MICROBIAL DIVERSITY AND USES OF MICROORGANISMS IN THE SOILS OF THIRUVARUR DISTRICT

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Bharathidasan University, Tiruchirappalli-24
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for the award of the degree of
DOCTOR OF PHILOSOPHY
IN
MICROBIOLOGY

By

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Under the Guidance of Dr. M. KANNAHI, M.Sc., M.Phil., Ph.D., B.Ed.,



"Arise, Awake and Stop Not Till the Goal is Reached"

PG AND RESEARCH DEPARTMENT OF MICROBIOLOGY

SENGAMALA THAYAAR EDUCATIONAL TRUST WOMEN'S COLLEGE (AUTONOMOUS)

(Affiliated to Bharathidasan University, Tiruchirappalli) (Accredited by NAAC; An ISO 9001:2015 Certified Institution)

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CERTIFICATE

This is to certify that the dissertation entitled "MICROBIAL DIVERSITY AND USES OF MICROORGANISMS IN THE SOILS OF THIRUVARUR DISTRICT" submitted to Bharathidasan University, Thiruchirappalli, for the award of the Degree of DOCTOR OF PHILOSOPHY IN MICROBIOLOGY, embodies the results of bonafide research work carried out by R.ARULMOZHI under my guidance and supervision in the PG and Research Department of Microbiology, Sengamala Thayaar Educational Trust Women's College, Mannargudi, Thiruvarur District, Tamil Nadu, India.

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ABBREVIATION

BCA - Bio control agent

CCD - Central composite design

CFU - Colony forming unit

EC - Electrical conductivity

EDAX - Energy dispersive x-ray analysis

EDX - Energy dispersive x-ray spectroscopy

EPA - Environmental protection agency

EU - European union

FE-TEM - Field emission – transmission electron microscopy

FT-IR - Fourier transform-infrared spectroscopy

GC - Gas chromatography

HBEF - Hubbard brook experimental forest

INM - Integrated nutrient management

IPM - Integrated Pest Management

K - Potassium

MFC - Microbial fuel cell

MIC - Minimum inhibitory concentration

MS - Mass spectrometry

N - Nitrogen

OC - Organic carbon

P - Phosphorus

PCR - Polymerase chain reaction

PDA - Potato dextrose agar

PGPR - Plant Growth Promoting Rhizobacteria

PPP - Plant protection products

PSB - Phosphate solublizing bacteria

RNA - Ribonucleic acid

RSM - Risk and safety management

S - Sulphur

SEM - Scanning electron microscopy

SNP - Silver nanoparticles

TDS - Total dissolved solid

TEM - Transmission electron microscope

TOC - Total organic carbon

US - United states of America

VWO - Verticillium wilt of olive

WS - Water shed

XRD - x-ray diffraction

CHAPTER-I

INTRODUCTION

1.1 Soil

Soil is defined as "The loose surface layer that covers the majority of land". Soil is made up of organic matter, minerals, gases, liquids, and organisms, all of which work together to support life. The pedosphere, or body of soil on Earth, serves four major functions: it serves as a substrate for plant growth, a source of water for storage, supply, and purification, a moderator of the atmosphere, and a habitat for species. Soil is an important part of the planet's ecosystem. The effects of soil processes on the world's ecosystems are far-reaching, ranging from ozone depletion and global warming to rainforest destruction and water contamination. Soil is a major carbon reservoir in the Earth's carbon cycle, and it may be one of the most sensitive to human disturbance and climate change. Due to increased biological activity at higher temperatures, soils are expected to add carbon dioxide to the atmosphere as the world warms, a positive feedback loop (amplification). However, in light of more recent research on soil carbon turnover, this forecast has been called into question (Davidson *et al.*, 2006).

Soil is a significant provider of ecosystem services since it serves as an engineering medium, a habitat for soil organisms, a recycling system for nutrients and organic wastes, a regulator of water quality, a modifier of atmospheric composition, and a medium for plant growth. Because soil has such a diverse range of niches and habitats, it holds the majority of the world's genetic diversity. A gram of soil can contain billions of creatures from thousands of different species, the majority of which are microbial and completely unknown.

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Table 1: Plants that grow well in the Thiruvarur Districts Soil types

S.No	Soil types	Suitable Plants
1	Sandy clay loam	Tomato, Beans, Sweet corn, Radish and
		greens
2	Clay loam saline alluvial	Rice, Black gram, Green gram, Tomato,
		Cotton, Sugar beet
3	Silty clay alluvial	Rice, Sugarcane, Tobacco, Cotton, Jute,
		Maize, Oil seeds, Vegetables and fruits
4	Loamy sand	Pulses, Oil seeds, Cotton, Sugar cane,
		Cucumbers, Onion
5	Clay	Rice, Green gram, Black gram, Vegetables
		and Fruits crop
6	Silty clay	Rice, Green gram, Black gram, Vegetables
		and Fruits crop
7	Saline alluvial	Tomato, Cotton, Sugar beet, Sugar cane,
		Beans and Peas
8	Saline alkaline	Tomato, Cotton, Sugar beet, Sugar cane,
		Beans and Peas

Natural attenuation refers to the ability of soils to effectively remove pollutants, eliminate disease pathogens, and decompose toxins. Soils, in general, maintain a net absorption of oxygen and methane while emitting carbon dioxide and nitrous oxide. Soils provide plants with physical support, as well as air, water, temperature regulation, nutrients, and toxin protection. Soils convert decaying organic matter into various nutritional forms, making nutrients easily available to plants and animals (Huggett, 1998).

1.2 Microbial diversity

The term "microbial diversity" or "biodiversity" has become so well-known that even a public servant knows what it means. The heterogeneity among living organisms is referred to as microbial diversity. Evolution is the primary driver of microbial diversity on Earth. Any cell's structural and functional variety is an evolutionary event that occurred as a result of Darwin's natural selection theory. Microbial diversity is an underappreciated national and international resource that requires more attention than it now receives. It refers to the range of variety found in all forms of microorganisms in the natural world, as well as how it has been influenced by human intervention. Understanding the microbial ecology in soil and other habitats necessitates microbial diversity research (Atlas, 1984).

It is significant in both natural and agricultural settings. Plant and animal diversity in forests and agro-ecosystems receives a lot of scientific attention, but microbe diversity is frequently overlooked. As a result, much more work needs to be done to better understand the role of microbes, inventory their diversity, and identify strategies to benefit from them. Soil bacteria are one of the most significant biotic components in terrestrial ecosystems that regulate decomposition and nutrient mineralization (Bardgett *et al.*, 2005).

Although there have been numerous studies on the factors that influence soil microbial communities in various ecosystems such as agricultural fields, grasslands, and forests, there is relatively little information on the relationship between soil properties and microbial communities in broadleaved forest soils, which are distinct from those in other terrestrial ecosystems. Microbial diversity must be studied not only for basic scientific inquiry, but also to comprehend the relationship between diversity and community structure and function (Nusslein and Tiedje, 1999).

Despite the strong link between plant and soil microbial communities, the relationship between plant variety and microbial processes has received little attention. Plant-microbe interactions are becoming more understood, but the intricacy of interconnecting biological, chemical, and physical components remains a mystery. Despite all attempts to quantify fluxes and gross microbial pools, the soil and its microbiota remain a mystery since the majority of soil microorganisms are unknown. The evaluation of soil physico-chemical parameters yielded useful information on microbial activity in the soil. In order to see the microbial activities, it is required to analyse the interplay between the physical and chemical features of soil (Meliani *et al.*, 2012).

1.3 Microbial synthesis of silver nano particles

Nanotechnology has the potential to transform both science and society. Nanotechnology entails experimenting with substances 1,00,000 times smaller than a strand of human hair at the atomic level in order to create useful materials and devices. It involves technologies on a billionth-of-a-meter scale. The word "NANO" comes from the Greek word "dwarf" (Parthiban *et al.*, 2010). One of the most active fields of research in modern material science is nanotechnology. Silver has a variety of uses, including spectrally selective coatings for solar

energy absorption and intercalation material for electrical batteries, biolabelling, and antibacterial compounds (Sharma *et al.*, 2009). Microbes prevalent in medical and industrial processes are inhibited by silver nanoparticles (Jose *et al.*, 2005).

Nanoparticles are becoming increasingly popular in a variety of fields of research, and they can help in the early identification and treatment of a variety of ailments. Silver nanoparticles were synthesized using *E. coli* in this study. This microbe can be found in nature and also in the human gut, where it aids digestion. When *E. coli* is exposed to silver ions in nature, it produces silver nanoparticles as part of its metabolism. After that, the silver ions are transformed into silver atoms. It was also discovered that temperature has an impact on the size of nanoparticles. At lower temperatures, larger nanoparticles are formed, while at higher temperatures, smaller nanoparticles are produced (Konish *et al.*, 2004).

Biological components are used in microbial nanomaterial creation, especially in prokaryotes and eukaryotes. Microorganisms are involved in a variety of biological processes, either directly or indirectly. For various types of nano particles, a variety of bacteria were utilized. Bacillus subtilis, Staphylococcus aureus, Micrococcus luteus, Bacillus cereus, Bacillus megaterium, Escherichia coli, Enterobacter aerogens and Klebsiella sp. that can be found. Silver nanoparticles were successfully produced through the synthesis of gold and silver nanoparticles by eukaryotic organisms such as Fusarium oxysporum, Aspergillus fumigatus and Aspergillus flavus (Mukherjee et al., 2001).

Silver nanoparticles are synthesized by microorganisms as a defense mechanism (resistance mechanism), and the nanoparticles created are valuable to mankind. The bacterial cell's resistance to silver ions in the environment is responsible for the production of

nanoparticles. In nature, silver ions are extremely poisonous to bacterial cells. As a result, their cellular machinery aids in the transformation of reactive silver ions to stable silver atoms. Temperature and pH play a part in their production as well. The size of nanoparticles at ambient temperature is 50 nm; at higher temperatures, such as 60°C, the size of nanoparticles decreases to 15 nm. This suggests that as the temperature rises, the size diminishes. The bacteria produce more nanoparticles in alkaline conditions than under acidic conditions. After pH 10, however, cell death occurs. *Pseudomonas stutzeri* AG259, a bacterial strain initially isolated from silver mine, provides the first proof of the synthesis. The amount of nanoparticles produced by *E. coli* changes as the concentration of AgNO₃ changes. The patented concentration is 1mM. Silver helps the organism create nanoparticles at lower concentrations, but at greater concentrations, it causes cell death (Mukherjee *et al.*, 2001).

1.4 Biocontrol agents

Biopesticides, which is an abbreviation for 'biological pesticides,' cover a wide range of pest management techniques, including predatory, parasitic, and chemical connections. Historically, the phrase has been associated with (biological control) and, by extension, the manipulation of living creatures. Because public perceptions might influence regulatory attitudes, biopesticides have been classified in the EU as "a type of pesticide based on microorganisms or natural materials." "Pesticidal substances produced by plants containing added genetic material (plant-incorporated protectants) or PIPs," according to the US EPA, "include naturally occurring pesticides (biochemical pesticides), microorganisms that control pests (microbial pesticides), and pesticidal substances produced by plants containing added genetic material (microbial pesticides)." Plants, bacteria and other microorganisms, nematodes,

and other species provide them. They're common in Integrated Pest Management (IPM) programmes, and they've gotten a lot of attention as alternatives to synthetic chemical Plant Protection Products (PPPs).

In agriculture, microorganisms play a critical role in promoting plant nutrient exchange and reducing the need of chemical fertilizers. Plant Growth Promoting Rhizobacteria (PGPR) promotes plant growth and development. In the rhizosphere, beneficial plant-soil microbial interactions can influence plant growth, yield, and soil fertility (Dastager *et al.*, 2011). Crop inoculants containing PGPR for biofertilization, phytostimulation, and biocontrol. It is appealing and a viable alternative to reducing the usage of chemical fertilizers, which have a negative impact on the environment (Ali *et al.*, 2010).

In agricultural soils, *Pseudomonas sp.* is a common bacterium. *Pseudomonas* strains that are most successful gram negative, motile, rod-shaped bacteria that have a variety of phytobeneficial effects. Plant pathogenic fungi that live in the soil cause massive crop losses all over the world. Agriculturalists have been dealing with the destructive actions of a variety of pests and pathogens, which have resulted in a decrease in productivity as well as aesthetic value. The use of chemicals to control plant diseases pollutes the environment, reduces soil production, and wastes water resources (Ayala and Rao, 2002).

Plant diseases, particularly those caused by soil-borne plant pathogens and nematodes, are controlled biologically. The use of microorganisms is seen as a more natural, renewable, and environmentally friendly alternative to the use of chemical pesticides. The revived interest in microbial biocontrol among agricultural biologists is owing to the fact that it provides

environmentally acceptable protection against weeds, insects, and plant diseases, as well as having a long-term effect and safety (Barker and Banfield, 2015).

It can outgrow them in terms of space and nutrition, creating a slew of potent plant-degrading enzymes like lytic enzymes, proteolytic enzymes, and more than 200 different antibiotics. The ability to synthesise numerous antibiotics can aid in biological control suppression and enhancement. Antibiotics such as 2,4-diacetyl phloroglucinol, generated by *Pseudomonas fluorescens* against *Pythium species* that cause damping off disease, have been hypothesised to be important in plant pathogen suppression. *Trichoderma virens* fights *Rhizoctonia solani* is a plant pathogenic fungus that has a wide range of hosts and is found all over the world. It is a soil transmitted pathogen that frequently appears as a hazard, such as growth on plants or in culture. Collar rot, root rat, damping of and wire stem are the most common plant diseases caused by it. Furthermore, biocontrol bacteria produce enzymes that can digest chitin, proteins, cellulose and hemicelluloses (Barker and Banfield, 2015).

1.5 Biofertilizers

Formulations based on beneficial and/or biological components are referred to as biofertilizers. It improves soil nutrient solubility and has the potential to increase crop productivity. It's biodegradable, non-toxic, and reasonably priced. It is quickly gaining traction as a viable alternative to chemical fertilizers. Although a large number of commercial biofertilizer manufacturing facilities exist in India, the overall required production capacity is still insufficient to meet demand.

It is proposed that biofertilizer be produced and used to raise agricultural productivity by using root nodule bacteria (Rhizobia), mycorrhizal fungi, and other microorganisms that can increase plant nutrient availability from soils. The most successful microbes for each crop will be determined for this purpose, for example, by measuring N₂ fixation activity with a nitrogen-15 isotope as a tracer and other means. The carriers of rhizobia and other biofertilizer microbes are sterilized using ionizing radiation. These microorganisms are chosen by pot and field trials, cultivated and packed with carrier materials, and commercially available for agricultural crops and forest rehabilitation. Quality control is critical, especially when dealing with a population of infected effective microorganisms and other pollutants, which can have negative consequences. Ionizing radiation carrier sterilization is one of the most effective ways to preserve biofertilizers in storage for a long time (Fasusi *et al.*, 2021).

Seed protein synthesis in legumes necessitates a lot of nitrogen. In addition to soil mineralized N and fertilizer N, nitrogen is obtained by symbiotic N₂ fixation with soil microbes. To increase seed yield of leguminous crops, especially in Asia, it is critical to promote N₂ fixation by inoculating with a highly efficient *Rhizobium* strain and improving soil management and cropping practices. It's critical to assess N₂ fixation in leguminous crops in order to choose effective rhizobia and enhance fertilizer application and crop management in ways that are compatible with N₂ fixation. Soybean, lupin, field pea, faba bean, common bean, lentil, and chick pea ranked first, second, and third, respectively, in terms of N₂ fixation (Unkovich and Pate, 2000).

Leguminous plants are typically maintained in test tubes, growth pouches, Leonard jars, or sterilized sand or vermiculite culture under controlled conditions for initial screening of

rhizobia species or for experimental purposes. Plants are frequently grown in greenhouse experiments using sterilized soil pots or a hydroponics system. Evaluation of N_2 fixation in experimental and farmer fields is also critical for final strain selection and agricultural management to optimize N_2 fixation and seed output. The percent Ndfa (percentage of N derived from atmospheric N_2) of a legume is a product of the interaction between the soil N environment and overall legume growth, rather as a feature regulated only by the legume genotype and rhizobia (Unkovich and Pate, 2000).

OBJECTIVES OF THE STUDY

Keeping all the information's in mind, the present study was planned with the following objectives,

- ➤ To collect the major seasonal (Monsoon, Post monsoon, Summer and Pre monsoon) soil types and to analyze physical characters, micronutrient, macronutrient and heavy metals of soil samples in Thiruvarur district
- > To isolate and identify seasonally varied microbial communities include bacteria, fungi and actinomycetes
- > To synthesis silver nanoparticle from certain bacteria isolated in primary soil types of bacteria
- To study the frequent distribution of bacterial, fungal and actinomycetal isolates which would support the degradation of organic and inorganic nutrients thereby influencing the growth of plant include, *Vigna mungo* (black gram), *Oryza sativa* (paddy) and *Vigna radiata* (green gram)
- To characterize predominant indigenous bacterial isolate by 16S rRNA sequencing
- > To produce microbicide against plant pathogens and formulate microbial fertilizer for plant growth

Microbial diversity and uses of microorganisms in the soils of Thiruvarur district

CHAPTER-II

REVIEW OF LITERATURE

2.1 Physico- chemical parameter analysis of soil

Soil pH, electrical conductivity (EC), organic carbon (OC), available nitrogen (N), phosphorus, potassium, and micronutrients are all factors in a physicochemical analysis. Alkalinity, pH, electrical conductivity, organic carbon, sodium, and potassium were all measured in five representative samples. Five soil samples were taken from 0–20 cm depth and examined for neutral to slightly alkaline soils. Soil pH was found to range from 7.60 to 8.81, conductivity from 0.50 to 0.73 dsm⁻¹, organic carbon from 0.52 to 0.72 percent, sodium from 0.52 to 0.97meq percent, and potassium from 125.31 to 630.15 kg/ha. Nitrogen availability ranged from 140.01 to 252.68 kg/ha, whereas Phosphorous availability ranged from 15.11 to 54.13 kg/ha. This data will assist farmers in determining the amount of fertilizer to apply to the soil in order to increase yield (Sangita Changdeo Dandwate, 2020).

The soil is the most critical component for human beings to be able to meet all of their fundamental needs. Soil is also an important part of our farming operations. Because plants rely on the soil for nutrients, water, and minerals, the soil type is a key component in deciding which plants will thrive in a given area. As a result, soil physico-chemical study is critical since both physical and chemical parameters influence soil production. The physico-chemical analysis of soil is based on a number of factors such as pH, electrical conductivity, organic carbon, accessible nitrogen, phosphorus, and potassium, to name a few. Soil samples were obtained from two districts in Himachal Pradesh, namely Shimla and Kinnaur, and the physicochemical analysis of soil was based on several parameters such as total Organic Carbon, Nitrogen (N),

Phosphorus (P), Potassium (K), pH, and electrical conductivity. This research reveals the amount of nutrients available in the soil of several apple orchard sites in Shimla and Kinnaur districts (Himachal Pradesh). The findings revealed that the minerals richness of these two districts' eight selected locations is medium or high. This information will assist farmers in resolving issues with soil nutrients and the amount of fertilizers to use in order to boost crop yields (Nirja Thakur *et al.*, 2019).

Soil samples were taken from agricultural lands in Sawai Madhopur tehsil for analysis. Fluorosis affects residents, animals, and some crop species sensitive to fluoride toxicity in this tehsil. Samples of soil were taken from 35 communities in the Sawai Madhopur Tehsil. A total of 175 samples were tested, including 5 samples from each community. Fluoride was measured using a specific ion meter. The quantity of fluoride ions in soil samples ranged from 1.0 ppm to 8.23ppm. One village is in the 0-1ppm range, seven villages are in the 1-1.5 ppm range, seven villages are in the 1.5-2.5 ppm range, sixteen villages are in the 2.5-5.0 ppm range, and four villages are in the 5.0-10.0 ppm range (Arshi Iram and Khan, 2018).

The results show that the soil in the Nakki-Lake area is moderately alkaline, with a pH of 7.11, Average Sand Content (75.12 %), Silt Content (11.23 %), Clay Content (6.25 %), Organic Matter (3.36 %), Permeability (27.66 mm/hr), Air Filled Porosity (14.33 percent), and other parameters showing low mean values, such as Nitrogen (0.23 mg/L), Phosphorus (52.33 mg/L), Potassium (732.67 mg/L), Magnesium (153.67 mg/L), Chloride (4108.33 mg/L), Sulphur (244.33 mg/L). Bulk Density (1453 kg/m3), Specific Gravity (2.62), Fusion Point (1245.67 °C), Total Combustible (0.22 %), Exchangeable Sodium (0.91 %), Calcium Carbonate (1.48 %), Effective Temperature of Destruction (971.33 °C), Electrical Conductivity - CaSO₄ Extract (2447)

S/cm) were all found in the soil samples, with average nitrate and sulphate levels of 31.19 mg. The nature of the soil of Nakki Lake and the surrounding area is alkaline, according to the quality characteristics of the soil analysis (Rakesh Gothwal and Govind Kumar Gupta, 2018).

Due to the increasing rise of industrialization and construction activities, soil availability for agriculture is reducing year after year. As a result, the quality of the soil has become a critical determinant in increasing the yield of any crop. Many physical and chemical parameters of soil Ladpura Tehsil headquarter and various diverse villages of Ladpura Tehsil of Kota district are the subject of this study. Kota is a very significant agricultural area, so we think that the current study would be valuable to farmers as well. We can recommend which nutrient is needed and in what amount to boost the production of a specific crop based on the findings of the study (Kirti Mohan Sharma and Hardev Singh Chaudhary, 2017).

The natural environment is clean, but it becomes polluted as a result of man's many actions, resulting in environmental pollution. The soil samples were investigated in the current study for physico-chemical investigation of various parameters. Fifteen representative samples were taken and their pH, EC, Phosphorus, Potassium, Sulfur, and Carbon levels were determined (Chandak Nisha, 2017).

Between January and July, soil samples were taken from three abattoirs in Port Harcourt (Agip, Iwofe, and Mile III). Physicochemical characteristics were determined in the samples using the appropriate probes. The pH of the soils was acidic, ranging from 4.59 ± 0.03 to 4.99 ± 0.14 , electrical conductivity from 208.00 ± 11.21 to 404.34 ± 7.18 S/cm, temperature from 33.14 ± 1.29 to 35.04 ± 0.96 °C, and salinity from 27.53 ± 1.91 to 58.65 ± 2.25 S/cm. The textural class

was sandy clay loam, which indicates that the soil has a larger amount of sand. Total moisture content was in the range of 16.66 ± 1.73 - 21.07 ± 2.05 %, chloride content was in the range of 17.10 ± 1.61 - 31.75 ± 2.00 %, and total nitrogen and nitrogen-based parameters were in the soil at extremely low concentrations. Total organic carbon ranged from 12.81 ± 0.15 - 16.41 ± 0.49 %, and total organic matter ranged from 22.33 ± 0.86 - 29.58 ± 0.72 mg/Kg, with extractable phosphorus content ranging from 0.66 ± 0.03 - 1.34 ± 0.33 %. The total hydrocarbon content of the samples ranged from 11.85 to 27.12 mg/kg. Human activities within the abattoir have altered the physicochemical speciation of the abattoirs, according to the findings. The abattoir's large content of organic components can be used as valuable manure for plant development. However, to avoid pollution of the environment, a continual check on the activities at the abattoirs should be implemented (Edori and Iyama, 2017).

The natural environment is clean, but it becomes polluted as a result of man's many actions, resulting in environmental pollution. The physico-chemical analysis of soil is based on a number of factors including pH, Electrical Conductivity (EC), Total Organic Carbon (TOC), Available Nitrogen (N), Available Phosphorus (P₂O₅), and available Potassium (K₂O). Representative samples from Fife were taken and tested for alkalinity, chloride, sulphate, pH, conductivity, sodium, and potassium. Alkalinity ranged from 20 to 64.0 meq/100 g, chloride concentration from 1.23 to 1.98 g/100 g, sulphate from 0.063 to 0.742 g, conductivity from 0.4 to 1.9 micro mohs, sodium from 150.6 to 50 ppm, and potassium from 100.9 to 135.5 ppm. For analysis, only a small portion of the massive soil mass is needed. This information will assist farmers in determining soil nutrient problems and the amount of fertilizer to be given to the soil to make production profitable (Marshal Soni, 2016).

The life layer of plants is formed by soil, which is a key component, a medium of unconsolidated nutrients and materials. It is a vital component of the biosphere's life support system. The physicochemical properties of soil influence how well it adapts to farming and how much biological activity it can support. The goal of this study was to look at some of the properties of soil samples collected in Katol Taluka, Nagpur. pH, conductivity, TDS, organic carbon, accessible nitrate, nitrogen, calcium, and magnesium were all measured during soil characterization. Because of the soil quality in different parts of the country, there was a fluctuation in values in the different places (Barkar and Banfield, 2015).

Total Organic Carbon (TOC), Nitrogen (N), Phosphorus (P₂O₅), Potassium (K₂O), pH, and Conductivity are all used in the physicochemical analysis of soil. This research leads to a conclusion on the amount of nutrients available in the soil of Bhusawal, District Jalgaon (Maharashtra). The results revealed that all eight of Bhusawal's selected locations have medium to high mineral richness. To investigate the effects of phosphate fertilizer, phosphorus, and nitrogen application on crop production percentages. This information will assist farmers in resolving issues linked to soil nutrients and the amount of fertilizers to use in order to boost crop yields (Kiran Chaudhari, 2013).

The University of Ilorin's main campus conducted a physico-chemical investigation of a soil near the microbiology laboratory. The study's goals were to assess pH, moisture content, organic matter content, water holding capacity, temperature, and soil texture in order to establish the soil's appropriateness for microbial growth and plant development. Six soil samples were taken, with a two-week delay between each sample. The pH ranged from 7.10 to 7.82, while the water retention capacity ranged from 0.28 to 0.53 ml/g of soil. The soil samples' organic matter

level ranged from 3.42 % to 4.70 %. The moisture content was found to fluctuate between 2.10 and 5.23 percent. The texture was identified as loamy sand, with an average composition of 89 percent sand, 7% silt, and 4% clay (Oyeyiola and Agbaje, 2013).

Soil is a natural body of mineral and organic material divided into horizons that differ in form, physical make-up, chemical composition, and biological properties from one another and from underlying materials. The soil in Pune's eastern section has been polluted as a result of industrialization and other anthropogenic activity. Because sewage water from the Mula - Mutha River flows through Manjari village, it was thought necessary to conduct a soil analysis to determine the extent of pollution in the soils in the surrounding area. Because plants rely on soils for nutrients, water, and minerals, the soil type plays an important role in deciding which plants will thrive in a given location. The investigation of soil samples obtained from the sugarcane fields of Manjari, Hadapsar, and Phursungi in the SE portion of Pune city, which is influenced by solid waste disposal and industrial effluents, was carried out in the current study. To begin, soil samples were gathered from 12 different places and analyzed. Chemical characteristics such as Phosphorus, Potassium, Copper, Iron, Manganese, Zinc, and Boron were analyzed along with physical factors such as pH, Electrical conductivity (EC), and organic carbon (%) (Wagh, 2013).

2.2 Microbial diversity

By comparing microbiomes from lands that have been under agronomic activity for over 50 years to those from uncultivated land, this study investigated the effects of long-term agriculture on bacterial diversity, composition, and putative function in the EFS using high-throughput 16S rRNA gene amplicon sequencing. Agriculture enhanced bacterial diversity,

according to the findings. These findings suggested that changes in bacterial diversity and potential function in the EFS were caused by edaphic variables induced by long-term agriculture (Joel Dube *et al.*, 2019).

The ability of soil fungi to increase and recover nitrogen, phosphorus, and potassium content in wet soil, as well as promote the growth of the host plant, has been tested. The host plant was grown in an optimal soil condition for two weeks in a mixture of fertile forest soil (nutrient-rich soil) and simulated flooded soil (nutrient-poor soil). Every day until two weeks after planting, a soil sample was taken and evaluated for nitrogen, phosphate, and potassium levels. Dilution plating was used to isolate soil fungus, which was then identified using Biology's Microbial Systems. The nitrogen, phosphorus, and potassium concentrations were found to be growing by two to three times from the original concentration after two weeks. *Aspergillus aculeatus* and *Paecilomyces lilacinus*, two fungal species, were identified with a probability of higher than 90%. Both detected fungus were found to be advantageous in improving plant development and increasing the availability of nutrient content in the soil, allowing the flooded soil to regain its nutritional content (Hazwani Aziz and Norazwina Zainol, 2018).

The study was carried out to determine the fungal diversity in soil samples taken from the Loyola College campus in Chennai. In this study, 25 isolates were isolated from soil samples. With the help of a standard key and a microbiological expert, 13 of the 28 isolates were recognized. The majority of the fungal isolates belonged to the genera Aspergillus and Mucor, with the genera Aspergillus and Mucor dominating. Aspergillus niger, Aspergillus clavatus, Aspergillus sydowii, Aspergillus variabilis, Aspergillus fumigatus, Penicillium chrysogenum, Colletotrichum gloeosporioides senu lato, Mucor sp., Rhizopus stolonifer, Rhizopus oryzae and

Cunninghamella bert. The Keratinophilic fungus Aspergillus niger has the highest number of individuals on campus, followed by Mucor sp (Raja et al., 2017).

For the isolation of fungi, 36 samples were obtained at random from 0-15 cm depth after removing the surface soil from various forest areas. For isolation, serial dilution approach and PDA media were utilized. Using relevant literature, eighty-two species belonging to thirty-two genera were identified. Deuteromycotina has 22 genera and 58 species, Zygomycotina has four genera and nine species, Oomycotina has three genera and five species, Ascomycotina has three genera and nine species, and NSF has none. *Penicillium* and *Aspergillus* are the most common fungi, with Chaetomium, Trichoderma, Fusarium, Absidia, Cladosporium, Phoma, Acremonium, Achyla, and Alternaria following closely after. Phomafemeti (83.33 %) had the highest percent incidence, while Myrothecium sps had the lowest percent occurrence (1.92 %). Fusarium oxysporum had the highest fungal frequency of 33.83 %, while other species had the lowest fungal frequency of 2.7 %. Because of the acidic pH of 4.63-5.05, high organic matter, and optimal moisture content, physicochemical investigation showed that the soil is rich in mycoflora. To summarize, the fundamental goal of fungi in nature is to recycle dead organic matter, making it available to future generations while also maintaining ecological balance in the ecosystem (Chandini and Rajeshwari, 2017).

Isolation and identification of fungus with the goal of reducing pesticide effects and plant disease caused by excessive use of chemical pesticides or fertilizers. The goal of this study was to isolate and identify fungi in order to improve soil fertility. The isolation and primary screening of fungi was carried out using a pure plate approach on PDA agar, a selective media. Several *Trichoderma* strains have been created as plant biocontrol agents. In some plants, biocontrol

bacteria have also been utilized as compost. Biological control, as a strategy for managing plant diseases, boosts output while also protecting the environment and biological resources, as well as providing a suitable agricultural system (Snehal, 2017).

The rising popularity of probiotics and prebiotics has prompted research into their actual activities in the human body. Microorganisms are known to play a critical role in the ecosystem, including nutrient recycling, trophic chain balancing, key physiological processes in plants and animals, and natural habitat conservation. These microscopic organisms help to the manufacture of antibacterial compounds and vitamins essential to live creatures in human food through flavoring products (Jeremias Pakulski Panizzon *et al.*, 2015).

Although soil bacterial communities are an essential biotic component that influences decomposition and nitrogen mineralization in terrestrial ecosystems, the variables that drive this biotic community in Meghalaya's broadleaved forest soils have not been thoroughly investigated. The role of physico-chemical characteristics in driving soil bacterial populations in Meghalaya's broadleaved forest stands of varying altitudes was investigated in this study. Soils were collected monthly for two years at two distinct depths (0-10 cm and 10-20 cm). Bacterial CFU were higher in the high altitude forest stand at 0-10 cm depth than in the low altitude forest stand at 10-20 cm depth, according to the findings. In both forest stands, it also demonstrated a substantial positive link with organic carbon and total nitrogen, indicating that these two are the key driving forces of bacterial communities in Meghalaya's broadleaved forest stand (Ruth Laldinthar and Dkhar, 2015).

In order to find new bioactive substances, researchers looked at maritime ecosystems, including sediments and organisms. The soil sample was obtained from Karankadu, which is located on the east coast of Thanjavur District, at four different seasons: post monsoon, summer, premonsoon, and monsoon, and research were conducted. Physico-chemical analysis was performed on four soil samples. The following were the seasonal fluctuations of the various parameters studied: pH (7.29-7.63), Electrical conductivity (0.26-0.52 Dsm⁻¹), Organic carbon (0.42-0.60 %), Clay (10.36-18.54 %), and other soil parameters such as available Nitrogen and Phosphorous (84.2-95.60 Kg/ac and 3.25-3.75 Kg/ac), available micronutrients (ppm) such as Zinc, Copper, Iron, Manganese (0.74-0.89, 0.78-1.05, 4.85-8.23, 3.15-3.48). At P<0.01, a link was found between pH, temperature, clay, and organic matter. Twenty-five key groups of bacterial isolates were assessed for spatial and temporal variations in marine sediments over various seasons, as well as soil physicochemical characteristics. Melissococcus sp., Marinococcus albus, Salinococcus sp., Rohella sp., Oscillospira sp., Saccharococcus sp., Sulfidobacillus sp., Brucella sp., Plannococcus sp., Edwardsiella sp., Brochothrix sp., Veillonella and Syntrophococcus sp (Kalaivani and Sukumaran, 2013).

Microorganisms in the soil have a crucial role in soil quality and plant productivity. For a better knowledge of soil health, effective methods for researching the diversity, distribution, and behaviour of microorganisms in soil habitats must be developed. The goal of this study is to critically analyze some of the most common methodologies and processes used in microbial ecological investigations of pot soils in order to better our understanding of the elements that influence measurement results and to help with experiment design. In potted soils, temperature and pH fluctuate. *Bacillus, Pseudomonas*, and *Cladosporium*. *A. flavus* were the bacteria with the

highest plate count in potted soil samples incubated at 20°C, while fungi such as *Cladosporium*, *A.flavus* were the fungi with the highest plate count in samples incubated at 20°C. Streptococcus, *Actinomycetes*, and *S.pyogenes*, *S.coelicolor* dominated the entire bacterial and fungus community. In fungus, decreased numbers were attained over time (Nandhini and Mary Josephine, 2013).

