8d | 337.5b | 436.3f | 116.7bc |
| Fungi | 10.0d | 308.6c | 527.2c | 121.0b |
| No inoculation (control) | 10.0d | 245.2f | 503.3e | 93.6d |
| **Interactions** | | | | |
| J * C | ** | ** | ** | ** |
| J * MI | ** | ** | ** | ** |
| C * MI | ** | ** | ** | ** |
| J * C * MI | ** | ** | ** | ** |

DHA – Dehydrogenase activity; GSA – beta-glucosidase activity; PHA – acid phosphomonoesterase activity; ASA – aryl sulphatase activity. *,** are levels of significance at the probability $P \leq 0.05$ and 0.01, respectively.
Within a parameter he values followed by different letters are significant different at ≥0.05 within a factor (J, C, MI)

Table 4.4: Interaction effect of burning, cropping and microbial communities on soil enzyme activities in 5 years *Jhum* cycle at 90 days growth stage of rice plant

| **Treatments** | DHA | GSA | PHA | ASA |
|---|---|---|---|---|
| | µg TPF $g^{-1}$ (dry) soil $h^{-1}$ | µg NP $g^{-1}$ (dry) soil $h^{-1}$ | | |
| **Jhumming (J)** | | | | |
| Burnt | 10.64b | 379.6b | 336.0b | 47.73b |
| Unburnt | 18.86a | 396.5a | 497.1a | 102.3a |
| **Cropping ( C )** | | | | |
| With rice | 17.97a | 405.1a | 402.8b | 88.70a |
| Without rice | 11.53b | 371.1b | 430.3a | 61.37b |
| **Microbial Inoculation (MI)** | | | | |
| PSB + Fungi | 16.1c | 426.4c | 420.1c | 66.2d |
| $N_2$ fixer + Fungi | 16.8bc | 345.6d | 363.6e | 82.0a |
| CDB + Fungi | 71.5b | 304.3f | 461.3a | 76.7b |
| PSB + $N_2$ fixer + CDB + Fungi | 18.9a | 321.0e | 424.0b | 72.3c |
| Fungi | 10.7d | 443.0b | 405.1d | 77.1b |
| No inoculation (control) | 8.4e | 488.0a | 426.0b | 75.8b |
| **Interactions** | | | | |
| J * C | ** | ** | ** | ** |
| J * MI | ** | ** | ** | ** |
| C * MI | ** | ** | ** | ** |
| J * C * MI | ** | ** | ** | ** |

DHA – Dehydrogenase activity; GSA – beta-glucosidase activity; PHA – acid phosphomonoesterase activity; ASA – aryl sulphatase activity. *,** are levels of significance at the probability $P \leq 0.05$ and 0.01, respectively.
Within a parameter he values followed by different letters are significant different at ≥0.05 within a factor (J, C, MI)

Table 4.5: Interaction effect of burning, cropping and microbial communities on soil enzyme activities in 5 years *Jhum* cycle at 120 days growth stage of rice plant

| **Treatments** | DHA | GSA | PHA | ASA |
|---|---|---|---|---|
| | µg TPF $g^{-1}$ (dry) soil $h^{-1}$ | µg NP $g^{-1}$ (dry) soil $h^{-1}$ | | |
| **Jhumming (J)** | | | | |
| Burnt | 07.475b | 308.9b | 351.397 | 68.12b |
| Unburnt | 20.356a | 425.2a | 323.021 | 81.54a |
| **Cropping ( C )** | | | | |
| With rice | 16.151a | 355.6b | 514.652 | 86.02a |
| Without rice | 11.680b | 378.6c | 159.766 | 63.64b |
| **Microbial Inoculation (MI)** | | | | |
| PSB + Fungi | 15.8a | 327.0f | 336.1c | 60.4e |
| $N_2$ fixer + Fungi | 15.3a | 337.1e | 296.8e | 76.5bc |
| CDB + Fungi | 13.1b | 371.7c | 350.2b | 83.6a |
| PSB + $N_2$ fixer + CDB + Fungi | 13.7b | 400.0b | 367.6a | 75.5bc |
| Fungi | 13.3b | 403.3a | 349.6b | 78.6b |
| No inoculation (control) | 12.2c | 363.3d | 322.7d | 74.4d |
| **Interactions** | | | | |
| J * C | ** | ** | ** | ** |
| J * MI | ** | ** | ** | ** |
| C * MI | ** | ** | ** | ** |
| J * C * MI | ** | ** | ** | ** |

DHA – Dehydrogenase activity; GSA – beta-glucosidase activity; PHA – acid phosphomonoesterase activity; ASA – aryl sulphatase activity. *,** are levels of significance at the probability $P \leq 0.05$ and 0.01, respectively.
Within a parameter he values followed by different letters are significant different at $\leq 0.05$ within a factor (J, C, MI)

Each of the microbial inoculation responds to soil enzymes activity differently. The inoculation of CDB + Fungi had impact to soil DHA, GSA and ASA enzyme activities where as inoculations of PSB + fungi effect the PHA activity at 45 days of rice plant growth.

The interaction between jhumming* cropping; jhumming * microbial innoculation; cropping * microbial inoculation and jhumming * cropping * microbial inoculation were significance at a level $P \leq 0.01$.

### 4.2.1.3 Soil enzymes activities at 90 days of rice plant growth

The soil enzymes such as DHA, GSA, ASA and PHA were strongly influence by the burning activity (Table 4.4. and annexure 4.9., 4.10., 4.11., 4.12.). The activities of DHA, GSA, and PHA were decrease in burnt soil where there was a slight increased in the activity of ASA in burnt soil.

Interestingly the activities of all the enzymes were found higher in soils where rice crop was grown as compared to bulk soils.

Each of the microbial inoculation responds to soil enzymes activity differently. The soil inoculation of PSB + $N_2$ fixer + CDB with fungi had a greater impact to soil DHA, inoculation of CDB and Fungi effect the GSA, inoculations of PSB + fungi influence the PHA activity and $N_2$ fixer + fungi had agreater impact to ASA at 90 days of rice plant growth.

The interaction between jhumming* cropping; jhumming * microbial innoculation; cropping * microbial inoculation and jhumming * cropping * microbial inoculation were significance at a level $P \leq 0.01$.

### 4.2.1.4. Soil enzymes activities at 120 days of rice plant growth

The soil enzymes such as DHA, GSA, ASA and PHA were strongly influence by the burning activity (Table 4.5. and appendix 4.13., 4.14., 4.15., 4.16.). The activities of DHA, GSA, and PHA were decrease in burnt soil where the activity of ASA was slightly increased in burnt soil.

Interestingly the activities of all the enzymes were found higher in soils where rice crop had grown increased and cropping and GSA were taken as an early indicator of soil processes.

The microbial inoculation responds was different to each enzymes activity. The inoculation of synthetic $N_2$ fixer had a greater impact to soil on DHAand CDB had a greater impact to GSA. PSB inoculants affect the PHA and sole fungi inoculation had a greater impact to ASA at 120 days of rice plant growth.

Each of the microbial inoculation responds to soil enzymes activity differently. The inoculation of synthetic $N_2$ fixer had a greater impact to soil DHA is impacted by inoculations of PSB + fungi and application of $N_2$ fixer + fungi and sole fungi had greater impact on GSA. PSB with $N_2$ fixer and CDB with fungi inoculants effect the PHA. CDB with Fungi inoculation had greater impact to ASA at 120 days of rice plant growth.

The interaction between jhumming* cropping; jhumming * microbial innoculation; cropping * microbial inoculation and jhumming * cropping * microbial inoculation were significance at a level $P \leq 0.01$.

### 4.2.2.1. Soil biochemical properties at 10 days growth stage of rice plant in response to burning, cropping and synthetic microbial inoculants

The soil biochemical properties such as SOC, pMN, POM MBC and DOC were studied and the result shows that this biochemical properties of soil were strongly affected by burning, cropping and synthetic microbial inoculation (Table 4.6. and annexure 4.17., 4.18., 4.19., 4.20. and 4.21.).

The higher amount of SOC, pMN, POM and MBC were observed in unburnt soils where a slight increase was observed in case of DOC.

In cropping conditions all the tested soil biochemical properties were found higher in a condition where rice crop was grown than the bulk soils.

The SOC was found to be highest in a condition where soils was inoculated with sole fungi and pMN was found highest where soil was inoculated with CDB + fungi. POM and MBC were found highest where soil was inoculated with PSB + fungi and the inoculation of $N_2$ fixer + fungi had a great impact on DOC content in soil.

The interaction between jhumming* cropping; jhumming * microbial innoculation; cropping * microbial inoculation and jhumming * cropping * microbial inoculation were significance at a level $P \leq 0.01$.

Table 4.6.: Interaction effect of burning, cropping and microbial communities on soil biochemical activities in 5 years *Jhum* cycle at 10 days growth stage of rice plant

| **Treatment** | SOC<br>% | pMN<br>µg $g^{-1}$(dw)soil | POM<br>% | MBC<br>µg /g | DOC<br>µg g soil |
|---|---|---|---|---|---|
| **Jhumming (J)** | | | | | |
| Burnt | 3.06b | 16.87a | 4.44a | 166.6b | 145.7a |
| Unburnt | 3.17a | 11.88b | 5.47b | 186.9a | 116.7b |
| **Cropping** | | | | | |
| Burnt | 3.10b | 18.92a | 6.42b | 201.3a | 134.3a |
| Unburnt | 3.14a | 09.84b | 6.48a | 152.1b | 128.1b |
| **Microbial Inoculation (MI)** | | | | | |
| PSB + Fungi | 3.01c | 13.18d | 7.24a | 212.9a | 136.8c |
| $N_2$ fixer + Fungi | 3.02c | 16.67b | 6.36c | 204.1b | 170.2a |
| CDB + Fungi | 3.18b | 18.00a | 6.94b | 178.0c | 143.2b |
| PSB + $N_2$ fixer + CDB + Fungi | 3.16b | 15.10c | 6.17c | 162.9d | 117.2d |
| Fungi | 3.29a | 10.49e | 5.99e | 160.2e | 110.9e |
| No inoculation (control) | 3.03c | 12.83d | 6.02e | 142.4f | 108.7f |
| **INTERACTION** | | | | | |
| J * C | ** | ** | ** | ** | ** |
| J * MI | ** | ** | ** | ** | ** |
| C * MI | ** | ** | ** | ** | ** |
| J * C * MI | | | | | |

SOC – Soil Organic Carbon; pMN; Potentially Mineralizable Nitrogen; POM – Particulate Organic Matter; SMBC – Soil Microbial Biomass Carbon DOC – Dissolve Organic Carbon *,** are levels of significance at the probability $P \leq 0.05$ and 0.01, respectively.
Within a parameter, the value followed by different letters are significantly differed at $P \leq 0.05$ within a factor (J, C, MI)

Table 4.7.: Interaction effect of burning, cropping and microbial communities on soil biochemical activities in 5 years *Jhum* cycle at 45 days growth stage of rice plant

| **Treatment** | SOC<br>% | pMN<br>µg $g^{-1}$(dw)soil | POM<br>% | MBC<br>µg /g | DOC<br>µg g soil |
|---|---|---|---|---|---|
| **Jhumming (J)** | | | | | |
| Burnt | 3.09b | 17.0a | 8.14b | 89.44b | 181.5a |
| Unburnt | 3.13a | 14.3b | 9.14a | 130.2a | 135.8b |
| **Cropping** | | | | | |
| Burnt | 3.14a | 21.1a | 8.22b | 133.2a | 194.7a |
| Unburnt | 3.07b | 10.1b | 9.06a | 86.37b | 122.6b |
| **Microbial Inoculation (MI)** | | | | | |
| PSB + Fungi | 2.93e | 08.8e | 8.51b | 129.6b | 230.9a |
| $N_2$ fixer + Fungi | 3.03d | 22.2a | 8.44bc | 134.7a | 148.1c |
| CDB + Fungi | 3.18b | 19.2b | 8.38bc | 117.4c | 145.9d |
| PSB + $N_2$ fixer + CDB + Fungi | 3.10c | 16.4c | 9.67a | 108.2d | 126.0e |
| Fungi | 3.37a | 11.9d | 8.27c | 93.99e | 154.5b |
| No inoculation (control) | 3.03d | 15.2c | 8.57b | 74.86f | 146.9cd |
| **INTERACTION** | | | | | |
| J * C | ** | ** | ** | ** | ** |
| J * MI | ** | ** | ** | ** | ** |
| C * MI | ** | ** | ** | ** | ** |
| J * C * MI | | | | | |

SOC – Soil Organic Carbon; pMN; Potentially Mineralizable Nitrogen; POM – Particulate Organic Matter; SMBC – Soil Microbial Biomass Carbon DOC – Dissolve Organic Carbon *,** are levels of significance at the probability $P \leq 0.05$ and 0.01, respectively.

Within a parameter, the value followed by different letters are significantly differed at P≤0.05 within a factor (J, C, MI)

Table 4.8: Interaction effect of burning, cropping and microbial communities on soil biochemical activities in 5 years *Jhum* cycle at 90 days growth stage of rice plant

| **Treatment** | SOC<br>% | pMN<br>µg $g^{-1}$(dw)soil | POM<br>% | MBC<br>µg /g | DOC<br>µg g soil |
|---|---|---|---|---|---|
| **Jhumming (J)** | | | | | |
| Burnt | 3.04b | 09.52a | 7.87a | 31.69b | 136.6b |
| Unburnt | 3.14a | 07.63b | 6.15b | 42.18a | 139.3a |
| **Cropping** | | | | | |
| Burnt | 3.15a | 10.30a | 6.78b | 61.79a | 143.9a |
| Unburnt | 3.02b | 06.86b | 7.24a | 12.08b | 132.0b |
| **Microbial Inoculation (MI)** | | | | | |
| PSB + Fungi | 3.04c | 08.91b | 6.72d | 41.22b | 157.1b |
| $N_2$ fixer + Fungi | 3.06c | 07.58c | 6.15e | 42.06ab | 125.0d |
| CDB + Fungi | 3.11b | 05.75d | 8.00a | 42.74a | 122.5e |
| PSB + $N_2$ fixer + CDB + Fungi | 3.20a | 06.16c | 7.73b | 38.99c | 119.3f |
| Fungi | 3.21a | 11.33a | 6.24e | 35.57d | 145.3c |
| No inoculation (control) | 2.90d | 11.75a | 7.21c | 21.04e | 158.7a |
| **INTERACTION** | | | | | |
| J * C | ** | ** | ** | ** | ** |
| J * MI | ** | ** | ** | ** | ** |
| C * MI | ** | ** | ** | ** | ** |
| J * C * MI | | | | | |

SOC – Soil Organic Carbon; pMN; Potentially Mineralizable Nitrogen; POM – Particulate Organic Matter; SMBC – Soil Microbial Biomass Carbon DOC – Dissolve Organic Carbon *,** are levels of significance at the probability $P \leq 0.05$ and 0.01, respectively.
Within a parameter, the value followed by different letters are significantly differed at P≤0.05 within a factor (J, C, MI)

Table 4.9.: Interaction effect of burning, cropping and microbial communities on soil biochemical activities in 5 years *Jhum* cycle at 120 days growth of rice plant

| **Treatment** | SOC<br>% | pMN<br>µg $g^{-1}$(dw)soil | POM<br>% | MBC<br>µg /g | DOC<br>µg g soil |
|---|---|---|---|---|---|
| **Jhumming (J)** | | | | | |
| Burnt | 2.50a | 15.98a | 7.43a | 54.56a | 204.7b |
| Unburnt | 2.36b | 14.55b | 5.56b | 53.96b | 208.6a |
| **Cropping** | | | | | |
| Burnt | 2.41b | 18.25a | 8.50a | 51.195b | 204.0b |
| Unburnt | 2.46a | 12.27b | 6.33b | 57.339a | 209.3a |
| **Microbial Inoculation (MI)** | | | | | |
| PSB + Fungi | 2.43b | 10.56d | 07.23c | 66.61a | 231.4a |
| $N_2$ fixer + Fungi | 2.37c | 13.94c | 07.74b | 54.87c | 220.6c |
| CDB + Fungi | 2.41c | 18.95a | 07.70b | 57.27b | 154.1f |
| PSB + $N_2$ fixer + CDB + Fungi | 2.49a | 16.47b | 08.07a | 66.33a | 224.2b |
| Fungi | 2.48a | 13.22c | 07.05c | 48.26d | 203.0e |
| No inoculation (control) | 2.42b | 18.43a | 06.70d | 32.24e | 206.9d |
| **INTERACTION** | | | | | |
| J * C | ** | ** | ** | ** | ** |
| J * MI | ** | ** | ** | ** | ** |
| C * MI | ** | ** | ** | ** | ** |
| J * C * MI | | | | | |

SOC – Soil Organic Carbon; pMN; Potentially Mineralizable Nitrogen; POM – Particulate Organic Matter; SMBC – Soil Microbial Biomass Carbon DOC – Dissolve Organic Carbon *,** are levels of significance at the probability $P \leq 0.05$ and 0.01, respectively.
Within a parameter, the value followed by different letters are significantly differed at P≤0.05 within a factor (J, C, MI)

### 4.2.2.2. Biochemical properties of soil at 45 days growth stage of rice plant in response to burning, cropping and microbial inoculants

The soil biochemical properties such as SOC, pMN, POM MBC and DOC were strongly affected by burning, cropping and microbial inoculation (Table 4.7. and annexure 4.22., 4.23., 4.24., 4.25. and 4.26.).

The higher amount of SOC, pMN, POM and MBC were observed in unburnt soils where a slight increase was observed in case of DOC.

In cropping conditions all the tested soil biochemical properties were found higher in a condition where rice crop was grown than the bulk soils.

The SOC was found to be highest in a condition where soils was inoculated with sole synthetic fungi.pMN was highest in soil was inoculated with $N_2$ fixer + fungi. POM was highest in soil inoculated with CDB, $N_2$ fixer and PSB + fungi. The MBC were found highest where soil was inoculated with $N_2$ fixer + fungi and the inoculation of PSB + fungi had a great impact on DOC content in soil.

The interaction between jhumming* cropping; jhumming * microbial innoculation; cropping * microbial inoculation and jhumming * cropping * microbial inoculation were significance at a level $P \leq 0.01$.

### 4.2.2.3 Biochemical properties of soil at 90 days growth stage of rice plant in response to burning, cropping and microbial inoculants

The soil biochemical properties such as SOC, pMN, POM MBC and DOC were strongly affected by burning, cropping and microbial inoculation (Table 4.8. and annexure 4.27., 4.28., 4.29., 4.30. and 4.31.).

At 90 days of rice growth there was changes in MBC and DOC content in soil. The higher amount of SOC, pMN, POM and DOC were observed in unburnt soils interestingly a slight increase was observed in case of MBC at burnt soil.

The cropping does had an effect on biochemical properties. In comparision with bulk soil higher amount of soil biochemical properties was recorded in soil where rice crop was grown.

The SOC and pMN was found to be highest in a condition where soils was inoculated with sole fungi and pMN was highest in soil inoculated with $N_2$ fixer + fungi, POM and MBC were highest in soil inoculated with CDB + fungi and at 90 days the microbial inoculation doesn't had any effect on DOC content in soil.

The interaction between jhumming* cropping; jhumming * microbial innoculation; cropping * microbial inoculation and jhumming * cropping * microbial inoculation were significance at a level $P \leq 0.01$.

### 4.2.2.4 Biochemical properties of soil at 120 days growth stage of rice plant in response to burning, cropping and microbial inoculants

The soil biochemical properties such as SOC, pMN, POM MBC and DOC were strongly affected by burning, cropping and synthetic microbial inoculation (Table 4.9. and annexure 4.32., 4.33., 4.34., 4.35. and 4.36.).

Higher amount of SOC, pMN, POM and MBC were observed in burnt soils where the DOC content shows higher value in an unburnt soil.

The cropping does had an effect on biochemical properties. In comparision with bulk soil higher amount of soil biochemical properties was recorded in soil where rice crop was grown however higher amount of DOC content was found in soil where rice crop was not grown.

The SOC was found to be highest in a condition where soils was inoculated with sole synthetic fungi, pMN in soil was inoculated with CDB + fungi, POM and MBC in soil inoculated with PSB + $N_2$ fixer + CDB + fungi and highest DOC content was recorded with soil inoculated with PSB + fungi.

The interaction between jhumming* cropping; jhumming * microbial innoculation; cropping * microbial inoculation and jhumming * cropping * microbial inoculation were significance at a level $P \leq 0.01$.

## OBJECTIVE- III

### 4.3.1 Relationship of soil properties with bacterial community

The relationship of soil properties with bacterial community profile was determined by super imposing soil data matrix on Multidimensional (MDS) plot. The weightage of individual soil properties in separating the bacterial communities was determined by Pearson co-relation co-efficient along with the MDS axis. The super impose soil data matrix on MDS plot shows that soil properties had played role in separating bacterial (Fig.4.16.). The bacterial community based MDS plot at 10 days of rice growth indicated that DHA, ASA, pMN, POM played significant role in separating bacterial communities in MDS axis 1 according to the presence and absence of rice. On the other hand MBC played significant role in separating burn and unburn soil along the MDS axis 2 (Table 4.10.). The other soil properties though they have show co-relation with MDS axis there effect was not significant.

### 4.3.2. Relationship of soil properties with Alpha proteobacteria at 45 days of rice growth stage

The relationship of soil properties with bacterial community profile was determined by super imposing soil data matrix on Multidimensional (MDS) plot. The weightage of individual soil properties in separating the bacterial communities was determined by Pearson co-relation co-efficient along with the MDS axis. The super impose soil data matrix on MDS plot shows that soil properties had played role in separating bacterial (Fig.4.17.). Alpha-Proteobacterial group based MDS plot at 45 days of rice growth indicated that pMN, POM and DOC played significant role in separating bacterial communities in MDS axis 1 according to the presence and absence of rice. On the other hand DHA played significant role in separating burn and unburn soil along the MDS axis 2 (Table 4.11.). The other soil properties though they have show co-relation with MDS axis there effect was not significant.

### 4.3.3. Relationship of soil properties with Alpha proteobacteria at 90 days of rice growth stage

The relationship of soil properties with bacterial community profile was determined by super imposing soil data matrix on Multidimensional (MDS) plot. The weightage of individual soil properties in separating the bacterial communities was determined by Pearson co-relation co-efficient along with the MDS axis. The super impose soil data matrix on MDS plot shows that soil properties had played role in

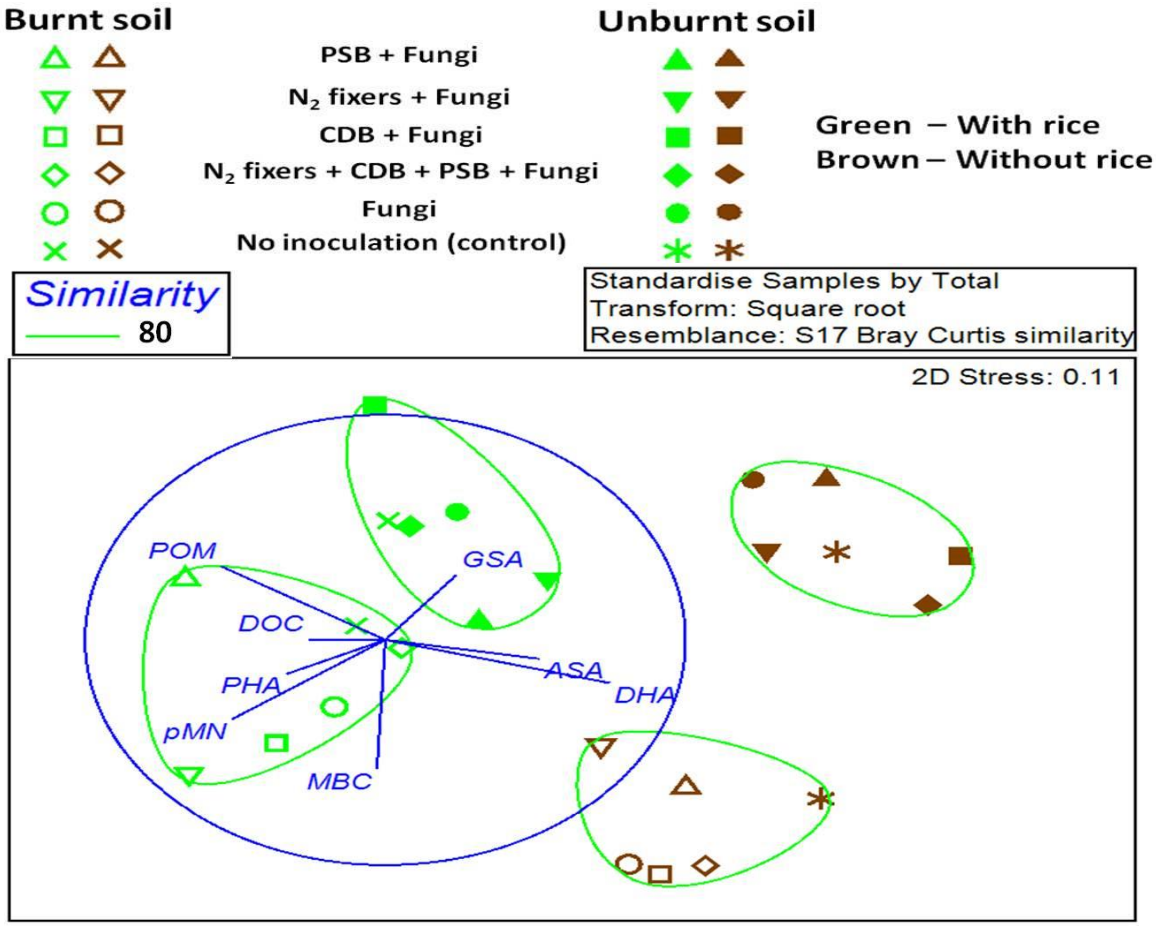


Fig.4.16: Principal Component Anlaysis plot showing relationship of bacterial community and soil properties at 10 days of rice growth

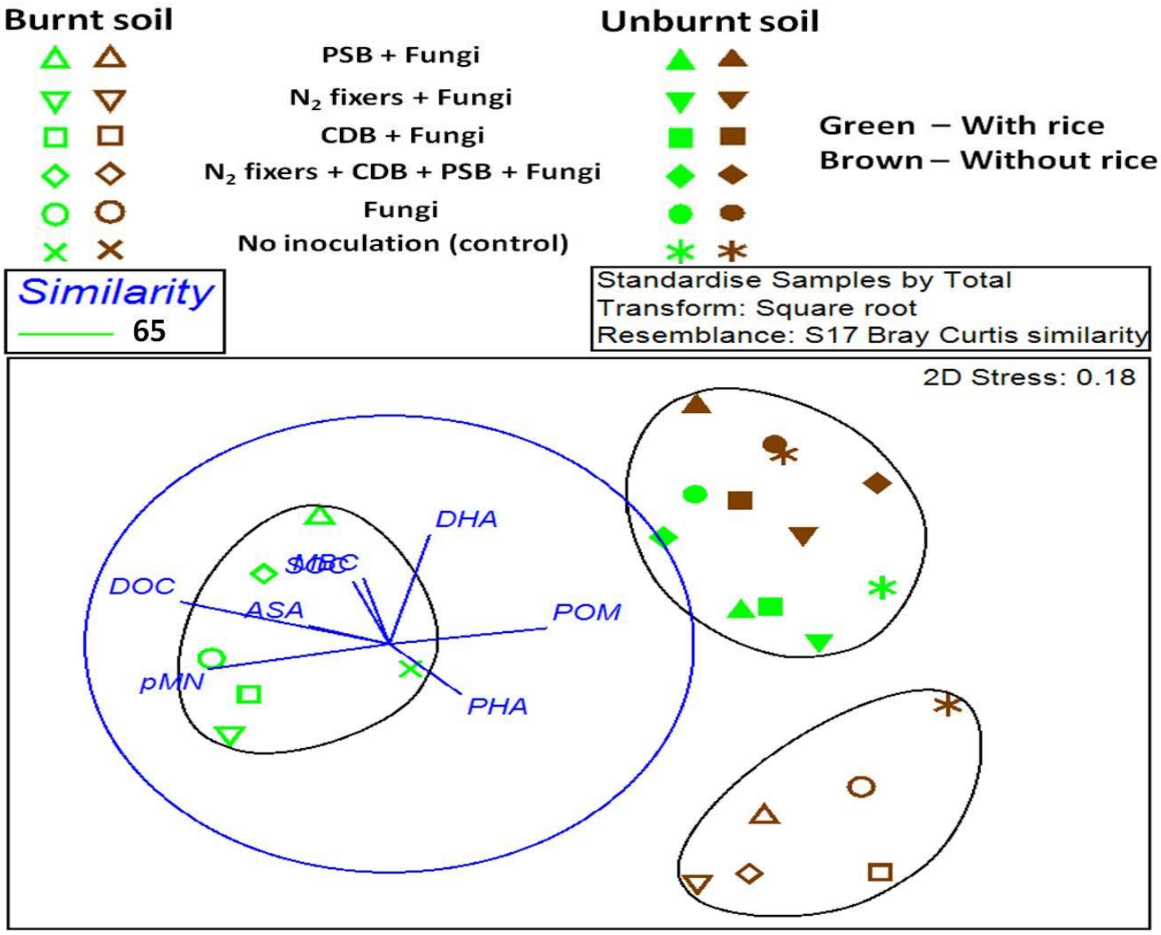


Fig.4.17: Principal Component Anlaysis based plot showing relationship of Alpha Proteobacterial community and soil properties at 45 days of rice growth

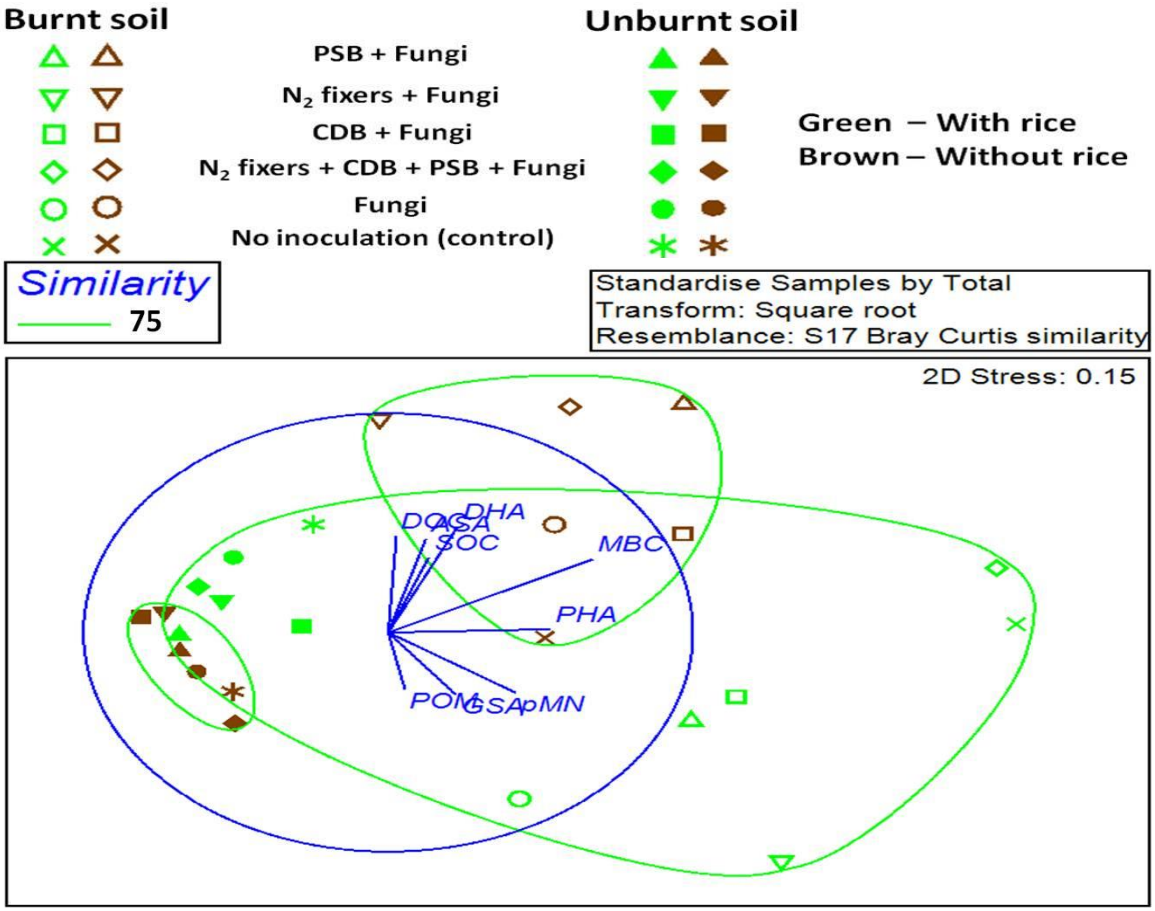


Fig.4.18: Principal Component Anlaysis based plot showing relationship of Alpha Proteobacterial community and soil properties at 90 days of rice growth