During three intervals from March to November 2011, 15 species of fungi belonging to six genera were isolated from agricultural areas in Salur Mandal. On Potato Dextrose Agar and Czapek's Dox Agar medium treated with appropriate antibiotics such as penicillin and streptomycin, the mycoflora were separated using soil dilution and soil plate techniques. Authentic fungus manuals were used to identify and characterize the mycoflora. They were isolated and characterised as Aspergillus flavus, Aspergillus fumigatus, Aspergillus niger, Aspergillus nidulans, Aspergillus terreus, Penicillium chrysogenum, Penicillium frequentans, Penicillium funiculosum, Trichoderma viride, Trichoderma harzianum, Fusarium oxysporum, Fusarium solani. Mycoflora seasonal variation and % frequency were statistically examined (Gaddeyya et al., 2012).

One of the most valuable resources for bioprospecting is microbial diversity. PCR-based genomic fingerprinting technologies are increasingly being used to examine the genetic diversity of bacteria. New species are discovered and former species are divided when more knowledge is gained and isolates from previously undiscovered environments, such as the soyabean rhizosphere, are examined. Since then, different researchers have used this technique extensively, and several new species have been discovered in the previous decade. The current investigation was designed with the role of rhizobacterial isolates in soybean plant growth

enhancement in mind. The application of phenotypic and molecular methods to research rhizobacteria from a major human food plant, such as soybean, could aid in the identification of robust functional rhizobacterial isolates. These rhizobacterial isolates would be used as a biocontrol agent against the most common pathogen that attacks the host plant. These efforts will lead to the discovery of a potent bioagent that can be used as a biofertilizer and a biocontrol agent by evaluating plant growth boosting activity and biocontrolling capabilities (Pavan Kumar Agrawal and Shuruthi Agarwal, 2011).

In the northeastern United States, soil Ca depletion due to acidic deposition-related soil chemistry changes has resulted in a reduction in forest productivity and carbon sequestration. To restore soil Ca pools, the acidic watershed (WS) 1 of the Hubbard Brook Experimental Forest (HBEF), NH, USA, was supplemented with Ca silicate in 1999. Soil samples from the Ca-amended (WS1) and reference watersheds (WS3) were obtained in 2006 to compare the bacterial community composition of the two watersheds. Before Ca amendment, the locations were roughly 125 metres apart and had similar stream chemistry and tree populations. In comparison to the reference soils, the Ca-amended soil had more Ca and P, but reduced Al and acidity. The bacterial community structure in the Ca-amended and reference soils was considerably different, and the differences were more obvious in the mineral soils, according to PhyloChip analysis of bacterial populations. The relative abundance of 300 taxa was impacted significantly in total. In the Ca-amended soils, the numbers of detectable taxa in families including Acidobacteriaceae, Comamonadaceae, and Pseudomonadaceae were fewer, whereas Flavobacteriaceae and Geobacteraceae were higher. Other functionally important groupings, such as the ammonia-

oxidizing Nitrosomonadaceae, have fewer taxa in the Ca-amended organic soil than in the mineral soil (Ganapathi Sridevi *et al.*, 2011).

The value of microbial diversity in soil ecosystems is gaining popularity. Because a wide range of microorganisms is involved in crucial soil functions, the diversity of microorganisms in soil is viewed as critical to the maintenance of soil health and quality. This study focuses on recent evidence on how plant type, soil type, and soil management regime affect soil microbial diversity, as well as the implications for disease suppressiveness of the soil. Plant type and soil type, the two main drivers of soil microbial community structure, are assumed to function in a complex way. We propose that the complexity of microbial interactions in soil, including interactions between microorganisms and soil and microorganisms and plants, is connected to the fact that in some instances soil and in others plant type is the major determinant driving soil microbial diversity. The relative strengths of the shaping forces exerted by plant and soil vs the ecological behaviour of microorganisms is used to create a conceptual framework (Garbeva *et al.*, 2004).

It is not necessary to determine the composition of microbial communities in soil in order to better quantify nutrient conversions. The holistic approach, which divides systems into pools and measures the flows that connect them, is the most efficient. Fumigation techniques have improved the quantification of nutrient dynamics in soil by determining microbial C, N, P, and S concentrations. However, further progress will necessitate the identification of new pools, such as active microbial biomass, using molecular approaches. Researchers recently used density-gradient centrifugation to separate 13C- and 12C-DNA isolated from soil treated with a 13C source. By multiplying the ratio between labeled and total DNA by the microbial biomass C

content of soil, this technique should allow for the calculation of the active microbial C pool. Furthermore, the taxonomic and functional characterization of 13C-DNA allows researchers to better understand how the C-substrate supplied to soil affects the composition of microbial communities (Nannipieri *et al.*, 2003).

2.3 Synthesis of silver nanoparticle

Silver is a dangerous yet valuable heavy metal that is used in a variety of biomedical and environmental fields. Widespread use of the metal has caused serious environmental concerns. *Bacillus cereus* was discovered in soil that had been polluted. Using central composite design (CCD) based on response surface approach, several experimental elements such as the amount of AgNO₃, inoculums size, temperature, time and pH were improved (RSM). In the form of optimum ramps, optimized values for AgNO₃ (1 mM) 10 ml, inoculum size (*Bacillus cereus*) 8.7 ml, temperature 48.5 °C, time 69 h, and pH 9 were shown. UV–visible spectrophotometer, Scanning Electron Microscopy, Fourier transform infrared spectrometer, particle size analyzer, and X-ray diffraction were used to characterize the produced nanoparticles. The spherical particles have a size range of 5 to 7.06 nm. The antibacterial efficacy of produced nanoparticles was examined using the disc diffusion method against five multidrug resistant microbial species, including *Staphylococcus epidermidis*, *Staphylococcus aureus*, *Escherichia coli*, *Salmonella sp.* and *Porteus mirabilis* (Saba Ibrahim *et al.*, 2021).

Some of the most important players affecting plant productivity are soil bacteria. Emerging contaminants, such as metal engineered nanoparticles, are now present in soil. The goal of this research was to determine the toxicological effects of silver and zinc oxide nanoparticles on microorganisms that promote plant development. Engineered nanoparticles were subjected to three types of bacteria: nitrogen fixers, phosphate solubilizers, and biofilm formers. The effect of silver and zinc oxide nanoparticles on pure bacteria cultures was first determined. These nanoparticles were then used to examine changes in bacterial community composition in soil. The effects of the nanoparticles were investigated using Illumina MiSeq 16S rRNA gene sequencing. In the presence of silver nanoparticles, relative abundances of the main and agriculturally important taxa, Proteobacteria, Actinobacteria, and Firmicutes, were altered in the soil. The abundance of the three phyla was altered by 25 to 45 % to silver nanoparticles. At the phylum level, zinc oxide nanoparticles had no effects. As a result, silver nanoparticles may have an impact on bacterial communities in soil, which could affect the processes carried out by soil bacteria (Sangeetha and Vigneshwaren, 2019).

The absorption peak in the ultraviolet-visible spectra was 420 nm. The generated SNPs had a mean diameter of 25 to 43 nm, according to transmission electron microscopy (TEM). The particles are crystalline in nature, with a spherical structure and sizes ranging from 32 to 86 nm, according to powder X-ray diffraction (XRD). The average SNP size was 63.39 nm, and the Zeta potential was 18.3 mV, according to DLS and Zeta potential analyses. The creation of SNPs was confirmed by energy-dispersive X-ray spectroscopy (EDX), which revealed a high signal in the silver area. There was also evidence of agglomeration in the SNPs. The produced SNPs are capable of suppressing, to varying degrees, often commercially plant pathogenic fungi, and the recorded values of MIC and MFC varied due to the type of fungi used, and they were in the range of 70 – 90, and 75 – 100 μg /l, respectively, from antifungal studies in vitro. *Bacillus*

pseudomycoides MT32 produces antifungal SNPs that can be used to solve a variety of problems in crop production (Mohamed El-Saadony et al., 2019).

Pseudomonas sp. THG-LS1.4, a soil-isolated Pseudomonas sp. strain, was used to make the AgNPs. Field Emission-Transmission Electron Microscopy (FE-TEM), X-ray diffraction (XRD), Fourier Transform-Infrared (FT-IR) spectroscopy, and particle size distribution were used to characterize the AgNPs (DLS). The AgNPs maximum absorbance was 412 nm, and their form was uneven, ranging from 10 to 40 nm. The crystalline nature of nanoparticles was verified by XRD spectroscopy measurements. Bacillus cereus, Staphylococcus aureus, Candida tropicalis, Vibrio parahaemolyticus, Escherichia coli, and Pseudomonas aeruginosa were all found to have antimicrobial activity. The AgNPs were also tested for increased antibacterial activity against Escherichia coli, Pseudomonas aeruginosa, and Salmonella enterica using various antibiotics. In addition, AgNPs have been shown to suppress biofilm formation. The biosynthesized AgNPs were found to be effective against the pathogens that were tested. More importantly, this research reveals AgNPs' potential as an antibacterial agent (Hina Singh et al., 2018).

UV/Vis Spectroscopy, Transmission Electron Microscope (TEM), X-Ray Diffraction (XRD), and Fourier Transform Infrared (FTIR) spectroscopy were used to analyze biosynthesized AgNPs. UV-vis spectroscopy revealed that maximal absorption occurred around 401-432 nm, which corresponds to AgNPs' distinctive surface plasmon resonance. The size range of these NPs was estimated to be between 7.8 and 13.4 nm using TEM. A number of Fcc structures of silver Bragg reflections corresponding to the (100), (110), (111), (200), and (220) planes were detected in the XRD pattern obtained for the AgNPs. The development of AgNPs

was indicated by a downward shift of absorption bands between 400 and 4000 cm1 in the FTIR data. Finally, the extracellular production of AgNPs by *Ochrobactrium sp.* (MAM-C9), *Achromobacter xylosoxidans* (MAM-29), *Pseudomonas aeruginosa* (MAM-42) and *Bacillus cereus* (MAM-I.11) was confirmed. This research found that bacterial production of AgNPs can help to avoid the negative consequences of chemical and physical procedures that aren't suited for medical use (Abo-State and Partila, 2018).

The ability to synthesize nanoparticles using bacteria is a boon for advanced research. Silver nanoparticles were created in this study utilizing the fungus *Aspergillus fumigatus* and an aqueous solution of AgNO₃. The UV-Visible Spectrophotometer was used to characterize the synthesized silver nanoparticles (Ag-NPs). In a visible zone, the maximum absorbance was measured at 435 nm. Silver ions were reduced due to amino groups in proteins and other functional groups in fungus cell-free filtrate. Because of the reduction of silver ions, the production of stable protein encapsulated with silver nanoparticles. Antimicrobial activity of Ag-NPs against *Bacillus cereus*, *Bacillus subtilis*, *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* has been demonstrated (Patil Rajshree *et al.*, 2018)

Typically, nanoparticles are created using a variety of compounds that are very hazardous, combustible, and have unethical environmental practices. This study uses *Bacillus sp.*, *Brevibacillus borstelensis* MTCC10642, to develop a more convenient and environmentally friendly process for synthesising silver nanoparticles from silver nitrate. UV-Vis Spectroscopy, X-Ray Diffraction (XRD), Fourier Transform Infrared Spectroscopy (FTIR), and Scanning Electron Microscopy (SEM) were used to establish the generation and characterization of Silver nanoparticles (Amar Kumar and Ashok Ghosh 2016).

The ability of a soil isolate of *Pseudomonas aeruginosa* to produce silver nanoparticles extracellularly using bacterial culture supernatant. The formation of silver nanoparticles was detected by a change in the colour of the bacterial supernatant, which was confirmed using UV-Vis spectroscopy and characterized using Scanning Electron Microscopy. A soil sample was used to isolate the test strain. The isolate was identified as a *Pseudomonas aeruginosa* strain by molecular analysis. Antibacterial activity of silver nanoparticles against *Escherichia coli* and *Staphylococcus aureus* has been demonstrated. In the field of nanotechnology, the development of bio-nanoparticles is a necessity. In the fields of biomedical nanotechnology and nanomedicine, silver nanoparticles are important (Sourath and Selven Subramanian, 2014).

A bacterial isolate collected from soil and identified as *Agrococcus sp.* generated silver nanoparticles. Enrichment culture with AgNO₃ in LB medium was used to isolate the bacterial culture. Transmission Electron Microscopy was used to examine silver nanoparticles. A bacterial isolate was found to create silver nanoparticles with sizes ranging from 5 to 80 nm. Silver nanoparticles had an average diameter of 555.1 microns, according to particle size analyzers. Furthermore, a UV-Visible Spectrophotometer revealed a silver surface Plasmon band at 311nm in culture broth. Four significant peaks were identified by FTIR (Fourier Transform Infrared spectroscopy) examination at 3450.47 cm⁻¹, 2077.67 cm⁻¹, 1636.91 cm⁻¹, and 1017.70 cm⁻¹ (Jangra Suman *et al.*, 2014).

The use of biologically generated silver nanoparticles in the creation of novel medicinal products has sparked a lot of attention. Physical and chemical approaches improve nanoscience by increasing safety and efficiency while reducing nanomaterials environmental and societal implications. When fungal biomass is subjected to an aqueous silver nitrate solution, silver

nanoparticles develop extracellularly. Visual inspection, UV-Vis absorption spectroscopy, and Transmission Electron Microscopy were used to analyze the silver nanoparticles (TEM). The growth of silver nanoparticles is shown by the colour change of silver nitrate solution to brown in visual analysis. The aqueous medium containing silver ion had a peak at 420 nm in the UV–visible spectrum. Polydisperse spherical and ellipsoid nanoparticles in the size range of 1-50 nm were seen in TEM micrographs. Silver nanoparticles produced by *Fusarium semitectum* were discovered to have significant antibacterial action against *K. pneumoniae* and *P. aeruginosa*. Silver nanoparticles may be biosynthesized in an environmentally sustainable, safe, and costeffective manner, and they have antimicrobial properties (Gitanjali Shelar and Ashok Chavan, 2014).

Because of their ability to synthesise nanoparticles of different size, shape, and morphology, biological production of silver nanoparticles utilizing microbes has piqued researchers' interest. A bacterial strain (CS 11) obtained from heavy metal contaminated soil was used to synthesize silver nanoparticles in the current work. The isolate was identified as a *Bacillus sp.* strain using molecular analysis. The bacterium was discovered to be able to generate silver nanoparticles extracellularly at room temperature after being treated with 1 mM AgNO₃. Visual observation and UV–Vis absorption at 450 nm corroborated this. The size of silver nanoparticles was validated in the 42–92 nm range by Transmission Electron Microscopy characterization. As a result, the current research shows that a *Bacillus* strain can efficiently synthesize stable silver nanoparticles (Vidhyalakshmi *et al.*, 2014).

Nanoparticles are at the forefront of nanotechnology's constantly evolving field. The production of nanoparticles with specified sizes and compositions is a hot topic in

nanotechnology research. The ability to produce nanoparticles of diverse material sizes and forms, as well as quickly assemble them into complex architecture, is critical to advances in nanotechnology. *Coryneybacterium sp.* was used to make silver nanoparticles in this work. UV-Visible Spectrophotometer was used to validate the creation of silver nanoparticles, and SEM and EDAX analysis were used to characterize them. The antibacterial activity of the silver nanoparticles produced was tested against certain human harmful microorganisms (Arun *et al.*, 2013).

2.4 Pot cultivation

The mung bean is a popular pulse crop. Crop production may be increased by managing inputs and selecting cultivars that are appropriate for diverse growing settings and seasons. An attempt was made to compile public data on crop management for maximum production. Methods: This research was carried out at Tamil Nadu Agricultural University's Department of Agronomy, Agricultural College and Research Institute, Madurai - 625104, Tamil Nadu, India. It was possible to comprehend a systematic and integrative assessment of study work conducted in many parts of the world, particularly in India. The importance of pulses, mung bean production and productivity status, zero-budget and low-budget management techniques, INM (Integrated Nutrient Management), IPM (Integrated Pest Management), weed management, and foliar nutrition for yield enhancement under various systems of cultivation, as well as cultivars details for various seasons and situations (Swaminathan *et al.*, 2021).

Soil texture, as well as the relationship between water regime and cultivar, had a substantial impact on rice grain yield. Continuous flooding produced significantly larger yields

than aerobic and saturated soil conditions, but the latter treatments were equivalent. Rondo's grain yield has dropped as a result of soil water regimes such as continual flooding, saturated treatments, and aerobic treatments. Across cultivars and water regimes, rice grain yield in clay soil was 46 percent higher than in sandy loam soil. The saturated and continual flooding treatments had more panicles than the aerobic condition. Furthermore, the number of panicles in clay soil was 25% higher than in sandy loam soil (Xiufen Li *et al.*, 2020).

Pulses are an important part of the human diet as a primary protein source (three times more than cereals) and are high in sulphur, calories, and vitamins, particularly the B-complex, as well as in our country's farm economy. They are an essential component of long-term agricultural productivity, particularly in rain-fed environments. Black gram (*Vigna mungo* (L.) Hepper), a highly regarded Leguminosae family pulse crop, is widely grown in India and is known as "Urad dal" (Raju, 2019).

Bangladesh, Afghanistan, Myanmar, and Pakistan are among the countries that grow black gram. Climates with moderate rainfall and loamy soil with high water retention capacity are ideal for black gram. Black gram is the third most significant pulse crop, and it is grown in rainfed, rice fallow, and irrigated environments during the kharif, rabi, and summer seasons. It matures in 90-100 days and nourishes the soil with nitrogen. Black gram is a major producer and consumer in India. It's used to make a variety of dishes, including Idli, Dosa, and non-fermented foods (Sivasubramanian *et al.*, 2015).

2.5 Molecular characterization

For cultivation – independent microbial diversity research, 16S rRNA gene amplicon analysis remains the gold standard. The choice of primers has a significant impact on the accuracy of these studies. In silico, the total coverage and phylum spectrum of 175 primers and 512 primer pairs were compared to the non-redundant SILVA 16S/18S rRNA reference dataset (SSUREF 108 NR). A selection of "best available" primer pairs for Bacteria and Archaea foe three amplicon size classes (100-400, 400-1000 and 1000bp) is supplied based on this study. By comparing the taxonomic distribution of 16S rDNA amplicons with 16S rDNA fragments from directly sequenced matagenomes, the most promising bacterial primer pair (S-D-Bact-0341-b-s-17/S-D-Bact-0785-a-A-21) was experimentally tested.

For decades, the 16S rRNA gene has been a mainstay of sequence-based bacterial study. However, high-throughput sequencing of the entire gene is only now becoming a viable option. In silico and sequence-based tests to re-evaluate the 16S gene's ability to offer taxonomic resolution at the species and strain level. We show that short-read sequencing systems can't attain the taxonomic resolution that sequencing the whole (1500 bp) gene (Jethro Johnson *et al.*, 2019).

Microbes in complicated biological mixes such as environmental samples and gut samples are widely identified, classified, and quantified using 16S rRNA gene sequencing. The 16S rRNA gene is a highly conserved component of all DNA-based life forms' transcriptional machinery, making it an ideal target gene for sequencing DNA in samples containing thousands of different species. Universal PCR primers can be constructed to target the conserved sections of the 16S gene, allowing the gene to be amplified in a variety of bacteria from a single sample.

With 16S rDNA fragments from directly sequenced metagenomes, the 16S rRNA gene contains both conserved and variable regions (Schmidt *et al.*, 1991).

2.6.1 Formulation of biocontrol agent

The use of biological control agents (BCAs) in an integrated management plan for *Verticillium* Wilt of Olive (VWO), a disease caused by the soil-borne fungus *Verticillium dahliae Kleb*, is of interest. Previous research has found that the root/rhizosphere of healthy olive plants is a significant reservoir of microorganisms with anti-VWO action (i.e., *Pseudomonas* strains PICF7 and PIC141). Furthermore, these BCAs have already evolved to fit the biological niche in which they are used. Three unique bacteria (strains PIC28, PIC73, and PIC167) were isolated from nursery-grown olive plants and characterized in detail using a previously developed in situ isolation method. *Bacillus* strain PIC28 is a member of the *Bacillus* genus. Some Bacillales members were shown to be compatible in vitro with previously reported BCAs (*Pseudomonas* spp. strains) from the olive rhizosphere, paving the way for the creation of bespoke bacterial consortia to combat VWO in the future (Carmen Gómez-Lama Cabanás *et al.*, 2018).

Chemical pesticides used in excess to battle pests harm the environment. Chemical insecticides are also resistant to plant diseases. Viruses like these can damage humans when they pile up in plants or soil. In agriculture, biological control is a non-chemical alternative to chemical control that reduces or eliminates the usage of pesticides. Biological regulation is also aided by microorganisms. The most prevalent sort of microorganism is bacteria. Because of their broad distribution in the soil, their capacity to endure changes in temperature, pH, and salinity, and their ability to create resistant endospore-forming species, *Bacillus* bacteria are used in

biological soil control. In soil and the rhizosphere, *Bacillus* species can be found in high numbers. These bacteria contribute in the treatment of plant diseases by producing siderophore, secreting enzymes, making antibiotics, and building systemic resistance (Mitra Aboutorabi, 2018).

Increasing yields while remaining ecologically friendly has been a fundamental problem for modern farming. As a result, environmentally friendly options are in high demand. Among the many species used as biocontrol agents, *Trichoderma* is a commonly used biocontrol agent against a range of plant illnesses. Asexual fungi known as *Trichoderma spp*. can be found in a range of agricultural soils as well as decaying wood. According to their hostile behaviour, *Trichoderma species* are parasitic on a variety of soil-borne and foliar plant diseases. According to new research, this fungus not only acts as a biocontrol agent but also improves plant resilience, growth, and development, resulting in higher agricultural yields. Antibiotics, mycoparasitism, nutrient competition, and plant systemic resistance are all instances of antagonistic activity. *Trichoderma spp*. is currently being used to control plant diseases as part of a long-term disease management strategy. The literature on *Trichoderma* as a biocontrol agent, its biocontrol activity, commercial production, and application in plant disease management programmes is summarized (Muhammad Usman Ghazanfar *et al.*, 2018).

Toxic fungicides are used without judgement, which has serious repercussions for human health and the environment. It has allowed us to design a strategy for alternative control techniques. Because of its mycolytic enzyme secretions, *Trichoderma species* has a lot of potential for fighting plant diseases. It competes for space and food with a competitive pathogen by halting its activity and keeling it, leading in a significant rise in the development of

economically important crops. A number of biocontrol-based fungicides have been created and distributed globally. This paper discusses the importance of *Trichoderma spp.*, its role as a biocontrol agent, and the global distribution of commercially available *Trichoderma spp* based bioproducts (Sajjad Hyder *et al.*, 2017).

Fungi biological control is thought to be a rapidly emerging natural phenomenon with implications for plant productivity and food supply in the studied area. They may contribute in the preservation of agricultural, food, and feed quality while decreasing the usage of toxic chemicals and pesticides. Fungal biological controls are a common and often crucial natural mortality factor in insect populations in natural environments. Unlike viruses and bacteria, fungi do not require ingestion to infect their insect hosts; instead, they may control all insects, including sucking insects, by penetrating straight through the insect cuticle. The current literature examines the history and current condition of fungal biological control, as well as our knowledge of the process (Jyoti and Singh, 2016).

A unique fungal isolate from high-salinity soil was isolated and identified for the prevention of soil-borne diseases. Among sixteen fungal isolates identified from Sugar beet rhizosphere samples taken from Al-Hosainia localities-El-Sharkia-Egypt, a robust isolate called SRBP ZSHSG1 was obtained. Traditional methods, in combination with phylogenetic analysis of 18S rRNA sequences, revealed that SRBP ZSHSG1 is identical in all *Trichoderma* strains, with *Trichoderma* asperellum being the most closely related. *Trichoderma* asperellum SRBP ZSHSG1 was proposed as a result (ID: KP336489). *T. roseum* and *Chaetomium globosum* were shown to be the most efficient inhibitors of the pathogens studied, followed by SRBP ZSHSG1. Experiments in the field backed up these conclusions. On rice straw, SRBP ZSHSG1 was able to

grow and produce the majority of active compounds (biostraw). The biostraw extract was the most efficient bioagent in terms of lowering pathogen numbers. GC/MS analysis of ethyl acetate extract revealed the presence of nine compounds. These compounds were recognized as four volatile alcohols (1-4) and fatty acid esters (5-9) (Eman Hamed, 2015).

The well diffusion method and MIC determination were used to test T. harzianum antibacterial activity. They produce or release a variety of compounds that trigger localized or systemic reactions in plants, explaining why they are not harmful. In SDA medium, the antimicrobial activity of T. harzianum culture broth extract was investigated. In an in vitro study, T. harzianum showed antimicrobial activity against the majority of the test species, including bacteria and fungi. It was most effective against A. terreus, A. fumigates, and A. clavatus, as well as clinical isolates such as Staphylococcus aureus, E. coli, and Klebsiella. On fungal isolates, T. harzianum has a minimum inhibitory concentration of 100 150 µl/ml, while on bacterial isolates, it has a minimum inhibitory concentration of 50-100 µl/ml of medium. T. harzianum extract had no antimicrobial action against A. niger and A. clavatus among fungal isolates, and Proteus among bacteria. In terms of resistance to other pathogenic organisms, T. harzianum use as a biocontrol agent is taking on a new dimension. Antagonistic reactions like as antibiosis, competition, and hyper parasitism are examples of antagonistic reactions that can lead to biological control. T. harzianum could be employed as an environmentally friendly biocontrol agent against harmful bacteria, according to the research (Leelavathi et al., 2014).

Biological management has emerged as a feasible alternative for controlling plant diseases while decreasing the use of agrochemicals and the health problems that come with them. Biocontrol agents are a class of naturally occurring soil bacteria that actively attack plant

illnesses and benefit plants by suppressing disease. Insect pests and weeds are also controlled with biocontrol solutions. Among the many biological control agents available, screening of potent biocontrol agents is essential for their future development and commercialization. Rhizosphere competency, antagonistic potential, and the ability to produce antibiotics, lytic enzymes, and toxins are all advantages of biocontrol agents. These biological control activities are carried out either directly or indirectly by producing a plant-mediated resistance response. Biocontrol techniques include antibiosis, parasitism, competition for nutrients and space, cell wall disintegration by lytic enzymes, and induced disease resistance. Many studies on various aspects of biological control have been conducted, but more research is required to support novel biocontrol technologies and applications by boosting the efficacy of biocontrol agents and their biocontrol potential. This article is intended to provide an overview of biological control, including its history, screening, mechanisms of action, biocontrol potential enhancement, and field application to treat major crop diseases (Singh *et al.*, 2014).

The probable antagonistic bacteria's antibacterial activity was tested in vitro against the most common and aggressive soft rot-causing bacterial strain Ecc P-138, which had previously been found. Only two isolates, E-45 and E-65, significantly inhibited Ecc P-138 *in vitro* growth. Physiological, biochemical, and carbon source utilization studies identified strain E-65 as *Bacillus* sp., while these tests identified isolate E-45 as *Lactobacillus sp.* Ecc P-138 was most effectively inhibited by E-65 in vitro screening and storage potatoes. E-65 reduced soft rot infection in 22-week storage potatoes of various types by 32.5–62.5 percent in a model experiment, indicating that it has a strong potential as a biological control agent for the primary

pectolytic bacteria Ecc. Isolate E-65 could be employed as a biocontrol agent for potato tubers, according to the findings (Rahman *et al.*, 2012).

Soil-borne plant pathogenic fungi are a major source of concern in agriculture. Biocontrol solutions that are non-toxic, cost-effective, and environmentally friendly are available. Because they produce siderophores, *Pseudomonas aeruginosa* MR-2, MR-5, MR-6, MR-9, MR-15, and MR-18 were chosen for this study. *Sclerotina sclerotiorum* was detected and described from an infected tomato plant after being cultured on the semi-selective medium "NEON." Antibacterial activity of *Pseudomonas aeruginosa* against *Sclerotina sclerotiorum* was investigated. When compared to control, all *Pseudomonas aeruginosa* strains suppressed *Sclerotina sclerotiorum* development by 62-83 percent inhibitory zone. The strains of *Pseudomonas* MR-18 demonstrated the highest inhibition. In an in vitro investigation, *Pseudomonas* strains effectively inhibited *Sclerotina sclerotiorum* growth (Vishal Kumar Deshwal and Punkajkumar, 2013).

The environmental damage caused by the widespread use of chemical pesticides inspired interest in integrated pest management, which use bio-pesticides rather than chemical pesticides to control plant pests and diseases. *Trichoderma spp.* is a fungus that can be used to fight a range of plant illnesses. The current work investigates the suitability of household rubbish, vegetable waste, and other wastes as substrates for mass growth of *Trichoderma viride* and proposes a cost-effective production technique. To generate biomass from fungal grain media, organic and non-synthetic media have been used. When cultivated in pulses, *Trichoderma spp.* produced the most biomass (19.98 gm in 250 ml) (Mridula Khandelwal *et al.*, 2012).

2.6.2 Formulation of bioferilizer

DJ-1-22 (Burkholderia sp Accession No. KY 859855), DJ-1-3 (Burkholderia sp Accession No. KY 636359), TS-3-15 (Stenotrophomonas sp Accession No. KY 636359), DS-2-10 (Herbaspirillum sp Accession No. KX587468), DJ-1-22 (Burkholderia sp Accession No. KY 85 When compared to the control, there is a considerable increase in yield (green leaf output) and plucking point. In terms of green leaf production (145 kg in the first year and 150.87 kg in the second year) and plucking point (88.75 in the first year and 91 in the second year), the DS-2-10, a bacterium of the genus Herbaspirillum sp, has shown the greatest response in comparison to the other five strains, both of which are statistically significant (P 0.001). The biggest increase in green leaf production with the application of biofertilizer in the first and second years, when compared to the control, is 20.81 percent and 25.40 percent, respectively. DS-1-20 had the strongest (24.6 mm diameter inhibition zone) positive response against Alternaria alternate, TS-3-15 and DS-1-20 had the strongest (15.4 mm diameter inhibition zone) positive response against Fomes lamaensis, and DS-1-20 had the strongest (15.5 mm diameter inhibition zone) positive response against Phomopsis theicola (Jayanta Bhaduri et al., 2018).

At monthly intervals, different carrier and liquid biofertilizers are collected from various production centres and research stations to monitor quality parameters such as moisture percentage, pH, consistency, contaminants levels, and microbial population of beneficial bacteria in liquid and carrier based biofertilizers. A progressive change in pH and consistency was detected in carrier and liquid Biofertilizers. When compared to liquid biofertilizers, the quality of carrier-based biofertilizers was too poor, and the decline in count was greater (Bhavya *et al.*, 2017).

Agriculture's decline is attributed to a loss of soil fertility, as well as an unfavorable distribution of rainfall, drought, storms, and floods. The high expense of inorganic fertilizers, which are necessary for plant growth, is one of the biggest issues that farmers face. Chemical fertilizers contaminate the ecosystems of the air, soil, and water. To combat this, scientists have discovered that "Bio fertilizer" is a great alternative to chemical fertilizers. Organic fertilizers, often known as bio fertilizers, provide nutrients to the soil. Organic matter in the soil can improve soil fertility while also slowing nitrogen release, assisting in the control of soil depletion and increasing the supply of other nutrients (Vidhya Devi and Judia Harriet Sumathy, 2017).

Plant Growth Promoting Rhizobacteria (PGPR) plays a vital part in the agriculture industry's sustainability. Growing need for crop output while reducing the usage of synthetic chemical fertilizers and pesticides is a major challenge today. PGPR has been shown to be an environmentally friendly method of improving agricultural yields by stimulating plant development via a direct or indirect process. PGPR regulates hormonal and nutritional balance, induces resistance against plant diseases, and solubilizes nutrients for easier uptake by plants, among other things. Furthermore, PGPR exhibits both synergistic and antagonistic interactions with microorganisms in the rhizosphere and in bulk soil, which improves plant growth rate indirectly. Many bacterial species that act as PGPR have been documented in the literature as effective in promoting plant growth. However, there is a disconnect between the PGPR's mode of action (mechanism) for plant growth and its role as a biofertilizer, emphasising the necessity of nano-encapsulation technology in enhancing PGPR efficacy. As a result, this analysis fills in the gaps and describes PGPR's mechanism as a biofertilizer for agricultural sustainability (Pravin Vejan et al., 2016).

Biofertilizers are microbial inoculants that aid plant growth and development by supplying nutrients to the plant. Biological nitrogen fixers and phosphate solubilizers are two common biofertilizers. PSBs are carrier-based preparations containing living cells of microorganisms such as bacteria, fungus, and actinomycetes that aid in crop productivity by assisting in the solubilization of insoluble phosphorus and encouraging plant growth by giving hormones, vitamins, and other growth factors. The goal of this study was to see how different formulations of phosphate solubilizing bacteria (PSB) performed in the nursery of cow pea (Vigna unguiculata (L.) Walp). The bioformulation was generated using several carrier materials such as composted coir pith, lignite, organic manure, vermicompost, and vermiculite after the selected top PSB strain was mass multiplied. The findings revealed that there were substantial changes in the growth and biochemical parameters of cow pea. The response differed depending on the carrier substance. Composted coir pith outperformed them all in terms of cow pea growth and biochemical responses (Tensingh Baliah et al., 2016).

Fertilizers provide important plant nutrients such as nitrogen (N), potassium (K), and phosphorus (P) to plants (P). These fertilizers boost crop yield, but they also pose a number of health risks. Consumer tastes are evolving toward organic farming, organic manure, and organic fertilizers as a result of these health risks. Biofertilizers have been a prominent component of biological nitrogen fixation in recent years. They provide a cost-effective and environmentally friendly method of supplying nutrients to plants. Biofertilizers are a low-cost, sustainable source of nutrients that can be used in conjunction with chemical fertilizers. Biofertilizers have acquired popularity among small and marginal farmers because to their inexpensive cost (Amit Kapoor *et al.*, 2015).

Due to their eco-friendly, easy-to-apply, non-toxic, and cost-effective characteristics, biofertilizers have emerged as a highly potent alternative to chemical fertilizers. They also operate as complements to agrochemicals by making nutrients that are naturally abundant in soil or the atmosphere useful for plants. Furthermore, they are a product that has the potential to be commercially viable in the long term once sufficient information is made available to producers and farmers through experience and communication. In India, the government is attempting to promote the use of biofertilizers in conjunction with contemporary agrochemicals. This paper emphasizes the need for high levels of innovation and active participation in scientific research and development, public awareness programmes to enhance the extra potential of sustainable agriculture development, as well as encouraging private organizations and policymakers to take an interest in this field in the Indian context (Mohd Mazid and Taqi Ahmed Khan, 2014).

Droughts, severe rainfalls, very high temperatures, cold damage, and storms have all occurred as a result of global warming and climate change in various regions throughout the world where such disasters had never occurred in previous decades. It is critical to establish an environmentally friendly co-existing mechanism on Earth. Agrochemicals have been widely used in recent years to increase yield. Intensive use of agrochemicals causes a slew of agricultural issues, as well as inadequate farming systems. For many crops, farmers use more chemical fertilizers than is suggested. Excessive use of chemical nitrogen fertilizers not only hastens soil acidification, but also puts groundwater and the atmosphere at risk of contamination. The development of a wide spectrum of bio-fertilizers has come from an extended research programme on beneficial bacteria and fungi, which met the nutrient requirements of crops while also increasing crop production. Different crops responded favourably to microbial inoculations

in numerous trials conducted in greenhouses and in the field. In order to boost yield and quality, effective rhizobial inoculants were applied to leguminous plants and AM fungus for muskmelons. Multifunctional bio-fertilizers have been created to reduce the use of chemical fertilizers by roughly 1/3 to 1/2. Enhancement and preservation of soil fertility through microorganisms will be a major challenge in the future (Swapna Latha Aggani, 2013).

Healthy wheat rhizosphere soil was used to isolate *Azotobacter* and *Azospirillum* strains, which were then bio-formulated in fly-ash (300 meshes). The bio-efficacy of a fly-ash-based *Azotobacter* and *Azospirillum* mixture alone and in combination with chemical fertilizer was tested on wheat. In treated soil, the populations of *Azotobacter* and *Azospirillum* were also assessed. Seed treatment with *Azotobacter* and *Azospirillum*, as well as soil treated with chemical fertilizer alone or in combination, significantly improved seed germination, plant height, plant biomass, and crop production when compared to control. Chemical fertilizer-treated wheat plants had higher bio-efficacy than bio-fertilizer-treated wheat plants; however the microbial community in the soil was reduced (destroyed). When compared to chemical fertilizer, *Azotobacter* and *Azospirillum* treated soil showed significantly increased microbial population with slightly lower plant growth. The use of fly-ash as a carrier in bio-fertilizer formulations was found to be a safe and effective option in the current investigation (Vipin Kumar Saini *et al.*, 2010).

Plant growth can be aided by a variety of bacteria and fungus. The final outcomes of the various pathways that PGPR possess and are the applicative goal of agricultural microbiology research are plant growth promoting activity and, more particularly, crop yield enhancement. sDespite the undeniable economic and environmental advantages of using some PGPR species as

biofertilizers, their usage must be carefully considered due to their role as opportunistic pathogens in nosocomial infections and patients with other disorders. On this premise, PGPR species for manufacturing safe biofertilizers must be chosen. The results of inoculation of different crops and cultivars with *Azospirillum* under field settings, as well as the number of bacterial cells and characteristics of the bacterial cultures utilized in the creation of biofertilizers, are also discussed (Luis Fuentes-Ramirez and Jesus Caballero-Mellado, 2005).

CHAPTER – III

MATERIALS AND METHODS

3.1.1 Topographical location of Sampling sites of Thiruvarur district

Thiruvarur district is one of the 32 districts in the Tamil Nadu state of India. The district occupies an area of 2161 Km². It lies between Nagapattinam district on the east and Thanjavur district on the west, and is bounded by the Palk Strait on the south. The district headquarters is at Thiruvarur town.

3.1.2 Geographical position

Date of District formation : 01.01.1997

Latitude (North – South) : Between 10°20' and 11°07'

Longitude (East – West) : Between 79°15 and 79°45'

Mean sea level : 10 meters

Area (sq. km) : 2161

3.1.3 Administrative Profile

There are 2 revenue divisions, 7 taluks, 10 community development blocks, 4 municipalities, 7 town panchayats, 430 village panchayats, 573 Revenue villages, 18 district panchayat wards and 3108 village panchayat wards in Thiruvarur district.

3.1.4 Meteorological information

The maximum temperature was around 35.19°C, while the minimum was around 26.39°C. The average relative humidity is around 73.2 %, with a range of 36.9 % to 95.6 %.

The pressure at the station ranges from 1008 to 999 hPa, with an average of 1017 hPa. In Tamil Nadu, there were four distinct seasons.

Summer – March, April and May

Pre monsoon — June, July and August

Monsoon – September, October and November

Post Monsoon – December, January and February

3.1.5 Sampling site and Collection of soil samples

Thanjavur, Thiruvarur and Nagapattinam districts were formed after the previous integrated Thanjavur district was divided into three. The district is located between the latitudes of 10.200 and 11.070 degrees north latitude. Nagapattinam district borders, the district on the east and north, Palk Strait on the south, and Thanjavur district on the west. Though the Delta districts are comprised of Thanjavur, Thiruvarur and Nagapattinam. Thiruvarur is located at the heart of the delta districts. The Cauvery is the district's main river, which has long supported agriculture and Tamil culture. With a total geographical area of 2097.09 square kilometres, it is a fairly small district.

This is only 1.6 percent of the total area of the state. Thiruvarur, Nannilam, Koradachery, Kudavasal, Valangaiman, Needamangalam, Mannargudi, Kottur, Thiruthuraipoondi, Nannilam, and Valangaiman revenue taluks and ten blocks of Thiruvarur, Nannilam, Koradachery, Kudavasal, Valangaiman, Needamangalam, Mannargudi, Kottur, Thiruthuraipoondi. The net area under cultivation is 1,50,900 hectares, out of a total geographical area of 2097.09 sq km.

Soil samples were obtained from the villages listed below in the Thiruvarur district of Tamil Nadu, India (Kannan Pandian *et al.*, 2011). In a plot, five areas were set aside for taking on a composite soil mixture. The field's surface was scraped away in order to acquire uniformly thick slices of soil from the plough depth in each location. To remove 1 to 2 cm of earth, a V-shaped cut was made with a shovel. The shovel blade sample was taken and placed in a clean bucket. Similarly, a sample was taken from each of the places chosen for one sampling unit. As a result, the samples were dumped onto clean paper and well mixed. After that, the samples were evenly distributed and divided into four equal halves. The remaining samples were combined after the two opposing quarters were rejected. The technique was continued until half a kilogram of soil was reached. The sample was taken in a clean bag and properly labeled. The bag's mouth was knotted with care.

The district has eight different types of soil, such as sand clay loam, clay loam saline alluvial, silty clay alluvial, loamy sand, clay, silty clay, saline alluvial, and saline alkaline soil are the different types. Sandy coastal alluvium and red loam are the most common soil types in the district. The alluvial soil can be found in the riverbed and neighboring parts of the Cauvery River, while the sand soil can be found along the beach. These soils are extremely fertile. The Cauvery River is the district's principal water source. Some of the seasonal rivers in this district include Vennar, Vettar, Koraiyar, Paminiyar, Mullaiyar, Harichandra Nadi, Arasalar, Vanchiar, Nattar, and others. The entire district is irrigated by canals that run for 612 kilometres and are supported by the Cauvery system. Clay soil covers the remaining portion of the district. Soil samples were collected over various seasons and analyzed for physico-chemical characteristics and collecting location, as shown in table 1.

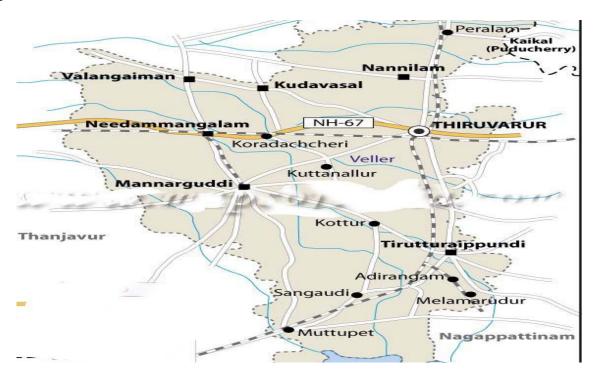
Table 1.1: Description of Sampling Sites Located in Thiruvarur District, Tamil Nadu (Kannan Pandian *et al.*, 2011)

S.No	Sample	Village name	S.No	Sample	Village name
	code			code	
1	SATpSI	Thirupattur	28	SDNSI	Chettichathram
2	SATpS2	Rayanallore	29	SDNS2	Bhagavathamangalam
3	SATpS3	Chettiyamolai	30	SDNS3	Munnavalkottai
4	SANSI	Kovilvenni	31	SENSI	Vadapathimangalam
5	SANS2	Nagar	32	SENS2	Rhishiyur
6	SANS3	Parappanamedu	33	SENS3	Laxmangudi
7	SAMSI	Muthalsethi	34	SEMSI	Palaiyur
8	SAMS2	Nalamsethi	35	SEMS2	Vengathangudi
9	SAMS3	Serankulam	36	SEMS3	Peruvidaimaruthur
10	SAKSI	Viswanathapuram	37	SEKS1	Paruthiyur
11	SAKS2	Mangudi	38	SEKS2	Thiyagarajapuram
12	SAKS3	Kalathur	39	SEKS3	Kamalapuram
13	SANaSI	Pandaravadai	40	SENaS1	Kollapuram
14	SANaS2	Nemmeli	41	SENaS2	Kurungulam
15	SANaS3	Thirunaichur	42	SENaS3	Kumarakudi
16	SAVSI	Valangaiman	43	SEVS1	Padagacheri
17	SAVS2	Regunathapuram	44	SEVS2	Puliyakudi
18	SAVS3	Melavidayal	45	SEVS3	Chandrasekarapuram
19	SBTpSI	Vellore	46	SFTS1	Vilamal
20	SBTpS2	Manali	47	SFTS2	Vijayapuram
21	SBTpS3	Keerakkolore	48	SFTS3	Thandalai
22	SCTpSI	Pamani	49	SGTS1	Alivalam
23	SCTpS2	Korukkai	50	SGTS2	Aamoor
24	SCTpS3	Desingurajapuram	51	SGTS3	Kalyanamahadevi
25	SDTpSI	Pinnathore	52	SHTS1	Thappalampulliyur
26	SDTpS2	Keelaperumazhai	53	SHTS2	Vengatesapuram
27	SDTpS3	Sanganthi	54	SHTS3	Karrappur



Fig -1: Location map of sampling site

S



3.2 Analysis of Physico-chemical parameters of soil

3.2.1 Determination of pH (Ghosh et al., 1983; Hanway and Heidal, 1952)

In a 50 to 100 mL beaker, 10 g of soil sample was weighed, and 20 mL of Calcium Chloride (CaCl₂) solution was added. The soil was allowed to absorb the CaCl₂ solution without stirring for 10 seconds before being thoroughly mixed with a glass rod. The pH of the suspension was measured using a calibrated pH metre after 30 minutes of stirring.

3.2.2 Determination of temperature (Van Bavel and Hillel, 1976)

The temperature probe was linked to the data-collection interface. The Temperature Probe was implanted to a depth of 10 cm in the soil. When the temperature reading stabilized, the displayed value was recorded as the soil temperature 10 cm below the sample surface (to the nearest 0.1°C).

3.2.3 Electrical conductivity (Richards, 1954)

Reagents

0.01M Potassium chloride solution: A small amount of potassium chloride was dried for two hours at 60 degrees Celsius. One litre of potassium chloride was created by dissolving 0.7456 g of potassium chloride in newly prepared distilled water. At 25°C, this solution has an electrical conductivity of 1411×10⁻³, or 1.412 mS/cm. choose a conductivity standard (KCl solution) that is similar to the sample value for the best results.

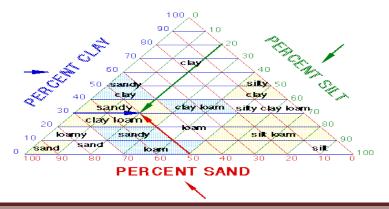
Procedure

1. In a 250 ml Erlenmeyer flask, 40 g of dirt was mixed with 80 ml distilled water. The flask was shaken for one hour on a reciprocating shaker before being filtered through Whatmann No.1 filter paper. The filtrate was now ready for conductivity testing.

- 2. The conductivity electrode was rinsed with normal KCl solution after being cleaned with distilled water.
- 3. A 25 ml beaker was filled with KCl solution, and the electrode was dipped in it. The conductivity meter was then calibrated to read 1.412 mS/cm at 25°C.
- 4. The electrode was rinsed before being dipped in soil extract. The digital display corrected to 25°C was recorded. The reading in mS/cm of electrical conductivity was measured of the soluble salt content in the extract and an indication of salinity status of this soil. The conductivity can also be expressed as mmhos/cm.

3.2.4 Determination of soil texture

The proportion content of groups of particles with distinct sizes in the soil can be characterized as the soil texture or particle size distribution. Soil texture determines the likelihood of finding a particle of a given size in a set of all particles (Bieganowski and Ryzak 2014). The spectral reflectance of soil was used to examine the soil properties. ASD Fieldspec 4 Spectroradiometer for spectral reflectance investigation of soil texture. In terms of soil texture, we can classify it using mineral particles such as sand, silt and clay (Snehal *et al.*, 2016). Silt particles have a diameter of 0.002 mm to 0.05 mm, sand particles have a diameter of 0.05 mm to 2.00 mm and clay particles have a diameter of less than 0.002 mm.



3.2.5 Determination of Moisture content (Muhr et al., 1965)

After removing the cover of the aluminium moisture box, 100 g of soil sample was placed inside and stored in the oven. The sample was held at 105°C until it reached a consistent weight (24-36 hours). The weight of the cooled moisture box was then calculated.

Calculation

Moisture (%) =
$$\frac{\text{Loss in weight}}{\text{Oven-dry weight of soil}} \times 100$$

$$\text{Moisture correction factor} = \frac{100 + \% \text{ Moisture}}{100}$$

3.2.6 Determination of organic carbon (Walkley and Black, 1934)

In a 500 ml conical flask, 0.1 g of the prepared soil sample was placed. The reaction was started with 10 ml of 0.16667 M K₂Cr₂O₇ solution and 20 ml concentrated H₂SO₄ and left to run for 30 minutes. 200 ml water and 10 ml H₃PO₄ were added to the reaction mixture. The solution was titrated using a standard 0.5M FeSO₄ solution after adding 100ml of NaF solution and 2 ml of diphenylamine indicator. The transition from a dull green to a turbid blue to a dazzling green. Simultaneously, a blank without a sample was run.

Calculation

% of organic carbon (X) =
$$\frac{10 (S-T) \times 0.003}{S} \times \frac{100}{\text{weight of soil}}$$

Where,

S = ml of FeSO₄ solution required for blank

 $T = ml \text{ of } FeSO_4 \text{ solution required for soil blank}$

3 = equivalent weight of Carbon

0.003 =Weight of Carbon

Percentage of organic matter = $Y \times 1.724$

3.2.7 Determination of Nitrogen (Subbiah and Asija, 1956)

Reagents

- a) A solution of sodium sulphate and 35 % sodium hydroxide was made by dissolving350 g of solid NaOH in one litre of water.
- b) In water, 0.1M NaOH was dissolved and compared to 0.1N potassium hydrogen phthalate or Standard H_2SO_4 .
- c) 0.1M HCl or 0.1M H₂SO₄ solution: The 0.1M acid solution was compared to the
 0.1M Sodium Carbonate solution.

Procedure

In a Kjeldhahl flask, 1 g of soil sample was inserted. 0.7 g CuSO₄, 1.5 g K₂SO₄, and 30 ml H₂SO₄ were added, and the mixture was heated for at least 30 minutes. The flask was taken off the heater and allowed to cool. Water was introduced to the distillation flask in the amount of 50 mL. The content was compared to 0.1 M NaOH in a titration.

Calculation

Percentage of nitrogen =
$$\frac{1.401 \text{ (V1M1 - V2M2)} - \text{ (V3M1 - V4M2)}}{\text{Weight of soil sample}} \times \text{df}$$

Where,

 V_1 = ml of standard acid taken in receiving flask for samples

 $V_2 = ml$ of standard NaOH taken in titration

 $V_3 = ml$ of standard acid taken to receiving flask for blank

 $V_4 = ml$ of standard NaOH used in titrating blank

 M_1 = molarity of standard acid

 M_2 = molarity of standard NaOH

df = Dilution factor of sample

3.2.8 Estimation of Nitrates (Subbiah and Asija, 1956)

Reagents

a) **Brusine sulphailic acid**: 1 g Brusine sulphate and 1 g Sulphanilic acid were dissolved in 50 ml warm distilled water, then 3ml concentrated HCl was added and the solution was diluted to 100 ml with distilled water.

b) **Sulphuric acid**: In 250 ml of distilled water, 1 lit of pure Sulphuric acid was added.

b) **Sodium chloride**: 30 g NaCl was dissolved in 100 ml distilled water.

Procedure

In an Erlenmeyer flask, 10 ml of filtered material and 2 ml of sodium chloride were shaken well before being placed in a cooling water bath. 10 ml H₂SO₄ and 0.5 ml brusine sulphanilic acid were added to the mixture and thoroughly mixed. The contents of the flask were placed in a hot water bath for 30 minutes and then allowed to cool. Finally, the absorbance in spectronic 20 was measured at 410 nm against a reagent blank. A conventional graph made using sodium nitrate was used to calculate the amount of nitrate.

3.2.9 Estimation of ammonia (Subbiah and Asija, 1956)

Reagents

- a) **Hypochloride stock**: Chlorine solution commercially available
- b) **Alkaline stock**: 100 g sodium citrate and 5 g sodium hydroxide were dissolved in distilled water and made up to 500 ml.
- b) **Nitroprusside reagent**: 1 g of nitroprusside was dissolved in distilled water and produced up to 200 ml.
- d) **Phenol reagent**: 100 mg of phenol was dissolved in 95 % ethanol and diluted with distilled water to make one lit.
- e) **Oxidizing reagent**: Prepared fresh in a stopper bottle with four parts Alkaline stock and one part Hypochloride stock.

Procedure

10 ml filtered sample + 0.4 ml phenol reagent + 0.4 ml nitroprusside reagent of the oxidizing reagent was added, properly mixed, and incubated for one hour at room temperature. In Spectronic 20, the absorption was measured at 630nm. A conventional graph was used to figure out how much ammonia there was.

3.2.10 Estimation of Phosphate (Olsen et al., 1954)

Reagent

Mixed reagent: A mixture of 25 ml H₂SO₄ and 7.5 ml Ammonium molybdate solution was made. 15 ml ascorbic acid and 2.5 ml potassium antimony tartarate were added to this mixture.

Procedure

10 ml filtered soil sample and 2 ml mixed reagent were added to 15 ml distilled water and diluted. After 10 minutes, the reading was obtained at 882 nm in Spectronic -20 against the reagent blank. A typical graph generated using K₂HPO₄ was used to calculate the amount of inorganic phosphate.

3.2.11 Estimation of available Potassium (Toth and Prince, 1949)

Reagents

Molar neutral ammonium acetate solution: 77 g of Ammonium acetate $(NH_4C_2H_3O_2)$ was dissolved in 1 lit of water.

Standard potassium solution: 1.908 g of pure KCl was dissolved in 1 lit of water. Then 10 ml of this solution was diluted into 1 lit with ammonium acetate solution.

Working Potassium standard solution: 0, 5, 10, 15 and 20 ml of the stock solution was taken separately and each sample was diluted with 100ml distilled water plus ammonium acetate solution.

Procedure

Standard curve preparation: The flame photometer was calibrated by atomizing 0 and 20 μ g K/ml solutions to a 0 to 100 reading. To create a standard curve, the values were plotted against the various potassium concentrations and the points were joined with a straight line.

Extraction: A conical flask fixed in a wooden rock containing 5 g of soil sample was filled with 25 ml of ammonium acetate extractant, agitated for 5 minutes, and then filtered. A flame photometer was used to determine the amount of potash in the filtrate.

Calculation

$$K\left(\frac{kg}{ha}\right) = A \times \frac{25}{5} \times \frac{2000000}{100000} = 10A$$

Where,

A = Content of K (μ g) in the sample, as read from the standard curve

Weight of 1 hectare of soil up to a plough depth is approximately 2 million Kg.

3.2.12 Estimation of available Sulphur (Chesnin and Yien, 1950)

Reagent

Mono Calcium Phosphate extracting solution (100mg P/litre): 2.035 g of Ca (H₂PO₄).H₂O was dissolved in 1 lit of distilled water.

Cum acacia-acetic acid solution: The solution was filtered using Whatmann No.42 filter paper after 5 g of chemically pure gum acacia powder was dissolved in 500 ml of hot water. One litre distilled water with acetic acid was used to dilute the cooled diluted solution.

Barium Chloride: BaCl₂ salt was passed through 1mm sieve and stored for use.

Standard stock solution (2000mg S/litre): 10.89 g of oven dried Potassium sulphate was dissolved in 1 lit water.

Standard working solution (10mg S/litre): 2.5 ml of the stock solution was diluted to 500 ml distilled water.

Barium sulphate seed suspension: 18 g BaCl₂ was dissolved in 44 ml hot water, followed by 0.5 ml standard stock solution. 4 ml of gum acacia-acetic acid solution was added to it. Every day, a new seed suspension was created for estimate.

Nitric acid (**Approximately 25%**): 250 ml of concentrated HNO₃ was diluted into one litre distilled water.

Acetic-phophoric acid: 900 ml of glacial acetic acid mixed with 300 ml of H₃PO₄.

Procedure

20 g of soil sample was dissolved in 100 ml of mono calcium phosphate extraction solution (500 mg P/litre) and shaken for one hour. Whatmann was used to filter the solution. A 25 ml volumetric flask was filled with 10ml of clear filtrate. 2.5 ml of 25% HNO₃ and 2 ml of acetic-phosphoric acid were added to the mixture. After shaking the BaSO₄ seed suspension, 0.5ml of this solution and 0.2 g of BaCl₂ crystals were added. A 1 ml solution of gum acacia-acetic acid was added. The solution was diluted to 25 ml, inverted three times, and set aside for 90 minutes. The turbidity was measured at 440nm after being inverted 10 times. 2.5, 5.0, 7.5, 10.5, 12.5, 15.0 ml of the working standard solution (10 mg S/litre) into a succession of 25 ml volumetric flasks to get 25, 50, 75, 100, 125, and 150 μg S. The turbidity was then measured, and a curve was created by graphing the turbidity versus the sulphur concentration (in g in a final volume of 25 ml).

Calculation

Available Sulphur (SO₄-S) (mg/Kg)
$$=\frac{W\times 100}{10\times 20}=\frac{W}{2}$$

Where,

W stands for the quantity of Sulphur in mg as obtained on X-axis against an absorbance reading Y axis on standard graph

20 is the weight of the soil sample in gram

100 is the volume of the extractant in ml

10 is the volume of extractant in ml in which turbidity is developed.

3.2.13 Determination of Calcium and Magnesium (Cheng and Bray 1951)

Reagents

EDTA or Versanate solution (0.01): 2 g of versanate was dissolved in distilled water and made the volume to 1 lit. It was titrated with 0.01N Calcium chloride solution.

Erichrome black T indicator: 10ml of ethanol was dissolved in 4.5 g of hydroxyl amine hydrochloride. 0.5 g of the indicator was added and prepared the solution.

Sodium cyanide solution: 2 % of Sodium diethyl di thio carbarbanate crystals were prepared. It was used to remove the interference of Copper, Cobalt and Nickel.

Procedure

In a 150 ml conical flask, 5 g of air dried soil sample was mixed with 25 ml of neutral normal water. The solution of ammonium acetate was added and agitated for 5 minutes on a mechanical shaker before being filtered through Whatmann No.1 filter paper. Not more than 0.1meq of Ca plus Mg was pipetted out of a 5ml aliquot. 2–5 Carbanate crystals and 5 ml ammonium chloride – ammonium hydroxide buffer solution, three to four drops of Erichrome black T-indicator were used. This solution was titrated with 0.01N versanate until the colour changed to vivid blue or green and there was no trace of wine red.

Calculation

$$N_1V_1=N_2V_2$$

$$N2 = N_2 V_2 \% \qquad V_1 = \frac{\textit{Normality of EDTA} \times \textit{Volume EDTA}}{\textit{ml of aliquot taken}}$$

Here,

 N_1 (Normality) = equivalent of Ca^{++} plus Mg^{++} present in one litre of aliquot

$$Ca + + plus \, Mg + + \, me/litre \, = \frac{Normality \, of \, EDTA \, \times Volume \, of \, EDTA}{ml \, of \, aliquot \, taken} \times 10$$

me of
$$Mg^{++} = me (Ca^{++} + Mg^{++}) - me$$
 of Ca^{++}

When expressed on soil weight basis

$$\text{Ca}^{++} \text{ plus Mg}^{++}/100 \text{g of soil} = \frac{100}{\textit{wieght of soil}} \times \frac{\textit{extract volume}}{1000} \times \textit{Ca} + + \textit{plus Mg} + + \textit{me/ltr}$$

3.2.14 Analysis of heavy metals

Heavy metal analysis was done at Biominin Laboratory, Sundarakkottai using Atomic Absorption Spectrophotomter (AAS) (Elia model).

Estimation on AAS

A unique hallow cathode lamp element was chosen and installed on AAS. Using blank solution, the flame was initiated and the instrument was set to zero. Standard solutions of various concentrations were inhaled one at a time and the results recorded. The standard curve was created by graphing the concentration of the element in question against its absorbance in various standard samples. When the operation was carried out correctly, a straight line relationship between the element's concentration and the absorbance on AAS was obtained, with a correlation efficient of nearly 1.0 aspirated soil extractant was obtained for estimation of nutrient element in the given soil sample, and the readings were observed.

Calculation

Content of micronutrient in the sample $(mg/Kg) = C \mu g/ml \times 2$ (dilution factor)

Where,

Dilution factor = 2.0 (soil sample taken = 10g and DTPA used = 20ml)

Absorbance readings on AAS of the soil extract being estimated for a $\mathsf{particular} \ \mathsf{element} = X$

Concentration of micronutrient as read from the standard curve for the given absorbance (X) = $C \mu g/ml$

3.2.14(a) Estimation of Zinc (Cheng and Bray 1951)

Reagents

Standard Zinc solution: In a beaker, 1g of pure zinc was weighed. A 20 ml (1:1) solution of HCl was added. The solution was poured into a 1 lit volumetric flask and filled with glass distilled water to make up the difference in volume. It was a zinc solution with a concentration of 1000 mg/ml. Refer to 1000 μ g/ml solution A for standard curve preparation. Standard B was created by diluting 1 ml of standard solution in 100 ml to obtain a 10 μ l/ml solution.

Glass-distilled or demineralized acidified water of pH 2.5 ± 0.5 : 1 ml of 10% sulphuric acid was diluted in one litre of distilled or mineralized water, and the pH was adjusted to 2.5 using a pH metre and 10% H₂SO₄ or NaOH. Acidified water was the name given to this solution.

Working Zn standard solution: To obtain 0.2, 0.4, 0.8, 1.2, 1.6, and 2.0 g/ml of Zinc, pipette 1, 2, 4, 6, 8, and 10ml of standard B solution into a 50ml numbered volumetric flask and make the volume with DTPA solution.

Procedure

The standards were atomized with flame solutions on AAS at a wavelength of 213.8nm (Zn line of the instrument). The absorbance value on the Y-axis was plotted against their individual zinc concentration on the X-axis to create a standard curve for the known concentration of zinc solution.

3.2.14(b) Estimation of Copper (Cheng and Bray, 1951)

Reagents

Standard Copper solution: A litre flask was filled with 1g of pure copper wire. The volume was up to the mark when 30ml of HNO₃ (1:1) was added. The flask was vigorously shaken. After that, 1ml of a 1000 g/ml copper solution was diluted to 1000ml to make a 10 g/ml standard copper solution.

Glass-distilled or demineralized acidified water of pH 2.5 \pm 0.5: Same as that done for Zn

Working standard solutions: 0.4, 0.6, 0.8, 1.0, 1.2, and 1.4 g/ml were obtained by pipetting 2, 3, 4, 5, 6, and 7 ml of 10 g/ml standard Cu solution into a 50 ml numbered volumetric flask and making the volume with DTPA solution.

Procedure

An atomic absorption Spectrophotometer was used to burn the standards at a wavelength of 324.8 nm (Cu line of the instrument). The standard curve was created by graphing the known copper concentration on the X-axis against the absorbance value on the Y-axis.

3.2.14(c) Estimation of Iron (Cheng and Bray, 1951)

Reagents

Standard iron solution: 1 g of pure iron wire was transferred to one flask and 30 ml of 6 M HCl was added then it was boiled. It was transferred to the beaker and made the volume up to the mark.

Glass-distilled or demineralized acidified water of pH 2.5 \pm 0.5: Same as that done for Zn.

Working iron standard solution: 10ml of iron stock solution was pipetted out in 100 ml volumetric flask and diluted with DTPA solution. 2, 4, 8, 12 and 16 ml of 100 μ g/ml of Fe solution was obtained.

Procedure

An Atomic Absorption Spectrophotometer was used to burn the standards at a wavelength of 248.3 nm (Fe line of the instrument). The standard curve was created by graphing the known copper concentration on the X-axis against the absorbance value on the Y-axis.

3.2.14(d) Estimation of Manganese (Cheng and Bray, 1951)

Reagent

Standard Mn solution: 3.0751 g of Manganese sulphate (MnSO₄.H₂O) was transferred into one litre flask and it was diluted with water and made the volume upto the mark.

Glass-distilled or demineralized acidified water of pH 2.5 \pm 0.5: Same as that done for Zn.

Working iron standard solution: Standard curve was prepared by taking lower concentrations of Mn in the range of 0-10 μ g/ml. 1, 2, 4, 6 and 8 ml of 50 μ g/ml solution was taken and made up the volume with DTPA solution to 50ml to obtain 1, 2, 4, 6 and 8 μ g/ml working standard.

Procedure

An Atomic Absorption Spectrophotometer was used to burn the standards at a wavelength of 279.5 nm (Mn line of the instrument). The standard curve was created by graphing the known copper concentration on the X-axis against the absorbance value on the Y-axis.

Procedure for extraction by DTPA

In a 100ml narrow mouth polypropylene vial, 10g of soil sample was obtained. A 20ml extraction solution of DTPA (Diethylene-tri-amine-penta-acetic acid) was added. At room temperature (25°C), the stopper bottle was shaken for 2 hours. Filter paper No. 1 or 42 was used to filter the content, and the filtrate was collected in polypropylene bottles. Except for the soil sample, the following steps were used to create a blank.

3.3 Isolation of Microbes from the collected soil samples

To isolate the bacteria and fungus, serial dilution was used with the soil samples collected. Following that, 1 g of soil sample was added to a tube holding 9 ml of sterile distilled water and well mixed to achieve a 1:10 dilution (10⁻¹). Then, using sterile pipettes, 1

ml of the diluted sample was transferred to the next tube and serially diluted into a succession of test tubes containing 9 ml of sterile distilled water up to 10⁻⁷ dilutions.

3.3.1 Bacteria and actinomycetes (Aneja, 2002)

From 10⁻⁴ to 10⁻⁷ dilutions, 0.1 ml of serially diluted sample was placed on nutrient agar plates and incubated at 37°C for 24 hours. The plates were examined for colony formation after incubation. The isolated organisms were then streaked on selective medium like Eosin Methylene Blue agar, MacConkey agar, Mannitol salt agar, and Violet red bile agar aseptically. Most bacteria and fungi were eliminated by drying the soil sample at 50°C for 15 minutes (in other cases, 2 % CaCO₃ was combined with the soil and incubated at 30-35°C for 10-15 days). The soil sample was then serially diluted, and 1ml of the soil suspension was dispersed across the surface of Starch Casein Agar (SCA) plates and incubated for 7 to 14 days at 30-35°C.

3.3.2 Fungi (Aneja, 2002)

From 10⁻² to 10⁻⁵ dilutions, 0.1 ml of serially diluted sample was placed over the prepared Potato Dextrose Agar (PDA) plated media, and the plates were incubated at 37 °C for 2-3 days.

3.3.3 Total Cell Count (Aneja, 2002)

Direct counting of cell suspension in a counting container of known volume using a microscope is the most popular way of enumerating total microbial cells. Neubauer counting chamber is one example of such a counting chamber. Colony counter, an electrical gadget, is another technique. The number of cells in this instrument is counted indirectly by measuring the loss of conductance as the cells move through a tiny passage. Total cell count can also be done using the membrane filtering method.

3.3.4 Identification of Bacteria and actinomycetes

Gram's staining technique, Motility test and Biochemical test were used to identify the isolated bacteria after incubation (Aneja, 2002).

3.3.4.1 Gram's staining (Hans Christain Gram, 1884)

On a clean glass slide, a thin smear of bacterial isolates was formed and heat fixed. The smear was then stained with crystal violet for one minute, rinsed with water, and finally stained with gram's iodine. The slide was washed again in tap water and decoloured with alcohol after one minute. After decolourization, the smear was counter stained for one minute with saffranin. The slide was washed and dried in the open air. It was then examined under a microscope.

3.3.4.2 Motility test (Bailey and Scott, 1966)

Around the hollow slide, petroleum jelly was placed. On the cover slip, a drop of culture was placed in the centre. Over the cover slip, petroleum jelly was placed to the concave slide surface facing down. The slide was then examined under a microscope. The bacterial isolates' motility was observed.

3.3.4.3 Biochemical test (Cappuccino and Shermann, 1998)

3.3.4.3(a) Indole Test

The indole test is used to determine whether bacteria can use the amino acid tryptophan. The peptone broth was made, sanitized, inoculated, and incubated for 24 to 48 hours at 37°C. After incubation, the existence of indole production was confirmed by the creation of a ruby pink ring caused by the addition of Kovac's reagent, indicating a positive indole test. The absence of ring development indicated that the indole test was negative.

3.3.4.3(b) Methyl Red Test

The methyl red test was used to determine whether a bacterium could create acid as a byproduct of glucose fermentation. The bacterial culture was inoculated into test tubes with MR-VP broth, which was subsequently incubated at 37°C for 24 to 48 hours. After incubation, 5 drops of methyl red reagent were added, and the medium's colour changed from yellow to red, indicating that the test was positive. The presence of yellow denotes a poor outcome.