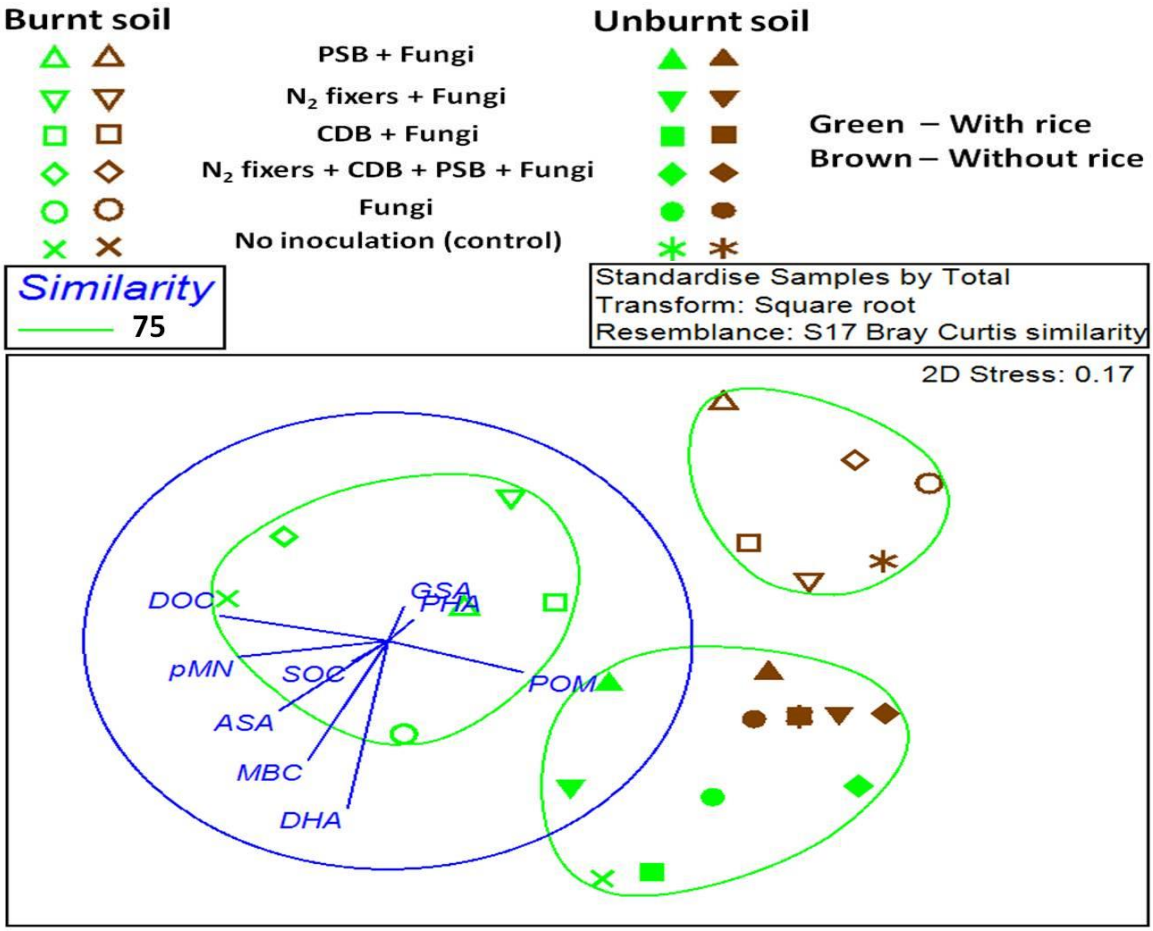


Fig.4.19: Principal Component Anlaysis based plot showing relationship of Beta Proteobacterial community and soil properties at 45 days of rice growth

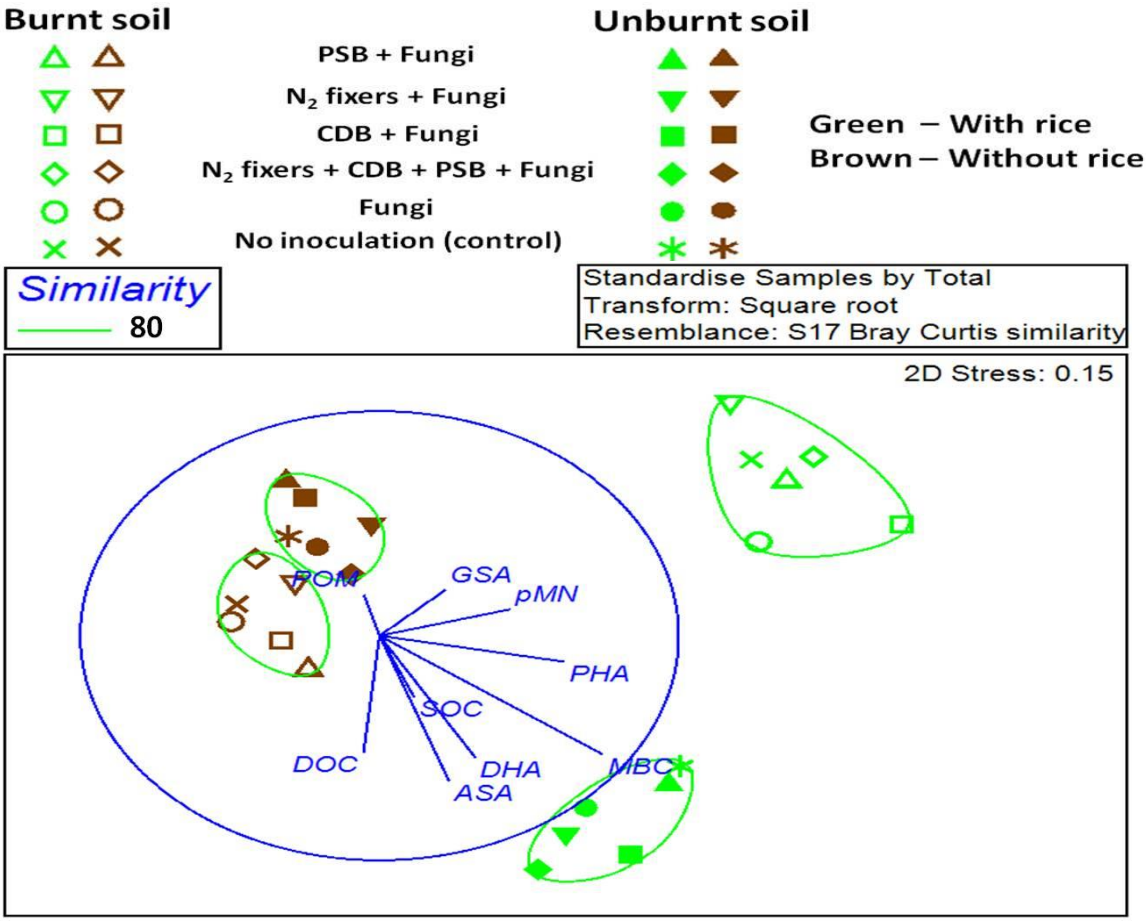


Fig. 4.20: Principal Component Anlaysis based plot showingrelationship of Beta Proteobacterial community and soil properties at 90 days of rice growth

Table 4.10: Pearson's correlation coefficient (r) for the relationship of bacterial community in MDS axis with soil propertiesat 10 days of rice plant growth

| | MDS 1 | MDS 2 |
|---|---|---|
| GSA | 0.24 | 0.29 |
| ASA | 0.51** | -0.08 |
| PHA | -0.33 | -0.15 |
| DHA | 0.75** | -0.19 |
| pMN | 0.51** | -0.35 |
| MBC | -0.03 | -0.57** |
| DOC | -0.25 | 0.00 |
| SOC | -0.07 | 0.10 |
| POM | -0.55** | 0.33 |

* and ** indicate level of significance at P≤0.005 and 0.01 respectively.

Table 4.11: Pearson's correlation coefficient (r) for the relationship alpha proteobacterial community along the MDS axis with soil propertiesat 45 days of rice plant growth

| | MDS 1 | MDS 2 |
|---|---|---|
| GSA | -0.06 | 0.05 |
| ASA | -0.26 | 0.08 |
| PHA | 0.24 | -0.22 |
| DHA | 0.13 | 0.48* |
| pMN | -0.60** | -0.11 |
| MBC | -0.09 | 0.29 |
| DOC | -0.69** | 0.19 |
| SOC | -0.12 | 0.27 |
| POM | 0.52** | 0.07 |

* and ** indicate level of significance at P≤0.005 and 0.01 respectively.

Table 4.12: Pearson's correlation coefficient (r) for the relationship alpha proteobacterial community along the MDS axis with soil propertiesat 90 days of rice plant growth

| | MDS 1 | MDS 2 |
|---|---|---|
| DOC | 0.03 | 0.44* |
| GSA | 0.22 | -0.28 |
| ASA | 0.12 | 0.43* |
| PHA | 0.53** | 0.01 |
| pMN | 0.42* | -0.27 |
| MBC | 0.67** | 0.33 |
| SOC | 0.13 | 0.34 |
| DHA | 0.23 | 0.48 |
| POM | 0.05 | -0.26 |

* and ** indicate level of significance at P≤0.005 and 0.01 respectively.

Table 4.13: Pearson's correlation coefficient (r) for the relationship beta proteobacterial community along the MDS axis with soil propertiesat 45 days of rice plant growth

| | MDS 1 | MDS 2 |
|---|---|---|
| GSA | 0.05 | 0.15 |
| ASA | -0.36 | -0.31 |
| PHA | 0.09 | 0.09 |
| pMN | -0.50* | -0.07 |
| SOC | -0.12* | -0.09 |
| DOC | -0.55** | 0.11 |
| DHA | -0.13 | -0.73** |
| MBC | -0.26 | -0.52** |
| POM | 0.44 | -0.14 |

* and ** indicate level of significance at P≤0.005 and 0.01 respectively.

Table 4.14: Pearson's correlation coefficient (r) for the relationship beta proteobacterial community along the MDS axis with soil propertiesat 90 days of rice plant growth

| | MDS 1 | MDS 2 |
|---|---|---|
| DOC | -0.05 | -0.52** |
| GSA | 0.22 | 0.20 |
| ASA | 0.23 | -0.65** |
| PHA | 0.62** | -0.12 |
| pMN | 0.44** | 0.12 |
| MBC | 0.75** | -0.53** |
| SOC | 0.12 | -0.27 |
| DHA | 0.32 | -0.54** |
| POM | -0.05 | 0.18 |

* and ** indicate level of significance at P≤0.005 and 0.01 respectively.

separating bacterial (Fig.4.18). Alpha-Proteobacterial group based MDS plot at 45 days of rice growth indicated that PHA, pMN, MBC played significant role in separating bacterial communities in MDS axis 1 according to the presence and absence of rice. On the other hand DOC and ASA played significant role in separating burn and unburn soil along the MDS axis 2 (Table 4.12.).The other soil properties though they have show co-relation with MDS axis there affect was not significant.

### 4.3.4. Relationship of soil properties with Beta proteobacteria at 45 days of rice growth stage

The relationship of soil properties with bacterial community profile was determined by super imposing soil data matrix on Multidimensional (MDS) plot. The weightage of individual soil properties in separating the bacterial communities was determined by Pearson co-relation co-efficient along with the MDS axis. The super impose soil data matrix on MDS plot shows that soil properties had played role in separating bacterial (Fig.4.19.). Beta-Proteobacterial group based MDS plot at 45 days of rice growth indicated that SOC, pMN, DOC played significant role in separating

bacterial communities in MDS axis 1 according to the presence and absence of rice. On the other hand DHA and SOC played significant role in separating burn and unburn soil along the MDS axis 2 (Table 4.13). The other soil properties though they have show co-relation with MDS axis there effect was not significant.

### 4.3.5. Relationship of soil properties with Beta- proteobacteria at 90 days of rice growth stage

The relationship of soil properties with bacterial community profile was determined by super imposing soil data matrix on Multidimensional (MDS) plot. The weightage of individual soil properties in separating the bacterial communities was determined by Pearson co-relation co-efficient along with the MDS axis. The super impose soil data matrix on MDS plot shows that soil properties had played role in separating bacterial (Fig.4.20.). Alpha-Proteobacterial group based MDS plot at 90 days of rice growth indicated that PHA, pMN, MBC played significant role in separating bacterial communities in MDS axis 1 according to the presence and absence of rice. On the other hand DOC, ASA, MBC and DHA played significant role in separating burn and unburn soil along the MDS axis 2 (Table 4.14.).The other soil properties though they have show co-relation with MDS axis there effect was not significant.

# Chapter-5
# Discussion

## 5.1 Soil Physio-chemical Properties

The burning event caused variations in the physico-chemical attributes of *jhum* soils. Burning activities have reduced the organic matter content from the secondary forests which were found to reduce the bulk density of soil (Alegre and Cassel 1996; Granged *et al.,* 2011; Biswas *et al.,* 2012). Rise in pH after burning was more prominent in acidic soils than in alkaline soils and was reported to be contributed by loss of OH, oxide formation and release of alkaline cations like Ca, Mg, and K (Certini, 2005). Results from this study also indicated that EC of the soil has increased immediately after burning. Similar increment in EC was previously observed by Terefe *et al.* (2008) when the soil was exposed to beyond 150°C. It was reported that the soil temperature rose up to 242°C± 10°C during burning of slashed biomass in *Jhum* fallows of NE India (Thakuria, 2015).

Decrease in SOC content after burning has been vividly described in the past (Nye and Greenland, 1960; Fernandez *et al*., 1997). Alteration in SOC content can be accounted for higher topsoil temperature (242°C± 10°C) during burning that causes burning of FFLs leading to limited incorporation of litter materials in burnt plots (Tinker *et al.,* 1996). At temperatures above 300°C, soil organic N is lost during the thermal oxidation of organic matter in the form of oxidized N gases and $N_2$ (Raison, 1979). The content of $NO_3$-N has a declining trend after burning (Ramakrishnan and Toky, 1981). In this study, soil Avl N content decreased after burning. Past findings indicated that burning activity decreased the content of soil Avl N. Depletion of N from the topsoil attributed to leaching loss caused by heavy monsoon rainfall and absorption by fast sprouting weed species (Wallbrink *et al.,* 2005), which is a common phenomenon in *jhum* fields across Northeast India. Loss of nitrogen at temperature as high as 100°C was reported by DeBano *et al*. (1979), which in the case of conventional *jhumming* usually exceed this threshold temperature. Increase in the content of Avl P after burning is a common phenomenon in *jhum* scenarios across Northeast India. Recently, Adeyolanu *et al*. (2014) has also cited an increase of Avl P while studying a slash and burn situation in tropical rainforest of Nigeria. The increase in Avl P can be attributed to the incorporation of P from the slashed biomass in the form of ash as indicated by Raison *et al*., 1985). Ramakrishnan and Toky (1981) reported increase in P and K concentrations after burning as well as an increasing

trend with increase in fallow length and summarized the phenomenon to be controlled by quantum of slashed and burned biomass of the above-ground plant species. Neff *et al*. (2005) have however reported about a mild shift in the K content after burning.

## 5.2. Responses of soil microbes to burnt and unburnt soils

In slash and burn agriculture burning activities play a major role in altering soil microbial community. Good indicator of soil biological activity i.e enzymes and soil health altered as soil microbial community structure change. Soil microbes are sensitive to fire. Structural differences of microbial communities from burnt to unburnt was well documented (Hamman *et al*., 2007; Xiang *et al*., 2014). The aboveground vegetation affects the size, abundance, diversity, composition and activity of microbial community in soils (Nusslein and Tiedji, 1999 and da Jesus *et al*., 2009; Zhao *et al*., 2014). The microbial structure gets affected with a change in ecosystem functions such as interaction between plants, soil and microorganisms which lead to manipulation in ecological processes (Singh *et al*., 2004). Land management, soil attributes and plant species were important for maintaining the structure and functions of bacterial communities (Nusslein and Tiedje, 1999; Wieland *et al*., 2001; Steenwerth *et al*., 2002; Hartman *et al*., 2008; Lauber *et al*., 2008; da Jesus *et al*., 2009 and Blasiak *et al*., 2014). The microbial community in soil can be affected by fire, land use and change in plant species which are the main component in shifting cultivation (Carson *et al*., 2010).

Soil microbial community composition and diversity was directly or indirectly affected by fire. Fire produces heat which kills the soil micro-organism and reduces the microbial biomass (Wang *et al*., 2012). Thus, fire become the threats to forest ecosystems (Bond and Keeley, 2005; Barcenas *et al.,* 2011; Xiang *et al*., 2014). Shift of Bacteroidetes and Betaproteobacteria with greater abundance. Alphaproteobacteria and Acidobacteria with reduced at boreal forest of China (Xiang *et al*., 2014). With a higher abundance of the genus Bradyrhizobium, shifts in bacterial community composition was also reported in slash and burn system. Betaproteobacteria was reported as most abundant bacterial group in slash and burn system (Blasiak *et al*., 2014).

From our present study using PCR-DGGE fingerprint, the soil bacterial community was found to be distinctly separated out between burnt and unburnt soils. In burnt and unburnt soils the bacterial communities cluster separately according to the presence or absence of rice crop. The stronger factor of variability in shaping the soil bacterial community at 10 days of rice plant growth and alpha-proteobacterial

community composition at 45 and 90 daysof rice plant growth was found to be in the order burning > cropping > microbial inoculation treatment. The beta-proteobacterialcommunity at 45 and 90 days of rice plant growth clustered separately according to the presence or absence of rice crop in burnt soil or unburnt soil. The stronger factor of variability in shaping the beta-proteobacterialcommunity composition was found to be in the order cropping> burning > microbial inoculation treatment. Hamman *et al*. (2007) reported the difference in structural soil microbial communities in burnt soils from unburnt soils of forest fire in central Colorado which was in aggrement with our findings. Our studies indicate that cropping/ presence of plants in soils shows a distinct separation in soil microbial community which could be due to the variation in secretion of root exudates by plants in a different quantity and quality leads to selection of rhizopheric microbes which in turn results in different microbial communities in soil (Nguyen, 2003 and Zhang *et al*., 2013). The presence of various plant species with special functional traits (C4 grasses, nitrogen-fixing legumes) effects the eco-system functioning (Balvanera *et al*., 2006; Fornara and Tilman, 2008) and improve the intricacy of soil microorganisms by rising the heterogeneity of organic substrates during decomposition of living roots and litter (Broughton and Gross, 2000). The restoration patterns of soil bacterial community differ under different vegetation (Zhang *et al.,* 2013). Deka and Mishra,1983 and Pandey *et al*., 2011) in their studies reported fire stimulates the actinomycetes population, fungi as the least affected group by fire and bacteria as the most affected group. Study conducted in Khasi hills of Megahalaya, India, reported that after two to three showers microbial population increased in the burnt plots as compared to unburnt (Sharma *et al*., 2004). With specific plant types the Mycorrhizal fungi and basidiomycota form symbiotic associations and the lignified plant detritus gets decomposed respectively and fungi are more sensitive to change in types of vegetation than soil bacteria (Bardgett and Mc Alister, 1999).

Microbial inoculation affect the soil microbial community, however, its effect was less prominent in our studies. Plant–soil-microorganism interaction results in a complex reactions. The inoculations of PGP (*Azospirillum brasilense*) with maize results in more number of roots in the soil (Dobbelaere *et al*., 2003), higher enzymes activity and microbial densities in the rhizospheric zone is due to the inoculation of soils with the beneficial micro-organism (Mawdsley & Burns, 1994 and Sowinski *et al*. 2007). When rhizobia (*Sinorhizobium meliloti)* was used as inoculants in field the diversity of bacterial community in the root zone was quantitatively and qualitatively affected. The proteobacteria groups largely get ffected by this inoculations which

results in reduction in numbers of $\gamma$-proteobacteria whereas the $\alpha$-proteobacteria were increased in numbers (Schwieger and Tebbe, 2000). Plant nutrient uptake, growth, development and yield of plants are effected by the inoculation of Rhizobium culture by different mechanism. As they are capable to fixing nitrogen, that accelerate the nitrogen-fixing free-living bacteria in soils which in turns results in increase the production of the essential nutrients such as phosphorus and iron for plants. Alterations of soil microbial community due to inoculation of various beneficial micro-organism may occur through secretion of antibiotic compound and their influence on rhizopheric bacterial communities. Spatial and temporal effects on rhizobacterial or fungal population noticed as the root zone was colonized with antibiotic-producing fluorescent pseudomonads, 2,4-diacetylphoroglucinol or phenazine compound produced (De Leij *et al*., 1995; Girlanda *et al*., 2001; Naseby & Lynch, 2001; Bakker *et al*., 2002 and Sowinski *et al*. 2007). The trifolitoxin-sensitive bacteria (Alphaproteobacteria) gets reduce in the root zone of bean due to secretions of trifolitoxin by *Rhizobium etlidue* (Robleto *et al*., 1998; Trabelsi and Mhamdi, 2013).

The importance of plant functions, nutrient cycling, primary productivity, litter decomposition and ecosystem stability and resistance to disturbance rates to ecosystem process was reported by (Madritch and Hunter, 2002 and Madritch *et al*., 2006). Change in litter quality was a result of alteration in plant community composition that disturbed soil conditions and nutrient cycling processes.

## 5.3. Effect of burning, cropping and microbial inoculation on soil enzymes activity as an indicator of soil processes

Soil enzymes get reduced as their hydrological enzyme gets disturbed by burning activities (Boerner *et al*., 2005). Change in their environment and oxidation of the available compounds by fire also directly affect the microbial activities in soil. Fire change the soil energy pathway which reflects in taxonomic shift in soil microbial communities (Bisset and Parkinson 1980).The soil enzymes such as DHA, GSA, ASA and PHA were strongly influenced by the burning, cropping and microbial inoculation throughout the rice crop growing season in our investigation. With the consequence of seasonal moisture changes, soil temperature and land management, soil and vegetation conditions the phosphatase activity in soil gets effected (Herbien and Neal, 1990; Speir and Cowling, 1991). It also reflects and feedback on community composition (Sinsabaugh *et al*., 2002). As PHA is directly affected by various factors the effect of PHA due by fire which results in decrease of PHA activity in soil(Ajwa *et al.,* 1999; Boerner *et al*., 2000). This past findings was concurrent with our present

finding that PHA enzymes activity decrease in burnt soil as comparison to the unburnt soils. The higher amount of PHA in soil with rice plant in comparisons to bulk soil was observed when there was P deficient in a soil plant roots secrete which enhance the solubilisation and remobilization of phosphate in soil and in bulk soil there was no such things which can release the phosphatase enzymes (Nakas *et al*., 1987; Chrost, 1991; Muchhal *et al*., 1996; Li *et al*., 1997; Daram *et al*., 1999; Kai *et al*., 2002; Versaw and Harrison, 2002). PHA enzymes activity was high in soils inoculated with functional PSB + synthetic fungi. Soil microclimate, SOC and the availability of P in the soil governed phosphatase enzyme and involved in P-cycling (Hamman *et al*., 2008).

GSA a good indicator of advanced changes in soil organic carbon(Dick, 1994; Wick *et al*., 1998). Thus, become a good biochemical indicator for measuring ecological changes. In present studies show a decreasing trend of GSA in burnt soil throughout the rice growing session and a similar results of decrease in GSA activity after burning was reported by (Ajwa *et al.,* 1999: Saplalrinliana *et al*., 2016 and Lungmuana *et al*., 2017). Under the influence of rice plant GSA activity was found higher throughout the rice growing session.This could be that most dominant glucosidase i.e β-glucosidase was released to the soil largely by plants, animals, fungi and bacteria (Esen, 1993).The most predominant source of β-D-glucosidase activity in soils was reported to be Fungi (Hayano and Katami, 1977; Hayano and Tubaki, 1985). This enzyme activity play a fundamental role in release of labile carbon to microorganism as well as C cycling in large scale (Acosta *et al*., 2007). GSA was found highest in soil inoculated with synthethic CDB + Fungi. CDB being involved in C-cycling this can be the result where highest GSA activity was found in soil inoculated with functional CDB + synthetic fungi.

The labile cellulose was broken down byβ - glucosidase, which involves in plant cell tissues decomposition at the first phases. This cell wall decompositions activities trigger the other enzymes such as proteases and phosphatases (Turner *et al*., 2000Sardans *et al*., 2008). Glucose as its final product it becomes an important C energy source to microbes in soil. (Esen, 1993). Its sensitivity to land management and soil pH was reported by (Dick *et al*., 1996; Bergstrom *et al*., 1998; Acosta-Martinez and Tabatabai, 2000; Ndiaye *et al*., 2000) and also reflects the past biological activity.

The decrease of DHA in burnt soils was observed throughout the rice growing session in comparison with unburnt soils. Our present study was in harmony with the past findings of (Ajwa *et al.,* 1999; Wolińska and Stępniewska, 2012; Saplalrinliana *et al*., 2016; Lungmuana *et al*., 2017) who reported the decrease of DHA after burning. Polluted soil with fly ash has lower DHA activity (Pitchel and Hayes,

1990). DHA as an intracellular enzymes it has a close relationship with microbial activity and is often used as an indicator of microbial activity in soil (Skujins, 1976:Nannipieri *et al*., 1990; Dick, 1994.). Both DHA and GSA activity patterns resembled the associated change in OC as a reflection of change in substrate availability for soil microbial community (Saha *et al*., 2011; Gispert *et al*., 2013).

Types and amount of organic matter content (Sarathchandra and Perrott, 1981) and change in soil pH (Acosta-Martínez and Tabatabai, 2000) contributes the reasons for change in ASA activity. Burning the biomass result in increase in soil pH which results to changes in ASA activity after burning and a similar change was also reported by (Vong *et al*., 2003) Microbial biomass in different soil systems is often correlated to the rate of S immobilisation (Klose and Tabatabai, 1999; Vong *et al*., 2003). With the introduction of rice crop ASA activity increases in comparison to bulk soil. This is due to the fact that where a crop is grown there was stress of available sulphur content in soil which results in increased secretion of sulphatase to cope up with the ecological demand thus results in higher ASA content in soils where rice crop was grown (Saplalrinliana *et al*., 2016; Lungmuana *et al*., 2017).

The possible causes of negative impact of burning on soil enzyme activities are: (1) depletion of hydrolytic enzyme pools due to breakdown of above- and below-ground community (2) sudden reduction in soil biota population and (3) nutrient enrichment in soils after burning reduce the dependency of crop plants on enzyme activities.

## 5.4. Burning, cropping, and microbial inoculation effect to soil biochemical properties

Soil biochemical properties get affected by burning activities. Our studies show that there was a decline in soil biochemical properties after burning. SOC, POM, MBC were gradually decreased during the cropping season. In first year of paddy cultivation by 17 to 31.3% the SOC decrease after burning in NE India (Ramakrishnan and Toky, 1981).The soil biochemical properties decreases throughout the cropping season by 6.1% after burning in Mizoram(Lungmuana *et al*., 2017). Burning of slash biomass results in alteration of SOC content which was reduced by 10 to 22.3% in *jhum* agriculture as burning activities accelerated soil erosion process greatly (Hatten *et al*., 2005; Choudhury *et al*., 2015). The decrease in SOC, MBC content after burning reflects the immediate degradation of soil by burning and as POM is sensitive to land management its amount decrease in soil after burning

(Aumtong *et al.,* 2009). Our study reveals that soil biochemical activities were higher where rice crop was grown in comparison to bulk soil. Higher microbial biomass in the ecosystem was a result of higher OM input normally due to rhizodeposition (Shao *et al*., 2015). Root mass, fine roots production from plants increased the accumulation of MBC, SOC become one of the major factors for increasing the soil microbial activity (Ajwa *et al*., 1999). The MBC and MBN was reduced by 82 and 71% respectively in the 1$^{st}$ year after burning (Xiang *et al*., 2014).

## 5.5. Relationship of soil properties with soil bacterial community

Affect of carbon pool by burning was reported by various scientists (Ramakrishnan and Toky, 1981; Aumtong *et al.,* 2009; Lungmuana *et al*., 2017). Our studies confirm the past findings in which the PCA studies also reveals that the carbon pool had a significant role in separating out the burnt soils and unburnt soils. Mainly MBC and DHA act as the main role in separating the soils from burnt to unburnt soils. DHA as an intracellular enzymes it has a close relationship with microbial activity and is often used as an indicator of microbial activity in soil (Nannipieri *et al*., 1990; Dick, 1994). Change in OC as a reflects changes in substrate availability for soil microbial community and DHA activity patterns resembled the associated chages in OC and substarte availability (Saha *et al*., 2011; Gispert *et al*., 2013). The relationship study of soil properties with bacterial community profile by super imposing soil data matrix on MDS plot shows that soil properties DHA, ASA, pMN, POM had significant role role in separating bacterial communities in MDS axis 1 according to the presence and absence of rice at 10 days where MBC played significant role in separating burn and unburn soil. In case of Alpha proteobacteria at 45 and 90 days of rice growth soil properties like pMN, POM, DOC PHA, MBC had significant role in separating bacterial communities according to the presence and absence of rice where as DHA, DOC, ASA played significant role in separating burn and unburn soil and with Beta proteobacteria at 45 and 90 days of rice growth SOC, pMN, DOC PHA, and MBC had significant role in separating bacterial communities according to the presence and absence of rice where as MBC and DHA played significant role in separating burnt and unburnt soil. In slash and burn agriculture due to biomass burning the soil pH shows a gradual increase after burning and also change in organic matter content. This could be the results for ASA activity for separating the burnt and unburnt soils. This finding is in concurrent with the past finding of (Sarathchandra and Perrott, 1981, Acosta-Martínez and Tabatabai, 2000 and Vong *et al*. (2003) who state that ASA activity

results in types, amount of organic matter content and change in soil pH As ASA activity gets affected by change in soil pH.

Soil enzymes activities along with carbon pool played a significant role in separating out the bacterial community in presence and absence of rice plant. This could be due to that change in land management, soil and vegetation conditions the phosphatase activity in soil gets effected (Herbien and Neal, 1990; Speir and Cowling, 1991). With a limitations of available P for plant uptake the plant roots secrete phosphatase which enhance the solubilisation and remobilization of phosphate in soil. (Versaw and Harrison, 2002). DHA as an intracellular enzymes is often used as an indicator of microbial activity in soil (Skujins, 1976, 1984; Nannipieri *et al*., 1990; Dick, 1994). Both DHA and GSA activity patterns resembled the associated change in OC as a reflection of change in the availability substrate for soil microbial community (Saha *et al*., 2011; Gispert *et al*., 2013).

Change in OC is the results of change in substrate availability which results in change in microbial activity. As the carbon pool are sensitive to land management burning activities results change in carbon pool. With the introduction of crops in shifting cultivation root mass, fine roots were produce from plants. The plants roots and fine roots release the exudates which results in selections of microbes in the root zone and with a monsoon shower the soil microbial activity in soils gradually increase. This could be the reason for which the soil carbon pool had a significant role in separating the soil bacterial community in presence and absence of rice crop. This findings was in concurrent with the past findings of sensitivity of carbon pool to land management (Aumtong *et al.,* 2009), increasement of rhizodeposition leads to higher microbial biomass (Shao *et al*., 2015), increased the accumulation of MBC, SOC from plants root mass, fine roots as major influential factors towards the increased of microbial activity (Ajwa *et al*., 1999).