3.3.4.3(c) Voges – Proskauer Test

The microorganism's ability to create acetoin (acetyl methyl carbinol) as a byproduct of glucose fermentation was determined using the Voges–Proskauer test. The bacterial culture was injected into MR-VP broth, which was put into test tubes and incubated at 37°C for 24 to 48 hours. 2 drops of VP-1 and VP-2 reagents were added after incubation. Following the addition of these reagents, the tube was gently shaken and exposed to oxygen before being left for 15-30 minutes to allow the reactions to occur. A favourable reaction is shown by the creation of pink red colour in the medium, while a negative reaction is indicated by the formation of weak brown colour.

3.3.4.3(d) Citrate Utilization Test

This test was carried out to see if the bacterium could use citrate as its only source of carbon. Simmon's citrate agar medium was produced, sanitized, and a slant in a test tube was created. The bacterial culture streaked over the slant's surface, and the tube was incubated at 37°C for 24 to 48 hours. The colour change from green to blue in the tube was noted after incubation. The colour shift was caused by a change in the medium's pH, which became

alkaline after citrate was added. No colour change in the medium suggests a negative reaction.

3.3.4.5(e) Urease test

The urea agar medium of Christensen was made, sanitized, and placed into a test tube. The bacterial culture was streaked on the slant's surface, and the tube was incubated for 24 hours at 37°C. The colour change from yellow to pink in the tube was noted during incubation. No colour change in the medium suggests a negative reaction.

3.3.4.6(f) Triple Sugar Iron Test

This test was used to distinguish between gram-negative and gram-positive bacteria. The isolates were stabbed and streaked over TSI agar slant for this test. For 24 hours, the tubes were incubated. The change in slope and butt coloration was noticed and documented.

3.3.5 Identification of Fungi

3.3.5(a) Wet mount Technique (Raper and Thom, 1968)

Preparation of lactophenol cotton blue stain

Cotton blue (Aniline blue) -0.125g, phenol crystals ($C_6H_5O_4$) -50 g, Glycerol -100 ml, lactic acid ($CH_3CHOHCOOH$) -50 ml, and 70% ethanol -50 ml were dissolved in 50 ml of distilled water. Lactophenol cotton blue solution was made for two days without disturbing the reagents to allow for dissolving and maturation.

Day 1: Cotton blue was dissolved in distilled water and allowed to sit overnight to remove any insoluble dye.

Day 2: Using protective gloves, phenol crystals were introduced to lactic acid in a glass beaker and swirled until the crystals dissolved using a magnetic stirrer. The glycerol was then added. The cotton blue was filtered and distilled water was added to the phenol + glycerol + lactic acid solution, which was thoroughly mixed. After that, keep it at room temperature.

Procedure

- ➤ A drop of 70% ethanol was placed on a clean microscopic glass slide.
- ➤ A sterile inoculating needle was used to introduce a fungus specimen to a drop of alcohol.
- > To ensure that the fungus sample mixed effectively with the alcohol, it was teased in alcohol with a needle mounter.
- ➤ Before the ethanol dried up, one or two drops of lactophenol cotton blue were added.
- ➤ Then, without producing air bubbles in the stain, cover it with a clean sterile cover slip.
- Fungal spores and other structures were visible on the slides with 40X magnification.

 Using standard manuals, the fungus were identified (Gilman, 2001; Nagamani *et al.*, 2006; Domsch *et al.*, 1980; Barnett and Hunter, 1972; Ellis, 1980).

3.4 Biosynthesis of silver nano particle

3.4.1 Synthesis of silver nano particles from bacteria (Arun et al., 2013)

The culture was centrifuged for 15 min at 5000 rpm, and the supernatant was used to make bacterial filtrate. 10 ml bacterial filtrate was combined with 90 ml silver nitrate solution (1 mm) and incubated at room temperature for 3 days. The metal-treated bacterial filtrate was centrifuged for 20 min at 8000 rpm. Petroleum ether was used to dry and powder the semi-

solid pellet. A few drops of petroleum ether were dropped into the semi-solid pellet and let to evaporate. The powdered pellet was kept at 4°C.

3.4.2 Extraction and Purification of Silver Nanoparticles

The examined organism was cultivated under optimal growth conditions using Nile Blue stain (NB) with pH 6.5 and a 20:30 mixing ratio of culture filtrate and AgNO₃ before being incubated at 30°C for 40 hours with a 140 rpm agitation speed. The SNPs were then purified using three ultracentrifugations at 17,000 rpm for 20 minutes at 4°C, followed by separation of the supernatant. To eliminate any remaining biomolecules, the clear supernatant suspension was redispersed in sterile deionized water. The purified solution was then dried overnight in a hot air oven at 60°C (Nagarajan and Kuppusamy, 2013). The dried powder of SNPs was then mixed with 10 ml deionized water and stored on a sonicator to prevent agglomeration of molecules before being utilized for characterization.

3.4.3 UV-Visible Spectrophotometric analysis

To confirm the decrease of silver ions, a UV-Visible Spectrophotometer was used to evaluate the supernatant qualitatively. After 24 hours, 1ml of sample supernatant was extracted and absorbance was measured using a UV-Visible Spectrophotometer between 400 and 600 nm.

3.4.4 Nitrate reductase assay

The enzyme nitrate reductase transforms nitrate to nitrite. The enzyme activity was determined according to Harley's technique (1993). After 1 hour, the activity was assessed by adding the enzyme's substrate (nitrate) and measuring the amount of nitrite produced. The amount of nitrate reductase activity is measured by the net increase in nitrite after 1 hour. 0.5 ml of phosphate buffer was pipetted into the test tubes and then 0.2 ml of standard potassium

nitrate solution was added and stirred thoroughly. The tubes were filled with 0.4 ml NADH and 0.7 ml distilled water.

0.2 ml of bacterial filtrate - silver nitrate mixture was added to this combination, whereas the control was kept without the silver nitrate mixture in the bacterial filtrate. For 15 minutes, the tubes were incubated in a water bath at 30°C. After that, 1 ml of N-(1-Naphthyl) Ethylene di amine (NED) reagent was added to the reaction mixture, and the tubes were incubated for 90 minutes. At 540 nm, the OD values were measured at regular intervals.

3.5 Pot cultivation (Stockler et al., 1994)

The cultivation took place at PG and Research Department of Microbiology, Sengamala Thayaar Educational Trust Women's College in Sundarakkottai. Two experiments were carried out. In Experiment 1, the soil water content was altered to 50% (-0.078 Mpa) Water Holding Capacity (WHC). The 50 percent WHC was chosen because plants thrived well at this water content in prior trials with this soil. After that, 400g soil (dry weight equivalent) was placed into pots and pre-germinated Black gram, rice and green gram, seeds were planted (*Vigna mungo, Oryza sativa* and *Vigna radiata*, 25 seeds per pot).

The experiment included eight treatments (sandy clay loam soil, clay loam saline alluvial, silty clay alluvial, loamy sand, clay, silty clay, saline alluvial and saline alkaline), each with three replicates, and each with a different watering schedule (Asch *et al.*, 2005). The treatment labels correspond to the number and order of weeks during which the soil was watered to 50% WHC and weeks during which it was not. The pots were placed in a light-filled glasshouse. During the moist periods, water content was kept at 50% WHC and weight was checked three times a day. During the dry periods, pots were let to dry until the water content reached 20% (after 2 days), after which it was maintained. Plant roots and shoots

were taken and their dry weight was assessed after four weeks. After removing all visible roots, soils were maintained at 4°C until available N and P, Water Extractable Organic Carbon (WEOC), and Microbial Biomass Carbon were determined (MBC).

The second experiment looked at how low soil water content affected microbial biomass, activity, and nutrient availability in both planted and unplanted soil. WHC was adjusted to 50% in the soil. After that, 16 pots were filled with soil (400g dry weight equivalent). Eight of the pots were densely planted with pre-germinated seeds to obtain planted soil (20 per pot). The high plant density was used to ensure a high root density, and as a result, roots influenced all soil in the planted pots. The remaining eight pots were left unplanted. To ensure steady soil water content during plant growth, the pots were put in natural light and watered three times a day. Weeds that germinated in the unplanted pots were pulled out.

Roots and shoots were removed four weeks after planting, when a dense plant cover had formed in the planted pots. Within 1-3 hours, the soil was dried to five water contents in a fan-forced oven at 40°C (10, 20, 30, 40 and 50 percent of WHC, equivalent to 0.037, 0.074, 0.11, 0.19 g water g⁻¹ soil and water potentials of -1.7, -0.7, -0.32, -0.16, 0.078 Mpa). Volumetric water contents of 0.048, 0.097, 0.14, 0.19, and 0.24gcm⁻³ correspond to these water contents. After that, 30g soil (dry weight equivalent) from each water content treatment (each water content with 12 repetitions, including planted and unplanted soils) was inserted into Polyvinyl Chloride (PVC) cores with a nylon mesh base (height cm, diameter 3.7 cm). By compressing the soil in the cores to the desired height, the bulk density of the soil was adjusted to 1.3 g cm⁻³.

The cores were then placed in a glass jar that was kept at 20-23°C in the dark. Every two days, the desired water content was maintained by weight. On days 5, 10, and 25, four

duplicates of cores were destructively collected for WEOC, accessible N and P, Microbial Biomass Carbon (MBC) and Microbial Biomass Nitrogen (MBN).

3.6 Molecular characterization (Sacchi et al., 2002; Ammann et al., 1995)

Monsoon, pre-monsoon, summer and post-monsoon soil samples from Thiruvarur district include a diverse range of microorganisms. *Bacillus subtilis* was discovered in abundance in all soil types and was sequenced using the 16S rRNA technique.

3.6.1 DNA preparation

Fresh pure *Bacillus subtilis* cells were treated with 100 µl of newly synthesized lysozyme (Madras Scientific) and incubated in a microfuge tube for 30 minutes at 35°C. Cells or incompletely lysed cells were recovered by centrifugation, and the pellet was lysed with 20 lit of 0.5 N NaOH and 20 lit of 1% SDS. The cell lysate was cooked for 10 minutes before being diluted with sterile water to 200 µl.

3.6.2 Amplification parameters

To amplify DNA, a minicycler with a heated lid thermocycler was employed. 8 pmol of each primer (0.8 µl of primer combination), 0.5 µl of DNA sample, 12.5 µl master mix, and pure sterile water were added to a 25 µl reaction. All amplification processes were heated for 3 minutes at 95°C. With short General primers, the PCR technique was 94°C 90 s, 48°C 35 s, 50°C 35 s, 72°C 105 s, and 33 cycles, with a final extension step at 72°C for 3 min and 4°C for 24 hours.

Sequencing protocol

Using below 16S rRNA universal primers, single-pass sequencing was done on each template. Using an ethanol precipitation technique, the fluorescent-labeled fragments were

separated from the unincorporated terminators. Electrophoresis was performed on the samples after they were resuspended in distilled water.

Bioinformatics protocol

The NCBI FASTA similarity search tool was used to examine the 16s rRNA sequence. Following the phylogenetic analysis of the query sequence with the closely related sequences of the FASTA findings, multiple sequence alignment was done.

3.7 Formulation of biocontrol agent (Pfallar et al., 1990)

3.7.1 Evaluation of biocontrol agents

The biocontrol effectiveness of all the isolates identified from the soil sample was assessed *in vitro* using the minimum inhibitory concentration method against the fungal pathogen *Rhizoctonia solani*. Potato Dextrose Agar medium was used to create the fungal lawn. With the use of a gel cutter, the four wells were created above the surface of the fungal lawn. In separate plates, 25 µl, 50 µl, 75 µl, and 100µl concentrations of biocontrol agents such as *Trichoderma viride*, *Pseudomonas fluorescence* and *Bacillus subtilis* were poured. The plates were incubated above them. After 5 days, 10 days, and 15 days of incubation, the plates were evaluated and inhibitory concentrations were measured.

3.8 Formulation of biofertilizer (Bhattacharia and Jha, 2012)

3.8.1 Azotobacter and Rhizobium

Azotobacter and Rhizobium bacterial strains were obtained from diverse places and cultured on slants for preservation as needed. To prepare starting culture, slant cultures were transferred to liquid broth of selective as well as optimal medium in the rotary shaker for 4 days. The starting cultures are then transferred to the fermenter in Biominin laboratory batch

culture mode, with correct temperature control at 30°C and constant agitation for 4–9 days. The broth was utilized as inoculants when the cell count reached 10⁸-10⁹ cells/ml.

Broth is mixed with an inert carrier substance that includes a sufficient amount of cells for convenient handling, packing, storing, and shipping. In this study, broth is mixed with unsterile soil, activated charcoal, and CaCO₃ in a 1:2:1 ratio, while another set is created by sprinkling unsterile soil, crude coal powder, and CaCO₃ in the same ratio over the carrier to preserve 40 percent moisture. The carrier containing inoculants was left for 7 days after correct mixing, and the above prepared microbial inoculants were utilized as biofertilizer.

3.8.2 Pot Cultivation

Vigna mungo Linn seed was obtained from State Seed Farms in Nedumbalam, Thiruthuraipoondi, Thiruvarur District. Vigna mungo Linn seeds were sown in 30 cm tall polythene bags of identical size. The culture media was made up of major soil types gathered from seven taluks in Thiruvarur District. The pots were equipped with a water supply. Three treatments were done,

T1- Azotobacter only

T2- Rhizobium only

T3- Azotobacter + Rhizobium

C - Control

In triplicates, all of the pots were put in a randomised pattern. The pots were kept at a temperature of 27-30°C in the open shade (Parvathi *et al.*, 1985).

3.8.3 Analysis of morphological parameters (Parvathi *et al.*, 1985)

The healthy seeds were chosen and used for laboratory experiment.

3.8.3(a) Germination percentage

By visual sight, germination refers to the initial manifestation of radical. Every day up to the seventh day following seeding, the number of seeds germinated in each treatment was counted. Germination percentage was calculated by using the following formula:

$$\textit{Germination percentage} = \frac{\textit{total number of seeds germinated}}{\textit{total number of seeds sown}} \times 100$$

3.8.3(b) Seedling length (cm/seedling)

On the seventh day, fifteen seedlings were chosen at random from each treatment to measure seedling length. The black gram seedlings' lengths were measured on a centimetre scale and the results were recorded.

3.8.3(c) Fresh weight and dry weight (g/seedling)

An electrical single pan balance was used to weigh fifteen seedlings and measure their fresh weight. They were dried for 24 hours at 80°C in a hot air oven, and their dry weights were measured with an electrical single pan balance and expressed in gram per seedling.

3.8.3(d) Vigour index

Vigour index of the seedlings was calculated by using the formula proposed by Abdul- Baki and Anderson (1973), as follows:

Vigour index = Germination percentage \times seedling length (root and shoot)

3.8.3(e) Tolerance index

Tolerance index of the seedlings were calculated by using the formula proposed by Turner and Marshal (1972) as follows:

$$Tolerance \text{ index} = \frac{\text{mean length of longest root in treatment}}{\text{mean length of longest root in the control}}$$

3.8.3(f) Shoot length and root length

Five plant samples were collected at 15, 30, 45 and 60 DAS (Days after Sowing) to record the shoot length and root length by using cm scale.

3.8.3(g) Number of root nodule

With the use of a digging fork, five plants with undamaged roots were taken from each allotment. To remove the soil, the root containing root nodules was gently detached from the soil and properly rinsed with tap water. Effective nodules were identified by their pink colour, and the number of nodules was recorded.

3.8.3(h) Total leaf area

The total leaf area was calculated by measuring the length and width of the leaf as described by Yoshida *et al.* (1972), as follows:

Leaf area (cm²) =
$$K \times length \times breadth$$

Where K = Kemp s constant (for dicot leaves 0.66)

3.8.3(j) Yield Parameters

(a) Number of pods per plant

In each pot, five plants were chosen at random and the quantity of pods per plant was recorded. The seeds were taken from the pods, and the total number of seeds was counted and expressed as number of seeds per pod.

(b) Dry weight of pods per plant

The pods were separated from the plant and their dry weights were measured by using an electrical single pan balance and it was expressed in g/plant.

(c) Hundred Seed weight

100 mature seeds were collected from test crop and their dry weights were recorded by using an electrical single pan balance.

(d) Seed yield

The yield of black gram was collected from which experimental pot and expressed in number of seeds per plant.

3.8.4 Phytochemical constituents' analysis of Vigna mungo Linn

3.8.4(a) Estimation of Total Chlorophyll (Arnon, 1949)

Each treatment received 200 mg of fresh leaves, which were pulverized in a mortar and pestle with 80 percent acetone. The supernatant was transferred to a volumetric flask after centrifugation (5000 rpm for 5 minutes). This operation was carried out again under the condition that the residue was colourless. The mortar and pestle were completely cleaned in 80 percent acetone, with the clear washing collected in the volumetric flask. The flask was

filled to a capacity of 10 ml with 80 percent acetone. Spectrophotometric analysis was performed on the solution, with measurements taken at 663nm and 645nm for chlorophyll 'a' and chlorophyll 'b', respectively.

The total chlorophyll, chlorophyll 'a' and chlorophyll 'b' contents were calculated by using the formula,

mg of chlorophyll 'a'/g of
$$= 12.7 \, (A_{663}) - 2.69 \, (A_{645}) \times \frac{V}{1000 \times W}$$

fresh leaves

mg of chlorophyll 'b' of =
$$22.9 (A_{645}) - 4.68 (A_{663}) \times \frac{V}{1000 \times W}$$

fresh leaves

$$\label{eq:moftotal} \text{m of total chlorophyll/g} \qquad = 20.2 \ (A_{645}) + 8.02 \ (A_{663}) \times \frac{V}{1000 \times W}$$

of fresh leaves

Where,

A = absorbance at specific wave lengths.

V = final volume of chlorophyll extract in 80% acetone.

W = fresh weight of tissue extracted

3.8.4(b) Estimation of Carbohydrate by Anthrone method (Hedge and Hofreiter, 1962)

A tube was filled with 100 mg of powdered plant leaves. It was hydrolyzed for three hours in a boiling water bath with 5 ml of 2.5 N-HCl before being cooled to room temperature. Solid sodium carbonate was used to neutralise it until the effervescence stopped. The volume was increased to 100 ml, then centrifuged. A 0.2 ml aliquot of the test sample

was obtained for analysis from the supernatant. The standards were made by diluting the working standard by 0, 0.2, 0.4, 0.6, 0.8, and 1ml. '0' was used as a place holder.

By adding distilled water to all test tubes, including the sample tubes, the volume was increased to 1 ml. After that, 4 ml of anthrone reagent was added to each tube and cooked in a boiling water bath for 8 minutes. Spectrophotometric analysis was performed on the test tubes, with results taken at 630 nm. The standard graph was used to calculate the amount of carbohydrate in the sample tube.

Amount of carbohydrate present in =
$$\frac{\text{Mg of glucose}}{\text{volume of the sample}} \times 100$$

3.8.4(c) Estimation of Protein (Lowry et al., 1951)

Extraction of protein from leaves

500 mg of the leaves were weighed and crushed in a pestle and mortar with 5-10 ml of the buffer. It was centrifuged and the supernatant was used for protein estimation.

Estimation of Protein

The working standard was pipetted into a succession of test tubes in increments of 0.2, 0.4, 0.6, 0.8, and 1ml. 0.2 ml of the sample extract was pipetted into other test tubes. With distilled water, the test tubes were filled to a capacity of 1 ml. The blank was a tube filled with 1 ml of water. Each tube, including the blank, received 5 ml of reagent C (alkaline copper solution). It was combined and set aside for ten minutes. Reagent D (Folin–ciocalteau reagent) was added and mixed in at a concentration of 0.5 ml. It was incubated for 30 minutes at room temperature in the dark. The colour blue was created. At 660 nm, the measurements were taken. The standard graph was used to calculate the amount of protein in the sample.

3.9.5 Statistical analysis (ANOVA)

To make it easier to compare the data of various growth metrics in all samples, a mean was generated (McDonald, 2014). The students't' test was used to see if the differences between the samples were significant.

The standard deviation of the samples mean is related to the chance of deviation from the population mean to compute the limits of mean. In other words, a confidence interval is used to compare the sample mean to the population mean. In this situation, a 't' value as well as the appropriate level of significance are required. In most biological investigations, a level of accuracy of 95 percent is considered adequate. When displaying the bounds of a mean, the level of significance of the investigated result should be included. To calculate the bounds of the mean, one needs follow the steps outlined below.

Step:1

The mean and standard deviation from the data representing the sample was found out.

Step:2

The degrees of freedom for a sample from the formula (d.f=n-1) (n=number of individual items) was determined.

Step:3

The level of significance say p=0.05 (i.e 5% chance of being wrong and 95% chance of being right) was determined.

Step:4

The value of "t" from the table against the degrees of freedom probability level was find out.

Step:5

Multiply that 't' value with Standard Error of Mean (SEM) and the product will be the quality that deviated on both sides of the sample mean. Symbolically X will have the limits of "t" and of the txSEM or the limit on the lower side X-txSEM.

The two limits are called the confidence interval. Thus the estimate would that there is only 5% chance that the population mean will be below or above the SEM value.

$$t = x \pm t (0.5p) \times SEM \text{ value}$$

The formula for calculating mean is $X = \frac{\sum X}{N}$

Where,

 $\sum x$ – sum of variables.

N - Total number of frequency.

The formula for calculating standard error of mean (SEM) is SEM = $\frac{\sigma}{\sqrt{n}}$

The formula for calculating standard deviation (s) is $\sigma = \sqrt{\in (X - X)2}s$

n-1

Where,

 $\sum (X-X)^2$ = The sum of the square of the deviation of each value from the mean, N= Number of observation.

CHAPTER IV

RESULTS

4.1 Soil sample collection

In the years 2014–2015, different seasonal (monsoon, post monsoon, summer and pre monsoon) soil samples were taken in the Thiruvarur district of Tamil Nadu. There were eight different soil types detected in this district (sandy clay loam, clay loam – saline alluvial, silty clay alluvial, loamy sand, clay, silty clay, saline alluvial, and saline alkaline) and their textural analysis was provided in the report (Table -1.2 and Plate-1 and 2).

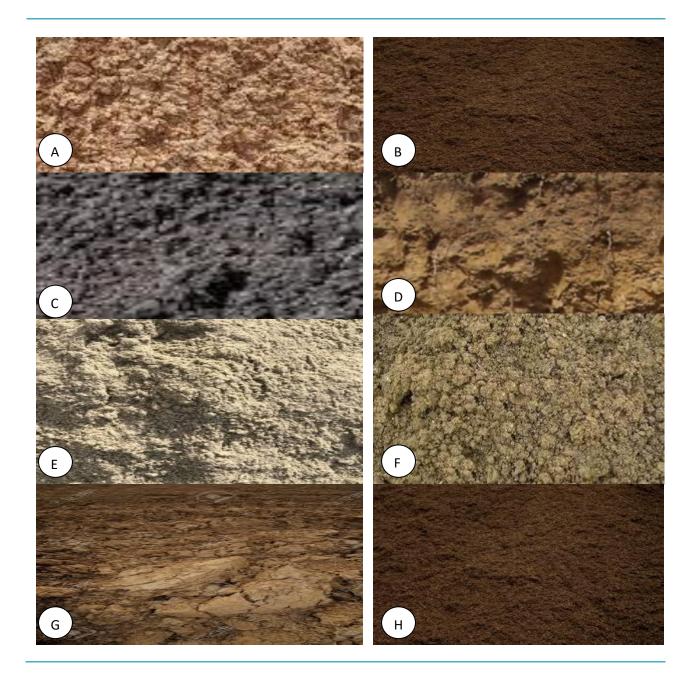
Table 1.2: Details of texture of soil collected from Thiruvarur district

S.No	Soil classes/	Range in relative % of soil samples				
	textural name	Sand	Silt	Clay		
1	Sandy soil	85-100	0-15	0-10		
2	Loamy sand	70-90	0-30	0-15		
3	Sandy loam	43-80	0-50	0-20		
4	Loam	23-52	28-50	7-27		
5	Silt loam	0-50	50-88	0-27		
6	Silt	0-20	88-100	0-12		
7	Sandy clay loam	45-80	0-28	20-35		
8	Clay loam	20-45	15-53	27-40		
9	Silty clay loam	0-20	40-73	27-40		
10	Sandy clay	45-65	0-20	35-45		
11	Silty clay	0-20	40-60	40-60		
12	Clay	0-45	0-40	40-100		

Plate-1
Collection of different of soils and sampling sites from Thiruvarur district, Tamil Nadu



Plate-2
Eight different soil types of Thiruvarur district



Note: A-Sandy clay loam, B-clay, C-silty clay, D-Saline-alkaline, E-Loamy sand, F-Silty clay alluvial, G-Clay loam – saline alluvial, H-Saline alkaline

4.2 Soil physico-chemical parameters analysis

There were eight different types of soil samples obtained in Thiruvarur districts, Tamil Nadu, including sandy clay loam, clay loam-saline alluvial, silty clay alluvial, loamy sand, clay, silty clay, saline alluvial, and saline-alkaline. Soil samples had their physico-chemical characteristics examined.

4.2.1 Soil colour

Four different seasonal (Monsoon, Post Monsoon, Summer and Pre Monsoon) soils were gathered in Thiruvarur districts, including sandy clay loam, clay loam-saline alluvial, silty clay alluvial, loamy sand, clay, silty clay, saline alluvial, and saline-alkaline. Dark grey, yellowish red, brownish yellow, greyish brown, dark brown, light grey, and pale brown were the most common colors (Table-2.1.1, 2.2.1, 2.3.1 and 2.4.1).

4.2.2 Size

Different seized sieves were used to measure different seasonal soil particle sizes, and the results were recorded (Table-2.1.1, 2.2.1, 2.3.1 and 2.4.1; Fig-1.1 and 1.2). The largest size of soil particle 596.80 μ m (monsoon) was found in Rhishiyur's (SENS2) loamy sand soil, while the smallest size of soil particle 321.67 μ m (summer) was found in Parappanamedu's (SANS3) sandy clay loam soil.

4.2.3 Physical analysis of soil sample

The pH, temperature, moisture content, loss of ignition, and electrical conductivity of distinct seasonal soil samples were measured using a standard process and the results were reported (Table-2.1.1, 2.2.1, 2.3.1 and 2.4.1, 2.5; Fig-1.1 and 1.2).

The salty alkaline soil of Bhagavathamangalam (SDNS2) and the silty clay soil of Pamani (SATpS1) had the highest soil pH of 8.3 (summer and premonsoon). Pandaravadai's (SANaS1) sandy clay loam had the lowest soil pH of 6.2 (post monsoon). The highest soil temperature was 41.9°C (Summer) in the Sandy clay loam soil of Nalamsethi (SAMS2), while the lowest soil temperature was 23°C (Monsoon) in the Loamy sand soil of Paruthiyur (SEKS1) and Kurungulam (SENaS2).

The maximum soil moisture content of 70.67% (Monsoon) was measured in Vilamal's silty clay alluvial soil (SFTS1), while the lowest soil moisture content of 21.67% (Summer) was measured in Vengatesapuram's saline alkaline soil (SHTS2). The largest loss of ignition 46.78% (Pre Monsoon) was observed in Muthalsethi's sandy clay loam soil (SAMS1), while the least loss of ignition 23.41% (Post Monsoon) was measured in Munnavalkottai's saline alkaline soil (SDNS3). The sandy clay loam soil at Serankulam (SAMS3) had the highest electrical conductivity 0.56 dsm⁻¹ (Pre Monsoon), while Muthalsethi (SAMS1) had the lowest electrical conductivity 0.18 dsm⁻¹ (Monsoon).

4.2.4 Macronutrient analysis

Nitrogen, nitrates, ammonium, phosphorus, potassium, sulphur, and hydrogen were tested using a conventional approach in four separate seasonal soil samples, and the results were recorded (Table-2.1.2, 2.2.2, 2.3.2 and 2.4.2, 2.5; Fig-2.1, 2.2 and 2.3).

The highest nitrogen concentration of 98 kg/ac (Monsoon) was found in Mangudi's sandy clay loam soil (SAKS2), while the lowest nitrogen concentration of 73.41 percent kg/ac (Summer) was found in Thinaichur's sandy clay loam soil (SANaS3). The sandy clay loam soil of Mangudi (SAKS2) had the maximum nitrates of 97 kg/ac (Monsoon), whereas the loamy sand

soil of Laxmangudi had the lowest nitrates of 71.89 kg/ac (Post Monsoon) (SENS3). The highest concentration of ammonium, 97.67 kg/ac (Monsoon), was found in the saline alkaline soil of Chettichathram (SDNS1), while the lowest concentration, 73 kg/ac (Monsoon) was found in the clay loam soil of Laxmangudi (SENS3). The saline alkaline soil of Thappalampulliyur (SHTS1) had the highest phosphorus content of 72 kg/ac (Post Monsoon), while the lowest concentration, 31.89 kg/ac (Pre Monsoon) was found in the silty clay soil of Pamani (SCTpS1).

The silty clay soil of Pamani (SCTpS1) had the maximum soil potassium of 58.34 kg/ac (Post Monsoon), whereas the loamy sand soil of Vengathangudi (SEMS2) had the lowest potassium of 31.23 kg/ac (Pre Monsoon). The highest sulphur concentration of 57.65 kg/ac (Post Monsoon) was found in Karrappur's salty alkaline soil (SHTS3), while the lowest sulphur content of 31.67 kg/ac (Pre Monsoon) was found in Vengathangudi's loamy sand soil (SEMS2). The highest hydrogen concentration (Monsoon) was found in the sandy clay loam soil of Nagar (SANS2), while the lowest hydrogen content 31.45 kg/ac (Summer) was found in the sandy clay loam soil of Valangaiman (SAVS1).

4.2.5 Micronutrient analysis

Iron, cobalt, chromium, iodine, manganese, zinc, molybdenum, and selenium were analyzed using a conventional approach in four separate seasonal soil samples, and the results were recorded (Table-2.1.3, 2.2.3, 2.3.3 and 2.4.3, 2.5; Fig-3.1, 3.2 and 3.3).

The clay soil of Keerakkolore (SBTpS3) and saline alkaline soil of Pinnathore (SDTpS1) had the greatest content of iron 7.53 µg/kg (Monsoon). The lowest concentration of 2.76 µg/kg (Summer) was found in Vijayapuram's silty clay alluvial soil (SFTS2). The maximum content of cobalt 5.21 µg/kg (Pre Monsoon) was found in saline alkaline soil of

Karrappur (SHTS3) while the lowest concentration 1.06 μg/kg (Monsoon) was found in clay soil of Manali (SBTpS2). The highest concentration of chromium 5.53 μg/kg (Monsoon) was found in Valangaiman's sandy clay loam soil (SAVS1), while the lowest concentration 2.46 μg/kg (Pre Monsoon) was found in Kurungulam's loamy sand soil (SENaS2). The maximum concentration of Iodine 7.60 μg/kg (Monsoon) was found in Vengathangudi's loamy sand soil (SEMS2), while the lowest concentration 1.89 μg/kg (Summer) was found in Nagar's sandy clay loam soil (SANS2).

The highest manganese concentration was 8.37 μg/kg (Monsoon) in Parappanamedu (SANS3) sandy clay loam soil, while the lowest was 2.45 μg/kg (Summer) in Sanganthi saline alkaline soil (SDTpS3). The maximum concentration of zinc 7.40 μg/kg (Monsoon) was found in Pandaravodai's sandy clay loam soil (SANaS1), while the lowest concentration 2.04 μg/kg (Pre Monsoon) was found in Pandaravodai's sandy clay loam soil (SANaS1). The highest concentration of Molybdenum 7.37 μg/kg (Monsoon) was found in the sandy clay loam soil of Chettiyamolai (SATpS3), while the lowest concentration 2.18 μg/kg (Summer) was found in the sandy clay loam soil of Rayanallore. The highest concentration of selenium 7.43 μg/kg (Monsoon) was found in Bhagavathamangalam's saline alkaline soil (SDNS2), while the lowest concentration 1.78 μg/kg (Summer) was found in Bhagavathamangalam's saline alkaline soil (SDNS2).