# Chapter-6

# Summary and Conclusion

Soil is the power house for all the terrestrial ecosystems. For biogeochemical cycles it is an essential and through thes cycle the soil functions. Both abiotic and biotic factors affect the soil functioning and its processes in soils. The major component of biological soil processes is soil enzymes activity. Soil enzymes play key role in decomposition of organic compounds, formation of organic matter in soil, their mineralization and recycling of nutrients. Due to different composition and activity of its living organisms, organic matter content and intensity of the biological processes, the enzymes level in soil vary. Understanding the relationship of soil enzymes activities, influence of crop plants to soil microbial community andits association to soil nutrient cycling processes has become one of ecology's primary goals in order to effectively maintain and sustain the functioning of an*jhum*agroecosystem. *Jhum* agroecosystem is the unique blending of forest ecology and agroecology in the sense that the fallow phase represents the secondary forest succession and rejuvenation of soils while the cropping phase represents the primitive forms of agricultural practices involving slashing and burning of above-ground forest biomass and breaking the functional linkages with the below-ground counterparts. As such above-ground and below-ground linkages in *jhum* agroecosystem can be influential mutual drivers, with both positive and negative impacts. Thus the impact assessment of *jhum* practices on soil biochemical processes as a reflection of the functioning of soil biota community and how the above-ground biological inputs like accumulated forest floor litters during fallow phase control over the functioning of soil biochemical processes were studied in this research.

The soil bacterial community composition altered significantly due to burning of slashed biomass on soil surface. The introduction of rice crop also altered the bacterial community composition in burnt/unburnt soil as evident from distinct cluster within the soil type. Though microbial inoculants treatment had impact on soil bacterial community composition, but such effect were obscured due to burn and crop factor.The Alpha proteobacterial communities of burnt and unburnt without rice crop clustered together and distinctly separated from the clusters of burnt and unburnt soil with rice crop at 45 days of rice growth. At 90 days of rice growth the impact of rice crop on composition of Alpha and beta proteobacterial community was more permanent in burnt soil then in unburnt soil. In absence of rice crop the beta

proteobacterial community of burnt and unburnt soil cluster together and there cluster was distinctly separated from the cluster of burnt and unburnt soil with rice crop at 45 days of rice growth. With the progress of time (90 days of rice growth) the effect of rice crop on beta proteobacterial community was more prominent than compared to burnt unburnt factor.

Burning had significant negative effect on the activity of enzymes such as DHA, GSA, PHA except ASA indicating higher activity in burnt soil. Introduction of rice crop had significant positive influenced on the activity of soil enzymes. There was significant positive interaction on burning and cropping on soil enzymes activities. There was a significant difference in the activity of soil enzymes among the microbial inoculants treatment. There was significant positive interaction between burnt and microbial inoculants or cropping and microbial inoculants. Burning had significant negative effect on SOC, pMN, POM, and MBC. Introduction of rice crop had significant positive influence on the activity on soil process indicators. There was significant positive interaction on burning and cropping on soil process indicators. There was significant differences in the activity of soil process indicators among the Microbial inoculants treatment. There was significant positive interaction between burnt and microbial inoculants or cropping and microbial inoculants

The change in bacterial community composition due to burning and cropping factor significantly influence soil process indicator like ASA, DHA, pMN, POM, and MBC as evident from their significant correlation with MDS 2. The change in alpha and beta proteobacterial community composition due to burning and cropping factor significantly influence soil process indicator like PHA, ASA, DHA, pMN, POM, SOC and MBC as evident from their significant correlation with MDS 1 and 2.

Burning of slash biomass on surface soil can altered soil bacterial community composition. The influence of rice crop on composition of soil bacterial community was more prominent in burnt soil than unburnt soil. The clustering behavior of soil bacterial community indicated that the greater influencing factors in shaping community composition is in order of burning > cropping > microbial inoculation. However, cropping seems to be greater influencing factor than burning in case of β-proteobacterial community. Burning had significant positive influence on rice growth yield. Therefore, it can be concluded that introduction of crop in burn soil along with microbial inoculation may positively influence soil processes as well as crop growth.

This research showed through pot experiment and laboratory analysis that burning of vegetative biomass does not change alpha and beta proto-bacterial

diversity; however cultivation of rice in the burnt soil cause a significant alteration of bacterial community. Perhaps, the gradual decomposition of the left over unburnt biomass through decomposition brings conspicuous change in soil microbial community upto 45 days of crop growth, as a result the influence of rice plant/ root activity is not seen conspicuously in the bacterial community. This is also reflected in different soil enzymes activities of the two systems i.e., burnt and unburnt. The influence of factor such as biomass burning, cropping and microbial inoculation in shaping microbial community composition is shown as burning cropping microbial inoculation. Thus in a burnt field cropping phase brings a positive change in microbial community and soil process and application of consortia of beneficial bacteria might help in enhcancing crop peoductivity. Such mechanistic studies may be directed in *jhum* system of varying fallow cycle in future research.

# BIBLIOGRAPHY


Acosta-Martínez, V. and Tabatabai, M.A. (2000). Enzyme activities in a limed agricultural soil.*Biol. Fert. Soils*, 31: 85-91.

Acosta-Martinez, V., Cruz, L., Sotomayor, R.D. and Perez-Alegrıa, L. (2007). Enzyme activities as affected by soil properties and land use in a tropical watershed. *Appl. Soil Ecol.*, 35: 35–45.

Aguilar-Fernández, M., Jaramillo, V.J., Varela, F.L. and Gavito, M.E. (2009).Short-term consequences of slash-and-burn practices on the arbuscular mycorrhizal fungi of a tropical dry forest. *Mycorrhiza*, 19: 179-186.

Ajwa, H.A., Dell, C.J. and Rice, C.W. (1999). Changes in enzyme activities and microbial biomass of tall grass prairie soil as related to burning and nitrogen fertilization. *Soil Biol. Biochem.,* 31: 769–777.

Alguacil, M.M., Torrecillas, E., García-Orenes, F. and Roldán, A. (2014). Changes in the composition and diversity of AMF communities mediated by management practices in a Mediterranean soil are related with increases in soil biological activity. *Soil Biol. and Biochem.,* 76: 34-44.

Allison S.D. and Treseder K.K. (2008). Warming and drying suppress microbial activity and carbon cycling in boreal forest soils. *Glob Chang Biol*., 14: 2898–2909.

Allison, S.D., Martiny, J.B.H. (2008). Resistance, resilience, and redundancy in microbial communities. *Proc. Natl. Acad. Sci*. U.S.A. 105: 11512–11519.

Allison, S.D. (2006). Soil minerals and humic acids alter enzyme stability: implications for ecosystem processes. *Biogeochem.*, 81: 361–373

Allison, S.D., and Vitousek, P.M. (2005). Responses of extracellular enzymes to simple and complex nutrient inputs.*Soil Biol. Biochem.,* 37: 937-944.

Altieri A.M. (1999). The ecological role of biodiversity in agroecosystem.Invertebrate Biodiversity as Bioindicators of Sustainable Landscapes. Practical Use of Invertebrates to Assess Sustainable Land Use.19-31.

Andriesse, J.P. and Schelaas, R.M. (1987). A monitoring study on nutrient cycles in soils under shifting cultivation under various climatic conditions in tropical Asia. III: The effect of land clearing through burning on fertility level. *Agr. Ecosyst. Environ.*, 19: 311-332.

Anjaneyulu, E., Balaji, M., Narasimha, G. and Ramgopal. M. (2011). Effect of pig iron slag particles on soil physico-chemical, biological and enzyme activities. *Iran. J. Energy Env.*, 2: 161-165.

Aon, M.A. and Colaneri, A.C. (2001). Temporal and spatial evolution of enzymatic activities and physico-chemical properties in a agricultural soil. *Appl. Soil Ecol.,* 18: 255–270.

Are, K.S., Oluwatosin, G.A., Adeyolanu, D.O. and Adebayo O.O. (2009). Slash and burn effect on soil quality of an Alfisol: Soil physical properties. *Soil & Tillage Research*, 103: 4–10.

Arunachalam, A. (2002). Dynamics of soil nutrients and microbial biomass during first year cropping in an 8-year jhum cycle. *Nutr. Cycl. Agroecosys.*, 64: 283–291.

Arunachalama, A., Kusum, M., Arunachalama, Pandey, H.N., and Tripathi, R. S. (1998).Fine litterfall and nutrient dynamics during forest regrowth in the humid subtropics of north-eastern India. *Forest Ecol. and Manag.,* 110: 209-219.

Aumtong, S., Magid, J., Bruun, S., and de Neergaard, N. (2009). Relating soil carbon fractions to land use in sloping uplands in northern Thailand. Agriculture, *Ecosys. Environ.*, 131: 229–239.

Awasthi, A., Singh, M., Soni S. K., Singh, R. and K, Alok. (2014). Biodiversity acts as insurance of productivity ofbacterial communities under abiotic perturbations.*The ISME J*., 1-8.

Bakker, P.A.H.M., Glandorf, D.C.M., Viebahn, M., Ouwens, T.W.M., Smit, E., Leeflang, P., Wernars, K., Thomashow, L.S., Thomas-Oates, J.E., and van Loon, L.C. (2002). Effects of Pseudomonas putida modified to produce phenazine-1-carboxylic acid and 2, 4-diacetylphloroglucinol on the microflora of field grown wheat. *Antonie van Leeuwenhoek.,* 81: 617–624.

Baldrian, P. (2008). Enzymes of Saprotrophic Basidiomycetes. In: Boddy L., Frankland J., van West P. (eds.): Ecology of Saprotrophic Basidiomycetes. Academic Press, New York, pp. 19–41.

Baldrian, P. (2009). Microbial enzyme-catalyzed processes in soils and their analysis.*Plant Soil Environ*., 55: 370–378.

Balvanera, P., Pfisterer, A.B., Buchmann, N., He, J.-S., Nakashizuka, T., Raffaelli, D., Schmid, B. (2006). Quantifying the evidence for biodiversity effects on ecosystem functioning and services. *Ecol. Lett*., 9: 1146–1156.

Bandick, A.K. and Dick, R.P. (1999). Field management effects on soil enzyme activities. *Soil Biol. Biochem.*, 31: 1471-1479.

Bárcenas-Moreno, G., García-Orenes, F., Mataix-Solera, J., Mataix-Beneyto, J., and Bååth, E. (2011).Soil microbial recolonisation after a fire in a Mediterranean forest. *Biol Ferti soils, 47*:261-272.

Bardgett, R. and Mc Alister, E. (1999).The measurement of soil fungal: bacterial biomass ratios as an indicator of ecosystem self-regulation in temperate meadow grassland. *Bio.Fertil. Soils*, 29: 282.

Bardgett, R.D., Freeman, C. and Ostle.N.J. (2008). Microbial contributions to climate change through carbon cycle feedbacks. The *ISME J*., 2: 805-814.

Baruah, M and Mishra, R.R. (1986). Effect of herbicides butachlor, 2, 4-d and oxyfluorfen on enzyme activities and CO2 evolution in submerged paddy field soil. *Plant Soil*, 96: 287-291.

Baruah, M and Mishra, R.R. (1984). Dehydrogenase and urease activities in rice field soils. *Soil Biol. Biochem*., 16: 423-424.

Baruah, T.C. and Barthakur, H.P. (1997). *A Text Book of Soil Analysis*, Vikas Publishing House Pvt. Ltd, Bangalore.

Batten, M.K., Scow, K.M., Davies, M,F., and Harrison, S.P. (2006): Two invasive plants alter soil microbial community composition in serpentine grasslands. *Biol. Invas.,* 8: 217–230.

Bell, T., Newman, J. A., Silverman, B. W., Turner, S. L. and Lilley, A.K. (2005) The contribution of species richness and composition to bacterial services. *Nature,* 436: 1157–1160.

Bergstrom, D.W., Monreal, C.M. and King, D.J. (1998). Sensitivity of soil enzyme activities to conservation practices. *SSSA J.,* 62: 1286-1295.

Bever, J. D., Morton, J. B., Antonovics, J and Schultz, P.A. (1996). Host-Dependent Sporulation and Species Diversity of Arbuscular Mycorrhizal Fungi in a Mown Grassland. *J. of Ecol.,* 84: 71-82.

Bisset , J. and Parkinson D (1980) Long term effects of fire on the composition and activity of the soil microflora of a subalpine, coniferous forest. *Can. J. Bot.,* 58: 1704–1721

Bissett, A., Burke, C., Cook, P.L.M., John P. and Bowman. (2007). Bacterial community shifts in organically perturbed sediments. *Environ. Microbiol*., 9: 46–60.

Blasiak, L.C. Alex W., et al. (2014). Bacterial Communities in Malagasy Soils with Differing Levels of Disturbance Affecting Botanical Diversity. *PLOS ONE*, 9: e85097

Boerner, R.E.J., and Brinkman, J.A. (2003). Fire frequency and soil enzyme activity in southern Ohio oak – hickory forests. *Appl. Soil Ecol*., 23: 137–146

Boerner, R.E.J., Decker,L.M., Kelly, Sutherland, and Elaine. (2000). Prescribed burning effects on soil enzyme activity in a southern Ohio hardwood forest: A landscape-scale analysis. *Soil Biol. Biochem*., 32: 899-908.

Boerner, R.E.J., Brinkman, J.A. and Smith, A. (2005). Seasonal variations in enzyme activity and organic carbon in soil of a burned and unburned hardwood forest.*Soil Biol. Biochem.,* 37: 1419–1426.

Boerner, R.E.J., Huang, J. and Hart, S.C. (2008). Fire, thinning, and the carbon economy:Effects of fire and fire surrogate treatments on estimated carbon storage and sequestration rate. *Fort. Ecol. Manag.,* 255: 3081-3097.

Bond, W.J. and Keeley, J.E. (2005). Fire as a global 'herbivore': the ecology and evolution of flammable ecosystems. *Trends Ecol Evol*., 20: 387-94.

Boserup, E., 1965. The Conditions of Agricultural Growth. Earthscan Publications Ltd., London.

Brady, N.C. (1996). Alternatives to slash-and-burn: A global imperative. *Agric. Ecosyst. Environ.*, *58*: 3–11.

Brand, J. and Pfund, J.L. (1998). Site-and watershed-level assessment of nutrient dynamics under shifting cultivation in eastern Madagascar. *Agr. Ecsyst. Environ.*, 71: 169-183.

Brand, J. and Pfund, J.L. (1998). Site-and watershed-level assessment of nutrient dynamics under shifting cultivation in eastern Madagascar. *Agr. Ecosyst. Environ.*, 71: 169-183.

Bray, J.R. and Curtis, J.T. (1957). An Ordination of the Upland Forest Communities of Southern Wisconsin.*Ecol. Monographs*, 27: 325-349

Bray, R.H. and Kurtz, L.T. (1945). Determination of total, organic and available forms of phosphorous in soils. *Soil Sci.,* 59: 39–45.

Brinkmann, W.L.F. and Nascimento, J.C. (1973). The effect of slash and burn agriculture on plant nutrients in the Tertiary Region of Central Amazonia.*Turrialba*, 23(3): 284-290.

Brookes, P.C. and Joergensen, R.G. (2006). Microbial biomass measurements by fumigation-extraction. In: Bloem, J., Hopkins, D.W. and Benedetti, A. (eds) Microbiological methods for assessing soil quality, CABI Publishing, Oxfordshire, UK, pp. 77-83.

Brookes, P.C., Landman, A., Pruden, G.and Jenkinson, D.S. (1985). Chloroform fumigation and the release of soil-nitrogen—a rapid direct extraction method to measure microbial biomass nitrogen in soil. *Soil Biol Biochem.,* 17: 837–842.

Brookfield, H., 2001. Exploring Agrodiversity. Columbia University Press, New York.

Broughton, L.C. and Gross, K.L. (2000). Patterns of diversity in plant and soil microbial communities along a productivity gradient in a Michigan old-field. Oecologia, 125: 420-427.

Bruun, T.B., Mertz, O. and Elberling, B. (2006). Linking yields of upland rice in shifting cultivation to fallow length and soil properties. *Agr. Ecosyst. Environ.*, 113: 139–149.

Brye, K.R. (2006). Soil physiochemical changes following 12 years of annual burning in a humid–subtropical tallgrass prairie: a hypothesis. Acta Oecologica, 30: 407-413

Burns, R.G. (1982). Enzyme-activity in soil—location and a possible role in microbial ecology.*Soil Biol Biochem*., 14: 423–427.

Burns, R.G. (1982). Enzyme activity in soil: location and possible role in microbial ecology. *Soil Biol. Biochem*., 14: 423-427.

Burns, R.G., De Forest, J.L., Marxsen, J., Sinsabaugh, R.L., Stromberger, M.E., Wallenstein, M.D., Weintraub, M.N. and Zoppini, A. (2013). Soil enzymes in a changing environment: Current knowledge and future directions. *Soil Biol. Biochem.*, 58: 216-234.

Cambardella, C. A., and Elliott, E. T. (1992). Particulate soil organic-matter changes across a grassland cultivation sequence. *Soil Science Society of America Journal*, 56: 777–783.

Carreiro, M.M., Sinsabaugh, R.L., Repert, D.A. and Parkhurst, D.F. (2000). Microbial enzyme shifts explain litter decay responses to simulated nitrogen deposition. *Ecology,* 81:2359–2365.

Carson, J.K., Gleeson, D.B., Clipson, N., Murphy, D.V. (2010). Afforestation alters community structure of soil fungi. *Fungal Biol*., 114: 580–584.

Casida, L., Klein, D. and Santoro, T. (1964). Soil Dehydrogenase Activity. *Soil Sci.,* 98: 371–376.

Certini, G. (2005). Effects of fire on properties of forest soils: a review. *Oecologia,* 143: 1–10

Chandler, D.P., Fredrickson, J.K., and Brockman, F.J. (1997). Effect of PCR template concentration on the composition and distribution of total community 16S rDNA clone libraries. *Mol. Ecol*., 6: 475-482.

Choromanska, U. and DeLuca, T.H. (2002). Microbial activity and nitrogen mineralization in forest mineral soils following heating: evaluation of post–fire effects. *Soil Biol. Biochem.,* 34: 263–271.

Choudhury, B.U., Fiyaz, A.R., Mohapatra, K.P., Ngachan, S., (2015). Impact of land uses, agrophysical variables and altitudinal gradients on soil organic carbon concentration of North-Eastern Himalayan Region of India. Land Degrad. Devel.

Chróst R.J. (1991). Environmental Control of the Synthesis and Activity of Aquatic Microbial Ectoenzymes. In: Chróst R.J. (eds) Microbial Enzymes in Aquatic Environments. Brock/Springer Series in Contemporary Bioscience. Springer, New York.

Clarke, R.K. (1993). Non-parametric multivariate analyses of changes in community structure. *Austral. Ecol.,* 18: 117-143.

Clarke, R.K. (1999). Nonmetric multivariate analysis in community-level ecotoxicology. *Environ Toxico Chem*., 18: 118-127.

Clemmensen, K.E., Bahr, A. et al. (2013). Roots and Associated Fungi Drive Long-Term Carbon Sequestration in Boreal Forest. *Science,* 339: 1615-1627.

Coleman, D. C. and CrossleyD. A. (1996). *Fundamentals of Soil Ecology*. Academic Press, London: pp. 205.

Comte, I., Davidson, R., Lucotte, M., de Carvalho, C.J.R., de Assis Oliveira, F., Da Silva, B.P. and Rousseau, G.X. (2012). Physicochemical properties of soils in the Brazilian Amazon following fire-free land preparation and slash-and-burn practices. *Agric. Ecosyst. Environ.*, 156: 108–115.

Creamer, C.A., de Menezes, A.B., Krull, E.S., Sanderman, J., Newton-Walters R. and Farrell M. (2015). Microbial community structure mediates response of soil C decomposition to litter addition and warming. *Soil Biol Biochem*., 80: 175–188.

Crutsinger, M.G., Collins D.M., Fordyce, A.J., Gompert, Z., Nice, C.C. and Sanders, J.N. (2006). Plant Genotypic Diversity Predicts Community Structure and Governs an Ecosystem Process. *Science,* 313: 966-968.

da Jesus, E.C., Marsh, T.L., Tiedje, J.M. and de Moreira F.M.S. (2009). Changes in land use alter the structure of bacterial communities in western Amazon soils. *The ISME J.*, 3: 1004–1011.

Dalal, R.C. (1982).Effect of plant growth and addition of plant residues on the phosphatase activity in soil. *Plant Soil*., 66: 265-269.

Daram, P., Brunner, S., Rausch, C., Steiner, C., Amrhein, N. and Buchera, M. (1999). Pht2; 1 Encodes a Low-Affinity Phosphate Transporter from Arabidopsis. *The Plant Cell*, 11: 2153–2166.

de Boer, W., Folman, L.B., Summerbell, R.C. and Boddy L. (2005). Living in a fungal world: Impact of fungi on soil bacterial niche development. *FEMS Microbiol. Rev.,* 29: 795–811.

De Leij, F.A.A.M., Sutton, E.J., Whipps, J.M., Fenlon, J.S. and Lynch, J.M. (1995). Impact of field release of genetically modified Pseudomonas fluorescens on indigenous microbial populations of wheat. *Appl. Environ. Microbiol.,* 61: 3443–3453.

DeBano, L.F., Neary, D.G. and Ffolliott, P.F. (1998). Fire's effects on ecosystems. John Wiley and Sons, New York.

DeBano, L.F., Rice, R.M., Conrad, C.E., (1979). Soil heating in chaparral fires: effects on soil properties, plant nutrients, erosion, and runoff. USDA Forest Service Research Paper PSW-145, pp 21.

DeForest, J.L., Zak, D.R. and Pregitzer, K.S. (2004). Atmospheric nitrate deposition and the microbial degradation of cellobiose and vanillin in a northern hardwood forest.*Soil Biol. Biochem*., 36: 965–971.

Deka HK and Mishra RR (1983). The effect of slash burning on soil microflora. Plant Soil 73:167–175.deposition affects soil concentrations of dissolved organic matter. *Ecosystems,* 9: 921–933.

Dick, R.P. (1994). Soil enzyme activities as indicators of soil quality. In: Doran, J.W., Coleman, D.C., Bezdicek, D.F. and Stewart, B.A. (eds) Defining Soil Quality for a Sustainable Environment. *Soil Sci. Soc. Am.*, Madison, Wisconsin, pp. 107–124.

Dick, R.P., Breakwell, D.P., Turco, R. F. (1996). Soil enzyme activities and biodiversity easurements as integrative microbiological indicators.as indicators of soil quality. *Soil Sci. Soc. Am.*, Madison, Wisconsin, pp. 247.

Dick, W.A. and Tabatabai, M.A. (1992).Significance and potential uses of soil enzymes. In: Metting, F.J.B. (Ed.). Soil Microbial Ecology: Applications in Agriculture and Environmental Management. Marcel Dekker, New York, pp. 95–125.

Dick, W.A. and Tabatabai, M.A. (1993). Significance and potential uses of soil enzymes. In: Metting, F.B. (ed) Soil Microbial Ecology: Application in Agricultural and Environment Management. Marcel Dekker, New York, pp. 95–125.

Dikici, H. and Yilmaz, C.H. (2006). Peat fire effects on some properties of an artificially drained peatland. *J. Env. Quality,* 35: 866–70.

Dilly, O. and Munch, J.C. (1998). Ratios between estimates of microbial biomass content and microbial activity in soils. *Biol. Fert. Soils,* 27: 374-379.

Dkhar, M.S. and Mishra, R.R. (1983). Dehydrogenase and urease activities of maize (*Zea mays* L.) field soils. *Plant Soil*, 70: 327-333.

Dobbelaere, S., Vanderleyden, J. and Okon, Y. (2003). Plant growthpromoting effects of diazotrophs in the rhizosphere. *CRC Crit Rev Plant Sci., 22*: 107–149.

Dodgson, K.S. and Rose, F.A. (1976). Sulfohydrolases. In: Metabolism of Sulfur Compounds Vol. 7, Metabolic Pathways (Greenberg DM. Ed.), Academic Press, London. pp. 359-431.

Dodgson, K.S. White, G. and Fitzgerald, J.W. (1982). Sulphatase Enzyme of Microbial Origin, Vol. I. CRC Press, Florida.

Doran, J.W. and Zeiss, M.R. (2000). Soil health and sustainability: managing the biotic component of soil quality. Appl. Soil Ecol., 15: 3–11.

Eivazi, F. and Bayan, M.R. (1996). Effects of long-term prescribed burning on the activity of select soil enzymes in an oak–hickory forest. *Can. J. For. Res.*, 26: 1799-1804.

Eivazi, F. and Tabatabai, M.A. (1977). Phosphates in soils. *Soil Biol. Biochem*., 9: 167-172.

Eivazi, F. and Tabatabai, M.A. (1988). Glucosidases and galactosidases in soils.*Soil Biol. Biochem.,* 20: 601-606.

Eric A., Wayne D. and Swank, T. (1987). Factors Limiting Denitrification in Soils from Mature and Disturbed Southeastern Hardwood Forests, Forest Science, 33: 135–144.

Erni, C. (2008). The Concept of indigenous peoples in Asia. A resource book, Copenhagen/Chiang Mai, IWGIA and AIPP

Esen, A. (1993). Beta-glucosidases: overview. In: Esen A (Ed.) Beta- glucosidases and molecular biology. American Chemical Society, Washington, DC, pp. 9-17.

Fernandez, I., Cabaneiro, A. and Carballas, T. (1997). Organic matter changes immediately after a wildfire in an Atlantic forest soil and comparison with laboratory soil heating. *Soil Biol. Biochem.,* 29: 1–11.

Finzi, A.C., Sinsabaugh, R.L., Long, T.M. and Osgood, M.P. (2006). Microbial community responses to atmospheric carbon dioxide enrichment in a warm-temperate forest. *Ecosys*., 9: 215–226

Fitzgeraid, J.W. and Stickland, T.C. (1987). Mineralization of organic sulphur in the O-horizon of a hardwood forest: involvement of sulphatase enzyme. *Soil Biol. Biochem*., 19: 779-781.

Fitzgerald, J.W. and Strickland, T.C. (1984). Formation and mineralization of organic sulphur in forest soils. *Biogeochem.*, 1: 79-95.

Fornara, D. A. and Tilman, D. (2008). Plant functional composition influences rates of soil carbon and nitrogen accumulation. *J Ecol*., 96: 314-322.

Franzluebbers, A.J., Haney, R.L. and Hons, F.M. (1999). Relationships of chloroform fumigation–incubation to soil organic matter pools. *Soil Biol. Biochem*., 31: 395-405.

Franzluebbers, A.J., Stuedemann, J.A., Schomberg, H.H. and Wilkinson, S.R. (2000).Soil organic C and N pools under long-term pasture management in the Southern Piedmont, USA. *Soil Biol. Biochem.,* 32: 469-478.

Frey, S.D., Knorr, M., Parrent, J.L. and Simpson, R.T. (2004). Chronic nitrogen enrichment affects the structure and function of the soil microbial community in temperate hardwood and pine forests. *For Ecol. Manage*., 196: 159–171.

Fritze, H., Smolander, A., Levula, T., Kitunen, V. and Malkonen, E. (1994). Wood–ash fertilization and fire treatments in a Scots pine forest stand: effects on the organic layer, microbial biomass and microbial activity. *Biol. Fert. Soils*, 17: 57–63.

Frizano, J., Vann, D.R., Johnson, A.H., Johnson, C.M., Vieira, I.C.G. and Zarin, D.J. (2003).Labile phosphorus in soils of forest fallows and primary forest in the Bragantina Region, Brazil. *Biotropica*, 35: 2-11.

Fukushima, M., Kanzaki, M., Hara, M., Ohkubo, T., Preechapanya, P. and Choocharoen, C. (2008). Secondary forest succession after swidden cultivation in the montane forest area in Northern Thailand. *Forest Ecol. Manage*. 255: 1994–2006.

Fukushima, M., Kanzaki, M., Hla, M.T. and Yazar, M. (2007). Recovery process of fallow vegetation in the traditional Karen swidden cultivation system in the Bago mountain range, Myanmar. Southe. *Asian Stud*., 45: 317–333.

Garcia, C. and Hernández, T. (1997). Biological and biochemical indicators in derelict soils subject to erosion.*Soil Biol. Biochem*., 29: 171-177

García-Oliva, F., Sanford, R.L. and Kelly, E. (1999a). Effect of burning tropical deciduous forest soil in Mexico on the microbial degradation of organic matter. *Plant and Soil*, 206: 29–36.

García-Oliva, F., Sanford, R.L. and Kelly, E. (1999b). Effects of slash-andburn management on soil aggregates, organic C and N in a tropical deciduous forest. *Geoderma*, 88:1–12.

Garrity, D.P. (1993). In: Ragland, J., Lal, R. (Eds.), Sustainable Land-Use Systems for Sloping Uplands in South East Asia. *ASA special publication*, 56: 41–66.

Giardina, C.P., Sanford Jr., Robert L., Døckersmith, I.C. and Jaramillo, V.J. (2000). The effects of slash burning on ecosystem nutrients during the land preparation phase of shifting cultivation. *Plant Soil,* 220: 247–260.

Gil, C., Ramos-Miras, J., Roca-Pérez, L., Boluda, R., 2010. Determination and assessment of mercury content in calcareous soils. *Chemosphere*, 78: 409–415.

Gilbert, N., Fulthorpe, R., and Kirkwood, A.E. (2012). Microbial diversity, tolerance, and biodegradation potential of urban wetlands with different input regimes.*Can J. Microbiol*., 58: 887–897.

Girlanda, M., Perotto, S., Moenne –Loccoz, Y., Bergero, R., Lazzari, A., Defago, G., Bonfante, P., and Luppi, A.M. (2001). Impact of biocontrol Pseudomonas fluorescens CHA0 and a genetically modified derivative on the diversity of culturable fungi in the cucumber rhizosphere. *Appl. Environ. Microbiol*., 67: 1851–1864.

Girvan, M.S. Bullimore, J., Pretty, J.N. Osborn, A.M. and Ball, A.S. (2003). Soil Type Is the Primary Determinant of the Composition of the Total and Active Bacterial Communities in Arable Soils. *Appl. Environ. Microbiol*., 69: 1800-1809.

Gispert, M., Emran, M., Pardini, G., Doni, S. and Ceccanti, B. (2013). The impact of land management and abandonment on soil enzymatic activity, glomalin content and aggregate stability. *Geoderma.,* 202-203: 51–61.

Gomes, N.C.M., Heuer, H., Schönfeld, J., Costa, R. , Mendonca-Hagler. L. and Smalla, K. (2001). Bacterial diversity of the rhizosphere of maize (*Zea mays*) grown in tropical soil studied by temperature gradient gel electrophoresis. *Plant Soil,* 232.

Gregorich E.G. and Beare, M.H. (2008). Soil sampling and methods of Analysis second edition Canadian society of soil science. Edited by Carter M.R and Gregorich E.G.Taylor and Francis.

Gregorich, E.G., and B.H. Ellert (1995). Light fraction and macroorganic matter in mineral soils. In M.R. Carter (Ed.), Soil Sampling and Methods of Analysis. Lewis Publishers, Boca Raton, FL, pp. 397–408.

Gregorich, E.G., Liang, B.C., Drury, C.F., Mackenzie, A.F., and McGill, W.B. (2000). Elucidation of the source and turnover of watr soluble and microbial biomass carbon in agricultural soil. *Soil Biol. Biochem.,* 32: 581-587.

Guan, S.Y. (1989). Studies on the factors influencing soil enzyme activities: Effect of organic manures on soil enzyme activities and N and P transformations. *Acta Pedol. Sinica*., 26: 72-78.

Guo, H. and Padoch, C. (1995). Patterns and management of agroforestry system in Yunnan, In: Brookfield, H. (eds) The United Nations University Collaborative Research Programme on People, Land Management and Environmental Change. *Global Environ. Chang.*, 5: 273–279

Gutknecht, J.L.M., Henry, H.A.L. and Balse, T.C. (2010). Inter-annual variation in soil extra cellular enzymes activity in response to simulated global change and fire structure. *Pedobiologia*, 53: 283-293.

Haifang Z., Gang L., Xiaolong S., Dianlin Y., Yujie Li., Jiang Q., Jingni Z. and Shulan Z. (2013). Changes in soil microbial functional diversity under different vegetation restoration patterns for Hulunbeier Sandy Land. *Acta Ecologica Sinica,* 33: 38–44

Hamman, S.T., Burke, I.C. and Knapp, E.E. (2008). Soil nutrients and microbial activity after early and late season prescribed burns in a Sierra Nevada mixed conifer forest. *Forest Ecol. Manag.*, 256: 367–374.

Hamman, S.T., Burke, I.C. and Stromberger, M.E. (2007). Relationships between microbial community structure and soil environmental conditions in a recently burned system.*Soil Biol. Biochem.*, 39: 1703–1711.

Haney, R.L., Franzluebbers, A.J., Hons, F.M., Hossner, L.R. and Zuberer, D.A. (2001). Molar concentration of K2SO4 and soil pH effect estimation of extractable C with chloroform fumigation extraction. *Soil Biol. Biochem*., 33: 1501–1507.

Hanson CA, Allison SD, Bradford MA, Wallenstein MD, Treseder KK (2008). Fungal taxa target different carbon sources in forest soil. *Ecosystem,* 11: 1157–1167

Hanway, J.J. and Heidel, H. (1952). Soil analysis methods as used in Iowa State College, Soil Testing Laboratory. *Iowa State Coll. Bull.,* 57: 1-131.

Hart, S.C., DeLuca, T.H., Newman, G.S., MacKenzie, M.D. and Boyle, S.I. (2005).Post-fire vegetative dynamics as drivers of microbial community structure and function in forest soils. *For. Ecol. Manag*., 220: 166–184.

Hartman, W.H., Richardson, C.J., Vilgalys, R., and Bruland, G.L. (2008). Environmental and anthropogenic controls over bacterial communities in wetland soils. *Proc. Natl. Acd. Sc. USA.,* 105: 17842-17847.

Hattenschwiler, S. et al. (2005) Biodiversity and litter decomposition in terrestrial ecosystems. *Annu. Rev. Ecol. Evol. Syst.,* 36: 191–218.

Hayano, K., and A. Katami (1977). Extraction of b-glucosidase activity from pea field soil. *Soil Biol. Biochem*., 9: 349–351.

Hayano, K., and K. Tubaki. (1985). Origin and properties of b-glucosidase activity of tomato-field *soil. Soil Biol. Biochem*., 17: 553–557.

Haynes, R.J. (2005). Labile organic matter fractions as central components of the quality of agricultural soils. *Adv. Agron*., 85: 221-268.

Heinemeyer, R. and Fitter, A.H. (2004). Impact of temperature on the arbuscular mychorrhizal (AM) symbiosis: growth responses of the host plant and its AM fungal partner. *J. Expiremt. Botany*, 55: 525-534.

Herbien, S.A. and Neal, J.L. (1990). Soil pH and phosphatase activity.*Communications in Soil Science and Plant Analysis*, 21: 439-456.

Hernández, T. and Garcia, C. (1997). Biological and biochemical indicators inderelict soils subject to erosion. *Soil Biol. Biochem*., 29: 171-177.

Heuer, H. and Smalla, K. (2007). Manure and sulfadiazine synergistically increased bacterial antibiotic resistance in soil over at least two months. Environ. Microbiol., 9: 657-666.

Heuer, H. and Smalla, K. (1999). Bacterial phyllosphere communities of *Solanum tuberosum* L. and T4-lysozyme-producing transgenic variants. *FEMS Microbiol. Ecol.,* 28: 357-371.

Hofrichter M. (2002). Review: Lignin conversion by manganese peroxidase (MnP). *Enzy. Microb. Technol*., 30: 454–466. doi: 10.1016/S0141-0229(01)00528-2.

Hoorman, J.J. (2011). The Role of Soil Fungus. Fact sheet: Agriculture and Natural Resource, The Ohio State University. SAG-14-11.

Hovig, E., Sorenson, B.S., Anne, B.A. and Borresen L. (1991). Constant denaturant gel electrophoresis, a modification of denaturing gradient gel electrophoredod, in mutation detection. *Mutation Research Lett.,* 262: 63-71.

Jordan D., Kremer R.J. (1994). Potential use of microbial activity as an indicator of soil quality. In: Pankhurst, C.E., Double, B.M., rew York, pp. 408-410.

Kauffman, J.B., Sanford, R.L., Cummings, D.L., Salcedo, I.H. and Sampaio, E.V.S.B. (1993). Biomass and nutrient dynamics associated with slash fires in Neotropical dry forests. *Ecology,* 74: 140–151.

Ketterings, Q.M., Bigham, J.M. and Laperche, V. (2000). Changes in soil mineralogy and texture caused by slash-and-burn fires in samatra, Indonesia. *Soil Sci. Soc. AM. J*., 64: 1108-1117.

Kiss, S., Dragan-Bularda, M. and Radulescu. D. (1975). Biological significance of enzymes accumulated in soil. *Adv. Agron*., 27: 25-87.

Kleinman, P., Bryant, R.B. and Pimentel, D. (1996). Assessing ecological sustainability of slash-and-burn agriculture through soil fertility indicators. *Agron. J., 88*: 122–127.

Klose, S. and M.A. Tabatabai. (1999). Urease activity of microbial biomass in soils.*Soil Biol. Biochem*., 31: 205–211.

Knoepp, J.D. and Swank, W.T. (1993). Site preparation burning to improve southern Appalachian pine-hardwood stands: nitrogen responses in soil, water, and streams. *Can. J. Res*., 23: 2263–2270.

Köhl, L., Oehl, F., van der Heijden, M.G.A. (2014). Agricultural practices indirectly influence plant productivity and ecosystem services through effects on soil biota. *Ecol. Appl*., 24: 1842–1853.

Kotroczó, Z., Veres, Z., Fekete, I., Krakomperger, Z., Tóth, A.J., Kate, L. and Tóthmérész, B. (2014). Soil enzyme activity in response to long-term organic matter manipulation.*Soil Biol. Biochem.,* 70: 237-243.

Kropf, S., Heuer H., Gruning M. and Smalla K. (2004). Significance test for comparing complex microbial community fingerprints using pairwise similarity measures. *J. Microbiological Methods*, 57: 187-195.

Krsek M. and Wellington E.M.H. (1999). Comparison of different methods for the isolation and purification of total community DNA from soil. *J Microbiol Meth.,* 39: 1-16.

Krsek, Martin & Wellington, E.m.h. (2000). Comparison of Different Methods for the Isolation and Purification of Total Community DNA from Soil. *J. of microbial. Methods,* 39: 1-16.

Kruskal, J.B. and Wish, M. (1978) Multidimensional Scaling. Sage University Paper Series on Quantitative Applications in the Social Sciences, No. 07-011, Sage Publications, Newbury Park.

Kumar, S. (2008). Report of the inter-ministerial national task force on rehabilitation of shifting cultivation areas. 20th September, New Delhi.

Kumar, S., chaudhuri, S. and Maiti, S.K. (2013). Soil Dehydrogenase Enzyme Activity in Natural and Mine Soil - *A Review. Middle-East Journal of Scientific Research,* 13: 898–906.

Ladd, J.N. (1978). Origin and range of enzymes in soil. In: Burns, R.G. (ed) Soil enzymes, Academic Press, New York, pp. 51-96.

Lane D.J. (1991) 16S/23S rRNA sequencing. In: E. Stackebrandt and M. Goodfellow (ed.), *Nucleic acid technology in bacterial systematics*. John Wiley and Sons, New York, N.Y. Pp. 115–175.

Lauber, C.L., Strickland, M.S., Bradford, M.A. and Fierer, N. (2008). The influence of soil properties on the structure of bacterial and fungal communities across land-use types. *Soil Biol Biochem*., 40: 2407–2415.

Lavelle, P. (1997). Faunal activities and soil processes: Adaptive strategies that determine ecosystem function. In: Beggan, M. and Fitter, A.H. (eds)*Advances In Ecological Research*, Elsevier Limited, Netherland, 27: 93-132.

Lawrence, D., and Schlesinger, W.H. (2001). Changes in soil phosphorus during 200 years of shifting cultivation in Indonesia. *Ecology*, 82: 2769–2780.

Lemos, L.N., Fulthorpe, R.R., Triplett, E.W., Roesch, L.F.W. (2011). Rethinking microbial diversity analysis in the high throughput sequencing era. *J. Microbiol. Methods*, 86: 42–51.

Li, M., Shinamo, T. and Tadano, T. (1997). Distribution of exudates of lupin roots in the rhizosphere under phosphorus deficient conditions, *Soil Sci. Plant Nutr*., 43: 237-245.

Li, P., Feng, Z., Jiang, L., Liao, C., and Zhang, J. (2014). A Review of Swidden Agriculture in Southeast Asia. *Remote Sens.*, 6: 1654-1683.

Liliensiek, K.A., Thakuria, D. and Clipson, N. (2012). Influences of Plant Species Composition, Fertilisation and Lolium perenne Ingression on Soil Microbial Community Structure in three Irish Grasslands. *Microb Ecol*., 63: 509–521.

Liu, L. and Greaver, T. (2010). A global perspective on belowground carbon dynamics under nitrogen enrichment. *Ecol. Lett*., 13: 819-828.

Liu, W., Xu, W., Hong, J. and Wan, S. (2010). Interannual variability of soil microbial biomass and respiration in responses to topography, annual burning and N addition in a semiarid temperate steppe. *Geoderma,* 158: 259–267.

Lugtenberg, B.J.J. and Kamilova, F. (2009). Plant growth promoting rhizobacteria. *Ann Rev Microbiol*., 63: 363–383.

Lungmuana, Singh, B.S., Vanthawmliana, Saha, S., Dutta, K.S. Rambuatsaiha, Akoijam R. Singh, R.A. and Boopathi, T. (2017). Impact of secondary forest fallow period on soil microbial biomass carbon and enzyme activity dynamics under shifting cultivation in North Eastern Hill region, India. *Catena*, 156: 10-17.

Maass, J.M., Jaramillo, V.J., Martínez-Yrizar, A., García-Oliva, F., Perez- Jimenez, A. and Sarukhan, J. (2002). Aspectos funcionales del ecosistema de selva baja caducifolia en Chamela, Jalisco. In: Noguera, F., Vega, J., García-Aldrete, A. and Quesada, M. (ed*s*) Historia natural de Chamela, Instituto de Biología, Universidad Nacional Autónoma de México, Mexico DF, pp. 525–542.

Madritch, M.D. and Hunter, M.D. (2002). Phenotypic diversity influences ecosystem functioning in an oak sandhills community. *Ecology,* 83: 2084–2090.

Madritch, M.D., Donaldson, J.R. and Lindroth, R.L. (2006). Genetic identity of Populus tremuloides litter influences decomposition and nutrient release in a mixed forest stand. *Ecosystem*s, 9: 528–537.

Magurran , A.E. (1988). Ecological diversity and its measurement.Princeton University Press, Princeton, New Jersey.

Makoi, Joachim, H.J.R. and Ndakidemi, P.A. (2008). Selected soil enzymes: Examples of their potential roles in the ecosystem. *Afr. J. Biotechnol.,* 7: 181-191.

Malmström, A. (2012). Life–history traits predict recovery patterns in Collembola species after fire: a 10 year study. *J. Appl. Soil Ecol.,* 56: 35–42.

Malmström, A., Persson, T., Ahlström, K., Gongalsky, and K.B., Bengtsson, J., (2009). Dynamics of soil meso–and macrofauna during a 5–year period after clear–cut burning in a boreal forest. *J. Appl. Soil Ecol.*, 43: 61–74.

Mawdsley, J.L. and Burns, R.G. (1994). Inoculation of plants with a Flavobacterium species results in altered rhizosphere enzyme activities. *Soil Biol Biochem*., 26: 871–882.

McCarthy, G.W., Siddaramappa, R., Reight, R.J., Coddling, E.E. and Gao G. (1994). Evaluation of coal combustion by products as soil liming materials: their influence on soil pH and enzyme activities. *Biol. Fert. Soils*., 17: 167-172.

McGill, W.B. and Colle, C.V. (1981). Comparative aspects of cycling of organic C, N, S and P through soil organic matter. Geoderma, 26: 267-286.

McGuire, K., Bent, E., Borneman, J., Majumder, A., Allison, S.D. and Treseder, K.K. (2010). Functional diversity in resource use by fungi.*Ecology,* 91: 2324–2332.

McLaren AD. (1975). Soil as a system of humus and clay immobilized enzymes. *Chem. Scripta*. 8: 97-99.

Mertz, O., Padoch, C., Fox, J., Cramb, R.A., Leisz, S.J., Nguyen, T.L. and Vien, T.D. (2009). Swidden change in Southeast Asia: understanding causes and consequences. *Hum. Ecol.*, 37: 269–280

Mertz, O., Wadley, R.L., et al. (2008). A fresh look at shifting cultivation: Fallow length an uncertain indicator of productivity. *Agricultural Systems*, 96: 75–84

Miki,T., Ushio, M., Fukui,S. and Kondoh, M.(2010). Functional diversity of microbial decomposers facilitates plant coexistence in a plant–microbe–soil feedback model. *Proceedings of the National Academy of Sciences*, 107: 14251-14256.

Miller, M., Palojarvi, A., Rangger, A., Reeslev, M. and Kjoller, A. (1998). The use of fluorogenic substrates to measure fungal presence and activity in soil. *Appl. and Environ. Microb.*, 64: 613–617.

Monokrousos, N., Papatheodorou, E.M., Diamantopoulos, J.D. and Stamou, G.P. (2006). Soil quality variables in organically and conventionally cultivated field sites. *Soil biol. biochem*., 38: 61282-1289

Muchhal, U.S., Pardo, J.M. and Raghothama, K.G. (1996). Phosphate transporters from the higher plant Arabidopsis thaliana. *Proc. Natl. Acad. Sci. USA*., 93: 10519-10523.

Muyzer, G., De Wall, E.C., and Uitterlinden, A.G. (1993). Profiling of Complex Microbial Populations by Denaturing Gradient Gel Electrophoresis Analysis of Polymerase Chain Reaction-Amplified Genes Coding for 16S rRNA. *Appl. Environ. Microbiol.,* 59: 695-700.

Nakas J.P., Gould W.D. and Klein, DA. (1987). Origin and expression of phosphatase activity in semi-arid grassland soil. *Soil Biol and Biochem.,* 19: 13-18.

Nannipieri P, Ascher J, Ceccherini MT, Landi L, Pietramellara G, Renella G. (2003). Microbial diversity and soil functions. *Eur. J. Soil. Sci.,* 54: 655–670.

Nannipieri, P. and Badalucco, L. (2003). Biological processes. In: Processes in the Soil–Plant System: Modelling Concepts and Applications (eds D.K. Bembi & R. Nieder). The Haworth Press, Binghamton, NY.

Nannipieri, P., Grego, S. and Ceccanti, B. (1990). Ecological significance of the biological activity in soils. In: Bollag, J.M. and Stotzky, G. (eds) Soil Biochemistry, Marcel Dekker, New York, pp. 293–355.

Naseby, D.C. and Lynch, J.M. (2001). Effect of 2, 4- diacetylphloroglucinol producing, overproducing, and nonproducing Pseudomonas fluorescens F113 in the rhizosphere of pea. *Microb. Ecol.,* 42: 193–200.

Navarrete, A., Cannavan, F.S., Taketani, R.G., Tsai, S.M. (2010). A molecular survey of the diversity of microbial communities in different Amazonian agricultural model systems. Diversity 2: 787–809.

Ndakidemi, P.A. (2006). Manipulating legume/cereal mixtures to optimize the above and below ground interactions in the traditional African cropping systems. *Afr. J. Biotechnol*., 5: 2526-2533.

Ndiaye, E.L., Sandeno, J.M., McGrath, D. and Dick, R.P. (2000). Integrative biological indicators for detecting change in soil quality. *Am. J. Alternative Agr.*, 15: 26–36.

Neary, D.G., Klopatek, C.C., DeBano, L.F. and Ffolliott, P.F. (1999). Fire effects on belowground sustainability: a review and synthesis. *Forest Ecol. Manag.*, 122: 51-71.

Nusslein, K., Tiedje, J.M. (1999) Soil bacterial community shift correlated with change from forest to pasture vegetation in a tropical soil. Appl. Environ. Microb., 65: 3622–3626

Nye, P.H. and Greenland, D.J. (1960). *The soil under shifting cultivation*.Common wealth Bureaux of Soils Technical Communication No. 51.Commonwealth Agricultural Dureaux, Farnham, UK. 156.

Ojima, D.S., Schimel, D.S., Patron, W.J., and Owensby, C.E. (1994). Long-and short-term effects of fire on nitrogen cycling in tallgrass prairie. *Biogeoche.,* 24: 67-84.

Oliveira, R.R. (2008). When the shifting agriculture is gone: functionality of Atlantic Coastal Forest in abandoned farming sites. *Bol. Mus. Para. Emílio Goeldi. Cienc. Hum.,* 3(2): 213-226.

Page, A.L., Miller, R.L. and Keeny, D.R. (1982). *Methods of soil analysis. Part-2 chemical and microbiological properties*, 2nd edition, Agronomy Monograph, 9: 961-1010, ASA, SSSA, CSSA, Madison.

Palm, C.A., Swift, M.J. and Woomer, P.L. (1996). Soil biological dynamics in slash-and-burn agriculture. *Agr. Ecosyst. Environ.*, 58: 61-74.

Pandey A., Chaudhry S., et al. (2011). Recovery of Bacillus and Pseudomonas spp. from the 'Fired Plots' Under Shifting Cultivation in Northeast India. *Curr Microbiol*., 62: 273–280

Pandey, A., Chaudhry, S. and Sharma, A. (2011). Recovery of *Bacillus* and *Pseudomonas* spp. from the 'Fired Plots' Under Shifting Cultivation in Northeast India. *Curr. Microbiol.*, 62: 273–280.

Pedroso-Jùnior, N.N., Murrieta, R.S.S. and Adams, C.A. (2008). Agricultura de corte e queima: um sistema em transformação. *Bol. Mus. Para. Emílio Goeldi. Cienc. Hum.*, 3: 153-174.

Pichtel J.R. and Hayes J.M., (1990). Influence of fly ash on soil microbial activity and populations. *J. Environ. Qual*., 19: 593-597.

Pitchel, J.R., Hayes, J.M. (1990). Influence of fly ash on soil microbial activity and populations. *J. Environ. Qual*., 19: 593-597.

Prieto-Fernández, A., Acea, M.J. and Carballas, T. (1998). Soil microbial and extractable C and N after wildfire. *Biol. Fert. Soils*, 27: 132–142.

Raison R.J., Khanna P.K. and Woods P.V. (1985). Mechanisms of element transfer to the atmosphere during vegetative fires. *Canadian J of Forest Research,* 15: 132-140.

Raison, R.J. (1979). Modification of the soil environment by vegetation fires, with particular reference to nitrogen transformations: A review. Plant and Soil*,* 51: 73-108.

Ram, M. and Singh, B.P. (1993). Soil fertility management in farming systems. In: Lectures Notes, Off Campus Training on Farming System, Aizawl, India.

Ramakrishnan, P.S. (1984). The science behind rotational bush fallow agriculture system (*jhum*).*Proc. Indian Acad. Sci.*, (*Section B*), 93: 379-400.

Ramakrishnan, P.S. (1992).Shifting agriculture and sustainable development: an interdisciplinary study from North-eastern India. Parthenon, Paris

Ramakrishnan, P.S. and Toky, O.P. (1981). Soil nutrient status of hill agro–ecosystems and recovery pattern after slash and burn agriculture (*jhum*) in North–eastern India*. Plant Soil,* 60: 41–64.

Rathore, S.S., Karunakaran, K. and Prakash, B. (2010). Alder based farming system a tradition farming practices in Nagaland for amelioration of *jhum* land. *Indian J. Trad. Knowledge*, 9(4): 677-680.

Reddy BV, Kallifidas D, Kim JH, Charlop-Powers Z, Feng Z, et al. (2012). Natural product biosynthetic gene diversity in geographically distinct soil microbiomes. Appl Environ Microbiol., 78: 3744–3752.

Rhee, Y.H., Y.C. Hah, and W. Hong. (1987). Relative contribution of fungi and bacteria to soil carboxymethylcellulase activity. Soil Biol. Biochem., 19: 479–481.

Robleto, E.A., Borneman, J. and Triplett, E. W. (1998). Effects of bacterial antibiotic production on rhizosphere microbial communities from a culture-independent perspective. Appl Environ Microbiol 64: 5020–5022.

Roder, W., Phengchanh, S., and Keoboulapha, B. (1995). Relationships between soil, fallow period, weeds and rice yield in slash-and-burn systems of Laos*. Plant Soil,* 176: 27–36.

Roldan, A. J. Salinas-García, M. Alguacil, F. Caravaca. (2005). Changes in soil enzyme activity, fertility, aggregation and C sequestration mediated by conservation tillage practices and water regime in a maize field, *Appl. Soil Ecol*., 30: 11-20.

Romanya, J., Casals, P., and Vallejo, V.R. (2001). Short-term effects of fire on soil nitrogen availability in Mediterranean grasslands and shrublands growing in old fields. *For Ecol Manag*., 147: 39–53.

Saha, S., Chakraborty, D., Lata, Pal. M. and Nagarajan, S. (2011). Impact of elevated CO2 on utilization of soil moisture and associated soil biophysical parameters in pigeon pea (Cajanas cajan L.). *Agric. Ecosyst. Environ*., 142: 213–221.

Saiya-Cork, K.R., Sinsabaugh, R.L. and Zak, D.R. (2002). The effects of long term nitrogen deposition on extracellular enzyme activity in an Acer saccharum forest soil. *Soil Biol. Biochem.,* 34: 1309–1315.

Sanchez, P.A. (1976). Properties and management of soils in the tropics. John Wiley, New York.

Sanchez, P.A. (1996). Introduction (Special Issue: Alternatives to Slash-and-Burn Agriculture). *Agric. Ecosyst. Environ.*, *58*: 1–2.

Sanchez, P.A., Bandy, D.E., Villachica, J.H., and Nicholaides, J.J. (1982). Amazon basin soils: management for continuous crop production. *Science,* 216: 821–827.

Saplalrinliana, H., Thakuria, D., Changkija., S. and Hazarika, S. (2016). Impact of Shifting Cultivation on Litter Accumulation and Properties of Jhum Soils of North East India.*J. Indian Soc. Soil Sci.,* 64: 650-1659.

Sarapatka, B. (2002). Phosphatase activity of eutric cambisols (Uppland, Sweden) in relation to soil properties and farming systems. *Scientia Agriculturae Bohemica*, 33: 18-24.

Sarapatka, B. and Kršková, M. (1997). Interactions between phosphatase activity and soil characteristics from some locations in the Czech Republic.Rostl.Výr. 43: 415–419

Sarathchandra, S.U. and Perrott, K.W. (1981). Determination of phosphatase and arylsulphatase activity in soils. *Soil Biol. Biochem*., 13: 543-545.

Sardans, J. Penuelas, J. and Estiarte, M. (2008). Changes in soil enzymes related to C and N cycle and in soil C and N content under prolonged warming and drought in a Mediterranean shrubland. *Appl. Soil Ecol*., 39: 223-235.

Satokari, R.M., Vaughan, E.E., Akkermans, A.D.L., Saarela, M., and de Vos, W.M. (2001). Bafidobacterial diversity in human feces detected by genus specific PCR and denaturing gradient gel electrophoresis. *Appl. Environ. Microbiol*., 67: 504-513.

Scheuner, E.T., Makeshin, F., Wells, E.D., and Catrer, P.Q. (2004). Short term impacts of harvesting and burning disturbances on physical and chemical characteristics of forest soils in Western New Foundland, Canada. *European. J. Forest Res*., 123: 321–330.

Schimel, J.P. and Weintraub, M.N. (2003). The implications of exoenzyme activity on microbial carbon and nitrogen limitation in soil: a theoretical model. *Soil Biol. Biochem*., 35: 549–563.

Schmidt, G. and Laskowski, Sr. M. (1961). Phosphate ester cleavage (Survey). In: Boyer PD, Lardy H, Myrback K (eds). The enzymes, 2nd edn. Academic Press, New York, pp. 3-35.

Schwieger, F. and. Tebbe, C. C "Effect of field inoculation with *Sinorhizobium meliloti* L33 on the composition of bacterial communities in rhizospheres of a target plant (*Medicago sativa*) and a non-target plant (*Chenopodium album*)—linking of 16S rRNA gene-based single-strand conformation polymorphism community profiles to the diversity of cultivated bacteria," *Applied and Environmental Microbiology*, vol. 66, no. 8, pp. 3556–3565, 2000.

Senthilkumar, K., Manian, S., Udaiyan, K. (1997). The effect of burning on soil enzyme activities in natural grasslands in southern India. *Ecol Res*., 12:21–25.

Shao, X., Yang, W. and Wu, M. (2015). Seasonal dynamics of soil labile organic carbon and enzyme activities in relation to vegetation types in Hangzhou bay tidal flat wetland. *PLoS One*, 10: 1–15.

Sharma GD (1980) Effect of fire on soil microorganisms in a Meghalaya pine forest. Folia Microbiol., 26(4): 321–327

Sharma, P., Rai, S.C., Sharma R. and Sharma, E. (2004). Effects of land use change on soil microbial C, N and P in a Himalayan watershed. *Pedobiologia*, 48: 83–92.

Sheffield, V.C., Cox, D.R., Lerman, L.S. and Myers R.M. (1989). Attachment of a 40 base-pair G+C-rich sequence (GC-Clamp) to genomic DNA fragments by the polymerase-chain reaction results in improved detection of single-base changes. *Proc. Natl. Acad. Sci. USA*, 86: 232-236.

Singh, B.K., Millard, P., Whiteley, A.S., Murrell, J.C. (2004). Unravelling rhizosphere-microbial interactions: opportunities and limitations. Trend Microbiol. 12: 386–393.

Sinsabaugh, R.L. (1994). Enzymic analysis of microbial pattern and process. *Biol. Fert. Soils,* 17: 69-74.

Sinsabaugh, R.L. (2010). Phenol oxidase, peroxidase and organic matter dynamics of soil.Review.*Soil Biol Biochem*., 42: 391-404.

Sinsabaugh, R.L., and Follstad Shah, J.J. (2012). Ecoenzymatic stoichiometry and ecological theory. *Annu Rev Ecol Evol Syst*., 43: 313–333.

Sinsabaugh, R.L., and Moorhead, D.L. (1994). Resource-allocation to extracellular enzyme-production—a model for nitrogen and phosphorus control of litter decomposition. *Soil Biol Biochem*., 26: 1305–1311.

Sinsabaugh, R.L., Antibus, R.K. and Linkins, A.E. (1991). An enzymic approach to the analysis of microbial activity during plant litter decomposition. *Agr. Ecosyst. Environ.*, 34: 43-54.

Sinsabaugh, R.L., Antibus, R.K., Linkins, A.E., McClaugherty, C.A., Rayburn, L., Repert, D. and Weiland, T. (1993). Wood Decomposition: Nitrogen and Phosphorus Dynamics in Relation to Extracellular Enzymes Activity. *Ecol.,* 75: -14.

Sinsabaugh, R.L., Carreiro, M.M., and Repert, D.A. (2002). Allocation of extracellular enzymatic activity in relation to litter composition, N deposition, and mass loss.*Biogeochemistry,* 60: 1–24.

Sinsabaugh, R.L., Gallo, M.E., Lauber, C., Waldrop, M.P. and Zak, D.R. (2005).Extracellular enzyme activities and soil organic matter dynamics for northern hardwood forests receiving simulated nitrogen deposition. *Biogeochem*., 75: 201–215.

Sinsabaugh, R.L., Hill, B.H., and Follstad shah, J.J. (2009). Ecoenzymatic stoichiometry of microbial organic nutrient acquisition in soil and sediment. *Nature*, 462: 795–798.

Sinsabaugh, R.L., Lauber, C., et al. (2008). Stoichiometry of soil enzyme activity at global scale. *Ecol Lett* ., 11: 1252–1264.

Six, J., Frey, S.D., Thiet, R.K. and Batten, K.M. (1999). Bacterial and Fungal Contributions to Carbon Sequestration In Agroecosystems. Soil Biol. And Biochem., 70: 555-569.

Skujins J. (1976). Extracellular enzymes in soil. *CRC Critical Review in Microbiology*. 4: 383-421.

Skujins J. (1984). Microbial Ecology of Desert Soils. Edited by K.C. Marshall. Advances in Microbial Ecology.vol 7. Springer, Boston, MA. PP 44-91.

Skujins, J. (1976). Extracellular Enzymes in Soil. *CRC Crit. Rev. Microbiol*., 4: 383-421.

Skujins, J. (1978). Soil enzymology and fertility index—a fallacy? History of abiontic soil enzyme research. In: Burns RG (Ed.), Soil Enzymes. Academic Press, London, pp. 1-49.

Šnajdr, J., Valaškova, V., Merhautova, V., Herinkova, J., Cajthaml, T. and Baldrian, P. (2008).Spatial variability of enzyme activities and microbial biomass in the upper layers of *Quercus petraea* forest soil. *Soil Biol. and Biochem*., 40: 2068–2075.

Sowinski, S,C., Herschkovitz, Y.,1, Okon, Y. and Jurkevitch, E. (2007). Effects of inoculationwith plant growth-promoting rhizobacteria on resident rhizosphere microorganisms. FEMS Microbiol Lett., 276: 1–11.

Speir, T.W., Cowling, J.C. (1991). Phosphatase activities of pasture plants and soils: Relationship with plant productivity and soil P fertility indices. *Biol Fertil Soils.,* 12, 189–194.

Speir, T.W. and Ross, D. J. 1978. “Soil phosphatase and sulphatase”. In *Soil Enzymes*, Edited by: Burns, R. G. 197–250. London, England: Academic Press.

Stach J.E.M., Bathe S., Clapp J.P. and Burns R.G. (2001). PCR-SSCP comparison of 16S rDNA sequence diversity in soil DNA obtained using different isolation and purification methods. *FEMS Microb. Ecol.,* 36: 139-151.

Starr, C.R. and William, G.R. (1993). Denitrification and Organic Carbon Availability in Two Aquifers. *Ground Water*, 31: 934 - 947.

Steenwerth, K.L., Jackson, L.E., Calderon, F.J., Stromberg, M.R., and Sow K.M. (2002). Soil microbial community composition and land use history in cultivated and grassland ecosystems of coastal California. *Soil Biol. Biochem.,* 34: 1599–1611.

Steffen, K.T., Cajthaml, T., Šnajdr, J. and Baldrian, P. (2007): Differential degradation of oak (Quercus petraea) leaf litter by litter-decomposing basidiomycetes. *Res. in Microb.,*158: 447–455.

Stephen, J.R., Kowalchuk, G.A., Bruns, M.A.V., Mccaig, A.E., Phillips, C.J., Embley, T.M. and Prosser, J.I. (1998). Analysis of beta-subgroup proteobacterial ammonia oxidizer populations in soil by denaturing gradient gel electrophoresis. *Appl. Environ. Microbiol.,* 64: 2958-2965.

Stevenson, F.J. (1982). Humus Chemistry, John Wiley & Sons, New York. Stevenson, F.J. (1994). Humus Chemistry, Genesis, Composition, Reactions, 2nd ed., John Wiley & Sons, New York.

Stevenson, F.J. (1986). Cycles of Soil: Carbon, Nitrogen, Phosphorus, Sulfur, Micronutrients. Wiley, New York, pp.380.