Table 2.1.1: Physical parameter Analysis of Monsoon Seasonal Soil Samples of Thiruvarur District, Tamil Nadu, India

S.No	Sample Code	Colour	Size (µm)	pН	Temperature (°C)	Moisture (%)	Loss of ignition	Electrical conductivity
						,	(%)	(dsm ⁻¹)
1	SATpS1	Dark grey	517.40±7.50	8.47 ± 0.97	25.33±1.68	47.67±2.30	35.61±1.99	0.26
2	SATpS2	Dark grey	425.60±6.34	8.37±0.96	25.00±1.67	47.00±2.28	39.67±2.09	0.25
3	SATpS3	Dark grey	325.63±6.05	8.43±0.96	27.00 ± 1.73	53.00±2.42	38.73±2.07	0.26
4	SANS1	Yellowish red	451.50±7.08	8.37±0.96	25.00±1.67	65.33±2.69	33.16±1.91	0.30
5	SANS2	Yellowish red	326.80±6.03	8.33±0.96	24.33±1.64	61.33±2.61	45.35±2.24	0.26
6	SANS3	Yellowish red	427.13±6.89	8.36±0.96	24.67±1.65	53.67±2.44	45.56±2.24	<mark>0.35</mark>
7	SAMS1	Dark grey	427.77±6.89	8.47 ± 0.97	23.33±1.61	54.00±2.44	36.47±2.01	0.18
8	SAMS2	Brownish yellow	532.73±7.69	8.33±0.96	24.00±1.63	67.33±2.73	33.05±1.91	0.24
9	SAMS3	Brownish Yellow	325.53±6.01	8.43±0.96	24.67±1.65	57.00±2.51	31.17±1.86	0.29
10	SAKS1	Yellow	425.90±6.88	7.43±0.90	25.00±1.67	65.33±2.69	33.84±1.93	0.28
11	SAKS2	Yellow	425.40±6.87	7.27±0.89	25.33±1.68	67.33±2.73	35.50±1.99	0.21
12	SAKS3	Yellow	338.50±6.13	7.50 ± 0.91	25.00±1.67	75.33±2.89	37.41±2.03	0.21
13	SANaS1	Greyish brown	344.23±6.18	7.57±0.91	23.67±1.62	59.33±2.56	41.75±2.15	0.21
14	SANaS2	Greyish brown	354.50±6.28	7.37±0.90	25.00±1.67	63.33±2.65	30.91±1.85	0.26
15	SANaS3	Greyish brown	475.27±7.27	7.37 ± 0.90	25.00±1.67	53.67±2.44	35.02±1.97	0.22
16	SAVS1	Greyish brown	539.13±7.73	7.20±0.89	24.33±1.64	58.67±2.55	35.59±1.99	0.22
17	SAVS2	Brownish yellow	448.00±7.05	7.30±0.90	23.00±1.59	55.67±2.49	39.15±2.08	0.31
18	SAVS3	Greyish brown	462.70±6.89	7.30±0.90	25.00±1.67	60.67±2.60	42.10±2.16	0.26
19	SBTpS1	Dark brown	537.50±7.72	7.80 ± 0.93	23.33±1.61	64.33±2.67	39.25±2.09	0.31
20	SBTpS2	Dark brown	529.47±7.67	8.03±0.71	25.00±1.67	60.33±2.58	36.41±2.01	0.28
21	SBTpS3	Dark brown	533.77±7.70	7.40 ± 0.90	24.33±1.64	60.33±2.58	34.15±1.95	0.24
22	SCTpS1	Dark yellowish brown	427.27±6.89	8.03±0.94	23.33±1.61	58.33±2.54	32.45±1.89	0.29
23	SCTpS2	Dark yellowish brown	427.10±6.89	8.17±0.95	25.00±1.67	54.33±2.45	39.23±2.08	0.23
24	SCTpS3	Dark yellowish brown	534.07±7.70	7.93±0.93	24.33±1.64	63.67±2.65	38.37±2.06	0.24
25	SDTpS1	Greyish brown	444.10±7.02	8.33±0.96	23.67±1.62	53.67±2.44	34.20±1.94	0.20
26	SDTpS2	Greyish brown	563.33±7.91	8.10±0.94	24.67±1.65	57.00±2.52	35.32±1.98	0.22
27	SDTpS3	Greyish brown	370.73±6.41	8.40±0.96	25.00±1.67	60.67±2.60	37.67±2.04	0.22

Conti.								
28	SDNS1	Pale brown	566.63±7.93	8.40±0.96	24.33±1.64	67.00±2.73	36.40±2.01	0.31
29	SDNS2	Pale brown	361.30±6.33	8.40±0.96	25.00±1.67	57.67±2.53	38.23±2.06	0.26
30	SDNS3	Pale brown	467.37±7.20	8.30±0.96	25.33±1.68	57.00±2.51	46.75±2.28	0.31
31	SENS1	Pale brown	538.73±7.73	6.46±0.84	24.00±1.63	57.00±2.51	26.81±1.72	0.27
32	SENS2	Pale brown	569.80±7.95	6.43±6.84	24.00±1.63	60.00±2.70	37.13±2.03	0.26
33	SENS3	Pale brown	434.67±6.94	6.56±0.85	23.67±1.62	54.33±2.45	30.83±1.85	0.23
34	SEMS1	Dark grey	463.63±6.17	7.67±0.92	23.33±1.61	56.67±2.50	34.31±1.95	0.22
35	SEMS2	Dark grey	470.63±7.23	7.50±0.91	24.33±1.64	57.67±2.53	31.05±1.85	0.31
36	SEMS3	Dark grey	376.00±6.46	7.47±0.91	25.00±1.67	63.33±2.65	33.49±1.92	0.30
37	SEKS1	Dark grey	469.70±7.22	7.53±0.91	23.00±1.59	63.33±2.65	38.33±2.08	0.22
38	SEKS2	Dark grey	357.43±6.30	7.53±0.91	25.67±1.69	64.33±2.67	34.79±1.97	0.25
39	SEKS3	Dark grey	379.67±6.49	7.53±0.91	24.00±1.63	58.00±2.54	38.48±2.06	0.22
40	SENaS1	Greyish brown	455.13±7.11	7.53±0.91	24.33±1.64	64.33±2.67	35.49±1.98	0.22
41	SENaS2	Greyish brown	473.13±7.25	7.53±0.91	23.00±1.59	60.33±2.58	32.54±1.90	0.22
42	SENaS3	Greyish brown	474.80±7.26	7.33±0.90	24.67±1.65	67.67±2.74	34.87±1.96	0.22
43	SEVS1	Greyish brown	525.73±7.64	7.43±0.90	27.00 ± 1.73	57.67±2.53	31.41±1.86	0.22
44	SEVS2	Greyish brown	378.17±6.45	7.57±0.92	25.67±1.69	63.67±2.66	35.05±1.97	0.28
45	SEVS3	Greyish brown	430.23±6.91	7.46±0.91	24.00±1.63	61.00±2.60	34.83±1.97	0.31
46	SFTS1	Dark grey	543.53±7.77	8.10±0.94	24.00 ± 1.63	70.67 ± 2.80	37.61±2.04	0.28
47	SFTS2	Dark grey	479.63±7.30	8.10±0.94	25.00±1.67	61.00±2.60	35.93±1.99	0.22
48	SFTS3	Dark grey	545.80±7.78	8.17±0.95	24.00±1.63	58.33±2.54	32.49±1.90	0.23
49	SGTS1	Dark greyish brown	475.67±7.26	8.10±0.94	25.00±1.67	62.00±2.62	38.93±2.07	0.28
50	SGTS2	Dark greyish brown	539.53±7.74	8.17±0.95	24.33±1.64	62.33±2.63	32.60±1.90	0.29
51	SGTS3	Dark greyish brown	561.97±7.90	8.07±0.94	24.33±1.64	64.00±2.67	33.95±1.94	0.25
52	SHTS1	Light grey	443.87±7.02	8.10±0.94	24.33±1.64	53.67±2.44	34.70±1.96	0.30
53	SHTS2	Light grey	439.70±6.98	8.10±0.94	26.00±1.69	64.00±2.67	32.17±1.89	0.28
54	SHTS3	Light grey	469.53±7.22	8.10±0.94	26.00±1.69	54.00±2.45	26.81±1.72	0.25

Table 2.1.2: Macronutrient Analysis of Monsoon Seasonal Soil Samples of Thiruvarur district, Tamil Nadu, India

S.No	Sample	N (kg/ac)	NO ₃ (kg/ac)	NH ₄ (kg/ac)	P (kg/ac)	K (kg/ac)	S (kg/ac)	H (kg/ac)
	Code							
1	SATpS1	96.67±3.28	84.67±3.07	76.00±2.90	63.00±2.64	38.67±2.04	35.00±1.97	67.00±2.73
2	SATpS2	84.67±3.06	86.33±3.09	76.00±2.90	55.33±2.69	40.33±2.12	43.33±2.19	69.33±2.77
3	SATpS3	93.00±3.21	94.33±3.23	75.33±2.89	53.00±2.42	36.33±2.01	34.00±1.94	66.33±2.77
4	SANS1	97.67±3.29	94.00±3.23	83.67±3.04	63.00±2.64	43.33±2.19	34.67±1.96	74.33 ± 2.87
5	SANS2	83.00±3.03	96.00±3.26	85.33±3.07	55.67±2.49	35.33±1.98	42.33±2.17	70.00±2.79
6	SANS3	75.33±2.89	84.00±3.05	88.00±3.12	64.33±2.67	43.67±2.20	43.67±2.20	45.67±2.25
7	SAMS1	87.67±3.12	84.00±3.05	79.33±2.96	53.67±2.44	36.00 ± 2.00	47.00±2.28	55.33±2.36
8	SAMS2	76.00±2.90	93.67±3.22	78.67±2.95	50.67±2.37	44.00±2.21	49.00 ± 2.33	55.30±2.36
9	SAMS3	93.00±3.21	94.00±3.23	84.33±3.06	55.67±2.49	38.67±2.07	45.00±2.23	51.00±2.38
10	SAKS1	96.67±3.28	97.00 ± 3.28	93.67±3.23	54.00±2.45	44.00±2.21	49.00±2.33	57.00±2.52
11	SAKS2	98.00 ± 3.29	85.33±3.08	94.33±3.23	45.33±2.24	36.00±2.00	40.67±2.12	69.67±2.78
12	SAKS3	83.00±3.03	85.67 ± 3.08	84.67±3.07	51.00±2.38	44.33±2.22	44.00±2.05	64.33±2.67
13	SANaS1	86.00±3.09	94.33±3.24	77.00±2.92	48.00±2.31	34.00±1.94	38.67±2.04	54.33±2.46
14	SANaS2	77.67±2.93	94.00±3.23	85.33±3.08	65.33 ± 2.69	35.33±1.98	42.00±2.16	53.00±2.43
15	SANaS3	85.33±3.08	84.33±3.06	85.33±3.08	47.67±2.30	43.67±2.20	38.67±2.07	55.67±2.48
16	SAVS1	94.00±3.23	89.00±3.14	94.00±3.23	53.00±2.43	36.00±2.00	47.67±2.30	45.67±2.25
17	SAVS2	97.00±3.28	94.33±3.23	84.33±3.06	57.00±2.51	41.67±2.15	42.00±2.16	45.67±2.25
18	SAVS3	86.33±3.09	96.00±3.26	85.00±3.07	62.00±2.62	33.67±1.93	38.67±2.07	62.67±2.63
19	SBTpS1	75.00±2.89	86.00±3.09	94.33±3.24	54.33±2.46	44.33±2.22	38.67±2.00	62.33±2.63
20	SBTpS2	74.00±2.86	84.33±3.06	84.33±3.06	57.67±2.53	36.00±2.00	48.67±2.32	54.00±2.45
21	SBTpS3	85.33±3.07	84.67±3.06	84.00±3.05	63.00±2.64	48.67 ± 2.32	48.00±2.31	59.67±2.57
22	SCTpS1	94.00±3.23	91.67±3.19	84.33±3.06	63.33±2.65	41.67±2.15	35.00±1.97	52.67±2.41
23	SCTpS2	94.33±3.24	86.67±3.10	93.00±3.21	48.67±2.32	41.33±2.14	45.67±2.25	62.00±2.62
24	SCTpS3	87.33±3.11	84.00±3.05	84.67±3.07	48.67±2.32	34.67±1.96	38.00±2.05	50.00±2.35
25	SDTpS1	84.67±3.06	74.33±2.87	84.67±3.07	52.67±2.42	48.00±2.30	46.67±2.28	54.33±2.45
26	SDTpS2	93.67±3.23	84.00±3.05	84.67±3.07	52.00±2.40	45.33±2.24	44.00±2.21	66.00±2.70
27	SDTpS3	85.67±3.08	84.33±3.06	94.33±3.24	52.33±2.41	43.67±2.20	34.33±1.95	54.00±2.44
			<u></u>	<u></u>				

Conti.								
28	SDNS1	85.33±3.07	78.33±2.95	97.67±3.29	51.67±2.39	41.67±2.15	46.67±2.28	57.33±2.52
29	SDNS2	74.33±2.87	83.00±3.03	94.67±3.24	61.00±2.60	35.33±1.98	38.67±2.07	61.00±2.60
30	SDNS3	82.00±3.01	87.33±3.11	94.00±3.23	65.00±2.69	47.67±2.30	46.67±2.28	61.67±2.60
31	SENS1	84.00±3.05	74.33±2.87	87.00±3.10	54.00±2.44	46.60±2.28	35.33±1.98	55.67±2.48
32	SENS2	93.00±3.21	76.00±2.90	75.00±2.59	54.33±2.45	43.00±2.18	45.67±2.25	62.67±2.63
33	SENS3	94.00±3.23	84.00±3.05	82.00±3.02	52.67±2.42	42.00±2.16	44.00±2.21	60.33±2.59
34	SEMS1	85.00±3.07	85.67±3.08	84.00±3.05	53.67±2.44	38.67±2.07	40.33±2.11	48.00±2.31
35	SEMS2	84.00±3.05	83.33±3.04	84.33±3.06	51.33±2.39	42.00±2.16	35.67±1.99	51.33±2.39
36	SEMS3	82.33±3.02	85.33±3.08	85.67±3.08	58.67±2.55	43.67±2.20	38.67±2.07	55.00±2.47
37	SEKS1	85.67±3.08	92.00±3.19	84.33±3.06	64.00±2.67	38.67±2.07	42.00±2.13	58.67±2.55
38	SEKS2	84.00±3.05	85.33±3.08	84.33±3.06	45.33±2.24	42.00±2.16	37.33±2.04	57.00±2.51
39	SEKS3	94.33±3.24	93.67±3.22	84.33±3.06	54.00±2.45	34.67±1.96	38.00±2.05	60.00±2.58
40	SENaS1	94.33±3.24	94.33±3.23	93.33±3.22	63.33±2.65	44.00±2.21	36.33±2.01	58.67±2.55
41	SENaS2	84.00±3.05	83.67±3.04	85.33±3.08	47.33±2.24	35.33±1.98	43.67±2.20	47.00±2.28
42	SENaS3	85.00±3.07	93.67±3.22	76.67±2.91	65.33 ± 2.69	43.67±2.20	34.33±1.95	65.33±2.69
43	SEVS1	83.00±3.03	94.33±3.24	82.00±3.02	47.00±2.28	47.67±2.30	44.00±2.21	54.33±2.45
44	SEVS2	76.00±2.90	96.33±3.27	86.33±3.10	63.00±2.64	35.67±1.99	35.33±1.98	50.67±2.37
45	SEVS3	74.33±2.87	85.33±3.08	93.00±3.21	47.67±2.30	45.67±2.25	40.67±2.12	62.00±2.62
46	SFTS1	84.00±3.05	83.67±3.05	93.33±3.22	45.33±2.24	50.00±2.35	42.00±2.16	57.33±2.52
47	SFTS2	94.00±3.23	83.00±3.03	73.67±2.86	55.33±2.48	45.33±2.24	38.33±2.06	60.00±2.58
48	SFTS3	84.00±3.05	93.00±3.21	85.00±3.07	56.00±2.49	45.67±2.25	33.00±1.91	52.00±2.40
49	SGTS1	76.67±2.91	85.33±3.08	85.33±3.08	64.00±2.67	42.00±2.16	45.67±2.25	62.00±2.62
50	SGTS2	85.00±3.07	84.33±3.06	75.33±2.89	50.00±2.36	47.67±2.30	33.67±1.93	54.67±2.46
51	SGTS3	76.00±2.90	83.67±3.05	73.00±2.84	57.67±2.53	46.67±2.28	42.33±2.17	61.00±2.40
52	SHTS1	83.00±3.04	84.33±3.06	74.00±2.86	49.33±2.34	46.67±2.28	38.67±2.07	59.67±2.57
53	SHTS2	84.67±3.06	93.67±3.22	84.33±3.06	65.00±2.69	44.33±2.22	43.67±2.20	59.67±2.57
54	SHTS3	94.00±3.23	84.00±3.05	84.67±3.07	63.033±2.65	43.00±2.18	41.80±2.13	65.00±2.6

Table 2.1.3: Micronutrient Analysis of Monsoon Seasonal Soil Samples of Thiruvarur District, Tamil Nadu, India

S.No	Sample	Fe (µg/Kg)	Co (µg/Kg)	Cr (µg/Kg)	I (µg/Kg)	Mn (µg/Kg)	Zn (µg/Kg)	Mb(µg/Kg)	Se (µg/Kg)
1	Code	4.52 : 0.71	2.52 : 0.52	2 20 . 0 60	4.52.0.71	1 22 : 0 60	4.40.070	2.40.0.61	4.40.0.70
1	SATpS1	4.53±0.71	2.53±0.53	3.30±0.60	4.53±0.71	4.33±0.69	4.40±0.70	3.40±0.61	4.40±0.70
2	SATpS2	3.57±0.63	3.23±0.60	3.57±0.63	4.47±0.70	5.43±0.78	5.37±0.77	4.30±0.60	3.60±0.63
3	SATpS3	4.83±0.73	2.20±0.49	4.30±0.69	5.10±0.75	4.53±0.71	4.53±0.71	7.37±0.90	5.40±0.77
4	SANS1	5.43±0.84	1.60±0.42	5.40±0.77	5.47±0.78	5.47±0.78	5.43±0.78	5.50±0.78	3.50±0.62
5	SANS2	6.40±0.80	1.40±0.39	4.16±0.68	4.47±0.70	5.10±0.75	5.90±0.80	5.30±0.77	5.27±0.76
6	SANS3	5.83±0.70	2.40±0.52	3.40±0.61	7.37±0.90	8.37 ± 0.96	7.36±0.90	4.36±0.70	4.33±0.69
7	SAMS1	4.40±0.71	3.53±0.62	2.67±0.54	6.33±0.83	5.43±0.78	4.13±0.68	5.40±0.77	3.60±0.63
8	SAMS2	4.53±0.71	2.53 ± 0.53	3.77±0.65	5.57±0.79	6.33±0.83	4.63±0.71	5.33±0.77	5.43±0.77
9	SAMS3	5.53±0.78	2.53 ± 0.53	4.37±0.70	6.40±0.84	4.50±0.71	5.37±0.77	6.30±0.83	4.70±0.72
10	SAKS1	6.43 ± 0.84	3.00 ± 0.58	3.57±0.63	4.53±0.71	3.60 ± 0.63	5.60±0.79	5.40±0.77	5.30±0.77
11	SAKS2	7.37±0.90	3.13 ± 0.59	6.27 ± 0.83	6.50±0.84	5.43 ± 0.78	7.37±0.90	4.37±0.70	5.37±0.77
12	SAKS3	5.47±0.78	3.40±0.61	5.53±0.78	5.37±0.77	4.37±0.70	5.53±0.78	5.70±0.79	4.33±0.69
13	SANaS1	7.40±0.91	4.13±0.68	6.40±0.84	4.40±0.70	5.37±0.77	7.40 ± 0.91	6.23±0.87	5.40±0.77
14	SANaS2	6.53±0.85	4.20 ± 0.68	5.37±0.77	4.53±0.71	4.77±0.73	6.50±0.84	6.53±0.87	3.73±0.64
15	SANaS3	7.37±0.90	3.00 ± 0.58	4.37±0.70	5.30±0.77	5.40±0.77	5.60±0.78	5.50±0.77	4.37±0.69
16	SAVS1	4.50±0.71	3.26±0.60	5.53±0.78	4.40±0.70	5.17±0.76	5.50±0.78	6.40±0.84	5.37±0.77
17	SAVS2	5.53±0.77	2.63±0.54	5.40±0.77	5.30±0.77	4.67±0.72	4.47±0.70	5.43±0.78	4.53±0.71
18	SAVS3	5.30±0.76	1.60±0.42	3.33±0.61	4.30±0.70	5.40±0.77	4.50±0.71	3.40±0.61	5.36±0.77
19	SBTpS1	4.50±0.71	1.40±0.40	3.70±0.64	5.40±0.77	5.70±0.79	4.30±0.70	3.73±0.64	5.63±0.79
20	SBTpS2	7.23±0.89	1.06±0.34	4.40±0.69	3.40±0.61	4.43±0.70	4.40±0.70	3.40±0.61	5.30±0.77
21	SBTpS3	7.53 ± 0.91	1.53±0.41	5.40±0.77	3.33±0.61	3.60±0.63	3.57±0.63	4.67±0.72	4.53±0.71
22	SCTpS1	6.27±0.83	1.53±0.41	5.43±0.77	4.37±0.70	2.71±0.55	3.60±0.63	4.47±0.70	4.43±0.70
23	SCTpS2	5.33±0.77	2.33±0.51	2.43±0.52	5.40±0.77	2.90±0.52	4.53±0.71	5.36±0.77	3.43±0.62
24	SCTpS3	4.27±0.69	1.60±0.42	4.46±0.70	5.37±0.77	3.46±0.62	5.30±0.77	3.70±0.64	4.30±0.70
25	SDTpS1	7.53 ± 0.91	2.40±0.51	4.30±0.62	5.36±0.77	4.36±0.70	3.70±0.64	4.43±0.70	5.40±0.78
26	SDTpS2	6.30±0.83	2.40±0.51	5.37±0.76	4.37±0.70	3.30±0.60	4.50±0.71	5.43±0.78	4.40±0.70
27	SDTpS3	5.50±0.78	3.40±0.61	4.83±0.73	5.37±0.77	4.43±0.70	5.40±0.77	3.77±0.65	5.53±0.78
28	SDNS1	7.37±0.91	4.40±0.70	5.33±0.75	4.53±0.71	5.43±0.78	5.40±0.77	5.43±0.78	6.40±0.84

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29	SDNS2	6.10±0.82	2.53±0.53	3.57±0.62	3.70±0.64	7.43±0.91	4.37±0.70	4.70±0.72	7.43 ± 0.91
30	SDNS3	4.60±0.71	1.50±0.41	4.40±0.70	4.40±0.70	6.77±0.87	3.37±0.61	5.43±0.78	5.43±0.78
31	SENS1	5.53±0.78	1.43 ± 0.40	5.40±0.77	3.53±0.63	5.53 ± 0.78	4.50±0.71	7.37 ± 0.90	5.43±0.78
32	SENS2	7.03±0.88	1.50 ± 0.41	6.47±0.84	4.37±0.69	5.13±0.75	4.30±0.69	6.27±0.83	4.43±0.70
33	SENS3	4.87±0.73	1.83±0.45	5.43±0.78	5.43±0.78	6.56 ± 0.85	3.40±0.61	5.43±0.78	3.40±0.61
34	SEMS1	6.77±0.87	2.50 ± 0.52	3.70 ± 0.64	7.33±0.90	5.67 ± 0.79	5.40±0.77	4.43±0.70	4.30±0.69
35	SEMS2	5.47±0.78	2.40 ± 0.52	3.76±0.64	7.60 ± 0.91	4.50±0.71	4.40±0.70	5.57±0.79	5.23±0.76
36	SEMS3	6.30±0.83	2.70 ± 0.55	3.70±0.64	6.47±0.85	3.53 ± 0.63	3.70±0.64	5.40±0.77	4.40±0.70
37	SEKS1	7.33±0.93	3.40 ± 0.61	5.37±0.77	5.30±0.77	4.50±0.71	4.40±0.70	3.47±0.62	3.67±0.64
38	SEKS2	6.13±0.82	2.50 ± 0.52	4.47±0.72	4.47±0.70	5.53 ± 0.78	5.37±0.71	4.37±0.70	3.30±0.61
39	SEKS3	7.37±0.91	3.27 ± 0.60	4.43±0.70	5.30±0.77	4.47 ± 0.70	4.26±0.69	4.73±0.72	4.40±0.70
40	SENaS1	6.40±0.84	1.63 ± 0.42	5.40±0.77	3.60±0.63	5.43 ± 0.78	5.40±0.77	4.70±0.72	5.40±0.77
41	SENaS2	7.37±0.91	1.47 ± 0.40	3.57±0.63	4.40±0.70	7.06 ± 0.88	3.70±0.64	4.37±0.70	4.53±0.71
42	SENaS3	5.70±0.79	2.80 ± 0.55	5.63±0.79	5.30±0.77	5.60±0.79	2.67±0.54	3.76±0.65	3.53±0.63
43	SEVS1	6.47 ± 0.84	2.83 ± 0.56	4.47±0.70	6.30±0.83	4.53±0.71	3.00±0.63	3.67±0.64	4.40±0.70
44	SEVS2	7.40±0.91	3.30 ± 0.60	5.40±0.77	5.40±0.77	3.77 ± 0.65	4.40±0.70	3.50 ± 0.62	5.53±0.78
45	SEVS3	5.53±0.78	4.30 ± 0.69	4.73±0.72	4.46±0.70	5.53±0.78	5.63±0.79	5.53±0.78	3.70±0.64
46	SFTS1	6.40 ± 0.84	3.47±0.62	5.53 ± 0.78	3.63±0.91	6.50 ± 0.84	6.30±0.84	6.20±0.83	4.50±0.71
47	SFTS2	5.50±0.78	2.70 ± 0.55	3.50 ± 0.62	7.40±0.91	5.50 ± 0.78	6.43±0.84	3.40±0.61	5.60±0.79
48	SFTS3	6.73±0.86	2.70 ± 0.55	3.63±0.63	6.50±0.84	5.70±0.79	5.38±0.77	4.37±0.70	4.70±0.72
49	SGTS1	7.40±0.91	3.57±0.63	4.37±0.70	5.40±0.78	4.60±0.71	5.40±0.77	5.40±0.77	5.30±0.77
50	SGTS2	4.53±0.71	1.80 ± 0.44	5.30±0.77	4.43±0.70	5.37±0.77	4.37±0.70	5.23±0.76	4.60±0.71
51	SGTS3	6.43±0.84	2.33±0.51	5.43±0.78	3.40±0.61	4.40 ± 0.70	5.70±0.79	3.90±0.66	3.40±0.61
52	SHTS1	7.67±0.92	3.33±0.61	5.43±0.78	4.30±067	5.53±0.78	6.30±0.86	4.40±0.70	3.43±0.62
53	SHTS2	7.43±0.91	4.10±0.67	4.70±0.72	5.37±0.77	6.60 ± 0.86	7.33±0.90	5.17±0.76	5.30±0.77
54	SHTS3	6.47 ± 0.85	3.53±0.63	5.40±0.74	5.33±0.77	5.40±0.77	6.40±0.84	4.57±0.71	4.47±0.70

Table 2.2.1: Physical parameter Analysis of Post Monsoon Seasonal Soil Samples of Thiruvarur District, Tamil Nadu, India

S.No	Sample	Colour	Size (µm)	pН	Temperature	Moisture	Loss of	Electrical
	Code			_	(∘ C)	(%)	ignition (%)	conductivity
								(dsm- ¹)
1	SATpS1	Dark grey	423.4±11.8	7.6±1.59	28.33±3.07	46.78±3.93	36.67±3.50	0.26
2	SATpS2	Dark grey	426.0±11.9	7.3 ± 1.55	27.98±3.05	43.67±3.81	38.45±3.59	0.43
3	SATpS3	Dark grey	423.3±11.8	7.7 ± 1.60	28.67±3.09	48.23±4.00	41.32±3.71	0.39
4	SANS1	Yellowish red	426.2±11.9	6.8 ± 1.50	30.01±3.16	51.39±4.13	43.62±3.81	0.32
5	SANS2	Yellowish red	346.8±10.7	7.8±1.61	30.02±3.16	56.43 ± 4.33	33.12±3.32	0.43
6	SANS3	Yellowish red	427.8±11.9	8.1 ± 1.64	30.50±3.19	48.67±4.02	32.45±3.29	0.27
7	SAMS1	Dark grey	532.6±13.3	8.2±1.65	28.67±3.09	42.89±3.78	33.54±3.34	0.32
8	SAMS2	Brownish yellow	465.7±12.4	$7.6\pm1,59$	27.89±3.05	40.23±3.66	31.45±3.23	0.32
9	SAMS3	Brownish Yellow	346.2±10.7	7.7±1.60	26.89±3.00	43.00±3.78	38.21±3.56	0.42
10	SAKS1	Yellow	423.0±11.8	7.0 ± 1.52	31.32±3.23	46.98±3.96	32.67±3.30	0.25
11	SAKS2	Yellow	347.8±10.7	7.0 ± 1.52	31.54±3.24	52.17±4.17	33.56±3.34	0.37
12	SAKS3	Yellow	465.2±12.4	7.2 ± 1.54	32.00 ± 3.26	42.89±3.78	28.43±3.07	0.28
13	SANaS1	Greyish brown	526.4±13.2	6.2±1.43	31.34±3.23	41.46±3.71	35.89±3.45	0.32
14	SANaS2	Greyish brown	367.9±11.1	6.8 ± 1.50	29.63±3.14	41.98±3.74	36.47±3.48	0.42
15	SANaS3	Greyish brown	432.7±12.0	7.6±1.59	32.56±3.29	50.69±4.11	34.98±3.41	0.42
16	SAVS1	Greyish brown	463.2±12.4	7.3±1.55	28.57±3.08	48.56±4.02	32.56±3.29	0.36
17	SAVS2	Brownish yellow	423.1±11.8	7.5±1.58	29.62±3.14	51.00±4.12	33.65±3.35	0.31
18	SAVS3	Greyish brown	462.3±12.4	6.9±1.51	32.00 ± 3.26	49.56±4.06	34.76±3.40	0.36
19	SBTpS1	Dark brown	356.1±10.8	6.8 ± 1.50	28.56±3.08	47.56±4.14	32.45±3.29	0.38
20	SBTpS2	Dark brown	372.6±11.1	7.3 ± 1.55	31.09±3.21	48.23±4.00	32.67±3.30	0.37
21	SBTpS3	Dark brown	432.8±12.0	7.5 ± 1.58	28.00±3.05	42.56±3.76	37.98±3.55	0.29
22	SCTpS1	Dark yellowish brown	456.1±12.3	8.2±1.65	27.00±3.00	46.34±3.93	36.56±3.49	0.28
23	SCTpS2	Dark yellowish brown	354.8±10.8	8.3±1.66	31.00±3.21	42.89±3.78	41.76±3.73	0.28
24	SCTpS3	Dark yellowish brown	465.2±12.4	7.6±1.59	30.56±3.19	43.67±3.81	42.41±3.75	0.22
25	SDTpS1	Greyish brown	432.1±12.0	7.7±1.60	31.42±3.23	47.63±3.98	29.45±3.13	0.24
26	SDTpS2	Greyish brown	386.1±11.3	7.3±1.55	29.78±3.15	43.56±3.81	23.56±2.80	0.23
27	SDTpS3	Greyish brown	473.2±12.5	6.7±1.49	27.89±3.04	52.63±4.18	31.45±3.24	0.34

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28	SDNS1	Pale brown	364.4±11.0	7.2±1.52	26.98±3.00	53.12±4.20	28.46±3.08	0.36
29	SDNS2	Pale brown	462.7±12.4	6.5±1.47	31.45±3.23	53.20±4.21	29.65±3.14	0.42
30	SDNS3	Pale brown	473.4±12.5	7.3±1.55	28.57±3.08	48.67±4.02	23.41±2.79	0.37
31	SENS1	Pale brown	463.6±12.4	7.2±1.55	28.42±3.07	47.89±4.00	31.56±3.24	0.31
32	SENS2	Pale brown	374.2±11.1	7.7±1.60	29.46±3.13	48.67±4.02	32.67±3.30	0.32
33	SENS3	Pale brown	465.2±12.4	8.2±1.65	32.00±3.26	43.89±3.82	27.98±3.05	0.28
34	SEMS1	Dark grey	467.2±12.4	8.3±1.66	31.67±3.25	44.28±3.84	28.54±3.08	0.27
35	SEMS2	Dark grey	473.2±12.5	7.6±1.59	30.67±3.19	43.56±3.81	29.56±3.13	0.42
36	SEMS3	Dark grey	367.2±11.1	6.7±1.49	31.00±3.21	44.27±3.84	29.56±3.13	0.31
37	SEKS1	Dark grey	452.0±12.3	6.5±1.47	29.78±3.15	47.38±3.97	35.14±3.42	0.43
38	SEKS2	Dark grey	462.9±12.4	7.2±1.55	28.92±3.10	46.42±3.93	34.17±3.37	0.41
39	SEKS3	Dark grey	432.7±12.0	7.5±1.58	27.63±3.03	43.58±3.82	32.45±3.28	0.42
40	SENaS1	Greyish brown	478.4±12.6	8.0±1.63	28.48±3.08	45.21±3.88	28.35±3.07	0.45
41	SENaS2	Greyish brown	387.2±11.3	8.1±1.64	26.43±2.97	47.23±3.97	31.65±3.25	0.32
42	SENaS3	Greyish brown	472.9±12.5	8.1±1.64	27.68±3.03	42.66±3.77	32.45±3.29	0.27
43	SEVS1	Greyish brown	472.3±12.5	7.4±1.57	30.42±3.18	46.34±3.93	33.45±3.34	0.29
44	SEVS2	Greyish brown	472.6±12.5	7.6±1.59	30.80±3.20	42.77±3.77	45.31 ± 3.89	0.31
45	SEVS3	Greyish brown	476.3±12.6	7.6±1.59	28.65±3.09	41.33±3.71	24.56±2.86	0.32
46	SFTS1	Dark grey	474.0±12.5	8.2±1.65	28.56 ± 3.08	44.65±3.85	26.43±2.97	0.35
47	SFTS2	Dark grey	476.3±12.6	8.0±1.63	27.63±3.03	43.12±3.79	25.63±2.92	0.36
48	SFTS3	Dark grey	476.2±12.6	8.2±1.65	28.41±3.07	42.10±3.74	27.31±3.01	0.34
49	SGTS1	Dark greyish brown	492.1±12.8	7.8±1.61	27.56±3.03	43.52±3.80	23.67±2.81	0.32
50	SGTS2	Dark greyish brown	482.2±12.7	7.6±1.59	30.45±3.18	44.58±3.85	26.62±2.98	0.32
51	SGTS3	Dark greyish brown	523.8±13.2	7.7±1.60	29.68±3.14	45.26±3.88	24.78±2.87	0.42
52	SHTS1	Light grey	476.4±12.6	8.2±1.65	29.41±3.13	46.27±3.92	26.31±2.96	0.32
53	SHTS2	Light grey	453.2±12.3	8.3±1.66	27.68±3.04	47.27±3.96	27.63±3.03	0.28
54	SHTS3	Light grey	423.1±11.9	8.4±1.67	29.56±3.14	46.26±3.92	24.81±2.87	0.24

Table 2.2.2: Macronutrient Analysis of Post Monsoon Seasonal Soil Samples of Thiruvarur district, Tamil Nadu

S.No	Sample Code	N (kg/ac)	NO ₃ (kg/ac)	NH ₄ (kg/ac)	P (kg/ac)	K (kg/ac)	S (kg/ac)	H (kg/ac)
1	SATpS1	92.65±5.56	86.23±5.36	80.32±5.17	45.56±3.90	38.34±3.57	42.56±3.77	36.78±3.50
2	SATpS2	86.43±5.37	83.21±5.27	81.26±5.20	48.67±4.03	36.32±3.48	43.87±3.82	32.46±3.29
3	SATpS3	91.63±5.53	83.34±5.27	80.21±5.17	52.78±4.19	34.67±3.40	38.41±3.58	36.78±3.50
4	SANS1	83.67±5.28	78.64±5.11	82.23±5.23	55.31±4.29	42.64±3.77	41.23±3.71	35.67±3.45
5	SANS2	75.89±5.03	81.67±5.22	76.48±5.05	54.32±4.25	46.67±3.94	42.00±3.74	40.28±3.66
6	SANS3	87.67±5.40	78.89±5.12	78.56±5.12	57.26±4.37	42.76±3.77	46.01±3.92	41.74±3.73
7	SAMS1	86.23±5.36	82.67±5.25	75.89±5.02	42.67±3.77	36.41±3.48	37.20±3.52	36.73±3.50
8	SAMS2	79.00±5.13	77.56±5.08	73.60±4.95	42.56±3.77	41.89±3.74	42.36±3.76	32.47±3.29
9	SAMS3	79.67±5.15	76.89±5.06	81.34±5.21	46.61±3.94	32.78±3.30	40.78±3.68	41.64±3.72
10	SAKSI	83.67±5.28	77.56±5.08	78.45±5.11	47.81±3.99	47.21±3.97	37.20±3.52	38.63±3.59
11	SAKS2	79.46±5.15	74.80±4.97	79.43±5.14	44.67±3.86	41.23±3.71	38.67±3.59	34.56±3.39
12	SAKS3	82.57±5.25	77.46±5.08	77.45±5.08	43.61±3.81	42.00±3.74	46.01±3.92	32.67±3.30
13	SANaSI	86.46±5.37	76.41±5.05	79.43±5.14	49.56±4.06	46.01±3.92	39.45±3.63	38.93±3.60
14	SANaS2	79.98±5.16	86.42±5.37	78.14±5.10	52.46±4.18	37.20±3.52	41.45±3.72	39.14±3.61
15	SANaS3	85.78±5.35	79.46±5.15	82.33±5.24	57.34±4.37	39.06±3.61	42.16±3.75	42.06±3.74
16	SAVSI	84.56±5.31	77.65±5.09	81.41±5.21	55.45±4.30	42.60±3.77	46.65±3.94	42.74±3.77
17	SAVS2	78.67±5.12	76.61±5.05	78.45±5.11	51.56±4.14	38.82±3.60	43.67±3.81	38.74±3.59
18	SAVS3	72.78±4.92	74.64±4.99	76.34±5.04	48.56±4.02	42.16±3.75	42.56±3.77	36.46±3.48
19	SBTpSI	83.67±5.28	72.63±4.92	84.00±5.29	49.45±4.06	43.21±3.79	41.76±3.73	38.46±3.58
20	SBTpS2	78.67±5.12	78.61±5.12	79.23±5.14	52.43±4.18	52.21±4.17	49.12±4.05	37.61±3.54
21	SBTpS3	73.43±4.95	76.89±5.06	78.34±5.11	57.43±4.37	52.34±4.18	53.56±4.22	35.65±3.45
22	SCTpSI	76.42±5.05	80. 34±5.17	77.92±5.10	61.96±4.54	58.34±4.41	52.89±4.20	42.30±3.75
23	SCTpS2	78.65±5.12	84.78±5.32	75.35±5.01	52.45±4.18	43.87±3.82	38.34±3.57	42.83±3.78
24	SCTpS3	72.65±4.92	78.98±5.13	76.34±5.04	54.64±4.27	42.42±3.76	36.32±3.48	44.42±3.85
25	SDTpSI	77.87±5.09	79.54±5.15	74.24±4.97	52.67±4.19	42.13±3.75	34.67±3.40	41.45±3.72
26	SDTpS2	76.67±5.05	81.67±5.22	78.23±5.11	49.89±4.08	41.48±3.72	43.63±3.81	38.45±3.58
27	SDTpS3	73.56±4.95	84.56±5.31	81.24±5.20	67.78±4.75	42.63±3.77	41.89±3.74	39.23±3.62
28	SDNSI	84.67±5.31	85.56±5.34	82.11±5.23	53.67±4.23	38.42±3.58	37.59±3.54	32.45±3.29

Microbial diversity and uses of microorganisms in the soils of Thiruvarur district

Conti								
29	SDNS2	83.41±5.27	81.56±5.21	81.26±5.20	55.56±4.30	34.57±3.39	41.43±3.72	35.62±3.44
30	SDNS3	78.65±5.12	77.45±5.08	82.11±5.23	52.34±4.18	32.41±3.29	43.58±3.81	38.46±3.58
31	SENSI	79.42±5.14	72.32±4.91	82.34±5.24	45.67±3.90	37.59±3.54	42.56±3.77	37.45±3.53
32	SENS2	78.31±5.11	78.34±5.11	84.34±5.30	51.46±4.14	38.45±3.58	36.41±3.48	36.61±3.49
33	SENS3	79.45±5.15	71.89±4.89	76.89±5.06	53.45±4.22	34.76±3.40	41.89±3.74	32.68±3.30
34	SEMSI	73.46±4.95	76.78±5.05	77.45 ± 5.08	61.45±4.52	36.71±3.50	32.78±3.30	33.89±3.36
35	SEMS2	74.56±4.98	74.86±4.99	79.34±5.14	66.87±4.72	38.63±3.59	37.59±3.54	37.67±3.54
36	SEMS3	78.67±5.12	73.78±4.96	77.65±5.09	57.73±4.39	41.43±3.72	45.56±3.90	36.67±3.50
37	SEKS1	83.67±5.28	76.94±5.06	79.68±5.15	56.35±4.33	44.67±3.86	42.87±3.78	37.23±3.52
38	SEKS2	88.45±5.43	75.67±5.02	80.32±5.17	57.34±4.37	42.32±3.75	41.72±3.73	41.06±3.70
39	SEKS3	81.46±5.21	75.67±5.02	81.32±5.21	61.00±4.51	48.53±4.02	36.71±3.50	42.06±3.74
40	SENaS1	78.46±5.11	75.45±5.01	88.56±5.43	58.46±4.41	42.87±3.78	41.43±3.72	43.56±3.81
41	SENaS2	74.64±4.99	73.45±4.94	85.34±5.33	62.67±4.57	37.76±3.55	44.67±3.86	38.56±3.58
42	SENaS3	83.23±5.27	72.56±4.91	75.34±5.01	58.45±4.41	36.65±3.49	42.32±3.75	36.57±3.49
43	SEVS1	78.00±5.10	77.62±5.08	78.45±5.11	57.43±4.37	34.57±3.39	42.34±3.76	39.42±3.62
44	SEVS2	74.67±4.99	78.56±5.12	77.56±5.08	61.89±4.54	38.68±3.59	47.71±3.99	41.06±3.70
45	SEVS3	82.23±5.23	77.67±5.10	78.45±5.11	52.45±4.18	39.68±3.64	50.42 ± 4.10	50.52 ± 4.10
46	SFTS1	81.67±5.21	79.12±5.13	76.74±5.06	58.34±4.41	40.62±3.68	46.32±3.93	38.65±3.59
47	SFTS2	79.56±5.14	74.89 ± 5.00	83.12±5.26	61.00±4.51	48.42±4.02	48.53±4.02	39.17±3.61
48	SFTS3	75.68 ± 5.02	75.67±5.02	88.46±5.43	44.78±3.86	44.32±3.84	45.21±3.88	38.56±3.58
49	SGTS1	79.67±5.15	77.66±5.09	82.76±5.25	48.35±4.01	41.90±3.73	44.67±3.86	31.78±3.25
50	SGTS2	78.68±5.12	79.56±5.15	76.34±5.04	58.45±4.41	39.42±3.62	42.34±3.76	33.05±3.32
51	SGTS3	81.78±5.22	79.67±5.15	78.34±5.11	63.21±4.59	37.56±3.54	44.67±3.86	32.67±3.30
52	SHTS1	83.57±5.28	78.66±5.12	86.72±5.38	72.00±4.90	36.54±3.49	48.93±4.04	36.74±3.50
53	SHTS2	79.69±5.15	79.78±5.16	83.14±5.26	66.45±4.71	32.61±3.30	39.68±3.64	35.67±3.45
54	SHTS3	78.62±5.12	73.78±4.96	82.00±5.23	62.89±4.58	37.34±3.53	57.65 ± 4.38	38.74±3.59

Table 2.2.3: Micronutrient Analysis of Post Monsoon Seasonal Soil Samples of Thiruvarur District, Tamil Nadu, India

S.No	Sample	Fe (µg/Kg)	Co (µg/Kg)	Cr (µg/Kg)	I (µg/Kg)	Mn (µg/Kg)	Zn (µg/Kg)	Mb(µg/Kg)	Se(µg/Kg)
1	Code	4.00 - 1.10	2 47 . 0 00	2.65.1.10	4.52 . 1.22	2.56.1.00	4.74 . 1.06	2.00 . 1.15	4.70 - 1.27
1	SATpS1	4.23±1.19	2.47±0.90	3.65±1.10	4.53±1.22	3.56±1.09	4.74±1.26	3.98±1.15	4.70±1.25
2	SATpS2	3.23±1.04	2.78±0.96	3.82±1.12	4.87±1.27	3.78±1.12	4.73±1.25	3.21±1.03	4.82±1.27
3	SATpS3	4.26±1.19	2.78±0.96	3.56±1.08	4.24±1.18	3.76±1.12	5.23±1.32	3.68±1.11	4.76±1.26
4	SANS1	3.45±1.07	2.76±0.96	3.68±1.10	4.78±1.26	3.41±1.07	4.76±1.25	3.81±1.13	5.04±1.30
5	SANS2	3.89±1.13	3.78±1.12	3.67±1.10	4.72±1.25	3.63±1.10	4.72±1.25	3.84±1.13	5.26±1.32
6	SANS3	4.53±1.22	3.27 ± 1.04	4.83±1.26	4.76±1.26	3.65±1.10	4.67±1.24	3.46±1.07	5.28 ± 1.33
7	SAMS1	3.45 ± 1.07	3.24 ± 1.03	4.34±1.20	4.67±1.25	3.59±1.09	4.83±1.27	3.69±1.11	3.78±1.12
8	SAMS2	3.76±1.11	3.67±1.10	4.87±1.27	3.89±1.14	3.72±1.11	4.31±1.20	3.28±1.04	3.56±1.08
9	SAMS3	3.43±1.06	4.02±1.15	3.03±1.00	3.42±1.07	3.66±1.10	4.21±1.18	3.87±1.13	3.23±1.03
10	SAKS1	3.23±1.03	4.27±1.19	2.78±0.96	3.46±1.07	3.47±1.07	3.78±1.12	4.26±1.19	3.74±1.12
11	SAKS2	3.67±1.10	3.78±1.12	2.62±0.93	3.34±1.05	3.67±1.11	3.67±1.11	4.83±1.27	3.62±1.10
12	SAKS3	4.12±1.17	2.87±0.97	2.68±0.95	3.89±1.14	3.45±1.07	3.66±1.10	4.27±1.19	3.88±1.14
13	SANaS1	4.00±1.15	2.78±0.96	2.96±0.99	3.78±1.12	3.86±1.13	3.71±1.11	4.21±1.18	4.00±1.15
14	SANaS2	3.29±1.04	2.45±0.90	2.83±0.97	3.67±1.11	3.57±1.09	3.56±1.09	3.41±1.07	4.24±1.19
15	SANaS3	2.86±0.98	2.67±0.94	2.89±0.98	3.78±1.12	3.81±1.13	3.68±1.11	3.78±1.12	4.26±1.19
16	SAVS1	5.34 ± 1.33	2.98±0.99	3.21±1.03	3.67±1.11	3.76±1.12	3.41±1.07	4.69±1.25	3.78±1.12
17	SAVS2	4.78±1.26	3.21±1.03	3.56±1.08	2.87±0.97	3.05±1.01	3.57±1.09	4.78±1.27	3.72±1.11
18	SAVS3	4.27±1.19	3.22±1.03	3.37±1.05	2.45±0.90	2.86±0.98	4.18±1.18	3.62±1.10	3.83±1.12
19	SBTpS1	4.32±1.20	3.42±1.06	4.24±1.19	2.46±0.91	2.89±0.98	4.13±1.17	3.46±1.07	3.46±1.07
20	SBTpS2	4.28±1.19	3.76±1.11	4.45±1.21	2.76±0.96	3.64±1.10	4.56±1.23	3.83±1.13	3.42±1.07
21	SBTpS3	5.21±1.31	4.21±1.18	4.21±1.18	2.87±0.98	3.32±1.05	4.87±1.27	3.76±1.12	3.38±1.06
22	SCTpS1	5.43±1.35	2.56±0.93	3.83±1.13	3.31±1.05	3.54±1.08	4.26±1.19	4.21±1.18	3.46±1.07
23	SCTpS2	4.78±1.26	2.46±0.90	3.78±1.12	3.26±1.04	3.65±1.10	4.67±1.25	3.81±1.13	3.42±1.07
24	SCTpS3	4.32±1.20	3.21±1.03	3.27±1.04	3.45±1.07	3.89±1.14	4.56±1.23	3.89±1.14	3.74±1.12
25	SDTpS1	4.34±1.20	3.42±1.07	3.06±1.00	3.56±1.09	4.64±1.24	3.78±1.12	4.69±1.25	3.68±1.11
26	SDTpS2	3.67±1.10	3.67±1.10	2.98±0.99	3.33±1.05	4.35±1.20	3.67±1.11	4.27±1.19	3.45±1.07
27	SDTpS3	3.78±1.12	4.21±1.18	2.87±0.98	3.21±1.03	4.21±1.18	3.72±1.11	4.21±1.18	3.76±1.12
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28	SDNS1	3.45±1.07	4.53 ± 1.22	3.56±1.09	3.67±1.22	3.81±1.13	3.18±1.03	3.46±1.07	3.67±1.11
29	SDNS2	3.89±1.14	4.44±1.22	3.67±1.11	3.46±1.07	3.96±1.15	3.16±1.03	3.29±1.05	3.44±1.07
30	SDNS3	3.67±1.10	3.62±1.10	2.89±0.98	3.83±1.13	3.68±1.11	3.21±1.03	3.21±0.77	3.67±1.11
31	SENS1	3.48±1.08	3.41±1.07	3.89±1.14	3.67±1.11	3.89±1.14	3.28±1.04	3.21±1.73	3.46±1.07
32	SENS2	3.18±1.03	3.21±1.03	4.38±1.21	4.67±1.25	4.19±1.18	3.49±1.08	3.46±1.07	3.42±1.07
33	SENS3	3.42±1.06	3.36±1.06	4.22±1.19	4.61±1.24	4.12±1.17	3.67±1.11	3.41±1.07	3.81±1.13
34	SEMS1	4.68±1.25	3.52±1.08	4.26±1.19	4.73±1.25	4.36±1.20	3.45±1.07	3.73±1.11	3.56±1.09
35	SEMS2	4.62±1.24	3.56±1.09	4.06±1.16	4.78±1.26	4.21±1.18	3.76±1.12	3.61±1.09	3.98±1.15
36	SEMS3	4.73±1.25	3.05±1.01	3.56±1.09	3.89±1.14	3.68±1.11	3.41±1.07	3.56±1.09	3.78±1.12
37	SEKS1	4.37±1.21	4.21±1.18	3.67±1.11	3.78±1.12	3.67±1.11	3.72±1.11	4.68±1.25	4.19±1.18
38	SEKS2	3.89±1.14	4.16±1.17	3.78±1.12	3.63±1.05	3.86±1.13	3.46±1.07	4.61±1.24	4.17±1.18
39	SEKS3	3.54±1.08	4.26±1.19	4.21±1.40	3.86±1.13	4.26±1.19	3.61±1.09	4.63±1.24	4.08±1.17
40	SENaS1	3.62±1.10	2.86±0.98	3.11±1.02	4.23±1.18	4.34±1.20	5.23±1.32	4.52±1.23	4.02±1.15
41	SENaS2	3.74±1.12	2.72±0.95	2.69±0.95	4.22±1.09	4.56±1.23	5.26±1.32	4.45±1.21	3.46±1.07
42	SENaS3	3.76±1.12	2.56±0.92	3.58±1.09	4.24±1.19	3.68±1.11	4.98±1.29	4.73±1.25	3.78±1.12
43	SEVS1	3.56±1.09	2.78±0.96	3.56±1.09	4.67±1.25	3.56±1.09	4.62±1.24	4.78±1.26	3.89±1.13
44	SEVS2	3.44±1.07	2.67±0.94	3.67±1.11	3.78±1.12	3.78±1.12	3.99±1.15	4.56±1.23	3.78±1.12
45	SEVS3	3.78±1.12	3.81±1.12	3.36±1.05	3.62±1.10	4.42±1.21	3.83±1.13	4.67±1.24	3.64±1.10
46	SFTS1	3.46±1.07	3.56±1.09	3.01±1.00	3.78±1.12	4.63±1.24	3.78±1.12	5.08±1.30	3.45±1.07
47	SFTS2	4.10±1.37	3.52±1.08	3.06±1.01	3.65±1.10	4.56±1.23	3.69±1.11	5.27 ± 1.32	3.12±1.02
48	SFTS3	4.28±1.43	3.57±1.09	3.78±1.12	3.78±1.12	3.76±1.12	4.67±1.25	5.23±1.32	3.76±1.12
49	SGTS1	3.78±1.12	3.67±1.06	4.02±1.15	3.28±1.05	3.68±1.11	4.91±1.28	4.21±1.18	3.47±1.07
50	SGTS2	3.52±1.08	3.71±1.11	3.45±1.07	3.62±1.10	3.78±1.12	5.02±1.29	4.28±1.19	3.43±1.14
51	SGTS3	3.69±1.11	4.06±1.07	3.78±1.22	3.89±1.30	3.82±1.13	5.03±1.29	4.23±1.19	3.76±1.12
52	SHTS1	4.87±1.27	4.02±1.16	4.94±1.28	3.56±1.09	4.83±1.27	5.26±1.32	5.23±1.32	4.67±1.25
53	SHTS2	4.26±1.19	3.89±1.14	4.89±1.28	3.82±1.13	4.46±1.22	5.34 ± 1.33	5.04±1.30	4.42±1.21
54	SHTS3	4.37±1.21	3.93±1.14	5.20 ± 1.11	3.67±1.11	4.53±1.23	5.06±1.30	5.46±1.35	4.76±1.25

Table 2.3.1: Physical parameter Analysis of Summer Seasonal Soil Samples of Thiruvarur District, Tamil Nadu

S.No	Sample	Colour	Size (µm)	pН	Temperature	Moisture	Loss of	Electrical
	Code				(°C)	(%)	ignition (%)	conductivity (dsm- ¹)
1	SATpS1	Dark grey	423.12±11.87	7.2±1.55	37.2±3.52	25.87±2.93	35.65±3.44	0.32
2	SATpS2	Dark grey	398.23±11.52	7.6±1.59	38.6±3.59	24.56±2.86	36.71±3.49	0.42
3	SATpS3	Dark grey	476.34±12.60	7.4±1.57	37.4±3.53	26.78±2.98	38.78±3,59	0.36
4	SANS1	Yellowish red	442.54±12.14	7.7±1.60	37.8±3.55	24.78±2.87	32.56±3.29	0.28
5	SANS2	Yellowish red	378.45±11.23	7.4±1.57	40.2±3.66	28.45±3.07	33.65±3.34	0.19
6	SANS3	Yellowish red	321.67±10.35	7.6±1.59	36.7±3.50	25.67±2.92	32.67±3.30	0.18
7	SAMS1	Dark grey	421.56±11.85	7.4±1.57	38.4±3.58	27.61±3.03	33.41±3.33	0.21
8	SAMS2	Brownish yellow	427.34±11.93	7.4±1.57	41.9±3.74	25.63±2.92	35.62±3.44	0.23
9	SAMS3	Brownish Yellow	426.34±11.92	7.3±1.55	38.3±3.57	28.64±3.08	33.76±3.35	0.24
10	SAKS1	Yellow	374.27±11.16	7.6±1.59	38.4±3.57	29.41±3.13	34.56±3.39	0.28
11	SAKS2	Yellow	384.50±11.32	7.4±1.57	37.5±3.53	28.45±3.07	36.67±3.49	0.32
12	SAKS3	Yellow	382.45±11.29	7.3±1.56	38.7±3.59	28.56±3.08	32.56±3.29	0.32
13	SANaS1	Greyish brown	421.67±11.85	7.5±1.58	38.6±3.58	25.89±2.93	34.67±3.39	0.42
14	SANaS2	Greyish brown	428.30±11.94	7.2±1.55	37.5±3.53	22.56±2.74	36.56±3.49	0.43
15	SANaS3	Greyish brown	387.21±11.36	7.7±1.60	38.4±3.57	23.78±2.81	35.42±3.43	0.36
16	SAVS1	Greyish brown	382.45±11.29	7.6±1.59	37.6±3.54	22.45±2.73	33.45±3.33	0.34
17	SAVS2	Brownish yellow	411.78±11.71	7.8±1.61	38.6±3.58	24.67±2.86	32.72±3.30	0.34
18	SAVS3	Greyish brown	387.31±11.36	7.2±1.55	37.3±3.52	28.56±3.08	31.09±3.21	0.37
19	SBTpS1	Dark brown	384.56±11.32	7.4±1.57	39.4±3.62	26.78±2.98	32.47±3,28	0.42
20	SBTpS2	Dark brown	322.57±10.36	7.5±1.58	36.7±3.49	27.43±3.02	33.76±3.35	0.42
21	SBTpS3	Dark brown	421.78±11.85	7.6±1.59	32.8±3.30	26.78±2.98	36.72±3.49	0.29
22	SCTpS1	Dark yellowish brown	431.56±11.99	7.6±1.59	36.7±3.49	25.61±2.92	37.68±3.54	0.28
23	SCTpS2	Dark yellowish brown	432.56±12.01	7.4±1.57	38.4±3.57	28.61±3.08	36.73±3.49	0.31
24	SCTpS3	Dark yellowish brown	446.67±12.20	7.4±1.57	38.5±3.57	22.89±2.76	34.42±3.38	0.34
25	SDTpS1	Greyish brown	456.67±12.33	7.4±1.57	36.7±3.49	23.67±2.80	36.42±3.48	0.28
26	SDTpS2	Greyish brown	431.63±11.99	7.6±1.59	34.2±3.76	24.62±2.86	31.67±3.24	0.29
27	SDTpS3	Greyish brown	408.17±11.66	7.4±1.57	38.7±3.59	28.73±3.09	37.63±3.54	0.31

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28	SDNS1	Pale brown	426.00±11.91	7.2±1.55	38.5±3.58	28.67 ± 3.09	32.46±3.28	0.33
29	SDNS2	Pale brown	356.67±10.90	8.3 ± 1.66	39.7±3.63	28.67±3.09	37.56±3.53	0.29
30	SDNS3	Pale brown	361.46±10.98	8.2±1.65	36.3±3.47	26.67±2.98	36.72±3.49	0.28
31	SENS1	Pale brown	426.44±11.92	7.7±1.60	39.4±3.62	24.87±2.87	32.45±3.28	0.31
32	SENS2	Pale brown	354.12±10.86	7.3±1.56	40.5±3.67	23.68±2.80	34.62±3.39	0.34
33	SENS3	Pale brown	378.23±11.23	7.3±1.56	41.8±3.73	23.54±2.80	35.51±3.44	0.31
34	SEMS1	Dark grey	364.32±11.02	7.0±1.52	38.6±3.58	23.41±2.79	36.32±3.47	0.29
35	SEMS2	Dark grey	378.41±11.23	7.0±1.52	37.6±3.54	25.62±2.92	35.67±3.44	0.43
36	SEMS3	Dark grey	384.45±11.32	7.0±1.52	32.8±3.30	27.62±3.03	32.56±3.29	0.42
37	SEKS1	Dark grey	421.56±11.85	7.6±1.59	38.7±3.59	26.45±2.96	35.45±3.43	0.35
38	SEKS2	Dark grey	465.45±12.45	7.2±1.55	38.6±3.57	29.45±3.13	33.56±3.34	0.32
39	SEKS3	Dark grey	438.41±12.09	7.2±1.55	37.9±3.55	26.67±2.98	32.67±3.30	0.34
40	SENaS1	Greyish brown	398.23±11.52	7.2±1.55	38.9 ± 3.60	25.63±2.92	34.67±3.39	0.41
41	SENaS2	Greyish brown	374.56±11.17	7.6±1.59	36.1±3.46	22.67±2.74	36.23±3.47	0.23
42	SENaS3	Greyish brown	368.45±11.08	7.6±1.59	38.5 ± 3.58	25.56±2.91	35.41±3.43	0.28
43	SEVS1	Greyish brown	382.34±11.28	7.6±1.59	37.2 ± 3.52	24.67±2.86	36.42±3.48	0.31
44	SEVS2	Greyish brown	365.42±11.03	7.4±1.57	38.2 ± 3.56	28.56±3.08	35.61±3.44	0.29
45	SEVS3	Greyish brown	372.34±11.14	7.6±1.59	37.7±3.54	25.45±2.91	37.54±3.53	0.28
46	SFTS1	Dark grey	387.28±11.36	7.4±1.57	38.2±3.56	24.56±2.86	32.65±3.29	0.28
47	SFTS2	Dark grey	402.23±11.58	7.5±1.58	38.5 ± 3.58	25.56±2.91	34.78±3.40	0.31
48	SFTS3	Dark grey	367.78±11.07	7.8±1.62	38.4±3.57	22.72±2.75	32.56±3.29	0.34
49	SGTS1	Dark greyish brown	358.34±10.92	7.8±1.62	37.9±3.55	23.56±2.80	36.21±3.47	0.42
50	SGTS2	Dark greyish brown	421.62±11.85	7.8±1.62	38.2±3.56	27.61±3.03	33.41±3.33	0.34
51	SGTS3	Dark greyish brown	446.36±12.20	7.9±1.62	39.4±3.62	28.62±3.08	34.56±3.39	0.42
52	SHTS1	Light grey	441.23±12.13	7.8±1.62	38.7±3.59	22.56±2.74	36.34±3.48	0.28
53	SHTS2	Light grey	423.03±11.87	7.8±1.62	36.4±3.48	21.67±2.68	33.56±3.34	0.25
54	SHTS3	Light grey	378.32±11.23	7.8±1.62	38.7±3.59	22.56±2.74	32.64±3.29	0.27

Table 2.3.2: Macronutrient Analysis of Summer Seasonal Soil Samples of Thiruvarur district, Tamil Nadu

S.No	Sample	N (kg/ac)	NO ₃ (kg/ac)	NH ₄ (kg/ac)	P (kg/ac)	K (kg/ac)	S (kg/ac)	H (kg/a)
	Code							
1	SATpSI	80.67±5.18	83.67±5.28	79.34±5.14	48.38±4.01	30.56±3.19	32.48±3.29	32.46±3.28
2	SATpS2	77.98±5.09	81.60±5.21	78.32±5.10	46.32±3.92	30.67±3.92	34.27±3.37	37.21±3.52
3	SATpS3	78.98±5.13	78.56±5.11	80.34±5.17	47.23±3.96	31.74±3.25	32.76±3.30	32.47±3.28
4	SANSI	81.89±5.22	76.45±5.04	81.67±5.21	44.78±3.86	32.46±3.28	37.45±3.53	37.45±3.53
5	SANS2	82.67±5.24	77.78±5.09	86.23 ± 5.36	46.37±3.93	37.41±3.53	34.78±3.40	36.41±3.48
6	SANS3	79.65±5.15	81.78±5.22	83.45±5.27	47.78±3.99	35.78±3.45	37.32±3.33	38.34±3.57
7	SAMSI	80.34±5.17	78.98±5.13	78.98±5.13	39.46±3.62	37.41±3.53	36.45±3.48	36.56±3.49
8	SATMS2	79.67±5.15	79.67±5.15	77.32±5.07	42.87±3.78	36.32±3.47	36.34±3.47	38.46±3.58
9	SAMS3	79.78±5.15	79.56±5.14	76.23±5.04	44.89±3.86	37.46±3.53	32.31±3.28	41.35±3.71
10	SAKSI	81.67±5.21	76.89±5.06	80.35±5.17	46.78±3.94	34.88±3.40	35.67±3.44	38.41±3.57
11	SAKS2	79.98±5.16	81.23±5.20	81.43±5.20	48.92±4.03	32.63±3.29	36.98±3.51	42.62±3.76
12	SAKS3	78.56±5.11	80.34±5.17	79.63±5.15	5084±4.11	34.56±3.39	35.56±3.44	46.21±3.92
13	SANaSI	74.67±4.98	82.78±5.25	76.23±5.04	48.45±4.01	37.42±3.53	40.32±3.66	38.48±3.58
14	SANaS2	75.45±5.01	79.34±5.14	78.45±5.11	54.76±4.27	37.56±3.53	39.45±3.62	35.23±3.42
15	SANaS3	73.41±4.94	78.45±5.11	80.32±5.17	53.67±4.22	32.57±3.29	36.67±3.49	32.41±3.28
16	SAVSI	78.56±5.11	78.00±5.09	81.79±5.22	51.89±4.15	38.41±3.57	38.32±3.57	31.45±3.23
17	SAVS2	79.67±5.15	73.56±4.95	78.45±5.11	48.56±4.02	37.21±3.52	35.67±3.44	37.51±3.53
18	SAVS3	78.56±5.11	72.62±4.92	77.56±5.08	43.89±3.82	36.45±3.48	32.68±3.30	35.23±3.42
19	SBTpSI	81.24±5.20	78.56±5.11	76.89±5.06	45.61±3.89	34.56±3.39	37.78±3.54	38.26±3.57
20	SBTpS2	79.78±5.15	77.67±5.08	84.56±5.30	42.78±3.77	32.45±3.28	38.45±3.58	34.34±3.38
21	SBTpS3	78.56±5.11	74.78±4.99	83.56±5.27	47.45±3.97	33.42±3.33	31.67±3.24	32.46±3.28
22	SCTpSI	80.67±5.18	80.78±5.18	81.25±5.20	46.78±3.94	32.56±3.29	32.41±3.28	36.34±3.48
23	SCTpS2	80.56±5.18	81.34±5.20	83.56±5.27	50.89±4.11	34.56±3.39	33.67±3.35	32.42±3.28
24	SCTpS3	78.56±5.11	82.78±5.25	80.84±5.19	51.78±4.13	35.56±3.44	37.68±3.54	34.61±3.39
25	SDTpSI	76.45±5.04	84.78±5.31	81.98±5.22	53.89±4.23	32.87±3.31	37.68±3.54	32.45±3.28
26	SDTpS2	79.78±5.15	83.67±5.28	80.45±5.17	52.96±4.20	33.65±3.34	36.67±3.49	32.47±3.28
27	SDTpS3	78.34±5.11	81.56±5.21	79.56±5.14	48.97±4.04	32.67±3.30	37.12±3.51	34.26±3.37
28	SDNSI	84.00±5.29	80.04±5.16	79.45±5.14	48.92±4.03	41.65±3.72	38.41±3.57	33.21±3.32

Conti								
29	SDNS2	83.78±5.28	80.34±5.17	80.56±5.18	44.67±3.85	33.61±3.34	36.67±3.49	36.42±3.48
30	SDNS3	84.56±5.30	82.45±5.24	78.67±5.12	43.78±3.82	35.63±3.44	37.41±3.53	31.92±3.26
31	SENSI	82.31±5.23	83.89±5.28	75.67±5.02	47.78±3.99	32.45±3.28	37.24±3.53	32.45±3.28
32	SENS2	78.52±5.11	78.91±5.12	80.34±5.17	49.64±4.06	34.52±3.39	38.64±3.58	36.41±3.48
33	SENS3	76.81±5.05	87.64±5.40	82.45±5.24	56.78±4.35	32.78±3.30	38.45±3.58	32.45±3.28
34	SEMSI	79.56±5.14	76.45±5.04	81.00±5.19	53.78±4.23	34.56±3.39	38.34±3.57	33.48±3.34
35	SEMS2	81.67±5.21	81.45±5.21	83.05±5.26	58.56±4.41	30.57±3.19	35.45±3.43	36.32±3.47
36	SEMS3	82.43±5.24	73.87±4.96	82.70±5.25	57.45±4.37	31.78±3.25	36.56±3.49	40.23±3.66
37	SEKS1	81.26±5.20	76.56±5.05	76.93±5.06	52.67±4.19	33.67±3.35	37.63±3.54	41.34±3.71
38	SEKS2	83.78±5.28	79.42±5.14	77.58±5.08	51.78±4.15	34.62±3.39	38.74±3.59	38.21±3.56
39	SEKS3	76.89±5.06	76.91±5.06	78.93±5.12	53.65±4.22	33.41±3.33	36.43±3.48	34.67±3.39
40	SENaS1	77.56±5.08	80.78±5.18	74.59±4.98	54.78±4.27	36.45±3.48	37.45±3.53	36.28±3.47
41	SENaS2	79.56±5.14	82.67±5.24	78.67±5.12	57.34±4.37	33.42±3.33	38.43±3.57	37.43±3.53
42	SENaS3	78.67±5.12	83.42±5.27	76.89±5.06	48.78±4.03	32.46±3.28	36.72±3.49	34.00±3.36
43	SEVS1	80.89±5.19	82.78±5.25	77.45±5.08	42.98±3.78	33.56±3.34	34.84±3.40	32.56±3.29
44	SEVS2	82.06±5.23	81.78±5.22	79.45±5.14	46.73±3.94	36.41±3.48	34.62±3.39	33.56±3.34
45	SEVS3	83.46±5.27	80.13±5.16	77.67±5.08	49.67±4.06	38.42±3.57	32.64±3.29	36.21±3.47
46	SFTS1	78.61±5.11	76.78±5.05	79.56±5.14	48.56±4.02	37.56±3.53	33.68±3.35	36.78±3.50
47	SFTS2	79.56±5.14	79.89±5.16	80.45±5.17	49.67±4.06	38.65±3.58	36.73±3.49	35.56±3.44
48	SFTS3	79.67±5.15	76.89±5.06	82.56±5.24	52.78±4.19	36.45±3.48	38.42±3.57	32.98±3.31
49	SGTS1	78.56±5.11	78.84±5.12	83.21±5.26	56.82±4.35	37.54±3.53	37.56±3.53	34.32±3.38
50	SGTS2	79.56±5.14	79.56±5.14	79.45±5.14	51.28±4.13	36.76±3.50	34.82±3.40	34.32±3.38
51	SGTS3	78.61±5.11	78.45±5.11	76.67±5.05	51.98±4.16	38.61±3.58	32.56±3.29	35.38±3.43
52	SHTS1	82.67±5.24	81.93±5.22	78.56±5.11	54.34±4.25	44.56±3.85	33.16±3.32	34.67±3.39
53	SHTS2	83.51±5.27	78.78±5.12	77.45±5.08	52.34±4.17	43.61±3.81	32.45±3.28	37.21±3.52
54	SHTS3	80.54±5.18	89.23±5.45	79.56±5.14	53.89±4.23	42.56±3.76	31.72±3.24	35.56±3.44

Table 2.3.3: Micronutrient Analysis of Summer Seasonal Soil Sample Located at Thiruvarur District, Tamil nadu