Strickland, T.C. and Fitzgerald, J.W. (1984). Formation and mineralization of organic sulphur in forest soils. *Biogeochem.*, 1: 79-95.

Stromgaard, P. (1986). Early succession on abandoned shifting cultivator's plots in the Miombo of South Central Africa. *Biotropica*, 18: 97-106.

Stursova, M., Crenshaw, C.L. and Sinsabaugh, R.L. (2006). Microbial responses to long term N deposition in a semi-arid grassland. *Microb Ecol*., 51: 90–98.

Styger, E., Fernandes, E.C.M., Rajaobelinirina, E. and Rakotondramasy, H.M. (2009). Degrading uplands in the rainforest region of Madagascar: Fallow biomass, nutrient stocks, and soil nutrient availability. *Agroforest. Syst*., 77: 107–122.

Subba Rao N.S. (1999) Soil Microbiology (4$^{th}$ Edition, Soil Microorganisms and Plant Growth), Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi.

Subbiah, B.V. and Asija, C.L. (1956).A rapid procedure for estimation of available nitrogen in soils. *Curr. Sci.,* 25: 259–260.

Subhramanyam, N.S. and Sambamurty, A.V.S.S. (2000). Ecology. Narosa Publishing House, New Delhi, 1-616

Suleiman, A.K.A., Manoelib, L., Boldoa, J.T., Pereirac, M.G. and Roescha, L.F.W. (2013). Shifts in soil bacterial community after eight years of land-use change. *Syst. Appl. Microb.,* 36: 137–144.

Sun, B., Dong, Z.X., Zhang, X.X., Li, Y., Cao, H., Cui, Z.L. (2011). Rice to vegetables: short versus long-term impact of land-use change on the indigenous soil microbial community, *Microb. Ecol*., 62: 474-485.

Susana Castro-Sowinski S.C., Herschkovitz Y., Okon Y. and Jurkevitch E. (2007). Effects of inoculation with plant growth-promoting rhizobacteria on resident rhizosphere microorganisms. *FEMS Microbiol Lett.,* 276: 1–11.

Tabatabai M.A. (1982). Soil enzymes, Dehydrogenases. In: Miller, R.H. and Keeney, D.R. (eds) Methods of Soil Analysis, Part 2. Chemical and Microbiolgical Properties. Agronomy

Tabatabai, M.A. (1994): Soil enzymes. In: Weaver, R.V., Angle, S., Bottomley, P.J., Bezdicek, D.F., Smith, S. and Tabatabai M.A. (eds.): Methods of Soil Analysis: Part 2 Microbiological and Chemical Properties. Soil Science Society of America, Madison, 903–947.

Tabatabai, M.A. and Bremner, J.M. (1969). Use of *p*–nitrophenyl phosphate for assay of soil phosphatase activity. *Soil Biol. Biochem.,* 1: 301–307.

Tabatabai, M.A. and Bremner, J.M. (1970). Arylsulphatase activity of soils. *Soil Sci. Soc. Am. J.,* 34: 225-229.

Tanaka, S., Ando, T., Funakawa, S., Sukhrun, C., Kaewkhongkha, T. and Sakurai, K. (2001). Effect of burning on soil organic matter content and N mineralization under shifting cultivation system of Karen people in northern Thailand. *Soil Sci. Plant Nutr.*, 47: 547–558.

Tardy, V., Aymé, S., et al. (2015). Shifts in microbial diversity through land use intensity as drivers of carbon mineralization in soil. *Soil Biol. Biochem*., 90: 204-213.

Tawnenga, S.U. and Tripathi, R.S. (1996). Evaluating second year cropping on jhum fallows in Mizoram, north-eastern India: phytomass dynamics and primary productivity. *J. Biosci.,* 21: 563–575.

Taylor, J. P., Wilson, B., Mills, M. S. and Burns, R. G. (2002): Comparison of microbial numbers

Thakuria D., Schmidt O., MacSuirtain M., Egan D. and Doohan F.M. (2008). Importance of DNA quality in comparative soil microbial community structure analyses. *Soil Biol. Biochem.,* 40: 1390-1403.

Thakuria, D. and Sharma, U.C. (2014). Shifting cultivation; coexistence of forest and agriculture.*NAAS News,* 14: 4–8.

Tilman, D. (1984). Plant dominance along an experimental nutrient gradient. *Ecol*., 65: 1445–53.

Tinker, P.B., Ingram, J.S.I. and Struwe, S. (1996). Effects of slash–and–burn agriculture and deforestation on climate change. *Agr. Ecosyst. Environ.,* 58: 13–22.

Tirol-Padre, A., Ladha, J.K., Regmi, A.P., Bhandari, A.L. and Inubushi, K. (2007). Organic amendments affect soil parameters in two long–term rice-wheat experiments. *Soil Sci. Soc. Am. J*., 71: 442-452.

Trabelsi, D., and Mhamdi R. (2013). Microbial Inoculants and Their Impact on Soil Microbial Communities: A Review. *BioMed Research International*, 2013: 1-11.

Treseder, K.K. (2008). Nitrogen additions and microbial biomass: a meta-analysis of ecosystem studies. *Ecol. Lett.,* 11: 1111-1120

Treseder, K.K. and Holden, S.R. (2013). Fungal carbon sequestration.*Science* 339:1528–1529.

Treseder, K.K. and Vitousek, P.M. (2001). Effects of soil nutrient availability on investment in acquisition of N and P in Hawaiian rain forests. *Ecol*., 82: 946–54.

Trevors, J.T. (1984). Dehydrogenase activity in soil: A comparison between the INT and TTC assay. *Soil Biol. Biochem*., 16: 673-674.

Turner, D.P., Cohen, W.B. and Kennedy, R.E. (2000). Alternative spatial resolutions and estimation of carbon flux over a managed forest landscape in western Oregon. *Land .Ecol*., 15: 441– 452.

Tyler, G. (1981). Heavy metals in soil biology and biochemistry. In: *Soil Biochem*., (Paul, E.A., Ladd, J.N. Eds), Dekker, New York pp. 371-414..

Uhl, C. (1987). Factors controlling succession following slash and burn agriculture in Amazonia. *Journal of Ecology*, 75: 377–407.

van der Heijden, M.G., Bardgett, R.D., and van Straalen, N.M. (2008). The unseen majority: soil microbes as drivers of plant diversity and productivity in terrestrial ecosystems. *Ecol Lett*., 11: 296–310.

van Vliet, N., Mertz, O., et al. (2012). Trends, drivers and impacts of changes in swidden cultivation in tropical forest-agriculture frontiers: A global assessment. *Glob. Environ. Chang.*, 22: 418–429

Vance, E.D., Brookes, P.C. and Jenkinson, D.S. (1987). An extraction method for measuring soil microbial biomass C. *Soil Biol. Biochem.,* 19: 703-707.

Veres, Z., Kotroczó, Z., Magyaros, K., Tóth, J.A. and Tóthmérész, B. (2013). Dehydrogenase Activity in a Litter Manipulation Experiment in Temperate Forest Soil. *Acta Silv. Lign. Hung.,* 9: 25–33.

Versaw, W.K. and Harrison, M.J. (2002).A Chloroplast Phosphate Transporter, PHT2; 1, Influences Allocation of Phosphate within the Plant and Phosphate-Starvation Responses.*Plant Cell*, 14: 1751-1766

Vong, P.C., Dedourge, O., Lasserre–Joulin, F. and Guckert, A. (2003). Immobilized–S, microbial biomass–S and soil arylsulphatase activity in the rhizosphere soil of rape and barley as affected by labile substrate C and N additions. *Soil Biol. Biochem.,* 35: 1651–1661.

Wakelin, S.A., Macdonald, L.M., Roger, S.L., Gregg, A.L., Bolger, T.P. and Baldock, J.A. (2008). Habitat selective factors influencing the structural composition and functional capacity of microbial communities in agricultural soils. *Soil Biol. Biochem*., 40: 803-813.

Waldrop, M.P. and Zak, D.R. (2006). Response of oxidative enzyme activities to nitrogen deposition affects soil concentrations of dissolved organic carbon. *Ecosystems*, 9:921–33.

Waldrop, M.P., Balser, T.C., and Firestone, M.K. (2000). Linking microbial community composition to function in a tropical soil. *Soil Biol. & Biochem.,* 32: 1837–1846

Waldrop, M.P., Zak, D.R., and Sinsabaugh, R.L. (2004). Microbial community response to nitrogen deposition in northern forest ecosystems. *Soil Biol Biochem.,* 36: 1443–1451

Walkley, A. (1947). Critical examination of rapid method for determining organic carbon in soils, effect of variation in digestion conditions and of inorganic soil constituents. *Soil Sci.*, 632: 251.

Wang, Q., Zhong, M. AND Wang S. (2012). A meta-analysis on the response of microbial biomas, dissolved ornagic matter, respiration and N mineralization in mineral sol to fire in forest ecosystems. *Fort. Ecol. Manage.*, 217: 91-97

Wardle, D.A. (2002). Communities and Ecosystems: Linking the Aboveground and Belowground Components, Princeton University Press, Princeton, NJ.

Weisburg , W. G., Barns, S.M., Pelletier, D.A and Lane DJ. (1991). 16S ribosomal DNA amplification for phylogenetic study*. J. Bacteriol.*, 173: 697-703.

Wick, B. (1998).Microbiological indicators for quality of soils at various stages of degradation in the forest-savanna-transition zone, south-western Nigeria. Dissertation submitted for Post- graduate Program of Studies in Agricultural Science in the Tropics and Subtropics, Faculty of Agriculture, University of Göttingen, Germany.

Wick, B., Kühne, R.F. and Vlek, P.L.G. (1998). Soil microbiological parameters as indicators of soil quality under improved fallow management systems in southwestern Nigeria.*Plant Soil*, 202: 97-107.

Wieland, G., Neumann, R., and Backhaus, H. (2001). Variation of microbial communities in soil, rhizosphere, and rhizoplane in response to crop species, soil type and crop development. *Appl. Environ. Microbiol.,* 67: 5849–5854.

Wolfe, B.E. and Kilrionomos, J.N. (2005). Breaking new ground: Soil communities and exotic plant invasion. *Biosci.*, 55: 477-487.

Wolińska, A. and Stępniewska, Z. (2012). *Dehydrogenase activity in the soil environment*.The John Paul II Catholic University of Lublin, Institute of Biotechnology, Department of Biochemistry and Environmental Chemistry, Lublin, Poland.

Wu, J., Joergensen, R.G., Pommerening, B., Chaussod, R. and Brookes, P.C. (1990). Measurement of soil microbial biomass C by fumigation-extraction—an automated procedure. *Soil Biol. Biochem.,* 22: 1167-1169.

Xiang, X.J., Shi, Y.U., Yang, J., Kong, J., Lin, X., Zhang and Zeng J. (2014). Rapid recovery of soil bacterial communities after wildfire in a Chinese boreal forest.*Sci. Rep*., 4: 3829.

Xiong, J. , Peng, F., Sun, H., Xue, X., and Chu, H. (2014). Divergent Responses of Soil Fungi Functional Groups to Short-term Warming. *Microb Ecol*., 68: 708–715.

Xu, Z. (1991). From shifting cultivation to agroforestry in the mountain areas of Yunnan tropics. In: Zhu, Z., Cai, M., Warg, S. and Jiang, Y. (eds) Agroforestry system in China. The Chinese Academy of Forestry, People's Republic of China and International Development Research Centre, Canada, (http://archive.idrc.ca/library/document/090916/chap32_e.html#32).

Xu, Z., Yu, G., Zhang, X., Ge, J., He, N., Wang, Q., and Wang, D. (2015). The variations in soil microbial communities, enzyme activities and their relationships with soil organic matter decomposition along the northern slope of Changbai Mountain. *Appl. Soil Ecol*, 86: 19–29

Yachi, S. and Loreau, M. (1999). Biodiversity and ecosystem functioning in a fluctuating environment: the insurance hypothesis*. Proc. Natl. Acad. Sci. USA,* 96: 1463–1468.

Yadav، P.K. (2013). Slash-and-Burn Agriculture in North-East India. Expert Opin Environ Biol, 2:1

Yang, C.H. and Crowley, D.E. (2000). Rhizosphere microbial community structure in relation to root location and plant iron nutritional status*. Appl. Environ. Microbiol.*, 66: 345-351.

Yano, Y., McDowell, W.H., and Aber, J.D., (2000). Biodegradable dissolved organic carbon in forest soil solution and effects of chronic nitrogen deposition. *Soil Biol. Biochem*., 32: 1743– 1751.

Yergeau, E, Bokhorst, S, Kang, S., Zhou, J., Greer, C.W., Aerts, R. and Kowalchuk, G.A. (2011). Shifts in soil microorganisms in response to warming are consistent across a range of Antarctic environments. *ISME J.,* 6: 692–702.

Yuan, Y., Dai, X., Xu, M., Wang, H., Fu, x., and Yang, F. (2015). Responses of microbial community structure to land-use conversion and fertilization in southern China. *European J. of Soil Biol*., 70: 1-.6.

Zak, D.R., Holmes, W.E., White, D.C., Peacock, A.D. and Tilman, D. (2003). Plant diversity, soil microbial communities, and ecosystem function: are there any links? *Ecology,* 84: 2042–2050.

Zeglin, L.H., Stursova, M., Sinsabaugh, R.L., and Collins, S.L. (2007). Microbial responses to nitrogen addition in three contrasting grassland ecosystems.*Oecologia*, 154: 349–359.

Zhang, H., Song, X., Wangd, C., Liu, H., Zhang, J., Li, Y., Li, G., Yang, D., Zhao, X. (2013). The effects of different vegetation restoration patterns on soil bacterial diversity for sandy land in Hulunbeier Acta *Ecologica Sinica*, 33: 211–216.

Zhang, Y.L., Sun, C.C.X., Chen, L.J., and Duan, Z.H. (2009). Catalytic potential of soil hydrolases in northeast China under different soil moisture conditions. *Revista de la Ciencia del Suelo y Nutrición Vegetal/ J. Soil Sci. Plant Nutr.*, 9: 116-124.

Zhao J, Ni T, Li Y, Xiong W, Ran W, Shen B, Shen Q and Zhang Q. (2014). Responses of Bacterial Communities in Arable Soils in a Rice-Wheat Cropping System to Different Fertilizer Regimes and Sampling Times. PLOS One 9: 1-11.

Zhou, J., Xue ,K., Xie, J., Deng, Y., Wu, L., Cheng, X., and *et al*. (2012). Microbial mediation of carbon-cycle feedbacks to climate warming. *Nat. Clim. Chang., 2*: 106–110.

Zhou, J.Z., Bruns, M.A., Tiedje, J.M. (1996). DNA recovery from soils of diverse composition. *Appl. Environ. Microbiol*., 62: 316 –322.

Zsolnay, A. (1996). Dissolved humus in soil waters. In: Piccolo, A. (Ed.), Humic Substances in Terrestrial Ecosystems. Elsevier, Amsterdam, pp. 171– 223.

Annexure 4.1. ASA Factorial ANOVA to test the significance of factors at 10 days

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | ASA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 39427.162[a] | 23 | 1714.224 | 133.110 | .000 |
| Intercept | 573653.312 | 1 | 573653.312 | 44544.481 | .000 |
| J | 16617.678 | 1 | 16617.678 | 1290.371 | .000 |
| C | 153.265 | 1 | 153.265 | 11.901 | .001 |
| MI | 2994.840 | 5 | 598.968 | 46.510 | .000 |
| J * C | 2375.325 | 5 | 475.065 | 36.889 | .000 |
| J * MI | 4337.312 | 1 | 4337.312 | 336.795 | .000 |
| C * MI | 6767.468 | 5 | 1353.494 | 105.099 | .000 |
| J * C * MI | 6181.274 | 5 | 1236.255 | 95.996 | .000 |
| Error | 618.154 | 48 | 12.878 | | |
| Total | 613698.628 | 72 | | | |
| Corrected Total | 40045.317 | 71 | | | |
| a. R Squared = .985 (Adjusted R Squared = .977) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 83.289 | C1MI1 | 99.712 | J1MI1 | 76.366 | C1J1MI1 | 87.017 |
| C1J2 | 98.150 | C1MI2 | 89.094 | J1MI2 | 112.439 | C1J1MI2 | 112.407 |
| C2J1 | 64.848 | C1MI3 | 81.932 | J1MI3 | 73.869 | C1J1MI3 | 65.716 |
| C2J2 | 110.755 | C1MI4 | 88.371 | J1MI4 | 96.433 | C1J1MI4 | 112.472 |
| | | C1MI5 | 98.630 | J1MI5 | 73.220 | C1J1MI5 | 86.402 |
| | | C1MI6 | 73.525 | J1MI6 | 98.936 | C1J1MI6 | 77.461 |
| | | C2MI1 | 94.895 | J2MI1 | 74.717 | C1J2MI1 | 61.336 |
| | | C2MI2 | 72.497 | J2MI2 | 92.675 | C1J2MI2 | 115.405 |
| | | C2MI3 | 85.412 | J2MI3 | 74.854 | C1J2MI3 | 82.699 |
| | | C2MI4 | 117.278 | J2MI4 | 127.837 | C1J2MI4 | 114.561 |
| | | C2MI5 | 83.736 | J2MI5 | 71.383 | C1J2MI5 | 63.740 |
| | | C2MI6 | 86.043 | J2MI6 | 98.395 | C1J2MI6 | 83.311 |
| | | | | | | C2J1MI1 | 86.155 |
| | | | | | | C2J1MI2 | 103.635 |
| | | | | | | C2J1MI3 | 63.279 |
| | | | | | | C2J1MI4 | 81.715 |
| | | | | | | C2J1MI5 | 82.814 |
| | | | | | | C2J1MI6 | 88.010 |
| | | | | | | C2J2MI1 | 66.894 |
| | | | | | | C2J2MI2 | 167.663 |
| | | | | | | C2J2MI3 | 74.645 |
| | | | | | | C2J2MI4 | 92.826 |
| | | | | | | C2J2MI5 | 68.122 |
| | | | | | | C2J2MI6 | 103.964 |

Annexure 4.2. Factorial ANOVA to test the significance of factors at 10 days of rice plant growth

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | DHA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 17.862[a] | 23 | .777 | 138.615 | .000 |
| Intercept | 64.878 | 1 | 64.878 | 11579.789 | .000 |
| J | 13.760 | 1 | 13.760 | 2455.949 | .000 |
| C | .145 | 1 | .145 | 25.869 | .000 |
| MI | 2.435 | 5 | .487 | 86.919 | .000 |
| J * C | .005 | 1 | .005 | .828 | .367 |
| J * MI | .941 | 5 | .188 | 33.604 | .000 |
| C * MI | .261 | 5 | .052 | 9.332 | .000 |
| J * C * MI | .315 | 5 | .063 | 11.245 | .000 |
| Error | .269 | 48 | .006 | | |
| Total | 83.009 | 72 | | | |
| Corrected Total | 18.131 | 71 | | | |

a. R Squared = .985 (Adjusted R Squared = .978)

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | .459 | C1MI1 | 1.033 | J1MI1 | .755 | C1J1MI1 | .654 |
| C1J2 | 1.350 | C1MI2 | 1.189 | J1MI2 | .827 | C1J1MI2 | .845 |
| C2J1 | .565 | C1MI3 | 1.085 | J1MI3 | .615 | C1J1MI3 | .500 |
| C2J2 | 1.423 | C1MI4 | .890 | J1MI4 | .588 | C1J1MI4 | .647 |
| | | C1MI5 | .657 | J1MI5 | .110 | C1J1MI5 | .070 |
| | | C1MI6 | .573 | J1MI6 | .177 | C1J1MI6 | .040 |
| | | C2MI1 | 1.217 | J2MI1 | 1.495 | C1J2MI1 | 1.412 |
| | | C2MI2 | 1.173 | J2MI2 | 1.534 | C1J2MI2 | 1.533 |
| | | C2MI3 | 1.027 | J2MI3 | 1.497 | C1J2MI3 | 1.670 |
| | | C2MI4 | .883 | J2MI4 | 1.185 | C1J2MI4 | 1.134 |
| | | C2MI5 | .839 | J2MI5 | 1.386 | C1J2MI5 | 1.243 |
| | | C2MI6 | .826 | J2MI6 | 1.222 | C1J2MI6 | 1.105 |
| | | | | | | C2J1MI1 | .857 |
| | | | | | | C2J1MI2 | .810 |
| | | | | | | C2J1MI3 | .730 |
| | | | | | | C2J1MI4 | .530 |
| | | | | | | C2J1MI5 | .150 |
| | | | | | | C2J1MI6 | .313 |
| | | | | | | C2J2MI1 | 1.578 |
| | | | | | | C2J2MI2 | 1.535 |
| | | | | | | C2J2MI3 | 1.324 |
| | | | | | | C2J2MI4 | 1.236 |
| | | | | | | C2J2MI5 | 1.528 |
| | | | | | | C2J2MI6 | 1.339 |

Annexure 4.3 . Factorial ANOVA to test the significance of factors at 10 days of rice plant growth

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | GSA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 1038187.437[a] | 23 | 45138.584 | 13734.848 | .000 |
| Intercept | 10102469.798 | 1 | 10102469.798 | 3073997.372 | .000 |
| C | 5577.317 | 1 | 5577.317 | 1697.076 | .001 |
| J | 81430.673 | 1 | 81430.673 | 24777.869 | .100 |
| MI | 192578.185 | 5 | 38515.637 | 11719.606 | .000 |
| C * J | 403667.309 | 5 | 80733.462 | 24565.721 | .000 |
| C * MI | 176519.053 | 5 | 35303.811 | 10742.306 | .000 |
| J * MI | 77201.380 | 1 | 77201.380 | 23490.972 | .000 |
| C * J * MI | 101213.520 | 5 | 20242.704 | 6159.486 | .000 |
| Error | 157.749 | 48 | 3.286 | | |
| Total | 11140814.983 | 72 | | | |
| Corrected Total | 955661.657 | 71 | | | |
| a. R Squared = .922 (Adjusted R Squared = .884) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 364.896 | C1MI1 | 331.954 | J1MI1 | 318.381 | C1J1MI1 | 212.037 |
| C1J2 | 317.009 | C1MI2 | 307.631 | J1MI2 | 326.904 | C1J1MI2 | 285.793 |
| C2J1 | 366.666 | C1MI3 | 383.337 | J1MI3 | 398.698 | C1J1MI3 | 336.277 |
| C2J2 | 449.759 | C1MI4 | 327.526 | J1MI4 | 312.438 | C1J1MI4 | 408.396 |
| | | C1MI5 | 380.780 | J1MI5 | 445.218 | C1J1MI5 | 558.975 |
| | | C1MI6 | 314.487 | J1MI6 | 393.049 | C1J1MI6 | 387.899 |
| | | C2MI1 | 524.196 | J2MI1 | 537.769 | C1J2MI1 | 451.871 |
| | | C2MI2 | 461.592 | J2MI2 | 442.319 | C1J2MI2 | 329.470 |
| | | C2MI3 | 521.631 | J2MI3 | 506.270 | C1J2MI3 | 430.396 |
| | | C2MI4 | 311.117 | J2MI4 | 326.205 | C1J2MI4 | 246.656 |
| | | C2MI5 | 304.665 | J2MI5 | 240.227 | C1J2MI5 | 202.585 |
| | | C2MI6 | 326.075 | J2MI6 | 247.513 | C1J2MI6 | 241.074 |
| | | | | | | C2J1MI1 | 424.724 |
| | | | | | | C2J1MI2 | 368.015 |
| | | | | | | C2J1MI3 | 461.120 |
| | | | | | | C2J1MI4 | 216.479 |
| | | | | | | C2J1MI5 | 331.461 |
| | | | | | | C2J1MI6 | 398.198 |
| | | | | | | C2J2MI1 | 623.668 |
| | | | | | | C2J2MI2 | 555.168 |
| | | | | | | C2J2MI3 | 582.143 |
| | | | | | | C2J2MI4 | 405.755 |
| | | | | | | C2J2MI5 | 277.869 |
| | | | | | | C2J2MI6 | 253.952 |

Annexure 4.4.Factorial ANOVA to test the significance of factors at 10 days growth stage of rice Plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | PHA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 976372.881[a] | 23 | 42450.995 | 20481.787 | .000 |
| Intercept | 24749250.354 | 1 | 24749250.354 | 11941036.185 | .000 |
| J | 48270.603 | 1 | 48270.603 | 23289.635 | .000 |
| C | 14866.365 | 1 | 14866.365 | 7172.734 | .000 |
| MI | 473112.176 | 5 | 94622.435 | 45653.501 | .000 |
| J * C | 135732.631 | 5 | 27146.526 | 13097.676 | .000 |
| J * MI | 43074.885 | 5 | 8614.977 | 4156.560 | .000 |
| C * MI | 159378.626 | 1 | 159378.626 | 76897.115 | .000 |
| J * C * MI | 101937.596 | 5 | 20387.519 | 9836.585 | .000 |
| Error | 99.486 | 48 | 2.073 | | |
| Total | 25725722.721 | 72 | | | |
| Corrected Total | 976472.367 | 71 | | | |
| a. R Squared = 1.000 (Adjusted R Squared = 1.000) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 498.982 | C1MI1 | 627.179 | J1MI1 | 612.326 | C1J1MI1 | 528.083 |
| C1J2 | 644.865 | C1MI2 | 594.284 | J1MI2 | 574.053 | C1J1MI2 | 501.647 |
| C2J1 | 621.819 | C1MI3 | 743.778 | J1MI3 | 601.581 | C1J1MI3 | 525.253 |
| C2J2 | 579.506 | C1MI4 | 509.002 | J1MI4 | 548.420 | C1J1MI4 | 504.410 |
| | | C1MI5 | 512.150 | J1MI5 | 563.502 | C1J1MI5 | 482.029 |
| | | C1MI6 | 445.150 | J1MI6 | 462.521 | C1J1MI6 | 452.471 |
| | | C2MI1 | 664.941 | J2MI1 | 679.793 | C1J2MI1 | 726.274 |
| | | C2MI2 | 659.180 | J2MI2 | 679.412 | C1J2MI2 | 686.921 |
| | | C2MI3 | 667.217 | J2MI3 | 809.415 | C1J2MI3 | 962.304 |
| | | C2MI4 | 550.445 | J2MI4 | 511.027 | C1J2MI4 | 513.593 |
| | | C2MI5 | 581.859 | J2MI5 | 530.507 | C1J2MI5 | 542.270 |
| | | C2MI6 | 480.332 | J2MI6 | 462.960 | C1J2MI6 | 437.828 |
| | | | | | | C2J1MI1 | 696.569 |
| | | | | | | C2J1MI2 | 646.458 |
| | | | | | | C2J1MI3 | 677.909 |
| | | | | | | C2J1MI4 | 592.430 |
| | | | | | | C2J1MI5 | 644.975 |
| | | | | | | C2J1MI6 | 472.571 |
| | | | | | | C2J2MI1 | 633.312 |
| | | | | | | C2J2MI2 | 671.902 |
| | | | | | | C2J2MI3 | 656.526 |
| | | | | | | C2J2MI4 | 508.460 |
| | | | | | | C2J2MI5 | 518.744 |
| | | | | | | C2J2MI6 | 488.093 |

Annexure 4.5: ASA Factorial ANOVA to test the significance of factors at 45 days

**Tests of Between-Subjects Effects**

| Dependent Variable: | ASA | | | | |
|---|---|---|---|---|---|
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 46459.539[a] | 23 | 2019.980 | 26.398 | .000 |
| Intercept | 945454.019 | 1 | 945454.019 | 12355.484 | .000 |
| J | 1031.631 | 1 | 1031.631 | 13.482 | .001 |
| C | 19799.873 | 1 | 19799.873 | 258.751 | .000 |
| MI | 9030.957 | 5 | 1806.191 | 23.604 | .000 |
| J * C | 2466.684 | 1 | 2466.684 | 32.235 | .000 |
| J * MI | 6605.108 | 5 | 1321.022 | 17.264 | .000 |
| C * MI | 3153.283 | 5 | 630.657 | 8.242 | .000 |
| J * C * MI | 4372.004 | 5 | 874.401 | 11.427 | .000 |
| Error | 3673.008 | 48 | 76.521 | | |
| Total | 995586.567 | 72 | | | |
| Corrected Total | 50132.547 | 71 | | | |

a. R Squared = .927 (Adjusted R Squared = .892)

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 121.537 | C1MI1 | 137.528 | J1MI1 | 115.810 | C1J1MI1 | 140.872 |
| C1J2 | 140.813 | C1MI2 | 131.700 | J1MI2 | 108.469 | C1J1MI2 | 128.970 |
| C2J1 | 100.077 | C1MI3 | 134.607 | J1MI3 | 120.100 | C1J1MI3 | 110.316 |
| C2J2 | 95.941 | C1MI4 | 129.704 | J1MI4 | 131.292 | C1J1MI4 | 137.079 |
| | | C1MI5 | 144.688 | J1MI5 | 107.834 | C1J1MI5 | 114.408 |
| | | C1MI6 | 108.824 | J1MI6 | 81.333 | C1J1MI6 | 97.575 |
| | | C2MI1 | 95.322 | J2MI1 | 117.040 | C1J2MI1 | 134.184 |
| | | C2MI2 | 87.751 | J2MI2 | 110.981 | C1J2MI2 | 134.429 |
| | | C2MI3 | 125.650 | J2MI3 | 140.156 | C1J2MI3 | 158.898 |
| | | C2MI4 | 103.772 | J2MI4 | 102.184 | C1J2MI4 | 122.329 |
| | | C2MI5 | 97.132 | J2MI5 | 133.986 | C1J2MI5 | 174.967 |
| | | C2MI6 | 78.425 | J2MI6 | 105.916 | C1J2MI6 | 120.073 |
| | | | | | | C2J1MI1 | 90.749 |
| | | | | | | C2J1MI2 | 87.969 |
| | | | | | | C2J1MI3 | 129.885 |
| | | | | | | C2J1MI4 | 125.506 |
| | | | | | | C2J1MI5 | 101.261 |
| | | | | | | C2J1MI6 | 65.092 |
| | | | | | | C2J2MI1 | 99.896 |
| | | | | | | C2J2MI2 | 87.534 |
| | | | | | | C2J2MI3 | 121.415 |
| | | | | | | C2J2MI4 | 82.038 |
| | | | | | | C2J2MI5 | 93.004 |
| | | | | | | C2J2MI6 | 91.759 |

Annexure 4.6. DHA factorial ANOVA to test the significance of factors at 45 days

**Tests of Between-Subjects Effects**

| Dependent Variable: | DHA | | | | |
|---|---|---|---|---|---|
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 2254.460[a] | 23 | 98.020 | 65.906 | .000 |
| Intercept | 10726.068 | 1 | 10726.068 | 7211.956 | .000 |
| J | 1094.338 | 1 | 1094.338 | 735.807 | .000 |
| C | 375.041 | 1 | 375.041 | 252.169 | .000 |
| MI | 329.313 | 5 | 65.863 | 44.284 | .000 |
| J * C | 244.727 | 5 | 48.945 | 32.910 | .000 |
| J * MI | 37.703 | 5 | 7.541 | 5.070 | .001 |
| C * MI | 11.643 | 1 | 11.643 | 7.829 | .007 |
| J * C * MI | 161.696 | 5 | 32.339 | 21.744 | .000 |
| Error | 71.389 | 48 | 1.487 | | |
| Total | 13051.917 | 72 | | | |
| Corrected Total | 2325.849 | 71 | | | |

a. R Squared = .969 (Adjusted R Squared = .955)