S.No	Sample	Fe (µg/Kg)	Co (µg/Kg)	Cr (µg/Kg)	I (µg/Kg)	Mn (µg/Kg)	Zn (µg/Kg)	Mb(µg/Kg)	Se(µg/Kg)
	Code								
1	SATpSI	4.23±1.18	3.78±1.12	4.01±1.15	2.64±0.93	3.56±1.08	4.21±1.18	2.78±0.96	3.01±1.00
2	SATpS2	4.02±1.15	3.67±1.10	4.32±1.12	2.08±0.83	3.82±1.12	4.35±1.20	2.18±0.85	3.28±1.04
3	SATpS3	4.26±1.19	3.39±1.06	4.21±1.18	2.67±0.94	3.41±1.06	2.89±0.98	2.76±0.95	3.29±1.04
4	SANSI	3.78±1.12	2.89±0.98	4.89±1.27	2.45±0.90	3.21±1.03	3.67±1.10	2.67±0.94	3.17±1.02
5	SANS2	3.56±1.08	2.78±0.96	5.03 ± 1.29	1.89±0.79	3.64±1.10	3.83±1.12	2.98±0.99	3.18±1.02
6	SANS3	3.82±1.27	2.73±0.95	4.89±1.27	2.05±0.82	3.56±1.08	4.56±1.23	2.78±0.96	2.98±0.99
7	SAMSI	3.67±1.10	3.67±1.10	3.45±1.07	2.05±0.82	4.56±1.23	3.78±1.12	2.68±0.94	2.86 ± 0.97
8	SAMS2	2.98±0.99	3.56±1.08	3.20±1.03	1.98±0.81	4.08±1.16	3.89±1.13	2.61±0.93	2.34±0.88
9	SAMS3	2.78±0.96	4.01±1.15	3.43±1.06	3.56±1.08	4.87 ± 1.27	3.91±1.14	2.56±0.92	3.78±1.12
10	SAKSI	3.01±1.00	4.22±1.18	3.57±1.09	3.13±1.02	4.67±1.24	4.06±1.16	2.56±0.92	3.21±1.03
11	SAKS2	3.04±1.01	4.67±1.24	3.44±1.07	4.02±1.15	2.89±0.98	5.02±1.29	2.78±0.96	3.27±1.04
12	SAKS3	3.28±1.04	3.67±1.10	3.89±1.13	4.32±1.20	2.87±0.97	4.82±1.26	3.01±1.00	2.98±0.99
13	SANaSI	3.67±1.10	3.56±1.08	4.00±1.15	3.78±1.12	2.69±0.94	3.89±1.13	2.97±0.99	2.24±0.86
14	SANaS2	3.87±1.13	3.87±1.13	4.02±1.15	3.26±1.04	2.78±0.96	3.67±1.10	3.08±1.01	3.78±1.12
15	SANaS3	4.67±1.24	3.45±1.07	4.05±1.16	3.56±1.08	2.57±0.92	3.21±1.03	2.89±0.98	3.46±1.07
16	SAVSI	4.62±1.24	3.78±1.12	3.89±1.13	2.87±0.97	2.87±0.97	3.67±1.10	3.11±1.01	3.56±1.08
17	SAVS2	2.89±0.98	3.98±1.15	3.98±1.15	2.36±0.88	2.94±0.98	4.56±1.23	2.34±0.88	4.02 ± 1.15
18	SAVS3	2.78±0.96	4.02±1.15	4.02±1.15	2.86±0.97	3.87±1.13	3.67±1.10	2.56±0.92	4.14±1.17
19	SBTpSI	2.89±0.98	4.12±1.17	2.88 ± 0.97	2.56±0.92	3.56±1.08	4.04±1.16	2.67±0.94	4.78±1.26
20	SBTpS2	3.13±1.02	2.89±0.98	2.76±0.97	2.81±0.96	3.63±1.10	3.78±1.12	2.78±0.96	3.98±1.15
21	SBTpS3	3.45±1.07	2.87±0.97	3.84±1.13	3.05±1.00	3.56±1.08	3.67±1.10	2.89±0.98	2.78 ± 0.96
22	SCTpSI	4.67±1.24	2.67±0.94	3.78±1.12	3.05±1.00	2.89±0.98	2.89±0.98	2.92±0.98	3.29±1.04
23	SCTpS2	3.67±1.10	2.83±0.97	3.67±1.10	3.12±1.01	2.78±0.96	2.67±0.94	2.83±0.97	3.67±1.10
24	SCTpS3	2.89±0.98	3.65±1.10	4.02±1.15	3.54±1.08	2.92±0.98	3.01±1.00	2.78±0.96	3.51±1.08
25	SDTpSI	2.78±0.92	3.44±1.07	4.12±1.17	3.25±1.04	2.56±0.92	3.07±1.01	2.68±0.94	3.67±1.10
26	SDTpS2	3.98±1.15	3.76±1.11	4.28±1.19	4.21±1.18	2.84±0.97	4.89 ± 1.27	3.03±1.00	2.89 ± 0.98
27	SDTpS3	4.02±1.15	3.78±1.12	4.02±1.15	4.21±1.18	2.45±0.90	3.89±1.13	3.92±1.14	2.87±0.97
28	SDNSI	4.28±1.19	3.56±1.08	2.78±0.96	3.34±1.05	2.78±0.96	3.78±1.12	3.78±1.12	1.98±0.81

Conti	Conti								
29	SDNS2	4.17±1.17	3.84±1.13	2.78±0.96	3.23±1.03	2.86±0.97	3.98±1.15	2.89±0.98	1.78±0.77
30	SDNS3	3.78±1.12	3.67±1.10	2.87±0.97	3.89±1.13	2.67±0.94	3.67±1.10	3.44±1.07	1.89±0.79
31	SENSI	3.63±1.10	3.45 ± 1.07	3.91±1.14	3.45±1.07	2.83±0.97	3.78±1.12	3.44±1.07	2.03±1.00
32	SENS2	3.67±1.10	3.67±1.10	3.45±1.07	3.43±1.06	2.89 ± 0.98	3.29 ± 1.04	3.44±1.07	2.89±0.98
33	SENS3	3.81±1.12	4.09±1.16	4.92±1.28	3.46±1.07	2.78±0.96	3.26±1.04	2.78±0.96	2.03±0.82
34	SEMSI	3.67±1.10	4.12±1.17	3.78±1.12	3.78±1.12	3.01±1.00	3.45 ± 1.07	2.78±0.96	2.78±0.96
35	SEMS2	4.04±1.16	4.28±1.19	4.02±1.15	4.91±1.27	3.15±1.02	2.88 ± 0.97	3.89±1.13	2.67±0.94
36	SEMS3	4.05±1.16	3.46±1.07	3.89±1.13	4.72±1.25	3.24±1.03	2.89 ± 0.98	3.89±1.13	2.98±0.99
37	SEKS1	3.78±1.12	5.02±1.29	4.02±1.15	4.34±1.20	3.28±1.04	2.34 ± 0.88	2.98±0.99	2.67±0.94
38	SEKS2	3.61±1.09	4.78±1.26	3.56±1.08	4.67±1.24	3.21±1.03	2.45±0.90	2.89±0.98	2.32±0.87
39	SEKS3	3.78±1.12	4.56±1.23	3.76±1.11	4.32±1.20	3.45±1.07	2.43±0.90	3.78±1.12	2.43±0.90
40	SENaS1	4.78±1.26	3.67±1.10	3.56±1.08	3.78±1.12	3.56±1.08	2.45±0.90	4.02±1.15	2.78±0.96
41	SENaS2	4.01±1.15	3.56±1.08	3.89±1.13	3.56±1.08	4.06±1.16	4.67±1.24	3.67±1.10	2.76±0.95
42	SENaS3	3.94±1.14	3.78±1.12	4.67±1.24	4.67±1.24	4.18±1.18	3.78±1.12	2.98±0.99	3.04±.100
43	SEVS1	3.67±1.10	4.67±1.22	4.62±1.24	4.53±1.22	4.67±1.24	3.81±1.12	4.78 ± 1.26	3.89 ± 1.13
44	SEVS2	3.54±1.08	4.52±1.22	3.89±1.13	3.89±1.13	4.42±1.21	3.56±1.08	4.29±1.19	3.78±1.12
45	SEVS3	3.07±1.01	3.67±1.10	3.78±1.12	3.78±1.11	3.89±1.13	3.23 ± 1.03	3.43±1.06	3.67±1.10
46	SFTS1	4.01±1.15	4.02±1.15	4.03±1.15	3.67±1.10	3.45±1.07	3.89 ± 1.13	3.28±1.04	3.23±1.03
47	SFTS2	2.76±0.95	4.98 ± 1.28	3.67±1.10	3.45±1.07	3.65±1.10	2.89 ± 0.98	2.76±0.95	3.67±1.10
48	SFTS3	2.94±0.98	5.05±1.29	3.56±1.08	3.67±1.10	3.76±1.11	2.67±0.94	2.67±0.94	2.88±0.97
49	SGTS1	2.87±0.95	4.35±1.20	4.06±1.16	4.05±1.16	3.78±1.12	2.78±0.96	2.89±0.98	2.67±0.94
50	SGTS2	3.05±1.00	2.96±0.99	4.78±1.26	3.87±1.13	2.98±0.99	3.89±1.13	3.45±1.07	3.09±1.01
51	SGTS3	3.78±1.12	3.67±1.10	3.98±1.15	4.32±1.20	2.56±0.92	3.67±1.10	3.02±1.00	3.21±1.03
52	SHTS1	3.82±1.38	4.45±1.21	3.03±1.00	4.38±1.20	2.78±0.96	3.45±1.07	3.67±1.10	3.67±1.10
53	SHTS2	4.80 ± 1.26	2.67±0.94	4.78±1.26	4.02±1.15	3.83±1.12	3.42±1.06	3.45±1.07	2.89±0.98
54	SHTS3	4.21±1.18	3.67±1.10	3.78±1.12	4.89±1.27	4.21±1.18	3.21±1.03	3.89±1.13	2.98±0.99

Table 2.4.1: Physical parameter Analysis of Pre Monsoon Seasonal Soil Samples of Thiruvarur District, Tamil Nadu, India

S.No	Sample	Colour	Size (µm)	pН	Temperature	Moisture	Loss of	Electrical
	Code				(° C)	(%)	ignition (%)	conductivity
								(dsm- ¹)
1	SATpS1	Dark grey	365.4±11.03	7.6±1.59	34.21±3.37	32.21±3.27	39.67±3.63	0.34
2	SATpS2	Dark grey	367.5±11.06	7.4±1.57	32.60±3.29	30.31±3.17	42.56±3.76	0.45
3	SATpS3	Dark grey	442.4±12.14	7.3±1.55	30.56±3.19	28.31±3.07	44.78±3.86	0.34
4	SANS1	Yellowish red	461.3±12.40	7.6±1.59	35.89±3.45	31.78±3.25	41.67±3.72	0.28
5	SANS2	Yellowish red	472.2±12.54	6.8±1.50	34.90±3.41	28.78±3.09	40.67±3.68	0.34
6	SANS3	Yellowish red	452.4±12.28	7.2±1.54	30.41±3.18	27.78±3.04	41.78±3.73	0.45
7	SAMS1	Dark grey	448.5±12.22	7.1±1.53	37.04±3.51	26.89±2.99	46.78±3.94	0.26
8	SAMS2	Brownish yellow	472.2±12.54	7.3±1.55	31.78±3.25	30.67±3.19	32.67±3.30	0.45
9	SAMS3	Brownish Yellow	462.4±12.41	7.5±1.58	35.76±3.45	31.78±3.25	31.78±3.25	<mark>0.56</mark>
10	SAKS1	Yellow	483.6±12.69	6.8±1.50	34.56±3.39	33.87±3.36	32.41±3.28	0.28
11	SAKS2	Yellow	436.4±12.06	6.5±1.47	32.42±3.28	31.56±3.24	39.21±3.61	0.26
12	SAKS3	Yellow	467.5±12.48	7.2±1.54	38.45±3.58	28.78±3.09	38.34±3.57	0.27
13	SANaS1	Greyish brown	476.2±12.59	7.3±1.55	37.42±3.53	22.43±2.73	36.46±3.48	0.27
14	SANaS2	Greyish brown	502.6±12.94	7.5±1.58	36.89±3.50	26.78±2.98	35.42±3.43	0.34
15	SANaS3	Greyish brown	512.4±13.06	7.4±1.57	37.67±3.54	27.63±3.03	34.57±3.39	0.42
16	SAVS1	Greyish brown	486.5±12.73	7.3±1.55	35.87±3.45	39.20 ± 3.61	33.78±3.35	0.28
17	SAVS2	Brownish yellow	472.5±12.54	7.4±1.57	36.78±3.50	30.56±3.19	34.67±3.39	0.26
18	SAVS3	Greyish brown	438.4±12.08	6.7±1.49	31.98±3.26	31.78±3.25	32.89±3.31	0.42
19	SBTpS1	Dark brown	389.5±11.39	6.8±1.50	34.67±3.39	23.98±2.82	38.46±3.58	0.43
20	SBTpS2	Dark brown	374.5±11.17	7.4±1.57	35.56±3.44	32.00±3.26	31.67±3.24	0.35
21	SBTpS3	Dark brown	387.2±11.36	6.4±1.46	34.67±3.39	34.17±3.37	35.67±3.44	0.35
22	SCTpS1	Dark yellowish brown	387.3±11.36	8.3 ± 1.66	36.89±3.50	32.67±3.30	37.42±3.53	0.42
23	SCTpS2	Dark yellowish brown	412.2±11.72	8.2±1.65	37.45±3.53	33.78±3.35	41.65±3.72	0.46
24	SCTpS3	Dark yellowish brown	387.3±11.36	8.1±1.64	37.45±3.53	32.78±3.30	35.67±3.44	0.41
25	SDTpS1	Greyish brown	412.6±11.72	8.2±1.65	36.56±3.49	28.78±3.09	36.56±3.49	0.46
26	SDTpS2	Greyish brown	387.5±11.36	7.8±1.61	37.45±3.53	34.71±3.40	38.67±3.59	0.27
27	SDTpS3	Greyish brown	362.6±10.99	7.4±1.57	35.89±3.45	32.34±3.28	37.78±3.54	0.31

Conti	Conti								
28	SDNS1	Pale brown	385.4±11.33	7.4±1.57	36.42±3.48	31.41±3.23	35.67±3.44	0.37	
29	SDNS2	Pale brown	472.6±12.55	7.7±1.60	34.54±3.39	26.32±2.96	33.41±3.33	0.31	
30	SDNS3	Pale brown	482.5±12.68	6.4±1.46	32.67±3.30	27.84±3.04	36.56±3.49	0.28	
31	SENS1	Pale brown	473.4±12.56	7.2±1.54	35.56±3.44	28.45±3.07	37.86±3.55	0.29	
32	SENS2	Pale brown	462.5±12.41	7.4±1.57	35.44±3.43	31.45±3.23	36.87±3.50	0.34	
33	SENS3	Pale brown	473.2±12.55	8.1±1.64	34.96±3.41	29.31±3.12	46.34±3.93	0.29	
34	SEMS1	Dark grey	461.7±12.40	7.8±1.61	37.89±3.55	30.21±3.17	46.76±3.94	0.28	
35	SEMS2	Dark grey	389.2±11.39	7.2±1.54	38.67±3.59	34.26±3.37	52.21±4.17	0.31	
36	SEMS3	Dark grey	402.6±11.58	7.3±1.55	31.34±3.23	35.56±3.44	35.67±3.44	0.34	
37	SEKS1	Dark grey	421.5±11.85	7.5±1.58	32.46±3.28	29.34±3.12	44.67±3.85	0.33	
38	SEKS2	Dark grey	389.5±11.39	7.6±1.59	33.42±3.33	27.45±3.02	42.78±3.77	0.36	
39	SEKS3	Dark grey	366.4±11.05	6.8±1.50	33.42±3.33	29.67±3.14	43.61±3.81	0.28	
40	SENaS1	Greyish brown	384.3±11.31	6.7±1.49	35.34±3.43	28.56±3.08	32.54±3.29	0.22	
41	SENaS2	Greyish brown	385.6±11.33	7.7±1.60	37.56±3.53	25.56±2.91	36.72±3.49	0.43	
42	SENaS3	Greyish brown	408.0±11.66	7.7±1.60	34.34±3.38	26.42±2.96	37.82±3.55	0.28	
43	SEVS1	Greyish brown	388.2±11.37	7.7±1.60	35.31±3.43	24.56±2.86	42.84±3.77	0.31	
44	SEVS2	Greyish brown	411.6±11.71	7.2±1.54	36.45±3.48	27.43±3.02	36.78±3.50	0.46	
45	SEVS3	Greyish brown	452.8±12.28	7.2±1.54	34.45±3.38	32.21±3.27	39.46±3.62	0.31	
46	SFTS1	Dark grey	398.4±11.52	7.2±1.54	35.45±3.43	30.11±3.16	38.00±3.55	0.34	
47	SFTS2	Dark grey	364.8±11.02	7.3±1.55	34.45±3.38	31.05±3.21	44.78±3.86	0.45	
48	SFTS3	Dark grey	417.8±11.80	7.3±1.55	32.31±3.28	32.08±3.27	41.78±3.73	0.41	
49	SGTS1	Dark greyish brown	387.6±11.36	7.4±1.57	33.34±3.33	29.00±3.10	32.67±3.30	0.38	
50	SGTS2	Dark greyish brown	432.3±12.00	7.2±1.54	35.43±3.43	28.06±3.05	43.56±3.81	0.41	
51	SGTS3	Dark greyish brown	467.3±12.48	7.1±1.53	36.21±3.47	29.34±3.12	42.17±3.74	0.28	
52	SHTS1	Light grey	413.8±11.74	7.1±1.53	35.68±3.44	30.10±3.16	35.65±3.44	0.26	
53	SHTS2	Light grey	426.5±11.92	7.3±1.55	34.35±3.38	28.32±3.07	41.00±3.69	0.22	
54	SHTS3	Light grey	389.4±11.39	7.3±1.55	36.72±3.49	29.34±3.12	35.65±3.44	0.27	

Table 2.4.2: Macronutrient Analysis of Pre Monsoon Seasonal Soil Samples of Thiruvarur district, Tamil Nadu

S.No	Sample	N (kg/ac)	NO ₃ (kg/ac)	NH ₄ (kg/ac)	P (kg/ac)	K (kg/ac)	S (kg/ac)	H (kg/ac)
	Code							
1	SATpS1	82.45±5.24	79.34±5.14	82.56±5.24	41.57±3.72	42.09±3.74	37.56±3.53	38.98±3.60
2	SATpS2	81.06±5.19	80.42±5.17	83.41±5.27	42.63±3.76	41.89±3.73	32.21±3.27	34.64±3.39
3	SATpS3	78.56±5.11	78.47±5.11	80.34±5.17	48.45±4.01	42.56±3.76	34.78±3.40	36.61±3.49
4	SANS1	79.56±5.14	77.45±5.08	82.34±5.23	52.61±4.18	41.67±3.72	31.78±3.25	42.87±3.78
5	SANS2	78.89±5.12	75.67±5.02	86.34 ± 5.36	48.52±4.02	38.93±3.60	30.87±3.20	41.78±3.73
6	SANS3	78.45±5.11	75.41±5.01	79.45±5.14	46.45±3.93	36.84±3.50	33.48±3.34	43.96±3.82
7	SAMS1	79.45±5.14	79.53±5.14	78.34±5.11	52.89±4.19	35.67±3.44	32.56±3.29	42.61±3.76
8	SAMS2	78.34±5.11	78.41±5.11	80.31±5.17	54.67±4.26	36.67±3.49	38.45±3.58	41.75±3.73
9	SAMS3	83.45±5.27	77.47±5.08	81.54±5.21	45.67±3.90	41.67±3.72	37.32±3.52	36.41±3.48
10	SAKS1	84.23±5.29	73.56±4.95	77.37±5.07	33.41±3.33	42.56±3.76	38.56±3.58	42.98±3.78
11	SAKS2	80.34±5.17	73.45±4.94	79.37±5.14	36.67±3.49	43.56±3.81	37.83±3.55	39.64±3.63
12	SAKS3	81.34±5.20	77.56±5.08	80.31±5.17	34.56±3.39	47.78±3.99	36.81±3.50	33.41±3.33
13	SANaS1	82.00±5.22	73.45±4.94	81.34±5.20	32.74±3.30	46.78±3.94	39.56±3.63	38.56±3.58
14	SANaS2	83.72±5.28	72.67±4.92	79.34±5.14	34.67±3.39	47.34±3.97	41.98±3.74	33.72±3.35
15	SANaS3	78.92±5.12	76.15±5.03	74.56±4.98	33.56±3.34	43.89±3.82	40.56±3.67	37.68±3.54
16	SAVS1	77.56±5.08	76.67±5.05	80.31±5.17	37.32±1.56	38.61±1.09	41.67±3.72	36.81±3.50
17	SAVS2	76.91±5.06	80.34±5.17	82.45±5.24	38.45±3.58	32.67±3.30	34.89±3.41	38.93±3.60
18	SAVS3	78.56±5.11	81.46±5.21	84.51±5.30	37.67±3.54	41.89±3.73	32.78±3.30	42.67±3.77
19	SBTpS1	78.43±5.11	78.45±5.11	78.00±5.09	36.67±3.49	37.67±3.54	34.78±3.40	41.23±3.70
20	SBTpS2	77.78±5.09	79.34±5.14	76.96±5.06	32.67±3.30	36.78±3.50	36.87±3.50	38.43±3.57
21	SBTpS3	79.56±5.14	76.45±5.04	78.92±5.12	34.67±3.39	37.45±3.53	32.78±3.30	32.14±3.27
22	SCTpS1	78.45±5.11	77.41±5.07	81.02±5.19	36.78±3.50	38.41±3.57	36.62±3.49	35.14±3.42
23	SCTpS2	76.45±5.04	78.45±5.11	82.06±5.23	31.89±3.26	37.34±3.52	38.92±3.60	45.21±3.88
24	SCTpS3	77.78±5.09	76.56±5.05	82.34±5.23	56.71±4.34	33.67±3.35	41.67±3.72	42.41±3.75
25	SDTpS1	76.56±5.05	78.34±5.11	79.56±5.14	43.78±3.82	36.61±3.49	44.67±3.85	43.67±3.81
26	SDTpS2	77.81±5.09	83.45±5.27	79.34±5.14	44.67±3.85	38.54±3.58	43.78±3.82	46.73±3.94
27	SDTpS3	72.98±4.93	82.64±5.24	75.89±5.02	48.92±4.03	39.43±3.62	42.78±3.77	43.62±3.81
28	SDNS1	80.95±5.19	77.58±5.08	81.34±5.20	52.52±4.18	37.67±3.54	37.56±3.53	38.91±3.60

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29	SDNS2	81.87±5.22	78.47±5.11	82.56±5.24	53.42±4.22	42.67±3.77	34.56±3.39	39.64±3.63
30	SDNS3	82.34±5.23	78.46±5.11	83.35±5.27	55.42±4.29	41.45±3.71	47.34±3.97	38.61±3.58
31	SENS1	83.45±5.27	76.91±5.06	82.32±5.23	54.72±4.27	42.67±3.77	44.67±3.85	34.63±3.39
32	SENS2	76.41±5.04	74.74±4.99	81.00±5.19	52.34±4.17	43.56±3.81	42.56±3.76	39.41±3.62
33	SENS3	78.92±5.12	77.78±5.09	82.04±5.22	56.78 ± 4.35	38.56±3.58	30.56±3.19	34.82±3.40
34	SEMS1	81.67±5.21	79.76±5.15	78.43±5.11	42.78±3.77	33.56±3.34	32.68±3.30	37.56±3.53
35	SEMS2	82.45±5.24	77.93±5.09	76.59±5.05	48.54±4.02	31.23±3.22	31.67±3.24	32.89±3.31
36	SEMS3	79.63±5.15	78.43±5.11	79.05±5.13	43.78±3.82	32.78±3.30	34.45±3.38	31.92±3.26
37	SEKS1	78.67±5.12	79.82±5.14	79.78±5.15	42.67±3.77	32.67±3.30	33.41±3.33	33.61±3.34
38	SEKS2	77.46±5.08	84.71±5.31	78.93±5.12	43.76±3.81	33.56±3.34	32.78±3.30	32.56±3.29
39	SEKS3	77.61±5.08	82.67±5.24	76.98±5.06	41.45±3.71	36.45±3.48	37.56±3.53	41.76±3.73
40	SENaS1	76.79±5.05	87.34±5.39	77.98±5.09	42.67±3.77	35.62±3.44	32.67±3.30	42.23±3.75
41	SENaS2	78.61±5.11	81.56±5.21	81.81±5.22	44.65±3.85	36.67±3.49	34.87±3.40	41.45±3.71
42	SENaS3	77.45±5.08	78.57±5.11	87.34±5.39	48.56±4.02	36.72±3.49	35.62±3.44	39.45±3.62
43	SEVS1	81.78±5.22	79.77±5.15	78.00 ± 5.09	52.21±4.17	32.45±3.28	36.51±3.48	38.61±3.58
44	SEVS2	86.45 ± 5.36	81.65±5.21	79.43±5.14	53.45±4.22	37.89±3.55	38.38±3.57	37.64±3.54
45	SEVS3	81.43±5.20	78.63±5.11	79.43±5.14	52.56±4.18	33.67±3.35	39.41±3.62	36.89±3.50
46	SFTS1	80.43±5.17	76.82±5.06	85.00 ± 5.32	55.56±4.30	45.65±3.90	48.21 ± 4.00	40.08±3.65
47	SFTS2	80.04±5.16	79.76±5.15	79.34±5.14	51.56±4.14	41.73±3.72	42.41±3.75	42.75±3.77
48	SFTS3	79.57±5.15	83.04±5.26	82.34±5.23	42.56±3.76	39.54±3.63	38.62±3.58	43.78±3.82
49	SGTS1	76.56±5.05	81.46±5.21	79.34±5.14	43.62±3.81	36.45±3.48	32.67±3.30	42.76±3.77
50	SGTS2	77.45±5.08	77.45±5.08	78.82±5.12	43.67±3.81	37.42±3.53	36.56±3.49	39.41±3.62
51	SGTS3	77.67±5.08	78.56±5.11	79.43±5.14	45.89±3.91	32.67±3.30	37.45±3.53	36.78±3.50
52	SHTS1	78.68±5.12	81.33±5.20	82.90±5.25	47.56±3.98	36.42±3.48	34.78±3.40	37.23±3.52
53	SHTS2	77.83±5.09	74.78±4.99	83.63±5.27	49.67±4.06	35.62±3.44	42.87±3.78	31.56±3.54
54	SHTS3	79.82±5.15	76.34±5.04	79.67±5.15	53.91±4.23	36.13±3.47	43.78±3.82	36.71±3.49

Table 2.4.3: Micronutrient Analysis of Pre Monsoon Seasonal Soil Samples of Thiruvarur District, Tamil Nadu

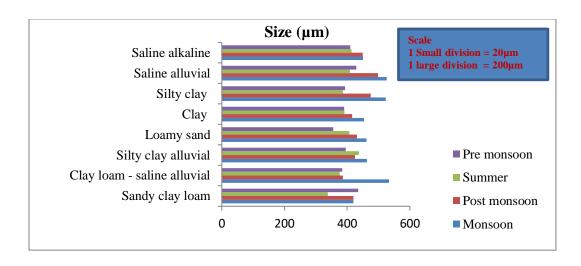
S.No	Sample	Fe (µg/Kg)	Co (µg/Kg)	Cr (µg/Kg)	I (µg/Kg)	Mn (µg/Kg)	Zn (µg/Kg)	Mb(µg/Kg)	Se(µg/Kg)
	Code								
1	SATpS1	3.88 ± 1.13	3.89±1.13	2.88 ± 0.97	3.56±1.08	2.61±0.93	3.89±1.13	3.67±1.10	4.36±1.20
2	SATpS2	3.56 ± 1.08	3.33±1.05	2.92 ± 0.98	3.65±1.10	2.73±0.95	3.62±1.09	3.58±1.09	4.34±1.20
3	SATpS3	3.45 ± 1.07	3.89±1.13	3.10±1.01	3.78±1.12	2.98±0.99	3.45±1.07	3.76±1.11	4.12±1.17
4	SANS1	3.78±1.12	3.47±1.07	3.08±1.01	4.56±1.23	2.62±0.93	3.81±1.12	3.84±1.13	3.26±1.04
5	SANS2	3.98±1.15	3.42±1.06	3.16±1.02	4.42±1.21	2.76±0.95	3.56±1.08	3.82±1.12	3.67±1.10
6	SANS3	3.42±1.06	3.67±1.10	3.18±1.02	4.67±1.24	2.67±0.94	3.54±1.08	3.56±1.08	3.89±1.13
7	SAMS1	4.67±1.24	3.83±1.12	3.48 ± 1.07	4.28±1.19	4.78±1.26	2.45±0.90	3.89±1.13	4.63±1.24
8	SAMS2	4.36±1.20	3.47±1.07	4.02±1.15	4.05±1.16	4.81±1.26	2.89±0.98	4.93±1.28	4.78±1.26
9	SAMS3	4.67±1.24	3.78±1.12	4.21±1.18	4.08±1.16	4.73±1.25	2.67±0.94	4.78±1.26	4.67±1.24
10	SAKS1	3.45±1.07	4.16±1.17	3.89±1.13	3.89±1.13	4.78±1.26	3.98±1.15	4.56±1.23	4.53±1.22
11	SAKS2	3.67±1.22	4.37±1.20	3.78±1.12	3.12±1.01	4.64±1.24	4.92±1.28	4.12±1.17	4.21±1.18
12	SAKS3	3.56±1.08	4.02±1.15	3.65±1.10	3.67±1.10	4.54±1.23	2.94±0.98	4.67±1.24	3.65±1.10
13	SANaS1	3.78±1.12	3.67±1.10	3.78±1.12	4.67±1.24	2.94±0.98	2.04±0.82	4.23±1.18	3.67±1.10
14	SANaS2	3.61±1.09	3.72±1.11	3.92±1.14	4.21±1.18	2.78±0.96	3.71±1.11	4.56±1.23	3.21±1.03
15	SANaS3	3.42±1.06	3.89±1.13	3.98±1.15	4.02±1.15	2.65±0.93	2.76±0.95	4.73±1.25	3.78±1.12
16	SAVS1	3.47±1.07	3.76±1.11	4.02±1.15	3.67±1.10	2.73±0.95	2.96±0.99	3.89±1.13	4.67±1.24
17	SAVS2	3.67±1.10	3.78±1.12	4.17±1.17	3.46±1.07	2.89±0.98	2.68±0.94	4.31±1.19	5.67±1.37
18	SAVS3	4.21±1.18	3.81±1.12	4.18±1.18	3.82±1.12	2.72±0.95	2.89±0.98	2.89±0.98	5.67±1.37
19	SBTpS1	4.67±1.24	4.72±1.25	4.67±1.24	2.67±0.94	3.89±1.13	3.41±1.06	2.93±0.98	5.24±1.32
20	SBTpS2	4.56±1.23	4.78±1.26	4.56±1.23	2.78±0.96	3.87±1.13	3.78±1.12	3.76±1.11	5.23±1.32
21	SBTpS3	4.21±1.18	4.28±1.19	4.45±1.21	2.89±0.98	3.67±1.10	3.72±1.11	3.47±1.07	5.03±1.29
22	SCTpS1	4.23±1.18	4.26±1.19	3.89±1.13	3.78±1.12	3.65±1.10	3.18±1.02	3.84±1.13	4.78±1.26
23	SCTpS2	4.61±1.23	4.56±1.23	3.76±1.11	3.84±1.13	3.46±1.07	3.76±1.11	3.67±1.10	4.46±1.21
24	SCTpS3	4.21±1.18	4.27±1.19	3.65±1.10	3.40±1.06	3.67±1.10	3.45±1.07	3.76±1.11	4.24±1.18
25	SDTpS1	4.67±1.24	4.28±1.19	3.86±1.13	2.67±0.94	4.67±1.24	3.78±1.12	3.65±1.10	3.67±1.10
26	SDTpS2	3.68±1.10	4.21±1.40	3.81±1.12	2.98±0.99	4.56±1.23	4.34±1.20	3.41±1.06	3.78±1.12
27	SDTpS3	3.56±1.08	4.37±1.45	3.76±1.11	2.78±0.98	4.72±1.25	2.89±0.98	2.67±0.94	3.98±1.15
28	SDNS1	4.61±1.23	4.26±1.19	3.41±1.06	2.73±0.95	4.89 ± 1.27	4.72±1.25	3.01±1.00	4.21±1.18