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 10.187 | C1MI1 | 15.656 | J1MI1 | 8.437 | C1J1MI1 | 12.603 |
| C1J2 | 18.789 | C1MI2 | 16.929 | J1MI2 | 8.944 | C1J1MI2 | 9.496 |
| C2J1 | 6.427 | C1MI3 | 18.709 | J1MI3 | 8.496 | C1J1MI3 | 9.238 |
| C2J2 | 13.420 | C1MI4 | 12.535 | J1MI4 | 8.913 | C1J1MI4 | 12.029 |
| | | C1MI5 | 11.276 | J1MI5 | 7.570 | C1J1MI5 | 7.926 |
| | | C1MI6 | 11.821 | J1MI6 | 7.482 | C1J1MI6 | 9.831 |
| | | C2MI1 | 9.384 | J2MI1 | 16.603 | C1J2MI1 | 18.708 |
| | | C2MI2 | 11.368 | J2MI2 | 19.354 | C1J2MI2 | 24.363 |
| | | C2MI3 | 12.662 | J2MI3 | 22.876 | C1J2MI3 | 28.181 |
| | | C2MI4 | 9.183 | J2MI4 | 12.805 | C1J2MI4 | 13.041 |
| | | C2MI5 | 8.732 | J2MI5 | 12.438 | C1J2MI5 | 14.627 |
| | | C2MI6 | 8.209 | J2MI6 | 12.549 | C1J2MI6 | 13.812 |
| | | | | | | C2J1MI1 | 4.270 |
| | | | | | | C2J1MI2 | 8.392 |
| | | | | | | C2J1MI3 | 7.754 |
| | | | | | | C2J1MI4 | 5.796 |
| | | | | | | C2J1MI5 | 7.215 |
| | | | | | | C2J1MI6 | 5.133 |
| | | | | | | C2J2MI1 | 14.498 |
| | | | | | | C2J2MI2 | 14.345 |
| | | | | | | C2J2MI3 | 17.570 |
| | | | | | | C2J2MI4 | 12.570 |
| | | | | | | C2J2MI5 | 10.249 |
| | | | | | | C2J2MI6 | 11.286 |

Annexure 4.7. Factorial ANOVA to test the significance of factors at 45 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | GSA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 879833.841[a] | 23 | 38253.645 | 8354.338 | .000 |
| Intercept | 7092739.452 | 1 | 7092739.452 | 1549006.388 | .000 |
| J | 4339.782 | 1 | 4339.782 | 947.779 | .000 |
| C | 20968.002 | 1 | 20968.002 | 4579.270 | .000 |
| MI | 272230.459 | 5 | 54446.092 | 11890.659 | .000 |
| J * C | 71399.992 | 1 | 71399.992 | 15593.276 | .000 |
| J * MI | 204323.936 | 5 | 40864.787 | 8924.594 | .000 |
| C * MI | 133090.370 | 5 | 26618.074 | 5813.208 | .000 |
| J * C * MI | 173481.301 | 5 | 34696.260 | 7577.429 | .000 |
| Error | 219.787 | 48 | 4.579 | | |
| Total | 7972793.080 | 72 | | | |
| Corrected Total | 880053.628 | 71 | | | |

a. R Squared = 1.000 (Adjusted R Squared = 1.000)

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 336.053 | C1MI1 | 230.607 | J1MI1 | 359.430 | C1J1MI1 | 294.417 |
| C1J2 | 257.544 | C1MI2 | 295.732 | J1MI2 | 187.950 | C1J1MI2 | 257.392 |
| C2J1 | 307.202 | C1MI3 | 402.460 | J1MI3 | 424.643 | C1J1MI3 | 507.041 |
| C2J2 | 354.656 | C1MI4 | 346.112 | J1MI4 | 309.929 | C1J1MI4 | 394.416 |
| | | C1MI5 | 235.638 | J1MI5 | 395.647 | C1J1MI5 | 303.106 |
| | | C1MI6 | 270.241 | J1MI6 | 252.163 | C1J1MI6 | 259.943 |
| | | C2MI1 | 366.079 | J2MI1 | 237.256 | C1J2MI1 | 166.796 |
| | | C2MI2 | 224.514 | J2MI2 | 332.296 | C1J2MI2 | 334.071 |
| | | C2MI3 | 464.167 | J2MI3 | 441.984 | C1J2MI3 | 297.878 |
| | | C2MI4 | 328.824 | J2MI4 | 365.007 | C1J2MI4 | 297.808 |
| | | C2MI5 | 381.679 | J2MI5 | 221.670 | C1J2MI5 | 168.170 |
| | | C2MI6 | 220.308 | J2MI6 | 238.386 | C1J2MI6 | 280.540 |
| | | | | | | C2J1MI1 | 424.444 |
| | | | | | | C2J1MI2 | 118.508 |
| | | | | | | C2J1MI3 | 342.245 |
| | | | | | | C2J1MI4 | 225.442 |
| | | | | | | C2J1MI5 | 488.188 |
| | | | | | | C2J1MI6 | 244.384 |
| | | | | | | C2J2MI1 | 307.715 |
| | | | | | | C2J2MI2 | 330.521 |
| | | | | | | C2J2MI3 | 586.089 |
| | | | | | | C2J2MI4 | 432.207 |
| | | | | | | C2J2MI5 | 275.170 |
| | | | | | | C2J2MI6 | 196.232 |

Annexure 4.8. Factorial ANOVA to test the significance of factors at 45 days of rice Plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | PHA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 578531.860[a] | 23 | 25153.559 | 13809.731 | .000 |
| Intercept | 18989196.940 | 1 | 18989196.940 | 10425391.292 | .000 |
| J | 9143.762 | 1 | 9143.762 | 5020.080 | .000 |
| C | 3540.037 | 1 | 3540.037 | 1943.541 | .000 |
| MI | 111556.868 | 5 | 22311.374 | 12249.323 | .000 |
| J * C | 37892.178 | 5 | 7578.436 | 4160.690 | .000 |
| J * MI | 120203.350 | 5 | 24040.670 | 13198.736 | .000 |
| C * MI | 263077.036 | 1 | 263077.036 | 144433.756 | .000 |
| J * C * MI | 33118.628 | 5 | 6623.726 | 3636.538 | .000 |
| Error | 87.429 | 48 | 1.821 | | |
| Total | 19567816.229 | 72 | | | |
| Corrected Total | 578619.289 | 71 | | | |
| a. R Squared = 1.000 (Adjusted R Squared = 1.000) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 471.389 | C1MI1 | 544.369 | J1MI1 | 573.710 | C1J1MI1 | 472.906 |
| C1J2 | 569.745 | C1MI2 | 559.944 | J1MI2 | 501.355 | C1J1MI2 | 514.234 |
| C2J1 | 578.260 | C1MI3 | 513.359 | J1MI3 | 538.151 | C1J1MI3 | 462.010 |
| C2J2 | 434.827 | C1MI4 | 510.900 | J1MI4 | 495.873 | C1J1MI4 | 484.077 |
| | | C1MI5 | 492.116 | J1MI5 | 530.013 | C1J1MI5 | 457.407 |
| | | C1MI6 | 502.715 | J1MI6 | 509.845 | C1J1MI6 | 437.702 |
| | | C2MI1 | 575.223 | J2MI1 | 545.882 | C1J2MI1 | 615.832 |
| | | C2MI2 | 462.588 | J2MI2 | 521.177 | C1J2MI2 | 605.654 |
| | | C2MI3 | 573.431 | J2MI3 | 548.639 | C1J2MI3 | 564.708 |
| | | C2MI4 | 361.678 | J2MI4 | 376.705 | C1J2MI4 | 537.723 |
| | | C2MI5 | 562.403 | J2MI5 | 524.507 | C1J2MI5 | 526.825 |
| | | C2MI6 | 503.935 | J2MI6 | 496.805 | C1J2MI6 | 567.727 |
| | | | | | | C2J1MI1 | 674.515 |
| | | | | | | C2J1MI2 | 488.475 |
| | | | | | | C2J1MI3 | 614.292 |
| | | | | | | C2J1MI4 | 507.669 |
| | | | | | | C2J1MI5 | 602.618 |
| | | | | | | C2J1MI6 | 581.988 |
| | | | | | | C2J2MI1 | 475.932 |
| | | | | | | C2J2MI2 | 436.701 |
| | | | | | | C2J2MI3 | 532.571 |
| | | | | | | C2J2MI4 | 215.688 |
| | | | | | | C2J2MI5 | 522.188 |
| | | | | | | C2J2MI6 | 425.882 |

Annexure 4.9. ASA Factorial ANOVA to test the significance of factors at 90 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | ASA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 78019.658[a] | 23 | 3392.159 | 382.665 | .000 |
| Intercept | 405353.632 | 1 | 405353.632 | 45727.431 | .000 |
| J | 53691.026 | 1 | 53691.026 | 6056.817 | .000 |
| C | 13436.847 | 1 | 13436.847 | 1515.794 | .000 |
| MI | 1676.564 | 5 | 335.313 | 37.826 | .000 |
| J * C | 2172.470 | 1 | 2172.470 | 245.074 | .000 |
| C * MI | 2638.540 | 5 | 527.708 | 59.530 | .000 |
| J * MI | 1661.840 | 5 | 332.368 | 37.494 | .000 |
| J * C * MI | 2742.372 | 5 | 548.474 | 61.873 | .000 |
| Error | 425.499 | 48 | 8.865 | | |
| Total | 483798.789 | 72 | | | |
| Corrected Total | 78445.157 | 71 | | | |

a. R Squared = .995 (Adjusted R Squared = .992)

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 55.893 | C1MI1 | 77.281 | J1MI1 | 39.766 | C1J1MI1 | 46.953 |
| C1J2 | 121.494 | C1MI2 | 93.159 | J1MI2 | 51.407 | C1J1MI2 | 64.791 |
| C2J1 | 39.557 | C1MI3 | 102.828 | J1MI3 | 43.731 | C1J1MI3 | 62.471 |
| C2J2 | 83.186 | C1MI4 | 84.782 | J1MI4 | 41.621 | C1J1MI4 | 48.611 |
| | | C1MI5 | 83.714 | J1MI5 | 52.673 | C1J1MI5 | 58.259 |
| | | C1MI6 | 90.398 | J1MI6 | 57.152 | C1J1MI6 | 54.274 |
| | | C2MI1 | 55.268 | J2MI1 | 92.783 | C1J2MI1 | 107.609 |
| | | C2MI2 | 70.802 | J2MI2 | 112.554 | C1J2MI2 | 121.527 |
| | | C2MI3 | 50.595 | J2MI3 | 109.692 | C1J2MI3 | 143.185 |
| | | C2MI4 | 59.924 | J2MI4 | 103.085 | C1J2MI4 | 120.954 |
| | | C2MI5 | 70.415 | J2MI5 | 101.456 | C1J2MI5 | 109.169 |
| | | C2MI6 | 61.226 | J2MI6 | 94.473 | C1J2MI6 | 126.522 |
| | | | | | | C2J1MI1 | 32.579 |
| | | | | | | C2J1MI2 | 38.024 |
| | | | | | | C2J1MI3 | 24.992 |
| | | | | | | C2J1MI4 | 34.631 |
| | | | | | | C2J1MI5 | 47.087 |
| | | | | | | C2J1MI6 | 60.029 |
| | | | | | | C2J2MI1 | 77.957 |
| | | | | | | C2J2MI2 | 103.581 |
| | | | | | | C2J2MI3 | 76.199 |
| | | | | | | C2J2MI4 | 85.216 |
| | | | | | | C2J2MI5 | 93.742 |
| | | | | | | C2J2MI6 | 62.423 |

Annexure 4.10. Factorial ANOVA to test the significance of factors at 90 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | DHA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 3468.161[a] | 23 | 150.790 | 110.276 | .000 |
| Intercept | 15671.129 | 1 | 15671.129 | 11460.678 | .000 |
| J | 1216.301 | 1 | 1216.301 | 889.511 | .000 |
| C | 745.478 | 1 | 745.478 | 545.186 | .000 |
| MI | 1054.789 | 5 | 210.958 | 154.279 | .000 |
| J * C | 261.629 | 5 | 52.326 | 38.267 | .000 |
| J * MI | 124.850 | 5 | 24.970 | 18.261 | .000 |
| C * MI | 40.710 | 1 | 40.710 | 29.772 | .000 |
| J * C * MI | 24.403 | 5 | 4.881 | 3.569 | .008 |
| Error | 65.634 | 48 | 1.367 | | |
| Total | 19204.924 | 72 | | | |
| Corrected Total | 3533.795 | 71 | | | |

a. R Squared = .981 (Adjusted R Squared = .973)

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 13.109 | C1MI1 | 18.905 | J1MI1 | 11.351 | C1J1MI1 | 14.380 |
| C1J2 | 22.833 | C1MI2 | 18.544 | J1MI2 | 11.911 | C1J1MI2 | 13.031 |
| C2J1 | 8.177 | C1MI3 | 21.733 | J1MI3 | 14.462 | C1J1MI3 | 18.194 |
| C2J2 | 14.894 | C1MI4 | 24.381 | J1MI4 | 11.447 | C1J1MI4 | 15.531 |
| | | C1MI5 | 14.043 | J1MI5 | 7.786 | C1J1MI5 | 9.675 |
| | | C1MI6 | 10.219 | J1MI6 | 6.901 | C1J1MI6 | 7.842 |
| | | C2MI1 | 13.382 | J2MI1 | 20.936 | C1J2MI1 | 23.430 |
| | | C2MI2 | 15.068 | J2MI2 | 21.701 | C1J2MI2 | 24.057 |
| | | C2MI3 | 13.297 | J2MI3 | 20.568 | C1J2MI3 | 25.271 |
| | | C2MI4 | 13.512 | J2MI4 | 26.445 | C1J2MI4 | 33.230 |
| | | C2MI5 | 7.293 | J2MI5 | 13.551 | C1J2MI5 | 18.412 |
| | | C2MI6 | 6.660 | J2MI6 | 9.979 | C1J2MI6 | 12.597 |
| | | | | | | C2J1MI1 | 8.321 |
| | | | | | | C2J1MI2 | 10.792 |
| | | | | | | C2J1MI3 | 10.730 |
| | | | | | | C2J1MI4 | 7.363 |
| | | | | | | C2J1MI5 | 5.897 |
| | | | | | | C2J1MI6 | 5.961 |
| | | | | | | C2J2MI1 | 18.442 |
| | | | | | | C2J2MI2 | 19.344 |
| | | | | | | C2J2MI3 | 15.865 |
| | | | | | | C2J2MI4 | 19.660 |
| | | | | | | C2J2MI5 | 8.690 |
| | | | | | | C2J2MI6 | 7.360 |

Annexure 4.11. Factorial ANOVA to test the significance of factors at 90 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | GSA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 931088.993[a] | 23 | 40482.130 | 15302.017 | .000 |
| Intercept | 10843347.884 | 1 | 10843347.884 | 4098724.347 | .000 |
| J | 5135.854 | 1 | 5135.854 | 1941.324 | .000 |
| C | 20797.441 | 1 | 20797.441 | 7861.316 | .000 |
| MI | 333728.872 | 5 | 66745.774 | 25229.526 | .000 |
| J * MI | 85709.132 | 5 | 17141.826 | 6479.514 | .000 |
| J * C | 182736.826 | 1 | 182736.826 | 69073.490 | .000 |
| C * MI | 144983.261 | 5 | 28996.652 | 10960.571 | .000 |
| J * C * MI | 157997.608 | 5 | 31599.522 | 11944.441 | .000 |
| Error | 126.986 | 48 | 2.646 | | |
| Total | 11774563.864 | 72 | | | |
| Corrected Total | 931215.979 | 71 | | | |
| a. R Squared = 1.000 (Adjusted R Squared = 1.000) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 447.003 | C1MI1 | 483.108 | J1MI1 | 441.884 | C1J1MI1 | 490.932 |
| C1J2 | 363.138 | C1MI2 | 386.677 | J1MI2 | 345.349 | C1J1MI2 | 423.756 |
| C2J1 | 312.255 | C1MI3 | 352.995 | J1MI3 | 347.798 | C1J1MI3 | 403.820 |
| C2J2 | 429.904 | C1MI4 | 368.292 | J1MI4 | 265.280 | C1J1MI4 | 367.794 |
| | | C1MI5 | 404.407 | J1MI5 | 437.440 | C1J1MI5 | 473.853 |
| | | C1MI6 | 434.945 | J1MI6 | 440.023 | C1J1MI6 | 521.865 |
| | | C2MI1 | 369.819 | J2MI1 | 411.043 | C1J2MI1 | 475.284 |
| | | C2MI2 | 304.614 | J2MI2 | 345.942 | C1J2MI2 | 349.598 |
| | | C2MI3 | 255.571 | J2MI3 | 260.767 | C1J2MI3 | 302.169 |
| | | C2MI4 | 273.665 | J2MI4 | 376.676 | C1J2MI4 | 368.790 |
| | | C2MI5 | 481.679 | J2MI5 | 448.646 | C1J2MI5 | 334.960 |
| | | C2MI6 | 541.128 | J2MI6 | 536.050 | C1J2MI6 | 348.025 |
| | | | | | | C2J1MI1 | 392.836 |
| | | | | | | C2J1MI2 | 266.942 |
| | | | | | | C2J1MI3 | 291.776 |
| | | | | | | C2J1MI4 | 162.767 |
| | | | | | | C2J1MI5 | 401.026 |
| | | | | | | C2J1MI6 | 358.181 |
| | | | | | | C2J2MI1 | 346.802 |
| | | | | | | C2J2MI2 | 342.286 |
| | | | | | | C2J2MI3 | 219.366 |
| | | | | | | C2J2MI4 | 384.563 |
| | | | | | | C2J2MI5 | 562.331 |
| | | | | | | C2J2MI6 | 724.074 |

Annexure 4.12. Factorial ANOVA to test the significance of factors at 90 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | PHA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 893521.208[a] | 23 | 38848.748 | 3002.159 | .000 |
| Intercept | 12495565.282 | 1 | 12495565.282 | 965633.910 | .000 |
| J | 466749.371 | 1 | 466749.371 | 36069.518 | .000 |
| C | 13619.452 | 1 | 13619.452 | 1052.486 | .000 |
| MI | 62480.850 | 5 | 12496.170 | 965.681 | .000 |
| J * C | 54833.532 | 5 | 10966.706 | 847.487 | .000 |
| J * MI | 195152.865 | 5 | 39030.573 | 3016.210 | .000 |
| C * MI | 83170.353 | 1 | 83170.353 | 6427.249 | .000 |
| J * C * MI | 17514.783 | 5 | 3502.957 | 270.702 | .000 |
| Error | 621.133 | 48 | 12.940 | | |
| Total | 13389707.623 | 72 | | | |
| Corrected Total | 894142.341 | 71 | | | |
| a. R Squared =.999 (Adjusted R Squared =.999) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 288.337 | C1MI1 | 468.929 | J1MI1 | 304.441 | C1J1MI1 | 332.693 |
| C1J2 | 517.341 | C1MI2 | 428.780 | J1MI2 | 271.641 | C1J1MI2 | 315.700 |
| C2J1 | 383.819 | C1MI3 | 412.208 | J1MI3 | 426.677 | C1J1MI3 | 315.903 |
| C2J2 | 476.874 | C1MI4 | 399.651 | J1MI4 | 316.844 | C1J1MI4 | 245.569 |
| | | C1MI5 | 345.249 | J1MI5 | 341.793 | C1J1MI5 | 261.943 |
| | | C1MI6 | 362.219 | J1MI6 | 355.073 | C1J1MI6 | 258.215 |
| | | C2MI1 | 371.933 | J2MI1 | 536.421 | C1J2MI1 | 605.165 |
| | | C2MI2 | 296.434 | J2MI2 | 453.573 | C1J2MI2 | 541.860 |
| | | C2MI3 | 510.419 | J2MI3 | 495.950 | C1J2MI3 | 508.512 |
| | | C2MI4 | 448.377 | J2MI4 | 531.185 | C1J2MI4 | 553.733 |
| | | C2MI5 | 464.939 | J2MI5 | 468.395 | C1J2MI5 | 428.554 |
| | | C2MI6 | 489.975 | J2MI6 | 497.121 | C1J2MI6 | 466.224 |
| | | | | | | C2J1MI1 | 276.189 |
| | | | | | | C2J1MI2 | 227.582 |
| | | | | | | C2J1MI3 | 537.450 |
| | | | | | | C2J1MI4 | 388.118 |
| | | | | | | C2J1MI5 | 421.643 |
| | | | | | | C2J1MI6 | 451.930 |
| | | | | | | C2J2MI1 | 467.677 |
| | | | | | | C2J2MI2 | 365.286 |
| | | | | | | C2J2MI3 | 483.387 |
| | | | | | | C2J2MI4 | 508.637 |
| | | | | | | C2J2MI5 | 508.235 |
| | | | | | | C2J2MI6 | 528.019 |

Annexure 4.13.ASA. Factorial ANOVA to test the significance of factors at 120 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | ASA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 24874.509[a] | 23 | 1081.500 | 72.587 | .000 |
| Intercept | 403225.345 | 1 | 403225.345 | 27063.227 | .000 |
| J | 3244.465 | 1 | 3244.465 | 217.758 | .000 |
| C | 9015.308 | 1 | 9015.308 | 605.079 | .000 |
| MI | 3646.446 | 5 | 729.289 | 48.948 | .000 |
| J * C | 2245.626 | 5 | 449.125 | 30.144 | .000 |
| J * MI | 1043.446 | 5 | 208.689 | 14.007 | .000 |
| C * MI | 3644.318 | 1 | 3644.318 | 244.595 | .000 |
| J * C * MI | 2034.899 | 5 | 406.980 | 27.315 | .000 |
| Error | 715.170 | 48 | 14.899 | | |
| Total | 428815.025 | 72 | | | |
| Corrected Total | 25589.679 | 71 | | | |

a. R Squared = .972 (Adjusted R Squared = .959)

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 72.198 | C1MI1 | 71.415 | J1MI1 | 47.245 | C1J1MI1 | 49.288 |
| C1J2 | 99.853 | C1MI2 | 91.260 | J1MI2 | 70.690 | C1J1MI2 | 79.529 |
| C2J1 | 64.047 | C1MI3 | 95.201 | J1MI3 | 80.376 | C1J1MI3 | 75.522 |
| C2J2 | 63.244 | C1MI4 | 89.787 | J1MI4 | 78.834 | C1J1MI4 | 84.201 |
| | | C1MI5 | 81.837 | J1MI5 | 67.385 | C1J1MI5 | 67.750 |
| | | C1MI6 | 86.653 | J1MI6 | 64.206 | C1J1MI6 | 76.897 |
| | | C2MI1 | 49.356 | J2MI1 | 73.525 | C1J2MI1 | 93.541 |
| | | C2MI2 | 61.656 | J2MI2 | 82.226 | C1J2MI2 | 102.991 |
| | | C2MI3 | 72.096 | J2MI3 | 86.921 | C1J2MI3 | 114.879 |
| | | C2MI4 | 61.241 | J2MI4 | 72.193 | C1J2MI4 | 95.372 |
| | | C2MI5 | 75.350 | J2MI5 | 89.802 | C1J2MI5 | 95.923 |
| | | C2MI6 | 62.175 | J2MI6 | 84.623 | C1J2MI6 | 96.410 |
| | | | | | | C2J1MI1 | 45.201 |
| | | | | | | C2J1MI2 | 61.851 |
| | | | | | | C2J1MI3 | 85.230 |
| | | | | | | C2J1MI4 | 73.467 |
| | | | | | | C2J1MI5 | 67.020 |
| | | | | | | C2J1MI6 | 51.514 |
| | | | | | | C2J2MI1 | 53.510 |
| | | | | | | C2J2MI2 | 61.461 |
| | | | | | | C2J2MI3 | 58.962 |
| | | | | | | C2J2MI4 | 49.015 |
| | | | | | | C2J2MI5 | 83.680 |
| | | | | | | C2J2MI6 | 72.836 |

Annexure 4.14. DHA factorial ANOVA to test the significance of factors at 120 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | DHA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 3917.031[a] | 23 | 170.306 | 149.255 | .000 |
| Intercept | 13942.756 | 1 | 13942.756 | 12219.318 | .000 |
| J | 2986.542 | 1 | 2986.542 | 2617.381 | .000 |
| C | 359.823 | 1 | 359.823 | 315.346 | .000 |
| MI | 108.772 | 5 | 21.754 | 19.065 | .000 |
| J * C | 72.256 | 5 | 14.451 | 12.665 | .000 |
| J * MI | 315.244 | 1 | 315.244 | 276.277 | .000 |
| C * MI | 38.024 | 5 | 7.605 | 6.665 | .000 |
| J * C * MI | 36.372 | 5 | 7.274 | 6.375 | .000 |
| Error | 54.770 | 48 | 1.141 | | |
| Total | 17914.558 | 72 | | | |
| Corrected Total | 3971.801 | 71 | | | |

a. R Squared = .986 (Adjusted R Squared = .980)

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 11.803 | C1MI1 | 17.601 | J1MI1 | 7.913 | C1J1MI1 | 10.875 |
| C1J2 | 20.499 | C1MI2 | 17.118 | J1MI2 | 7.585 | C1J1MI2 | 11.219 |
| C2J1 | 3.147 | C1MI3 | 16.318 | J1MI3 | 7.333 | C1J1MI3 | 12.466 |
| C2J2 | 20.213 | C1MI4 | 15.235 | J1MI4 | 7.738 | C1J1MI4 | 12.316 |
| | | C1MI5 | 16.681 | J1MI5 | 7.159 | C1J1MI5 | 12.015 |
| | | C1MI6 | 13.955 | J1MI6 | 7.124 | C1J1MI6 | 11.930 |
| | | C2MI1 | 13.954 | J2MI1 | 23.642 | C1J2MI1 | 24.328 |
| | | C2MI2 | 13.418 | J2MI2 | 22.951 | C1J2MI2 | 23.017 |
| | | C2MI3 | 10.070 | J2MI3 | 19.055 | C1J2MI3 | 20.170 |
| | | C2MI4 | 12.136 | J2MI4 | 19.633 | C1J2MI4 | 18.154 |
| | | C2MI5 | 10.018 | J2MI5 | 19.539 | C1J2MI5 | 21.347 |
| | | C2MI6 | 10.485 | J2MI6 | 17.317 | C1J2MI6 | 15.981 |
| | | | | | | C2J1MI1 | 4.951 |
| | | | | | | C2J1MI2 | 3.951 |
| | | | | | | C2J1MI3 | 2.200 |
| | | | | | | C2J1MI4 | 3.159 |
| | | | | | | C2J1MI5 | 2.304 |
| | | | | | | C2J1MI6 | 2.319 |
| | | | | | | C2J2MI1 | 22.957 |
| | | | | | | C2J2MI2 | 22.886 |
| | | | | | | C2J2MI3 | 17.940 |
| | | | | | | C2J2MI4 | 21.112 |
| | | | | | | C2J2MI5 | 17.732 |
| | | | | | | C2J2MI6 | 18.652 |

Annexure 4.15. Factorial ANOVA to test the significance of factors at 120 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | ASA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 46459.539[a] | 23 | 2019.980 | 26.398 | .000 |
| Intercept | 945454.019 | 1 | 945454.019 | 12355.484 | .000 |
| J | 1031.631 | 1 | 1031.631 | 13.482 | .001 |
| C | 19799.873 | 1 | 19799.873 | 258.751 | .000 |
| MI | 9030.957 | 5 | 1806.191 | 23.604 | .000 |
| J * C | 2466.684 | 1 | 2466.684 | 32.235 | .000 |
| J * MI | 6605.108 | 5 | 1321.022 | 17.264 | .000 |
| C * MI | 3153.283 | 5 | 630.657 | 8.242 | .000 |
| J * C * MI | 4372.004 | 5 | 874.401 | 11.427 | .000 |
| Error | 3673.008 | 48 | 76.521 | | |
| Total | 995586.567 | 72 | | | |
| Corrected Total | 50132.547 | 71 | | | |
| a. R Squared = .927 (Adjusted R Squared = .892) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 121.537 | C1MI1 | 137.528 | J1MI1 | 115.810 | C1J1MI1 | 140.872 |
| C1J2 | 140.813 | C1MI2 | 131.700 | J1MI2 | 108.469 | C1J1MI2 | 128.970 |
| C2J1 | 100.077 | C1MI3 | 134.607 | J1MI3 | 120.100 | C1J1MI3 | 110.316 |
| C2J2 | 95.941 | C1MI4 | 129.704 | J1MI4 | 131.292 | C1J1MI4 | 137.079 |
| | | C1MI5 | 144.688 | J1MI5 | 107.834 | C1J1MI5 | 114.408 |
| | | C1MI6 | 108.824 | J1MI6 | 81.333 | C1J1MI6 | 97.575 |
| | | C2MI1 | 95.322 | J2MI1 | 117.040 | C1J2MI1 | 134.184 |
| | | C2MI2 | 87.751 | J2MI2 | 110.981 | C1J2MI2 | 134.429 |
| | | C2MI3 | 125.650 | J2MI3 | 140.156 | C1J2MI3 | 158.898 |
| | | C2MI4 | 103.772 | J2MI4 | 102.184 | C1J2MI4 | 122.329 |
| | | C2MI5 | 97.132 | J2MI5 | 133.986 | C1J2MI5 | 174.967 |
| | | C2MI6 | 78.425 | J2MI6 | 105.916 | C1J2MI6 | 120.073 |
| | | | | | | C2J1MI1 | 90.749 |
| | | | | | | C2J1MI2 | 87.969 |
| | | | | | | C2J1MI3 | 129.885 |
| | | | | | | C2J1MI4 | 125.506 |
| | | | | | | C2J1MI5 | 101.261 |
| | | | | | | C2J1MI6 | 65.092 |
| | | | | | | C2J2MI1 | 99.896 |
| | | | | | | C2J2MI2 | 87.534 |
| | | | | | | C2J2MI3 | 121.415 |
| | | | | | | C2J2MI4 | 82.038 |
| | | | | | | C2J2MI5 | 93.004 |
| | | | | | | C2J2MI6 | 91.759 |

Annexure 4.16. Factorial ANOVA to test the significance of factors at 120 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | PHA | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 2505635.592[a] | 23 | 108940.678 | 68952.941 | .000 |
| Intercept | 8187116.006 | 1 | 8187116.006 | 5181955.303 | .000 |
| J | 14494.305 | 1 | 14494.305 | 9174.029 | .000 |
| C | 2267002.404 | 1 | 2267002.404 | 1434877.083 | .000 |
| MI | 37081.178 | 5 | 7416.236 | 4694.034 | .000 |
| J * C | 40219.604 | 5 | 8043.921 | 5091.321 | .000 |
| J * MI | 35906.124 | 5 | 7181.225 | 4545.286 | .000 |
| C * MI | 72829.979 | 1 | 72829.979 | 46097.025 | .000 |
| J * C * MI | 38101.999 | 5 | 7620.400 | 4823.258 | .000 |
| Error | 75.837 | 48 | 1.580 | | |
| Total | 10692827.435 | 72 | | | |
| Corrected Total | 2505711.428 | 71 | | | |
| a. R Squared = 1.000 (Adjusted R Squared = 1.000) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 560.645 | C1MI1 | 528.686 | J1MI1 | 368.947 | C1J1MI1 | 613.277 |
| C1J2 | 468.660 | C1MI2 | 451.993 | J1MI2 | 278.288 | C1J1MI2 | 448.331 |
| C2J1 | 142.150 | C1MI3 | 565.494 | J1MI3 | 388.688 | C1J1MI3 | 665.633 |
| C2J2 | 177.382 | C1MI4 | 552.067 | J1MI4 | 395.471 | C1J1MI4 | 617.788 |
| | | C1MI5 | 501.959 | J1MI5 | 331.042 | C1J1MI5 | 515.606 |
| | | C1MI6 | 487.716 | J1MI6 | 345.947 | C1J1MI6 | 503.236 |
| | | C2MI1 | 143.635 | J2MI1 | 303.373 | C1J2MI1 | 444.094 |
| | | C2MI2 | 141.705 | J2MI2 | 315.410 | C1J2MI2 | 455.655 |
| | | C2MI3 | 134.935 | J2MI3 | 311.740 | C1J2MI3 | 465.354 |
| | | C2MI4 | 183.225 | J2MI4 | 339.821 | C1J2MI4 | 486.346 |
| | | C2MI5 | 197.351 | J2MI5 | 368.268 | C1J2MI5 | 488.312 |
| | | C2MI6 | 157.744 | J2MI6 | 299.512 | C1J2MI6 | 472.196 |
| | | | | | | C2J1MI1 | 124.618 |
| | | | | | | C2J1MI2 | 108.245 |
| | | | | | | C2J1MI3 | 111.743 |
| | | | | | | C2J1MI4 | 173.154 |
| | | | | | | C2J1MI5 | 146.479 |
| | | | | | | C2J1MI6 | 188.658 |
| | | | | | | C2J2MI1 | 162.652 |
| | | | | | | C2J2MI2 | 175.165 |
| | | | | | | C2J2MI3 | 158.126 |
| | | | | | | C2J2MI4 | 193.295 |
| | | | | | | C2J2MI5 | 248.223 |
| | | | | | | C2J2MI6 | 126.829 |

Annexure 4.17. Factorial ANOVA to test the significance of factors at 10 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | DOC | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 129384.178[a] | 23 | 5625.399 | 1539.756 | .000 |
| Intercept | 1239373.320 | 1 | 1239373.320 | 339234.991 | .000 |
| J | 15077.614 | 1 | 15077.614 | 4126.968 | .000 |
| C | 708.223 | 1 | 708.223 | 193.851 | .000 |
| MI | 28924.849 | 5 | 5784.970 | 1583.433 | .000 |
| J * C | 33788.739 | 5 | 6757.748 | 1849.697 | .000 |
| J * MI | 21306.964 | 5 | 4261.393 | 1166.407 | .000 |
| C * MI | 4193.881 | 1 | 4193.881 | 1147.928 | .000 |
| J * C * MI | 25383.907 | 5 | 5076.781 | 1389.591 | .000 |
| Error | 175.365 | 48 | 3.653 | | |
| Total | 1368932.863 | 72 | | | |
| Corrected Total | 129559.543 | 71 | | | |
| a. R Squared = .999 (Adjusted R Squared = .998) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 156.440 | C1MI1 | 134.450 | J1MI1 | 145.737 | C1J1MI1 | 161.647 |
| C1J2 | 112.233 | C1MI2 | 182.959 | J1MI2 | 211.661 | C1J1MI2 | 193.356 |
| C2J1 | 134.903 | C1MI3 | 136.752 | J1MI3 | 157.648 | C1J1MI3 | 180.693 |
| C2J2 | 121.225 | C1MI4 | 90.162 | J1MI4 | 109.739 | C1J1MI4 | 94.146 |
| | | C1MI5 | 134.276 | J1MI5 | 149.981 | C1J1MI5 | 184.643 |
| | | C1MI6 | 127.422 | J1MI6 | 99.262 | C1J1MI6 | 124.153 |
| | | C2MI1 | 139.152 | J2MI1 | 127.866 | C1J2MI1 | 107.254 |
| | | C2MI2 | 157.598 | J2MI2 | 128.896 | C1J2MI2 | 172.562 |
| | | C2MI3 | 149.763 | J2MI3 | 128.866 | C1J2MI3 | 92.810 |
| | | C2MI4 | 144.259 | J2MI4 | 124.681 | C1J2MI4 | 86.177 |
| | | C2MI5 | 87.645 | J2MI5 | 71.940 | C1J2MI5 | 83.909 |
| | | C2MI6 | 89.967 | J2MI6 | 118.127 | C1J2MI6 | 130.690 |
| | | | | | | C2J1MI1 | 129.827 |
| | | | | | | C2J1MI2 | 229.966 |
| | | | | | | C2J1MI3 | 134.602 |
| | | | | | | C2J1MI4 | 125.333 |
| | | | | | | C2J1MI5 | 115.319 |
| | | | | | | C2J1MI6 | 74.371 |
| | | | | | | C2J2MI1 | 148.478 |
| | | | | | | C2J2MI2 | 85.229 |
| | | | | | | C2J2MI3 | 164.923 |
| | | | | | | C2J2MI4 | 163.185 |
| | | | | | | C2J2MI5 | 59.971 |
| | | | | | | C2J2MI6 | 105.563 |

Annexure 4.18 factorial ANOVA to test the significance of factors at 10 days growth of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | SMBC | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 112640.634[a] | 23 | 4897.419 | 1379.911 | .000 |
| Intercept | 2250059.376 | 1 | 2250059.376 | 633983.247 | .000 |
| J | 7442.610 | 1 | 7442.610 | 2097.051 | .000 |
| C | 43596.616 | 1 | 43596.616 | 12283.909 | .000 |
| MI | 44478.205 | 5 | 8895.641 | 2506.462 | .000 |
| J * C | 202.709 | 1 | 202.709 | 57.116 | .000 |
| C * MI | 6078.064 | 5 | 1215.613 | 342.515 | .000 |
| J * MI | 5448.673 | 5 | 1089.735 | 307.047 | .000 |
| J * C * MI | 5393.756 | 5 | 1078.751 | 303.952 | .000 |
| Error | 170.356 | 48 | 3.549 | | |
| Total | 2362870.365 | 72 | | | |
| Corrected Total | 112810.990 | 71 | | | |
| a. R Squared = .998 (Adjusted R Squared = .998) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 189.541 | C1MI1 | 235.962 | J1MI1 | 190.093 | C1J1MI1 | 198.647 |
| C1J2 | 213.231 | C1MI2 | 236.002 | J1MI2 | 186.895 | C1J1MI2 | 207.213 |
| C2J1 | 143.683 | C1MI3 | 201.875 | J1MI3 | 175.843 | C1J1MI3 | 203.320 |
| C2J2 | 160.661 | C1MI4 | 166.025 | J1MI4 | 161.717 | C1J1MI4 | 175.180 |
| | | C1MI5 | 193.965 | J1MI5 | 157.477 | C1J1MI5 | 195.373 |
| | | C1MI6 | 174.488 | J1MI6 | 127.647 | C1J1MI6 | 157.513 |
| | | C2MI1 | 189.948 | J2MI1 | 235.817 | C1J2MI1 | 273.277 |
| | | C2MI2 | 172.272 | J2MI2 | 221.378 | C1J2MI2 | 264.790 |
| | | C2MI3 | 154.158 | J2MI3 | 180.190 | C1J2MI3 | 200.430 |
| | | C2MI4 | 154.418 | J2MI4 | 158.727 | C1J2MI4 | 156.870 |
| | | C2MI5 | 131.942 | J2MI5 | 168.430 | C1J2MI5 | 192.557 |
| | | C2MI6 | 110.293 | J2MI6 | 157.135 | C1J2MI6 | 191.463 |
| | | | | | | C2J1MI1 | 181.540 |
| | | | | | | C2J1MI2 | 166.577 |
| | | | | | | C2J1MI3 | 148.367 |
| | | | | | | C2J1MI4 | 148.253 |
| | | | | | | C2J1MI5 | 119.580 |
| | | | | | | C2J1MI6 | 97.780 |
| | | | | | | C2J2MI1 | 198.357 |
| | | | | | | C2J2MI2 | 177.967 |
| | | | | | | C2J2MI3 | 159.950 |
| | | | | | | C2J2MI4 | 160.583 |
| | | | | | | C2J2MI5 | 144.303 |
| | | | | | | C2J2MI6 | 122.807 |

Annexure 4.19. Factorial ANOVA to test the significance of factors at 10 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | pMN | | | | |
| Source | Type III Sum of Squares | df | Mean Square | F | Sig. |
| Corrected Model | 4861.047[a] | 23 | 211.350 | 101.299 | .000 |
| Intercept | 14890.519 | 1 | 14890.519 | 7136.971 | .000 |
| J | 448.706 | 1 | 448.706 | 215.063 | .000 |
| C | 1483.318 | 1 | 1483.318 | 710.949 | .000 |
| MI | 454.832 | 5 | 90.966 | 43.600 | .000 |
| J * C | 491.516 | 5 | 98.303 | 47.116 | .000 |
| J * MI | 734.281 | 1 | 734.281 | 351.938 | .000 |
| C * MI | 547.025 | 5 | 109.405 | 52.437 | .000 |
| J * C * MI | 701.370 | 5 | 140.274 | 67.233 | .000 |
| Error | 100.147 | 48 | 2.086 | | |
| Total | 19851.713 | 72 | | | |
| Corrected Total | 4961.194 | 71 | | | |
| a. R Squared = .980 (Adjusted R Squared = .970) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 24.610 | C1MI1 | 14.115 | J1MI1 | 17.582 | C1J1MI1 | 24.500 |
| C1J2 | 13.230 | C1MI2 | 26.325 | J1MI2 | 22.193 | C1J1MI2 | 38.500 |
| C2J1 | 9.145 | C1MI3 | 24.098 | J1MI3 | 23.079 | C1J1MI3 | 34.995 |
| C2J2 | 10.539 | C1MI4 | 18.873 | J1MI4 | 15.705 | C1J1MI4 | 20.997 |
| | | C1MI5 | 13.233 | J1MI5 | 9.123 | C1J1MI5 | 12.667 |
| | | C1MI6 | 16.875 | J1MI6 | 13.582 | C1J1MI6 | 16.000 |
| | | C2MI1 | 12.247 | J2MI1 | 8.780 | C1J2MI1 | 3.730 |
| | | C2MI2 | 7.026 | J2MI2 | 11.158 | C1J2MI2 | 14.150 |
| | | C2MI3 | 11.913 | J2MI3 | 12.932 | C1J2MI3 | 13.200 |
| | | C2MI4 | 11.332 | J2MI4 | 14.500 | C1J2MI4 | 16.750 |
| | | C2MI5 | 7.747 | J2MI5 | 11.857 | C1J2MI5 | 13.800 |
| | | C2MI6 | 8.788 | J2MI6 | 12.082 | C1J2MI6 | 17.750 |
| | | | | | | C2J1MI1 | 10.663 |
| | | | | | | C2J1MI2 | 5.887 |
| | | | | | | C2J1MI3 | 11.163 |
| | | | | | | C2J1MI4 | 10.413 |
| | | | | | | C2J1MI5 | 5.580 |
| | | | | | | C2J1MI6 | 11.163 |
| | | | | | | C2J2MI1 | 13.830 |
| | | | | | | C2J2MI2 | 8.165 |
| | | | | | | C2J2MI3 | 12.663 |
| | | | | | | C2J2MI4 | 12.250 |
| | | | | | | C2J2MI5 | 9.913 |
| | | | | | | C2J2MI6 | 6.413 |

Annexure 4.20. POM factorial ANOVA to test the significance of factors at 10 daysof rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | POM | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 193.657[a] | 23 | 8.420 | 1351.783 | .000 |
| Intercept | 3001.052 | 1 | 3001.052 | 481809.988 | .000 |
| J | 70.010 | 1 | 70.010 | 11239.874 | .000 |
| C | .071 | 1 | .071 | 11.440 | .001 |
| MI | 16.153 | 5 | 3.231 | 518.649 | .000 |
| J * C | 4.997 | 5 | .999 | 160.452 | .000 |
| J * MI | 65.872 | 1 | 65.872 | 10575.558 | .000 |
| C * MI | 4.044 | 5 | .809 | 129.862 | .000 |
| J * C * MI | 32.510 | 5 | 6.502 | 1043.865 | .000 |
| Error | .299 | 48 | .006 | | |
| Total | 3195.008 | 72 | | | |
| Corrected Total | 193.956 | 71 | | | |
| a. R Squared = .998 (Adjusted R Squared = .998) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 8.367 | C1MI1 | 7.401 | J1MI1 | 8.693 | C1J1MI1 | 10.471 |
| C1J2 | 4.482 | C1MI2 | 6.666 | J1MI2 | 7.235 | C1J1MI2 | 8.420 |
| C2J1 | 6.517 | C1MI3 | 6.974 | J1MI3 | 7.708 | C1J1MI3 | 9.654 |
| C2J2 | 6.458 | C1MI4 | 6.016 | J1MI4 | 6.974 | C1J1MI4 | 7.856 |
| | | C1MI5 | 5.904 | J1MI5 | 6.781 | C1J1MI5 | 6.754 |
| | | C1MI6 | 5.586 | J1MI6 | 7.261 | C1J1MI6 | 7.049 |
| | | C2MI1 | 7.081 | J2MI1 | 5.789 | C1J2MI1 | 4.331 |
| | | C2MI2 | 6.056 | J2MI2 | 5.487 | C1J2MI2 | 4.911 |
| | | C2MI3 | 6.916 | J2MI3 | 6.182 | C1J2MI3 | 4.295 |
| | | C2MI4 | 6.331 | J2MI4 | 5.372 | C1J2MI4 | 4.176 |
| | | C2MI5 | 6.081 | J2MI5 | 5.204 | C1J2MI5 | 5.055 |
| | | C2MI6 | 6.461 | J2MI6 | 4.786 | C1J2MI6 | 4.124 |
| | | | | | | C2J1MI1 | 6.915 |
| | | | | | | C2J1MI2 | 6.050 |
| | | | | | | C2J1MI3 | 5.763 |
| | | | | | | C2J1MI4 | 6.093 |
| | | | | | | C2J1MI5 | 6.808 |
| | | | | | | C2J1MI6 | 7.474 |
| | | | | | | C2J2MI1 | 7.246 |
| | | | | | | C2J2MI2 | 6.063 |
| | | | | | | C2J2MI3 | 8.070 |
| | | | | | | C2J2MI4 | 6.568 |
| | | | | | | C2J2MI5 | 5.353 |
| | | | | | | C2J2MI6 | 5.448 |

Annexure 4.21.SOC factorial ANOVA to test the significance of factors at 10 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | SOC | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 9.900[a] | 23 | .430 | 223.242 | .000 |
| Intercept | 700.837 | 1 | 700.837 | 363470.419 | .000 |
| J | .189 | 1 | .189 | 97.852 | .000 |
| C | .027 | 1 | .027 | 14.022 | .000 |
| MI | .771 | 5 | .154 | 79.989 | .000 |
| J * C | .196 | 1 | .196 | 101.464 | .000 |
| J * MI | 3.083 | 5 | .617 | 319.805 | .000 |
| C * MI | 2.453 | 5 | .491 | 254.473 | .000 |
| J * C * MI | 3.181 | 5 | .636 | 329.979 | .000 |
| Error | .093 | 48 | .002 | | |
| Total | 710.830 | 72 | | | |
| Corrected Total | 9.993 | 71 | | | |
| a. R Squared = .991 (Adjusted R Squared = .986) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 3.101 | C1MI1 | 2.991 | J1MI1 | 2.883 | C1J1MI1 | 2.847 |
| C1J2 | 3.100 | C1MI2 | 2.805 | J1MI2 | 3.014 | C1J1MI2 | 2.742 |
| C2J1 | 3.036 | C1MI3 | 2.949 | J1MI3 | 3.354 | C1J1MI3 | 3.135 |
| C2J2 | 3.243 | C1MI4 | 3.394 | J1MI4 | 3.322 | C1J1MI4 | 3.912 |
| | | C1MI5 | 3.574 | J1MI5 | 2.833 | C1J1MI5 | 2.906 |
| | | C1MI6 | 2.889 | J1MI6 | 3.006 | C1J1MI6 | 3.066 |
| | | C2MI1 | 3.039 | J2MI1 | 3.148 | C1J2MI1 | 3.135 |
| | | C2MI2 | 3.237 | J2MI2 | 3.028 | C1J2MI2 | 2.868 |
| | | C2MI3 | 3.431 | J2MI3 | 3.025 | C1J2MI3 | 2.762 |
| | | C2MI4 | 2.935 | J2MI4 | 3.008 | C1J2MI4 | 2.877 |
| | | C2MI5 | 3.010 | J2MI5 | 3.751 | C1J2MI5 | 4.243 |
| | | C2MI6 | 3.184 | J2MI6 | 3.067 | C1J2MI6 | 2.712 |
| | | | | | | C2J1MI1 | 2.918 |
| | | | | | | C2J1MI2 | 3.286 |
| | | | | | | C2J1MI3 | 3.573 |
| | | | | | | C2J1MI4 | 2.732 |
| | | | | | | C2J1MI5 | 2.761 |
| | | | | | | C2J1MI6 | 2.945 |
| | | | | | | C2J2MI1 | 3.161 |
| | | | | | | C2J2MI2 | 3.187 |
| | | | | | | C2J2MI3 | 3.288 |
| | | | | | | C2J2MI4 | 3.138 |
| | | | | | | C2J2MI5 | 3.259 |
| | | | | | | C2J2MI6 | 3.422 |

Annexure 4.22. Factorial ANOVA to test the significance of factors at 45 days

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | DOC | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 399334.080[a] | 23 | 17362.351 | 3497.156 | .000 |
| Intercept | 1813573.369 | 1 | 1813573.369 | 365293.207 | .000 |
| J | 37530.840 | 1 | 37530.840 | 7559.529 | .000 |
| C | 93498.119 | 1 | 93498.119 | 18832.559 | .000 |
| MI | 80507.330 | 5 | 16101.466 | 3243.186 | .000 |
| J * C | 85710.371 | 1 | 85710.371 | 17263.937 | .000 |
| J * MI | 40311.251 | 5 | 8062.250 | 1623.913 | .000 |
| C * MI | 39909.809 | 5 | 7981.962 | 1607.741 | .000 |
| J * C * MI | 21866.360 | 5 | 4373.272 | 880.872 | .000 |
| Error | 238.306 | 48 | 4.965 | | |
| Total | 2213145.755 | 72 | | | |
| Corrected Total | 399572.386 | 71 | | | |
| a. R Squared = .999 (Adjusted R Squared = .999) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 252.078 | C1MI1 | 303.686 | J1MI1 | 304.478 | C1J1MI1 | 441.089 |
| C1J2 | 137.411 | C1MI2 | 165.182 | J1MI2 | 160.013 | C1J1MI2 | 217.622 |
| C2J1 | 111.002 | C1MI3 | 210.287 | J1MI3 | 172.394 | C1J1MI3 | 283.710 |
| C2J2 | 134.344 | C1MI4 | 141.460 | J1MI4 | 136.279 | C1J1MI4 | 173.185 |
| | | C1MI5 | 172.720 | J1MI5 | 160.677 | C1J1MI5 | 194.028 |
| | | C1MI6 | 175.133 | J1MI6 | 155.400 | C1J1MI6 | 202.836 |
| | | C2MI1 | 157.966 | J2MI1 | 157.175 | C1J2MI1 | 166.283 |
| | | C2MI2 | 131.099 | J2MI2 | 136.268 | C1J2MI2 | 112.743 |
| | | C2MI3 | 81.373 | J2MI3 | 119.267 | C1J2MI3 | 136.864 |
| | | C2MI4 | 110.352 | J2MI4 | 115.533 | C1J2MI4 | 109.735 |
| | | C2MI5 | 136.391 | J2MI5 | 148.434 | C1J2MI5 | 151.412 |
| | | C2MI6 | 118.857 | J2MI6 | 138.590 | C1J2MI6 | 147.430 |
| | | | | | | C2J1MI1 | 167.866 |
| | | | | | | C2J1MI2 | 102.405 |
| | | | | | | C2J1MI3 | 61.077 |
| | | | | | | C2J1MI4 | 99.372 |
| | | | | | | C2J1MI5 | 127.326 |
| | | | | | | C2J1MI6 | 107.964 |
| | | | | | | C2J2MI1 | 148.066 |
| | | | | | | C2J2MI2 | 159.794 |
| | | | | | | C2J2MI3 | 101.669 |
| | | | | | | C2J2MI4 | 121.331 |
| | | | | | | C2J2MI5 | 145.456 |
| | | | | | | C2J2MI6 | 129.750 |

Annexure 4.23. Factorial ANOVA to test the significance of factors at 45 days growth of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | SMBC | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 113875.924[a] | 23 | 4951.127 | 2725.849 | .000 |
| Intercept | 868557.600 | 1 | 868557.600 | 478185.423 | .000 |
| J | 29920.417 | 1 | 29920.417 | 16472.721 | .000 |
| C | 39622.247 | 1 | 39622.247 | 21814.075 | .000 |
| MI | 30594.579 | 5 | 6118.916 | 3368.776 | .000 |
| J * C | 1601.444 | 1 | 1601.444 | 881.677 | .000 |
| C * MI | 1867.247 | 5 | 373.449 | 205.603 | .000 |
| J * MI | 3585.029 | 5 | 717.006 | 394.748 | .000 |
| J * C * MI | 6684.960 | 5 | 1336.992 | 736.083 | .000 |
| Error | 87.185 | 48 | 1.816 | | |
| Total | 982520.709 | 72 | | | |
| Corrected Total | 113963.109 | 71 | | | |
| a. R Squared = .998 (Adjusted R Squared = .998) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 108.190 | C1MI1 | 159.676 | J1MI1 | 108.076 | C1J1MI1 | 121.042 |
| C1J2 | 158.393 | C1MI2 | 167.158 | J1MI2 | 106.854 | C1J1MI2 | 126.392 |
| C2J1 | 70.705 | C1MI3 | 146.290 | J1MI3 | 91.925 | C1J1MI3 | 108.205 |
| C2J2 | 102.044 | C1MI4 | 125.788 | J1MI4 | 90.782 | C1J1MI4 | 113.792 |
| | | C1MI5 | 110.631 | J1MI5 | 80.139 | C1J1MI5 | 103.348 |
| | | C1MI6 | 90.208 | J1MI6 | 58.911 | C1J1MI6 | 76.363 |
| | | C2MI1 | 99.651 | J2MI1 | 151.250 | C1J2MI1 | 198.309 |
| | | C2MI2 | 102.406 | J2MI2 | 162.710 | C1J2MI2 | 207.924 |
| | | C2MI3 | 88.618 | J2MI3 | 142.983 | C1J2MI3 | 184.375 |
| | | C2MI4 | 90.677 | J2MI4 | 125.683 | C1J2MI4 | 137.783 |
| | | C2MI5 | 77.364 | J2MI5 | 107.856 | C1J2MI5 | 117.914 |
| | | C2MI6 | 59.531 | J2MI6 | 90.828 | C1J2MI6 | 104.053 |
| | | | | | | C2J1MI1 | 95.111 |
| | | | | | | C2J1MI2 | 87.316 |
| | | | | | | C2J1MI3 | 75.645 |
| | | | | | | C2J1MI4 | 67.771 |
| | | | | | | C2J1MI5 | 56.929 |
| | | | | | | C2J1MI6 | 41.459 |
| | | | | | | C2J2MI1 | 104.192 |
| | | | | | | C2J2MI2 | 117.495 |
| | | | | | | C2J2MI3 | 101.591 |
| | | | | | | C2J2MI4 | 113.583 |
| | | | | | | C2J2MI5 | 97.798 |
| | | | | | | C2J2MI6 | 77.602 |

Annexure 4.24. Factorial ANOVA to test the significance of factors at 45 days

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | pMN | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 5250.586[a] | 23 | 228.286 | 31.858 | .000 |
| Intercept | 17592.461 | 1 | 17592.461 | 2455.044 | .000 |
| J | 134.863 | 1 | 134.863 | 18.820 | .000 |
| C | 2179.041 | 1 | 2179.041 | 304.087 | .000 |
| MI | 1396.206 | 5 | 279.241 | 38.968 | .000 |
| J * C | 261.137 | 1 | 261.137 | 36.442 | .000 |
| J * MI | 311.203 | 5 | 62.241 | 8.686 | .000 |
| C * MI | 777.471 | 5 | 155.494 | 21.699 | .000 |
| J * C * MI | 190.664 | 5 | 38.133 | 5.321 | .001 |
| Error | 343.960 | 48 | 7.166 | | |
| Total | 23187.008 | 72 | | | |
| Corrected Total | 5594.547 | 71 | | | |
| a. R Squared = .939 (Adjusted R Squared = .909) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 24.406 | C1MI1 | 12.832 | J1MI1 | 7.955 | C1J1MI1 | 11.664 |
| C1J2 | 17.860 | C1MI2 | 32.666 | J1MI2 | 26.832 | C1J1MI2 | 42.000 |
| C2J1 | 9.594 | C1MI3 | 28.832 | J1MI3 | 22.122 | C1J1MI3 | 35.000 |
| C2J2 | 10.666 | C1MI4 | 18.666 | J1MI4 | 17.500 | C1J1MI4 | 21.000 |
| | | C1MI5 | 15.164 | J1MI5 | 13.704 | C1J1MI5 | 18.664 |
| | | C1MI6 | 18.635 | J1MI6 | 13.886 | C1J1MI6 | 18.106 |
| | | C2MI1 | 4.789 | J2MI1 | 9.666 | C1J2MI1 | 14.000 |
| | | C2MI2 | 11.664 | J2MI2 | 17.498 | C1J2MI2 | 23.332 |
| | | C2MI3 | 9.538 | J2MI3 | 16.248 | C1J2MI3 | 22.664 |
| | | C2MI4 | 14.250 | J2MI4 | 15.416 | C1J2MI4 | 16.332 |
| | | C2MI5 | 8.705 | J2MI5 | 10.165 | C1J2MI5 | 11.664 |
| | | C2MI6 | 11.833 | J2MI6 | 16.582 | C1J2MI6 | 19.164 |
| | | | | | | C2J1MI1 | 4.246 |
| | | | | | | C2J1MI2 | 11.664 |
| | | | | | | C2J1MI3 | 9.244 |
| | | | | | | C2J1MI4 | 14.000 |
| | | | | | | C2J1MI5 | 8.744 |
| | | | | | | C2J1MI6 | 9.666 |
| | | | | | | C2J2MI1 | 5.332 |
| | | | | | | C2J2MI2 | 11.664 |
| | | | | | | C2J2MI3 | 9.832 |
| | | | | | | C2J2MI4 | 14.500 |
| | | | | | | C2J2MI5 | 8.666 |
| | | | | | | C2J2MI6 | 14.000 |

Annexure 4.30.POM factorial ANOVA to test the significance of factorsat 45 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | POM | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 133.954[a] | 23 | 5.824 | 126.758 | .000 |
| Intercept | 5381.127 | 1 | 5381.127 | 117117.238 | .000 |
| J | 17.843 | 1 | 17.843 | 388.353 | .000 |
| C | 12.933 | 1 | 12.933 | 281.488 | .000 |
| MI | 15.795 | 5 | 3.159 | 68.754 | .000 |
| J * C | 32.275 | 5 | 6.455 | 140.488 | .000 |
| J * MI | 9.291 | 1 | 9.291 | 202.217 | .000 |
| C * MI | 29.543 | 5 | 5.909 | 128.595 | .000 |
| J * C * MI | 16.274 | 5 | 3.255 | 70.837 | .000 |
| Error | 2.205 | 48 | .046 | | |
| Total | 5517.287 | 72 | | | |
| Corrected Total | 136.159 | 71 | | | |
| a. R Squared = .984 (Adjusted R Squared = .976) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 7.364 | C1MI1 | 7.862 | J1MI1 | 8.679 | C1J1MI1 | 7.626 |
| C1J2 | 9.078 | C1MI2 | 9.179 | J1MI2 | 8.132 | C1J1MI2 | 7.780 |
| C2J1 | 8.930 | C1MI3 | 8.428 | J1MI3 | 8.612 | C1J1MI3 | 7.780 |
| C2J2 | 9.208 | C1MI4 | 8.497 | J1MI4 | 9.119 | C1J1MI4 | 8.115 |
| | | C1MI5 | 7.737 | J1MI5 | 7.545 | C1J1MI5 | 6.997 |
| | | C1MI6 | 7.625 | J1MI6 | 6.797 | C1J1MI6 | 5.887 |
| | | C2MI1 | 9.166 | J2MI1 | 8.349 | C1J2MI1 | 8.098 |
| | | C2MI2 | 7.710 | J2MI2 | 8.757 | C1J2MI2 | 10.578 |
| | | C2MI3 | 8.350 | J2MI3 | 8.166 | C1J2MI3 | 9.076 |
| | | C2MI4 | 10.846 | J2MI4 | 10.223 | C1J2MI4 | 8.878 |
| | | C2MI5 | 8.817 | J2MI5 | 9.009 | C1J2MI5 | 8.477 |
| | | C2MI6 | 9.525 | J2MI6 | 10.353 | C1J2MI6 | 9.362 |
| | | | | | | C2J1MI1 | 9.732 |
| | | | | | | C2J1MI2 | 8.484 |
| | | | | | | C2J1MI3 | 9.443 |
| | | | | | | C2J1MI4 | 10.123 |
| | | | | | | C2J1MI5 | 8.093 |
| | | | | | | C2J1MI6 | 7.707 |
| | | | | | | C2J2MI1 | 8.599 |
| | | | | | | C2J2MI2 | 6.936 |
| | | | | | | C2J2MI3 | 7.257 |
| | | | | | | C2J2MI4 | 11.569 |
| | | | | | | C2J2MI5 | 9.541 |
| | | | | | | C2J2MI6 | 11.344 |

Annexure 4.26. SOC factorial ANOVA to test the significance of factors at 45 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | SOC | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 11.239[a] | 23 | .489 | 136.330 | .000 |
| Intercept | 696.828 | 1 | 696.828 | 194407.161 | .000 |
| J | .029 | 1 | .029 | 8.203 | .006 |
| C | .098 | 1 | .098 | 27.447 | .000 |
| MI | 1.453 | 5 | .291 | 81.048 | .000 |
| J * C | .150 | 1 | .150 | 41.786 | .000 |
| J * MI | 2.371 | 5 | .474 | 132.290 | .000 |
| C * MI | 5.112 | 5 | 1.022 | 285.247 | .000 |
| J * C * MI | 2.026 | 5 | .405 | 113.047 | .000 |
| Error | .172 | 48 | .004 | | |
| Total | 708.240 | 72 | | | |
| Corrected Total | 11.411 | 71 | | | |
| a. R Squared = .985 (Adjusted R Squared = .978) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 3.173 | C1MI1 | 2.991 | J1MI1 | 2.883 | C1J1MI1 | 2.847 |
| C1J2 | 3.123 | C1MI2 | 2.805 | J1MI2 | 3.031 | C1J1MI2 | 2.742 |
| C2J1 | 3.008 | C1MI3 | 2.949 | J1MI3 | 3.354 | C1J1MI3 | 3.135 |
| C2J2 | 3.140 | C1MI4 | 3.512 | J1MI4 | 3.271 | C1J1MI4 | 4.010 |
| | | C1MI5 | 3.741 | J1MI5 | 3.000 | C1J1MI5 | 3.239 |
| | | C1MI6 | 2.889 | J1MI6 | 3.006 | C1J1MI6 | 3.066 |
| | | C2MI1 | 2.871 | J2MI1 | 2.980 | C1J2MI1 | 3.135 |
| | | C2MI2 | 3.254 | J2MI2 | 3.028 | C1J2MI2 | 2.868 |
| | | C2MI3 | 3.431 | J2MI3 | 3.025 | C1J2MI3 | 2.762 |
| | | C2MI4 | 2.694 | J2MI4 | 2.935 | C1J2MI4 | 3.014 |
| | | C2MI5 | 3.011 | J2MI5 | 3.752 | C1J2MI5 | 4.243 |
| | | C2MI6 | 3.184 | J2MI6 | 3.067 | C1J2MI6 | 2.712 |
| | | | | | | C2J1MI1 | 2.918 |
| | | | | | | C2J1MI2 | 3.320 |
| | | | | | | C2J1MI3 | 3.573 |
| | | | | | | C2J1MI4 | 2.532 |
| | | | | | | C2J1MI5 | 2.761 |
| | | | | | | C2J1MI6 | 2.945 |
| | | | | | | C2J2MI1 | 2.825 |
| | | | | | | C2J2MI2 | 3.187 |
| | | | | | | C2J2MI3 | 3.288 |
| | | | | | | C2J2MI4 | 2.855 |
| | | | | | | C2J2MI5 | 3.261 |
| | | | | | | C2J2MI6 | 3.422 |

Annexure 4.27. Factorial ANOVA to test the significance of factors at 90 days

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | DOC | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 97177.259[a] | 23 | 4225.098 | 1148.631 | .000 |
| Intercept | 1370835.585 | 1 | 1370835.585 | 372673.938 | .000 |
| J | 134.947 | 1 | 134.947 | 36.686 | .000 |
| C | 2535.820 | 1 | 2535.820 | 689.385 | .000 |
| MI | 19268.386 | 5 | 3853.677 | 1047.657 | .000 |
| J * C | 8432.671 | 5 | 1686.534 | 458.499 | .000 |
| J * MI | 37593.994 | 1 | 37593.994 | 10220.264 | .000 |
| C * MI | 14247.182 | 5 | 2849.436 | 774.645 | .000 |
| J * C * MI | 14964.259 | 5 | 2992.852 | 813.634 | .000 |
| Error | 176.562 | 48 | 3.678 | | |
| Total | 1468189.407 | 72 | | | |
| Corrected Total | 97353.821 | 71 | | | |
| a. R Squared = .998 (Adjusted R Squared = .997) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 119.699 | C1MI1 | 138.548 | J1MI1 | 164.942 | C1J1MI1 | 117.851 |
| C1J2 | 168.137 | C1MI2 | 124.528 | J1MI2 | 134.328 | C1J1MI2 | 112.556 |
| C2J1 | 153.530 | C1MI3 | 129.573 | J1MI3 | 99.022 | C1J1MI3 | 100.335 |
| C2J2 | 110.567 | C1MI4 | 140.698 | J1MI4 | 121.086 | C1J1MI4 | 93.555 |
| | | C1MI5 | 148.185 | J1MI5 | 145.065 | C1J1MI5 | 122.910 |
| | | C1MI6 | 181.975 | J1MI6 | 155.242 | C1J1MI6 | 170.985 |
| | | C2MI1 | 175.586 | J2MI1 | 149.192 | C1J2MI1 | 159.246 |
| | | C2MI2 | 125.526 | J2MI2 | 115.726 | C1J2MI2 | 136.501 |
| | | C2MI3 | 115.372 | J2MI3 | 145.923 | C1J2MI3 | 158.812 |
| | | C2MI4 | 97.929 | J2MI4 | 117.541 | C1J2MI4 | 187.840 |
| | | C2MI5 | 142.343 | J2MI5 | 145.463 | C1J2MI5 | 173.459 |
| | | C2MI6 | 135.536 | J2MI6 | 162.270 | C1J2MI6 | 192.966 |
| | | | | | | C2J1MI1 | 212.034 |
| | | | | | | C2J1MI2 | 156.101 |
| | | | | | | C2J1MI3 | 97.710 |
| | | | | | | C2J1MI4 | 148.617 |
| | | | | | | C2J1MI5 | 167.220 |
| | | | | | | C2J1MI6 | 139.498 |
| | | | | | | C2J2MI1 | 139.138 |
| | | | | | | C2J2MI2 | 94.951 |
| | | | | | | C2J2MI3 | 133.034 |
| | | | | | | C2J2MI4 | 47.242 |
| | | | | | | C2J2MI5 | 117.466 |
| | | | | | | C2J2MI6 | 131.573 |

Annexure 4.28. Factorial ANOVA to test the significance of factors at 90 days growth of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | SMBC | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 55665.691[a] | 23 | 2420.247 | 1056.338 | .000 |
| Intercept | 98240.419 | 1 | 98240.419 | 42877.874 | .000 |
| J | 1980.535 | 1 | 1980.535 | 864.421 | .000 |
| C | 44472.044 | 1 | 44472.044 | 19410.205 | .000 |
| MI | 4040.724 | 5 | 808.145 | 352.722 | .000 |
| J * C | 2452.548 | 1 | 2452.548 | 1070.436 | .000 |
| C * MI | 75.352 | 5 | 15.070 | 6.578 | .000 |
| J * MI | 2326.956 | 5 | 465.391 | 203.124 | .000 |
| J * C * MI | 317.533 | 5 | 63.507 | 27.718 | .000 |
| Error | 109.976 | 48 | 2.291 | | |
| Total | 154016.086 | 72 | | | |
| Corrected Total | 55775.667 | 71 | | | |
| a. R Squared = .998 (Adjusted R Squared = .997) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 50.710 | C1MI1 | 71.229 | J1MI1 | 37.360 | C1J1MI1 | 64.732 |
| C1J2 | 72.872 | C1MI2 | 69.835 | J1MI2 | 37.047 | C1J1MI2 | 56.481 |
| C2J1 | 12.677 | C1MI3 | 72.024 | J1MI3 | 35.722 | C1J1MI3 | 56.651 |
| C2J2 | 11.494 | C1MI4 | 64.684 | J1MI4 | 33.882 | C1J1MI4 | 53.239 |
| | | C1MI5 | 58.713 | J1MI5 | 29.586 | C1J1MI5 | 47.507 |
| | | C1MI6 | 34.262 | J1MI6 | 16.566 | C1J1MI6 | 25.653 |
| | | C2MI1 | 11.212 | J2MI1 | 45.082 | C1J2MI1 | 77.727 |
| | | C2MI2 | 14.258 | J2MI2 | 47.045 | C1J2MI2 | 83.190 |
| | | C2MI3 | 13.461 | J2MI3 | 49.763 | C1J2MI3 | 87.397 |
| | | C2MI4 | 13.314 | J2MI4 | 44.116 | C1J2MI4 | 76.130 |
| | | C2MI5 | 12.435 | J2MI5 | 41.562 | C1J2MI5 | 69.920 |
| | | C2MI6 | 7.834 | J2MI6 | 25.530 | C1J2MI6 | 42.871 |
| | | | | | | C2J1MI1 | 9.988 |
| | | | | | | C2J1MI2 | 17.614 |
| | | | | | | C2J1MI3 | 14.793 |
| | | | | | | C2J1MI4 | 14.524 |
| | | | | | | C2J1MI5 | 11.665 |
| | | | | | | C2J1MI6 | 7.479 |
| | | | | | | C2J2MI1 | 12.436 |
| | | | | | | C2J2MI2 | 10.901 |
| | | | | | | C2J2MI3 | 12.129 |
| | | | | | | C2J2MI4 | 12.103 |
| | | | | | | C2J2MI5 | 13.204 |
| | | | | | | C2J2MI6 | 8.190 |

Annexure 4.29. Factorial ANOVA to test the significance of factors at 90 days

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | pMN | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 987.500[a] | 23 | 42.935 | 38.322 | .000 |
| Intercept | 5304.500 | 1 | 5304.500 | 4734.595 | .000 |
| J | 64.222 | 1 | 64.222 | 57.322 | .000 |
| C | 213.556 | 1 | 213.556 | 190.612 | .000 |
| MI | 390.833 | 5 | 78.167 | 69.769 | .000 |
| J * C | 128.778 | 5 | 25.756 | 22.988 | .000 |
| J * MI | 143.778 | 5 | 28.756 | 25.666 | .000 |
| C * MI | 24.500 | 1 | 24.500 | 21.868 | .000 |
| J * C * MI | 21.833 | 5 | 4.367 | 3.898 | .005 |
| Error | 53.778 | 48 | 1.120 | | |
| Total | 6345.778 | 72 | | | |
| Corrected Total | 1041.278 | 71 | | | |
| a. R Squared = .948 (Adjusted R Squared = .924) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 11.833 | C1MI1 | 8.333 | J1MI1 | 8.833 | C1J1MI1 | 10.000 |
| C1J2 | 8.778 | C1MI2 | 10.500 | J1MI2 | 8.167 | C1J1MI2 | 11.667 |
| C2J1 | 7.222 | C1MI3 | 6.833 | J1MI3 | 6.167 | C1J1MI3 | 7.667 |
| C2J2 | 6.500 | C1MI4 | 7.167 | J1MI4 | 5.833 | C1J1MI4 | 7.000 |
| | | C1MI5 | 13.500 | J1MI5 | 15.000 | C1J1MI5 | 17.667 |
| | | C1MI6 | 15.500 | J1MI6 | 13.167 | C1J1MI6 | 17.000 |
| | | C2MI1 | 9.500 | J2MI1 | 9.000 | C1J2MI1 | 6.667 |
| | | C2MI2 | 4.667 | J2MI2 | 7.000 | C1J2MI2 | 9.333 |
| | | C2MI3 | 4.667 | J2MI3 | 5.333 | C1J2MI3 | 6.000 |
| | | C2MI4 | 5.167 | J2MI4 | 6.500 | C1J2MI4 | 7.333 |
| | | C2MI5 | 9.167 | J2MI5 | 7.667 | C1J2MI5 | 9.333 |
| | | C2MI6 | 8.000 | J2MI6 | 10.333 | C1J2MI6 | 14.000 |
| | | | | | | C2J1MI1 | 7.667 |
| | | | | | | C2J1MI2 | 4.667 |
| | | | | | | C2J1MI3 | 4.667 |
| | | | | | | C2J1MI4 | 4.667 |
| | | | | | | C2J1MI5 | 12.333 |
| | | | | | | C2J1MI6 | 9.333 |
| | | | | | | C2J2MI1 | 11.333 |
| | | | | | | C2J2MI2 | 4.667 |
| | | | | | | C2J2MI3 | 4.667 |
| | | | | | | C2J2MI4 | 5.667 |
| | | | | | | C2J2MI5 | 6.000 |
| | | | | | | C2J2MI6 | 6.667 |

Annexure 4.35. POM factorial ANOVA to test the significance of factors at 90 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | POM | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 241.661[a] | 23 | 10.507 | 109.177 | .000 |
| Intercept | 3541.753 | 1 | 3541.753 | 36801.966 | .000 |
| J | 52.872 | 1 | 52.872 | 549.385 | .000 |
| C | 3.781 | 1 | 3.781 | 39.287 | .000 |
| MI | 35.368 | 5 | 7.074 | 73.501 | .000 |
| J * C | 30.740 | 5 | 6.148 | 63.884 | .000 |
| J * MI | .494 | 1 | .494 | 5.138 | .028 |
| C * MI | 66.204 | 5 | 13.241 | 137.583 | .000 |
| J * C * MI | 52.201 | 5 | 10.440 | 108.484 | .000 |
| Error | 4.619 | 48 | .096 | | |
| Total | 3788.032 | 72 | | | |
| Corrected Total | 246.280 | 71 | | | |
| a. R Squared = .981 (Adjusted R Squared = .972) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 7.559 | C1MI1 | 6.454 | J1MI1 | 8.435 | C1J1MI1 | 7.757 |
| C1J2 | 6.010 | C1MI2 | 7.480 | J1MI2 | 7.139 | C1J1MI2 | 9.932 |
| C2J1 | 8.183 | C1MI3 | 8.047 | J1MI3 | 9.602 | C1J1MI3 | 9.428 |
| C2J2 | 6.303 | C1MI4 | 7.569 | J1MI4 | 8.186 | C1J1MI4 | 8.412 |
| | | C1MI5 | 5.909 | J1MI5 | 6.802 | C1J1MI5 | 5.179 |
| | | C1MI6 | 5.246 | J1MI6 | 7.060 | C1J1MI6 | 4.643 |
| | | C2MI1 | 7.003 | J2MI1 | 5.023 | C1J2MI1 | 5.152 |
| | | C2MI2 | 4.834 | J2MI2 | 5.176 | C1J2MI2 | 5.028 |
| | | C2MI3 | 7.957 | J2MI3 | 6.402 | C1J2MI3 | 6.667 |
| | | C2MI4 | 7.906 | J2MI4 | 7.289 | C1J2MI4 | 6.726 |
| | | C2MI5 | 6.579 | J2MI5 | 5.686 | C1J2MI5 | 6.639 |
| | | C2MI6 | 9.178 | J2MI6 | 7.364 | C1J2MI6 | 5.850 |
| | | | | | | C2J1MI1 | 9.112 |
| | | | | | | C2J1MI2 | 4.345 |
| | | | | | | C2J1MI3 | 9.775 |
| | | | | | | C2J1MI4 | 7.960 |
| | | | | | | C2J1MI5 | 8.425 |
| | | | | | | C2J1MI6 | 9.477 |
| | | | | | | C2J2MI1 | 4.894 |
| | | | | | | C2J2MI2 | 5.323 |
| | | | | | | C2J2MI3 | 6.138 |
| | | | | | | C2J2MI4 | 7.851 |
| | | | | | | C2J2MI5 | 4.733 |
| | | | | | | C2J2MI6 | 8.879 |

Annexure 4.31. SOC factorial ANOVA to test the significance of factors at 90 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | SOC | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 4.863[a] | 23 | .211 | 209.862 | .000 |
| Intercept | 688.140 | 1 | 688.140 | 683019.017 | .000 |
| J | .157 | 1 | .157 | 155.970 | .000 |
| C | .305 | 1 | .305 | 303.118 | .000 |
| MI | .813 | 5 | .163 | 161.469 | .000 |
| J * C | .729 | 5 | .146 | 144.714 | .000 |
| J * MI | .152 | 1 | .152 | 150.578 | .000 |
| C * MI | 1.077 | 5 | .215 | 213.717 | .000 |
| J * C * MI | 1.630 | 5 | .326 | 323.532 | .000 |
| Error | .048 | 48 | .001 | | |
| Total | 693.051 | 72 | | | |
| Corrected Total | 4.911 | 71 | | | |
| a. R Squared = .990 (Adjusted R Squared = .985) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 3.064 | C1MI1 | 3.064 | J1MI1 | 3.011 | C1J1MI1 | 3.033 |
| C1J2 | 3.249 | C1MI2 | 3.215 | J1MI2 | 2.983 | C1J1MI2 | 3.080 |
| C2J1 | 3.026 | C1MI3 | 2.950 | J1MI3 | 3.185 | C1J1MI3 | 3.134 |
| C2J2 | 3.027 | C1MI4 | 3.312 | J1MI4 | 3.201 | C1J1MI4 | 3.265 |
| | | C1MI5 | 3.438 | J1MI5 | 2.967 | C1J1MI5 | 2.834 |
| | | C1MI6 | 2.961 | J1MI6 | 2.922 | C1J1MI6 | 3.038 |
| | | C2MI1 | 3.020 | J2MI1 | 3.072 | C1J2MI1 | 3.094 |
| | | C2MI2 | 2.906 | J2MI2 | 3.137 | C1J2MI2 | 3.350 |
| | | C2MI3 | 3.283 | J2MI3 | 3.048 | C1J2MI3 | 2.766 |
| | | C2MI4 | 3.105 | J2MI4 | 3.216 | C1J2MI4 | 3.359 |
| | | C2MI5 | 2.994 | J2MI5 | 3.465 | C1J2MI5 | 4.043 |
| | | C2MI6 | 2.851 | J2MI6 | 2.890 | C1J2MI6 | 2.884 |
| | | | | | | C2J1MI1 | 2.988 |
| | | | | | | C2J1MI2 | 2.887 |
| | | | | | | C2J1MI3 | 3.236 |
| | | | | | | C2J1MI4 | 3.137 |
| | | | | | | C2J1MI5 | 3.101 |
| | | | | | | C2J1MI6 | 2.805 |
| | | | | | | C2J2MI1 | 3.051 |
| | | | | | | C2J2MI2 | 2.925 |
| | | | | | | C2J2MI3 | 3.330 |
| | | | | | | C2J2MI4 | 3.073 |
| | | | | | | C2J2MI5 | 2.888 |
| | | | | | | C2J2MI6 | 2.896 |

Annexure 4.32. Factorial ANOVA to test the significance of factors at 120 days

**Tests of Between-Subjects Effects**

| Dependent Variable: | DOC | | | | |
|---|---|---|---|---|---|
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 171944.502[a] | 23 | 7475.848 | 2166.091 | .000 |
| Intercept | 3075903.584 | 1 | 3075903.584 | 891228.269 | .000 |
| J | 268.382 | 1 | 268.382 | 77.762 | .000 |
| C | 520.344 | 1 | 520.344 | 150.767 | .000 |
| MI | 46690.600 | 5 | 9338.120 | 2705.675 | .000 |
| J * C | 21231.576 | 5 | 4246.315 | 1230.349 | .000 |
| J * MI | 3870.293 | 1 | 3870.293 | 1121.399 | .000 |
| C * MI | 54409.132 | 5 | 10881.826 | 3152.957 | .000 |
| J * C * MI | 44954.176 | 5 | 8990.835 | 2605.051 | .000 |
| Error | 165.663 | 48 | 3.451 | | |
| Total | 3248013.749 | 72 | | | |
| Corrected Total | 172110.165 | 71 | | | |

a. R Squared = .999 (Adjusted R Squared = .999)

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 209.403 | C1MI1 | 228.729 | J1MI1 | 223.020 | C1J1MI1 | 229.609 |
| C1J2 | 198.601 | C1MI2 | 225.369 | J1MI2 | 207.649 | C1J1MI2 | 227.326 |
| C2J1 | 200.116 | C1MI3 | 99.370 | J1MI3 | 170.279 | C1J1MI3 | 163.757 |
| C2J2 | 218.641 | C1MI4 | 243.938 | J1MI4 | 245.316 | C1J1MI4 | 230.093 |
| | | C1MI5 | 234.036 | J1MI5 | 204.524 | C1J1MI5 | 228.876 |
| | | C1MI6 | 192.569 | J1MI6 | 177.770 | C1J1MI6 | 176.757 |
| | | C2MI1 | 234.013 | J2MI1 | 239.722 | C1J2MI1 | 227.849 |
| | | C2MI2 | 215.759 | J2MI2 | 233.479 | C1J2MI2 | 223.412 |
| | | C2MI3 | 208.792 | J2MI3 | 137.883 | C1J2MI3 | 34.983 |
| | | C2MI4 | 204.545 | J2MI4 | 203.167 | C1J2MI4 | 257.783 |
| | | C2MI5 | 172.008 | J2MI5 | 201.520 | C1J2MI5 | 239.197 |
| | | C2MI6 | 221.155 | J2MI6 | 235.954 | C1J2MI6 | 208.381 |
| | | | | | | C2J1MI1 | 216.430 |
| | | | | | | C2J1MI2 | 187.972 |
| | | | | | | C2J1MI3 | 176.801 |
| | | | | | | C2J1MI4 | 260.539 |
| | | | | | | C2J1MI5 | 180.173 |
| | | | | | | C2J1MI6 | 178.782 |
| | | | | | | C2J2MI1 | 251.595 |
| | | | | | | C2J2MI2 | 243.546 |
| | | | | | | C2J2MI3 | 240.783 |
| | | | | | | C2J2MI4 | 148.551 |
| | | | | | | C2J2MI5 | 163.844 |
| | | | | | | C2J2MI6 | 263.527 |

Annexure 4.33. Factorial ANOVA to test the significance of factors at 120 days growth of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | SMBC | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 13350.654[a] | 23 | 580.463 | 520.031 | .000 |
| Intercept | 212033.974 | 1 | 212033.974 | 189958.908 | .000 |
| J | 6.413 | 1 | 6.413 | 5.746 | .020 |
| C | 679.310 | 1 | 679.310 | 608.586 | .000 |
| MI | 9942.329 | 5 | 1988.466 | 1781.445 | .000 |
| J * C | 12.976 | 1 | 12.976 | 11.625 | .001 |
| C * MI | 1771.046 | 5 | 354.209 | 317.332 | .000 |
| J * MI | 527.065 | 5 | 105.413 | 94.438 | .000 |
| J * C * MI | 411.514 | 5 | 82.303 | 73.734 | .000 |
| Error | 53.578 | 48 | 1.116 | | |
| Total | 225438.206 | 72 | | | |
| Corrected Total | 13404.232 | 71 | | | |
| a. R Squared = .996 (Adjusted R Squared = .994) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 51.918 | C1MI1 | 58.958 | J1MI1 | 62.852 | C1J1MI1 | 52.467 |
| C1J2 | 50.472 | C1MI2 | 50.806 | J1MI2 | 49.653 | C1J1MI2 | 47.585 |
| C2J1 | 57.213 | C1MI3 | 56.081 | J1MI3 | 66.131 | C1J1MI3 | 67.696 |
| C2J2 | 57.465 | C1MI4 | 67.264 | J1MI4 | 66.833 | C1J1MI4 | 71.217 |
| | | C1MI5 | 43.979 | J1MI5 | 52.639 | C1J1MI5 | 46.636 |
| | | C1MI6 | 30.084 | J1MI6 | 29.285 | C1J1MI6 | 25.910 |
| | | C2MI1 | 74.276 | J2MI1 | 70.382 | C1J2MI1 | 65.450 |
| | | C2MI2 | 58.947 | J2MI2 | 60.100 | C1J2MI2 | 54.027 |
| | | C2MI3 | 58.461 | J2MI3 | 48.411 | C1J2MI3 | 44.467 |
| | | C2MI4 | 65.398 | J2MI4 | 65.829 | C1J2MI4 | 63.311 |
| | | C2MI5 | 52.546 | J2MI5 | 43.886 | C1J2MI5 | 41.322 |
| | | C2MI6 | 34.404 | J2MI6 | 35.203 | C1J2MI6 | 34.258 |
| | | | | | | C2J1MI1 | 73.238 |
| | | | | | | C2J1MI2 | 51.722 |
| | | | | | | C2J1MI3 | 64.566 |
| | | | | | | C2J1MI4 | 62.448 |
| | | | | | | C2J1MI5 | 58.641 |
| | | | | | | C2J1MI6 | 32.660 |
| | | | | | | C2J2MI1 | 75.315 |
| | | | | | | C2J2MI2 | 66.173 |
| | | | | | | C2J2MI3 | 52.356 |
| | | | | | | C2J2MI4 | 68.347 |
| | | | | | | C2J2MI5 | 46.450 |
| | | | | | | C2J2MI6 | 36.149 |

Annexure 4.34. Factorial ANOVA to test the significance of factors at 120 days

**Tests of Between-Subjects Effects**

| Dependent Variable: | pMN | | | | |
|---|---|---|---|---|---|
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 4254.792[a] | 23 | 184.991 | 39.313 | .000 |
| Intercept | 16778.779 | 1 | 16778.779 | 3565.678 | .000 |
| J | 36.832 | 1 | 36.832 | 7.827 | .007 |
| C | 642.990 | 1 | 642.990 | 136.642 | .000 |
| MI | 637.000 | 5 | 127.400 | 27.074 | .000 |
| J * C | 1254.303 | 5 | 250.861 | 53.311 | .000 |
| J * MI | 51.946 | 1 | 51.946 | 11.039 | .002 |
| C * MI | 774.261 | 5 | 154.852 | 32.908 | .000 |
| J * C * MI | 857.459 | 5 | 171.492 | 36.444 | .000 |
| Error | 225.871 | 48 | 4.706 | | |
| Total | 21259.441 | 72 | | | |
| Corrected Total | 4480.662 | 71 | | | |

a. R Squared = .950 (Adjusted R Squared = .925)

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 18.120 | C1MI1 | 14.916 | J1MI1 | 7.916 | C1J1MI1 | 8.832 |
| C1J2 | 18.388 | C1MI2 | 17.500 | J1MI2 | 15.166 | C1J1MI2 | 21.000 |
| C2J1 | 13.842 | C1MI3 | 28.166 | J1MI3 | 12.166 | C1J1MI3 | 14.500 |
| C2J2 | 10.713 | C1MI4 | 17.082 | J1MI4 | 20.027 | C1J1MI4 | 23.832 |
| | | C1MI5 | 12.498 | J1MI5 | 17.998 | C1J1MI5 | 16.332 |
| | | C1MI6 | 19.361 | J1MI6 | 22.611 | C1J1MI6 | 24.222 |
| | | C2MI1 | 6.222 | J2MI1 | 13.222 | C1J2MI1 | 21.000 |
| | | C2MI2 | 10.388 | J2MI2 | 12.722 | C1J2MI2 | 14.000 |
| | | C2MI3 | 9.748 | J2MI3 | 25.748 | C1J2MI3 | 41.832 |
| | | C2MI4 | 15.861 | J2MI4 | 12.916 | C1J2MI4 | 10.332 |
| | | C2MI5 | 13.943 | J2MI5 | 8.443 | C1J2MI5 | 8.664 |
| | | C2MI6 | 17.500 | J2MI6 | 14.250 | C1J2MI6 | 14.500 |
| | | | | | | C2J1MI1 | 7.000 |
| | | | | | | C2J1MI2 | 9.332 |
| | | | | | | C2J1MI3 | 9.832 |
| | | | | | | C2J1MI4 | 16.222 |
| | | | | | | C2J1MI5 | 19.664 |
| | | | | | | C2J1MI6 | 21.000 |
| | | | | | | C2J2MI1 | 5.444 |
| | | | | | | C2J2MI2 | 11.444 |
| | | | | | | C2J2MI3 | 9.664 |
| | | | | | | C2J2MI4 | 15.500 |
| | | | | | | C2J2MI5 | 8.222 |
| | | | | | | C2J2MI6 | 14.000 |

Annexure 4.32. Factorial ANOVA to test the significance of factors at 120 days growth of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | POM | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 226.316[a] | 23 | 9.840 | 108.156 | .000 |
| Intercept | 3964.515 | 1 | 3964.515 | 43576.553 | .000 |
| J | 60.987 | 1 | 60.987 | 670.352 | .000 |
| C | 84.703 | 1 | 84.703 | 931.030 | .000 |
| MI | 15.609 | 5 | 3.122 | 34.313 | .000 |
| J * C | 19.386 | 5 | 3.877 | 42.618 | .000 |
| J * MI | 2.101 | 1 | 2.101 | 23.088 | .000 |
| C * MI | 22.558 | 5 | 4.512 | 49.589 | .000 |
| J * C * MI | 20.972 | 5 | 4.194 | 46.103 | .000 |
| Error | 4.367 | 48 | .091 | | |
| Total | 4195.198 | 72 | | | |
| Corrected Total | 230.683 | 71 | | | |
| a. R Squared = .981 (Adjusted R Squared = .972) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 7.414 | C1MI1 | 8.432 | J1MI1 | 6.716 | C1J1MI1 | 7.644 |
| C1J2 | 9.596 | C1MI2 | 10.005 | J1MI2 | 7.328 | C1J1MI2 | 9.510 |
| C2J1 | 5.586 | C1MI3 | 8.564 | J1MI3 | 7.383 | C1J1MI3 | 9.033 |
| C2J2 | 7.085 | C1MI4 | 8.914 | J1MI4 | 6.513 | C1J1MI4 | 7.434 |
| | | C1MI5 | 7.880 | J1MI5 | 5.533 | C1J1MI5 | 5.552 |
| | | C1MI6 | 7.237 | J1MI6 | 5.527 | C1J1MI6 | 5.311 |
| | | C2MI1 | 6.042 | J2MI1 | 7.758 | C1J2MI1 | 9.219 |
| | | C2MI2 | 5.482 | J2MI2 | 8.159 | C1J2MI2 | 10.500 |
| | | C2MI3 | 6.849 | J2MI3 | 8.029 | C1J2MI3 | 8.094 |
| | | C2MI4 | 7.240 | J2MI4 | 9.641 | C1J2MI4 | 10.394 |
| | | C2MI5 | 6.237 | J2MI5 | 8.584 | C1J2MI5 | 10.207 |
| | | C2MI6 | 6.164 | J2MI6 | 7.873 | C1J2MI6 | 9.162 |
| | | | | | | C2J1MI1 | 5.788 |
| | | | | | | C2J1MI2 | 5.147 |
| | | | | | | C2J1MI3 | 5.733 |
| | | | | | | C2J1MI4 | 5.592 |
| | | | | | | C2J1MI5 | 5.515 |
| | | | | | | C2J1MI6 | 5.743 |
| | | | | | | C2J2MI1 | 6.297 |
| | | | | | | C2J2MI2 | 5.818 |
| | | | | | | C2J2MI3 | 7.964 |
| | | | | | | C2J2MI4 | 8.889 |
| | | | | | | C2J2MI5 | 6.960 |
| | | | | | | C2J2MI6 | 6.585 |

Annexure 4.36. SOC factorial ANOVA to test the significance of factors at 120 days of rice plant

| Tests of Between-Subjects Effects | | | | | |
|---|---|---|---|---|---|
| Dependent Variable: | SOC | | | | |
| Source | Type III SS | df | Mean Square | F | Sig. |
| Corrected Model | 1.553[a] | 23 | .068 | 34.407 | .000 |
| Intercept | 428.226 | 1 | 428.226 | 218233.542 | .000 |
| J | .349 | 1 | .349 | 177.774 | .000 |
| C | .058 | 1 | .058 | 29.725 | .000 |
| MI | .118 | 5 | .024 | 12.072 | .000 |
| J * C | .311 | 5 | .062 | 31.668 | .000 |
| J * MI | .024 | 1 | .024 | 12.420 | .001 |
| C * MI | .456 | 5 | .091 | 46.453 | .000 |
| J * C * MI | .236 | 5 | .047 | 24.097 | .000 |
| Error | .094 | 48 | .002 | | |
| Total | 429.874 | 72 | | | |
| Corrected Total | 1.647 | 71 | | | |
| a. R Squared = .943 (Adjusted R Squared = .915) | | | | | |

| | C*J | | C*MI | | J*MI | | C*J*MI |
|---|---|---|---|---|---|---|---|
| C1J1 | 2.462 | C1MI1 | 2.357 | J1MI1 | 2.425 | C1J1MI1 | 2.355 |
| C1J2 | 2.359 | C1MI2 | 2.424 | J1MI2 | 2.394 | C1J1MI2 | 2.424 |
| C2J1 | 2.555 | C1MI3 | 2.327 | J1MI3 | 2.508 | C1J1MI3 | 2.324 |
| C2J2 | 2.379 | C1MI4 | 2.396 | J1MI4 | 2.525 | C1J1MI4 | 2.337 |
| | | C1MI5 | 2.423 | J1MI5 | 2.596 | C1J1MI5 | 2.588 |
| | | C1MI6 | 2.535 | J1MI6 | 2.603 | C1J1MI6 | 2.741 |
| | | C2MI1 | 2.519 | J2MI1 | 2.451 | C1J2MI1 | 2.358 |
| | | C2MI2 | 2.333 | J2MI2 | 2.363 | C1J2MI2 | 2.424 |
| | | C2MI3 | 2.502 | J2MI3 | 2.321 | C1J2MI3 | 2.330 |
| | | C2MI4 | 2.590 | J2MI4 | 2.461 | C1J2MI4 | 2.455 |
| | | C2MI5 | 2.552 | J2MI5 | 2.379 | C1J2MI5 | 2.258 |
| | | C2MI6 | 2.307 | J2MI6 | 2.239 | C1J2MI6 | 2.329 |
| | | | | | | C2J1MI1 | 2.495 |
| | | | | | | C2J1MI2 | 2.364 |
| | | | | | | C2J1MI3 | 2.692 |
| | | | | | | C2J1MI4 | 2.712 |
| | | | | | | C2J1MI5 | 2.604 |
| | | | | | | C2J1MI6 | 2.465 |
| | | | | | | C2J2MI1 | 2.544 |
| | | | | | | C2J2MI2 | 2.301 |
| | | | | | | C2J2MI3 | 2.312 |
| | | | | | | C2J2MI4 | 2.468 |
| | | | | | | C2J2MI5 | 2.500 |
| | | | | | | C2J2MI6 | 2.150 |

# VITA

Carolyn Zothansiami d/o K. Hrangzuala was born in 4th April, 1988 at Chhingchhip, Serchip district, Mizoram. She passed her HSLC in the year 2005 under Mizoram Board of School Education and HSSLC (Science) in the year 2007 under Mizoram Board of School Education. She persued her B.Sc. (Agriculture) in the same year from HNB Garhwal university, Uttarankhand and passed in 2011. She further continued her M.Sc. (Agriculture) in Soil Science and Agricultural Chemistry from College of Post Graduate Studies, Central Agriculture University Imphal and completed in the year 2013. In the same year she continue pursuing her Ph.D. programme in Soil Science and Agricultural Chemistry from College of Post Graduate Studies, Central Agriculture University Imphal. In 2015, she joined as Subject Matter Specialist (Soil Science) at Krishi Vigyan Kendra, Kolasib district, Mizoram. Till date she is currently serving as Subject Matter Specialist (Soil Science) at Krishi Vigyan Kendra, Kolasib district, Mizoram.

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