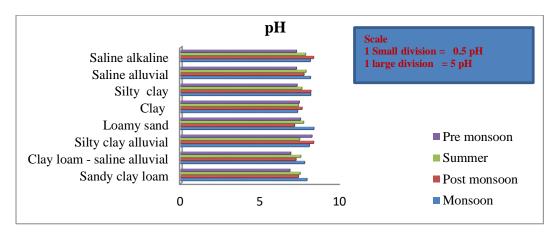
Conti									
29	SDNS2	4.28±1.19	4.28±1.19	3.46±1.07	2.89±0.98	4.82±1.26	3.98±1.15	3.42±1.06	3.18±1.02
30	SDNS3	4.57±1.23	4.26±1.19	3.57±1.09	2.89±0.98	4.63±1.24	3.67±1.10	3.45±1.07	4.12±1.17
31	SENS1	4.62±1.24	3.56 ± 1.08	3.87±1.13	4.94±1.28	4.67±1.24	4.24±1.18	3.42±1.06	4.89±1.27
32	SENS2	4.75±1.25	3.47 ± 1.07	3.48±1.07	4.01±1.15	4.03±1.15	4.08±1.16	3.54±1.08	4.67±1.24
33	SENS3	4.61±1.23	3.96±1.14	3.67±1.10	4.42±1.21	3.67±1.10	3.89 ± 1.13	4.64±1.24	3.98±1.15
34	SEMS1	4.73±1.25	3.68 ± 1.10	2.92±0.98	4.78±1.25	3.87±1.13	2.94 ± 0.98	4.78±1.26	4.89±1.27
35	SEMS2	4.64±1.24	3.61±1.09	2.98±0.99	4.51±1.22	3.62±1.09	2.94 ± 0.98	4.67±1.24	3.89±1.13
36	SEMS3	4.12±1.17	3.78 ± 1.12	2.94±0.98	4.78±1.25	3.48±1.07	2.89 ± 0.98	5.21±1.31	3.78±1.12
37	SEKS1	3.09±1.01	3.67±1.10	2.65±0.93	5.34 ± 1.33	3.78±1.12	4.31±1.19	5.78 ± 1.92	3.67±1.10
38	SEKS2	3.89±1.13	3.74±1.11	2.74±0.95	5.23±1.32	4.08±1.16	4.54±1.23	5.23±1.32	3.65±1.10
39	SEKS3	3.61±1.09	3.78 ± 1.12	2.76±0.95	4.67±1.24	4.13±1.17	4.06±1.16	5.34 ± 1.33	3.45±1.07
40	SENaS1	3.57±1.09	4.15±1.17	2.57±0.92	4.48±1.22	4.21±1.18	3.46 ± 1.07	5.56±1.36	5.81±1.39
41	SENaS2	3.69±1.10	4.12±1.17	2.46±0.90	4.62±1.24	4.63±1.24	3.18 ± 1.02	5.31±1.33	5.26±1.32
42	SENaS3	3.23±1.03	4.50 ± 1.22	2.67±0.94	4.82±1.26	4.72±1.25	3.08 ± 1.01	4.53±1.22	5.23±1.32
43	SEVS1	3.45±1.07	3.91±1.14	2.67±0.94	4.67±1.24	3.69±1.10	4.18±1.18	4.67±1.24	4.67±1.24
44	SEVS2	3.67±1.10	3.96±1.14	3.78±1.12	4.10±1.16	3.58±1.09	4.16±1.17	4.67±1.24	4.32±1.20
45	SEVS3	3.87±1.13	3.85±1.13	3.45±1.07	4.26±1.19	3.61±1.09	4.12±1.17	3.79±1.12	4.34±1.20
46	SFTS1	4.02±1.15	4.67±1.24	3.56±1.08	3.41±1.06	3.68±1.10	3.45±1.07	3.67±1.10	3.83±1.12
47	SFTS2	4.76 ± 1.25	4.78±1.26	3.61±1.09	3.68±1.10	3.76±1.11	3.21±1.03	3.45±1.07	4.08±1.16
48	SFTS3	3.68±1.10	4.92±1.28	3.71±1.11	3.67±1.10	4.03±1.15	3.24±1.03	3.78±1.12	4.27±1.19
49	SGTS1	3.67±1.10	4.77±1.26	3.64±1.10	3.78±1.02	4.45±1.21	3.26±1.04	3.75±1.11	4.89±1.27
50	SGTS2	3.78±1.12	4.78±1.26	3.81±1.12	4.02±1.15	4.68±1.24	3.21±1.03	3.72±1.11	4.67±1.24
51	SGTS3	3.71±1.11	4.67±1.24	3.67±1.10	4.23±1.18	4.01±1,15	3.78±1.12	3.78±1.12	4.48±1.22
52	SHTS1	3.82±1.12	5.14±1.30	3.62±1.09	4.67±1.24	3.26±1.04	3.45±1.07	4.67±1.55	5.56±1.36
53	SHTS2	3.64±1.10	5.09±1.30	3.48±1.07	5.02±1.29	3.64±1.10	3.02 ± 1.00	4.52±1.22	5.89 ± 1.40
54	SHTS3	3.82±1.12	5.21 ± 1.31	3.56±1.08	5.30±1.32	3.87±1.13	2.67 ± 0.94	4.63±1.24	5.26±1.32

Table 2.5: The highest parameter found in the Thiruvarur District's seasonal soil sample

S.No	Name of the Taluk	Highest parameter
1	Thiruthuraipoondi	pН
		Potassium
		Iron
		Molybdenum
2	Mannargudi	рН
		Temperature
		Loss of ignition
		Electrical conductivity
		Iodine
3	Needamangalam	Size
		Ammonium
		Hydrogen
		Manganese
		Selenium
4	Thiruvarur	Moisture
		Phosphorus
		Sulphur
		Cobalt
		Chromium
5	Kudavasal	Nitrogen
6	Valangaiman	Chromium
7	Nannilam	Zinc

Figure 1.1: Physical parameter (Size, pH and Temperature) analysis of different seasonal soil samples in Thiruvarur district





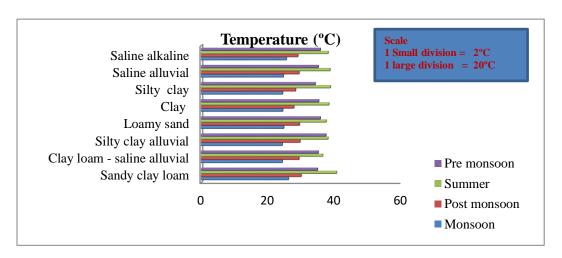
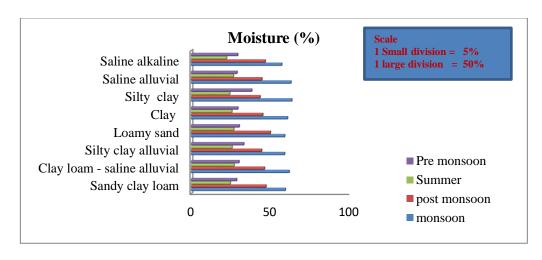
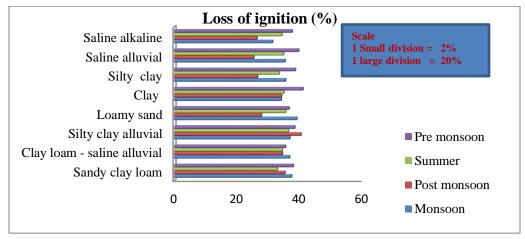


Figure 1.2: Physical parameter (Moisture, Loss of ignition and Electrical conductivity) analysis of different seasonal soil samples in Thiruvarur district





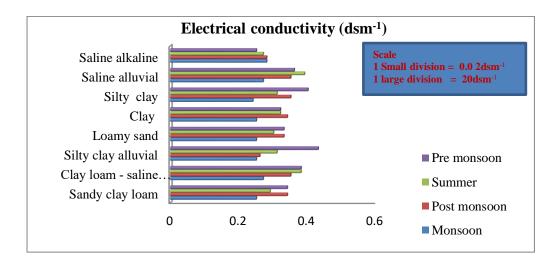
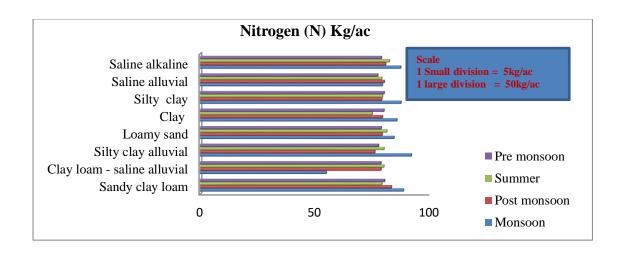
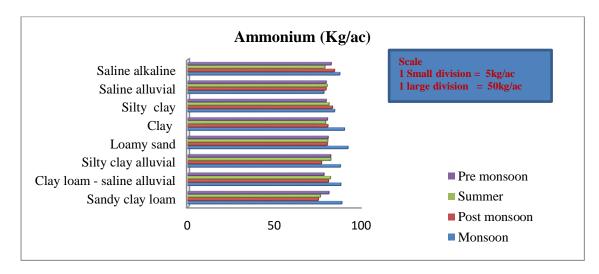


Figure 2.1: Macronutrient (N, NH_4 and NH_3) analysis of different seasonal soil samples in Thiruvarur district





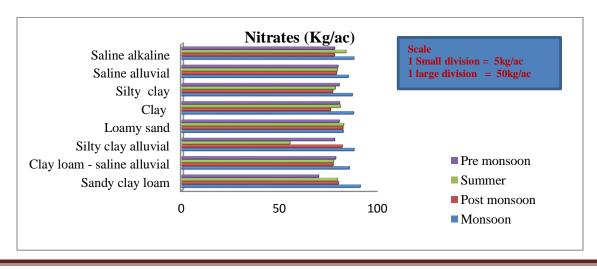
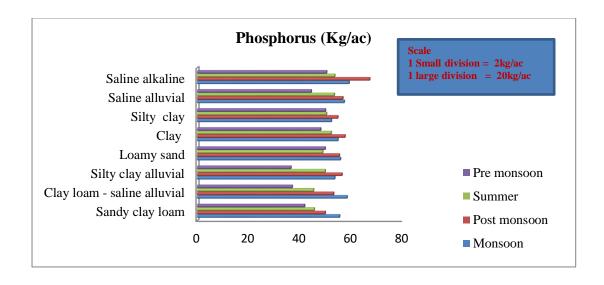


Figure 2.2: Macronutrient (P and K) analysis of different seasonal soil samples in

Thiruvarur district



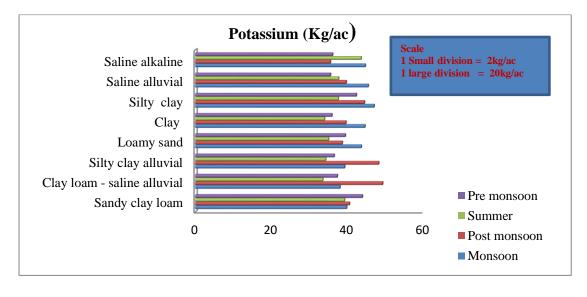
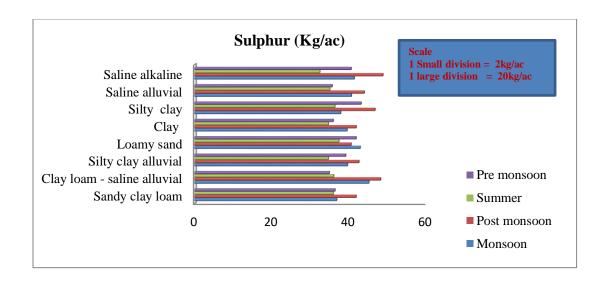


Figure 2.3: Macronutrient (S and H) analysis of different seasonal soil samples in Thiruvarur district



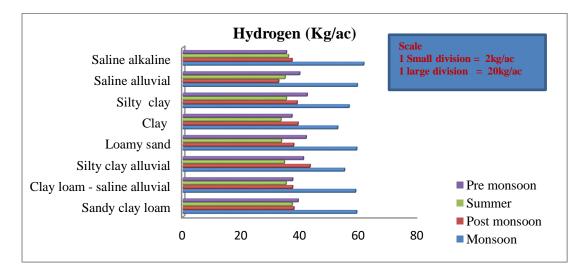
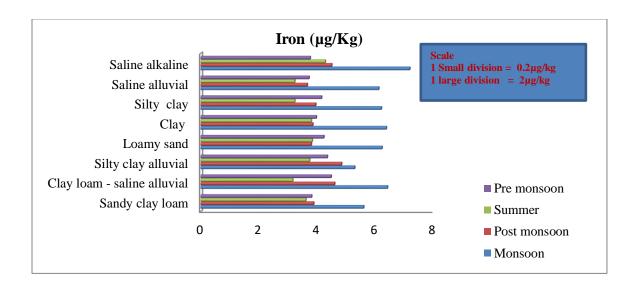


Figure 3.1: Micronutrient (Fe, Cr and Co) analysis of different seasonal soil samples in

Thiruvarur district



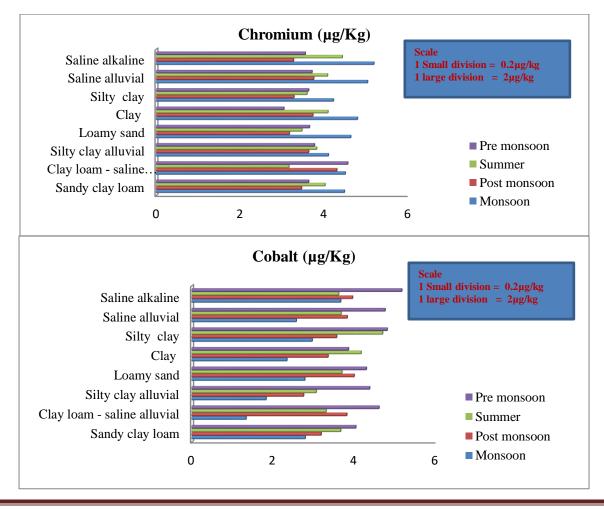
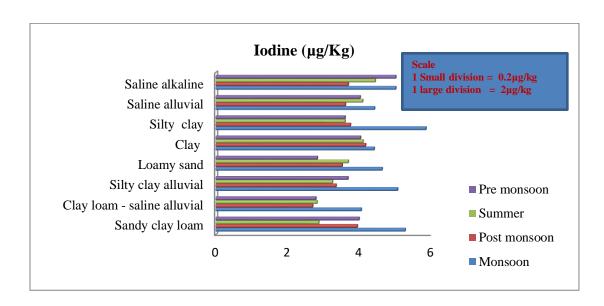


Figure 3.2: Micronutrient (I and Mn) analysis different seasonal soil samples of

Thiruvarur district



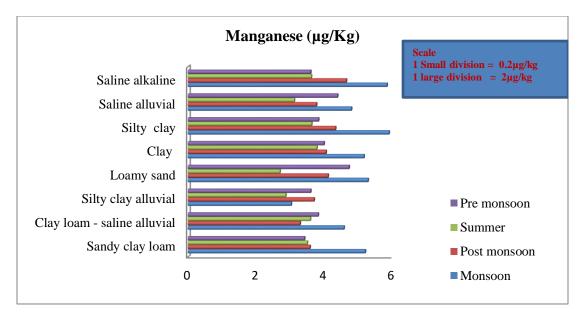
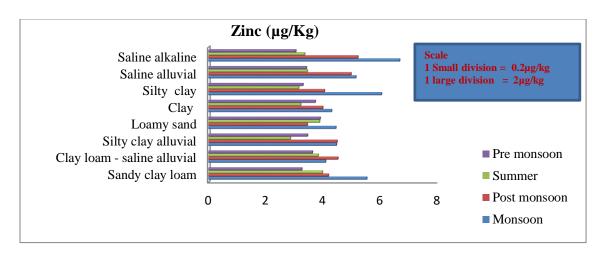
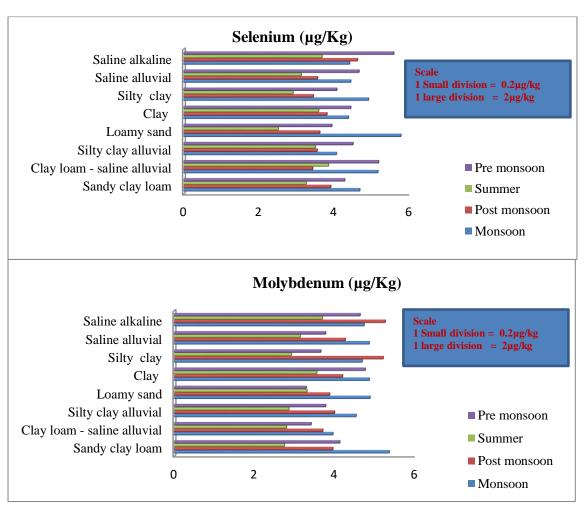


Figure 3.3: Micronutrient (Zn, Se and Mb) analysis different seasonal soil samples of

Thiruvarur district





4.3 Microbial diversity

4.3.1 Isolation and identification of bacteria and actinomycetal species

Thiruvarur district has eight different (Sandy clay loam, Clay loam –saline alluvial, Silty clay alluvial, Loamy sand, Clay, Silty clay, Saline alluvial and Saline alkaline) soil types, according to the study. *Bacillus, Pseudomonas, Escherichia, Nitrobacter, Nitrosomonas, Clostridium, Xymomonas, Corneybacterium, Rhizobium, Thiobacillus, Enterobacter, Serratia, Proteus, Streptococcus, Staphylococcus, Azospirillum, Mycobacterium, Vibrio Salmonella, and Erwinia.* There were over fifteen bacteria and one actinomyces present in all monsoon seasonal soil types. Except for saline-alkaline soil, *Staphylococcus aureus* was found in seven different soil types. Except for loamy sand and saline alkaline soil, ten bacterial and two actinomycetal species were found in six soil types. *Clostridium* species were found in four different soil types, including sandy clay loam, clay, silty clay, and silty clay alluvial soil. *Micromonospora* species (Actinomycetes) were discovered in four different soil types: sandy clay loam, clay, silty clay, and saline alluvial soil (Fig 4.1; Table 3.1.1, 3.1.2, 3.1.3, 3.1.4, 3.2.1 and 3.2.2; Plate-2,3,4,5,6,7,8,9,10,11,12,13 and 14).

Twelve bacterial and two actinomycetes were found in all soil types during the postmonsoon season. Except for saline alkaline soil, four bacterial species were found in seven soil types. Except for saline alkaline and loamy sand, eight bacteria and actinomycetes were found in six soil types.

Only five bacterial species and an actinomycetes were found in all summer seasonal soil types. Except for loamy sand, seven soil types included two actinomycetes and four bacteria. In six soil types, four bacteria were found: sandy clay loam, clay, silty clay, and saline alluvial. Clay, silty clay, saline-alluvial, clay loam-saline alluvial, and saline alkaline soil types all had

Micromonospora and Salmonella species. Clay, silty clay, saline alluvial, and sandy clay loam were all shown to include Actinomyces. Xymomonas sps, Rhizobium leguminosorum, Rhizobium trifoli and Serratia marsecence were found in all soil types during the pre-monsoon season. In sandy clay loam, clay, silty clay, loamy sand, saline alkaline, and saline alluvial soil, Nitrobacter, Corneybacterium, Proteus mirabilis, Streptococcus, and Actinomyces were found. Clay, loamy sand, and saline alkaline soil all had Microbispora species (Fig 4.2 Table 3.1.1, 3.1.2, 3.1.3, 3.1.4, 3.2.1 and 3.2.2; Plate- 3,4,5,6,7,8,9,10,11,12,13,14 and 15).

Table 3.1.1: Microbial Density of Monsoon Seasonal Soil Samples of Thiruvarur District, Tamil Nadu, India

S.No	Sample	Bacteria			Fungi			Actinomycetes		
	Code	10-4	10-5	10-6	10-2	10	10-4	10-2	10-3	10-4
						3				
1	SATpSI	86	<mark>98</mark>	84	72	78	93	76	73	83
2	SATpS2	85	92	89	76	78	92	72	76	72
3	SATpS3	78	83	90	83	84	90	83	72	78
4	SANSI	82	98	93	82	83	94	86	73	84
5	SANS2	86	87	82	92	96	83	82	78	72
6	SANS3	83	96	82	84	86	88	76	74	82
7	SAMSI	83	86	82	76	77	82	74	72	73
8	SATMS2	78	72	82	84	88	84	84	82	76
9	SAMS3	83	92	88	93	92	89	93	84	92
10	SAKSI	92	94	93	86	87	88	85	86	82
11	SAKS2	86	96	89	73	76	77	73	76	70
12	SAKS3	82	85	80	93	94	<mark>96</mark>	82	82	86
13	SANaSI	86	92	88	84	85	<mark>96</mark>	73	87	76
14	SANaS2	76	83	86	84	86	87	76	78	79
15	SANaS3	84	92	95	93	96	92	72	76	80
16	SAVSI	83	96	88	76	74	76	72	76	72
17	SAVS2	82	94	92	84	86	82	76	78	78
18	SAVS3	86	92	84	92	86	94	76	89	72
19	SBTpSI	86	84	80	86	87	83	73	78	70
20	SBTpS2	92	86	90	94	92	<mark>96</mark>	83	84	86
21	SBTpS3	94	82	93	86	87	88	76	72	72
22	SCTpSI	<mark>95</mark>	86	<mark>98</mark>	93	94	<mark>96</mark>	84	82	83
23	SCTpS2	86	82	82	86	93	92	86	88	82
24	SCTpS3	86	84	86	82	86	83	76	78	76

25	SDTpSI	93	82	90	76	74	78	73	74	83
26	SDTpS2	89	86	86	72	74	75	82	86	82
27	SDTpS3	78	73	76	86	74	83	76	78	72
28	SDNSI	84	92	94	84	84	93	84	82	86
29	SDNS2	83	82	84	<mark>96</mark>	<mark>97</mark>	94	76	78	84
30	SDNS3	78	78	73	93	94	92	83	82	76
31	SENSI	76	74	73	83	84	86	73	76	74
32	SENS2	86	82	85	87	88	84	91	93	78
33	SENS3	92	84	86	93	96	94	92	84	88
34	SEMSI	88	82	89	89	84	82	<mark>96</mark>	72	78
35	SEMS2	83	86	88	76	78	93	83	84	82
36	SEMS3	92	86	87	84	88	89	86	84	86
37	SEKS1	88	82	89	74	78	93	73	76	82
38	SEKS2	83	84	86	76	73	84	74	82	84
39	SEKS3	93	87	86	93	96	82	76	72	74
40	SENaS1	84	86	82	78	93	82	83	82	76
41	SENaS2	88	82	86	78	76	78	86	84	82
42	SENaS3	93	94	90	83	84	78	<mark>96</mark>	93	94
43	SEVS1	83	88	90	84	86	78	83	82	86
44	SEVS2	82	86	92	82	86	82	83	85	93
45	SEVS3	83	96	94	76	74	83	78	76	78
46	SFTS1	73	88	86	76	84	86	83	84	80
47	SFTS2	83	76	89	72	86	83	76	73	78
48	SFTS3	73	82	90	82	84	86	89	82	81
49	SGTS1	83	84	86	76	73	72	86	83	76
50	SGTS2	77	78	83	82	86	83	92	<mark>96</mark>	<mark>94</mark>
51	SGTS3	84	86	92	72	76	74	82	<mark>96</mark>	82
52	SHTS1	82	84	91	82	86	93	83	84	83
53	SHTS2	92	93	96	92	94	90	<mark>96</mark>	82	83
54	SHTS3	86	87	88	76	93	89	92	86	87

Table 3.1.2: Microbial Density of Post Monsoon Seasonal Soil Samples of Thiruvarur District, Tamil Nadu, India

S.No	Sample	Bacteria			Fungi			Actinomycetes		
	Code	10-4	10-5	10-6	10-2	10	10-4	10-2	10-	10-4
						3			3	
1	SATpSI	89	<mark>88</mark>	82	73	<mark>88</mark>	<mark>93</mark>	78	76	82
2	SATpS2	79	82	79	78	72	<mark>93</mark>	72	76	74
3	SATpS3	91	73	80	82	74	90	84	79	82
4	SANSI	87	<mark>88</mark>	83	83	83	82	76	73	80
5	SANS2	78	77	75	82	86	86	82	72	78
6	SANS3	86	86	72	84	83	82	86	79	80
7	SAMSI	78	76	84	73	87	83	84	78	78
8	SATMS2	87	62	87	82	82	82	84	82	76
9	SAMS3	78	82	82	83	82	79	73	87	82
10	SAKSI	76	84	83	82	89	78	75	79	82
11	SAKS2	67	76	82	78	<mark>88</mark>	87	73	75	70
12	SAKS3	87	75	70	83	84	86	83	81	76
13	SANaSI	83	82	78	74	75	86	75	83	86
14	SANaS2	76	73	76	94	76	77	72	68	74
15	SANaS3	77	82	82	73	86	82	71	66	73
16	SAVSI	72	86	80	76	84	74	71	86	75
17	SAVS2	73	84	82	83	82	82	73	<mark>88</mark>	77
18	SAVS3	82	82	64	82	84	84	72	80	72
19	SBTpSI	84	64	60	82	86	81	83	79	74
20	SBTpS2	75	76	86	84	82	86	84	82	82
21	SBTpS3	68	72	78	<mark>86</mark>	86	83	67	78	78
22	SCTpSI	<mark>92</mark>	84	82	83	84	86	82	85	80
23	SCTpS2	82	82	83	84	83	82	84	82	80
24	SCTpS3	77	82	83	80	76	81	86	77	76
25	SDTpSI	72	72	89	76	72	72	83	78	80
26	SDTpS2	78	76	82	78	76	78	72	83	82
27	SDTpS3	73	73	78	80	75	87	86	77	77
28	SDNSI	79	82	84	82	82	83	74	<mark>88</mark>	81
29	SDNS2	86	86	74	76	78	84	86	77	82
30	SDNS3	82	71	63	83	84	82	73	83	78
31	SENSI	78	70	83	<mark>86</mark>	74	88	78	86	70
32	SENS2	82	72	75	82	82	83	83	83	77
33	SENS3	82	86	80	83	86	84	95	82	82
34	SEMSI	81	82	82	79	74	92	<mark>91</mark>	79	72
35	SEMS2	88	83	82	72	88	73	82	82	80
36	SEMS3	78	82	83	82	86	89	85	82	81

37	SEKS1	81	80	85	72	78	83	73	75	85
38	SEKS2	82	81	82	77	72	83	72	<mark>88</mark>	83
39	SEKS3	79	67	83	83	86	83	74	74	79
40	SENaS1	76	76	81	73	83	84	82	86	73
41	SENaS2	81	72	82	75	86	74	85	82	77
42	SENaS3	79	74	78	73	84	72	86	83	83
43	SEVS1	82	78	80	74	82	74	73	83	79
44	SEVS2	86	76	82	72	87	83	73	86	83
45	SEVS3	73	86	84	66	78	89	88	73	78
46	SFTS1	68	76	76	66	82	82	82	80	82
47	SFTS2	81	86	79	72	87	83	71	83	81
48	SFTS3	63	84	80	72	85	87	86	81	<mark>86</mark>
49	SGTS1	73	82	76	<mark>86</mark>	78	82	88	<mark>88</mark>	77
50	SGTS2	72	<mark>88</mark>	73	82	82	82	89	76	84
51	SGTS3	80	82	82	72	86	84	86	86	83
52	SHTS1	84	74	81	72	82	84	84	82	73
53	SHTS2	72	83	86	82	84	92	76	83	81
54	SHTS3	78	78	88	<mark>86</mark>	83	82	82	82	82

Table 3.1.3: Microbial Density of Summer Seasonal Soil Samples of Thiruvarur District, Tamil Nadu, India

S.No	Sample	I	Bacteria	a		Fungi		Acti	nomyce	etes
	Code	10-4	10-5	10-6	10-2	10-3	10-4	10-2	10-3	10-4
1	SATpSI	68	63	67	75	66	67	68	72	75
2	SATpS2	72	68	62	69	69	66	73	72	<mark>78</mark>
3	SATpS3	70	71	73	76	65	71	74	75	77
4	SANSI	66	72	77	<mark>78</mark>	67	<mark>78</mark>	75	78	73
5	SANS2	62	73	72	68	73	71	77	72	74
6	SANS3	68	77	<mark>79</mark>	71	75	73	73	76	75
7	SAMSI	75	70	68	67	72	61	75	74	76
8	SAMS2	71	72	65	58	67	68	76	77	<mark>78</mark>
9	SAMS3	68	69	63	67	66	69	71	74	77
10	SAKSI	62	64	62	68	<mark>79</mark>	74	67	78	71
11	SAKS2	63	66	66	74	67	72	71	76	75
12	SAKS3	73	63	67	71	73	75	63	64	68
13	SANaSI	<mark>78</mark>	59	72	68	75	71	75	76	73
14	SANaS2	73	62	73	62	<mark>79</mark>	76	72	74	<mark>78</mark>
15	SANaS3	65	63	77	63	72	64	71	67	68

16	SAVSI	63	65	74	64	76	<mark>78</mark>	69	71	74
17	SAVS2	72	68	67	67	63	<mark>78</mark>	72	77	73
18	SAVS3	76	71	72	74	78	69	66	68	67
19	SBTpSI	68	77	71	74	75	76	77	78	69
20	SBTpS2	61	73	78	72	71	71	73	68	67
21	SBTpS3	58	72	77	<mark>78</mark>	69	71	65	63	64
22	SCTpSI	56	71	73	68	67	67	65	63	69
23	SCTpS2	67	68	67	71	73	71	77	<mark>79</mark>	76
24	SCTpS3	59	63	72	77	74	74	59	62	76
25	SDTpSI	62	64	68	76	77	76	68	67	72
26	SDTpS2	63	69	61	77	76	74	69	66	68
27	SDTpS3	71	71	65	74	71	71	72	68	64
28	SDNSI	72	79	68	73	66	63	71	76	72
29	SDNS2	73	73	66	67	68	69	76	77	73
30	SDNS3	68	62	69	62	69	67	72	75	71
31	SENSI	64	65	67	63	65	79	69	68	70
32	SENS2	59	<mark>79</mark>	68	64	62	77	76	75	<mark>78</mark>
33	SENS3	62	73	66	66	75	73	77	71	72
34	SEMSI	72	62	78	62	78	72	71	64	69
35	SEMS2	77	67	72	59	79	69	69	67	68
36	SEMS3	63	65	74	68	68	77	69	69	65
37	SEKS1	68	62	72	66	68	79	62	63	66
38	SEKS2	59	66	76	68	64	69	73	72	71
39	SEKS3	68	63	69	67	62	64	72	69	71
40	SENaS1	71	66	68	<mark>78</mark>	73	63	67	68	66
41	SENaS2	68	74	66	77	75	68	74	71	77
42	SENaS3	69	73	67	72	75	73	75	76	76
43	SEVS1	71	72	78	68	67	72	69	65	64
44	SEVS2	72	71	79	62	57	73	72	68	65
45	SEVS3	<mark>78</mark>	66	71	69	78	76	77	76	71
46	SFTS1	77	69	74	62	76	67	71	74	72
47	SFTS2	68	72	77	64	71	69	72	76	75
48	SFTS3	64	77	68	66	74	68	76	77	73
49	SGTS1	62	68	63	67	72	69	67	73	<mark>78</mark>
50	SGTS2	68	67	75	75	77	68	66	69	69
51	SGTS3	71	71	77	71	68	69	69	65	68
52	SHTS1	73	69	74	73	69	68	67	71	69
53	SHTS2	66	67	69	72	76	<mark>78</mark>	76	<mark>79</mark>	<mark>78</mark>
54	SHTS3	69	68	66	71	74	72	<mark>78</mark>	74	<mark>78</mark>

Table 3.1.4: Microbial Density of Pre Monsoon Seasonal Soil Samples of Thiruvarur District, Tamil Nadu, India

S.No	Sample]	Bacteri	a		Fungi		Acti	nomyce	etes
	Code	10-4	10-5	10-6	10-2	10-3	10-4	10-2	10-3	10-4
1	SATpS1	73	76	67	67	63	76	76	68	71
2	SATpS2	72	71	74	58	65	78	75	72	77
3	SATpS3	71	70	72	68	62	67	67	67	73
4	SANS1	68	69	73	63	67	68	78	74	68
5	SANS2	67	74	76	65	69	65	76	72	70
6	SANS3	62	71	78	67	<mark>79</mark>	71	67	65	68
7	SAMSI	63	73	71	78	67	77	71	72	76
8	SATMS2	67	73	67	72	72	78	67	67	78
9	SAMS3	63	68	77	76	76	74	78	78	74
10	SAKSI	68	66	78	67	73	72	67	69	68
11	SAKS2	69	64	73	63	69	76	63	78	77
12	SAKS3	75	62	<mark>79</mark>	67	68	76	69	75	75
13	SANaS1	74	61	68	<mark>78</mark>	65	78	78	74	69
14	SANaS2	73	58	67	57	67	<mark>79</mark>	70	65	<mark>78</mark>
15	SANaS3	76	60	75	78	71	73	71	<mark>79</mark>	67
16	SAVS1	72	62	72	74	<mark>79</mark>	77	73	73	75
17	SAVS2	77	67	77	76	76	73	73	78	76
18	SAVS3	71	72	73	77	77	71	74	69	67
19	SBTpSI	74	74	67	75	76	72	78	77	72
20	SBTpS2	<mark>79</mark>	76	66	76	73	74	68	78	74
21	SBTpS3	67	61	68	77	74	72	67	75	<mark>78</mark>
22	SCTpSI	68	67	64	<mark>78</mark>	65	73	63	66	75
23	SCTpS2	69	73	69	68	67	77	67	67	76
24	SCTpS3	72	77	74	69	68	64	74	73	<mark>78</mark>
25	SDTpSI	77	72	72	67	64	63	<mark>79</mark>	77	72
26	SDTpS2	78	76	75	62	67	62	78	66	77
27	SDTpS3	67	62	68	61	66	66	68	67	73
28	SDNSI	65	61	76	68	67	65	72	62	59
29	SDNS2	69	64	77	64	68	62	71	65	65
30	SDNS3	78	68	67	76	72	76	68	65	62
31	SENSI	72	77	59	72	77	76	78	63	63
32	SENS2	71	<mark>78</mark>	68	67	64	67	69	66	63
33	SENS3	68	76	66	66	64	62	65	67	65
34	SEMSI	69	77	65	64	59	63	<mark>79</mark>	64	66
35	SEMS2	71	73	68	77	76	77	73	65	64
36	SEMS3	77	71	66	74	76	75	75	76	66
37	SEKS1	73	67	68	76	72	73	77	73	65

38	SEKS2	72	65	76	61	63	67	71	62	72
39	SEKS3	68	63	75	74	71	72	68	65	76
40	SENaS1	65	64	72	68	67	64	69	66	77
41	SENaS2	74	57	73	68	78	67	77	78	<mark>78</mark>
42	SENaS3	76	75	77	67	77	78	78	72	67
43	SEVS1	71	76	74	71	70	68	67	77	<mark>78</mark>
44	SEVS2	73	69	72	78	76	77	71	76	67
45	SEVS3	74	66	73	75	76	77	73	77	77
46	SFTS1	73	69	67	76	73	71	72	67	76
47	SFTS2	72	68	76	66	65	67	69	73	67
48	SFTS3	71	67	67	68	65	62	68	67	56
49	SGTS1	74	76	78	73	75	78	69	76	66
50	SGTS2	73	73	73	76	77	73	78	77	67
51	SGTS3	65	77	74	73	75	71	74	72	77
52	SHTS1	68	71	68	64	64	68	74	75	73
53	SHTS2	66	67	69	72	76	78	76	<mark>79</mark>	<mark>78</mark>
54	SHTS3	69	68	66	71	74	72	78	74	<mark>78</mark>

Table 3.1.5: The highest microbial count found in the Thiruvarur district's seasonal soil sample

S.No	Name of the Microorganisms	Name of the taluk
01	Bacteria	Thiruthuraipoondi
02	Fungi	Needamangalam
03	Actinomycetes	Mannargudi,
		Thiruvarur,
		Nannilam

Table 3.2.1: Isolation of bacteria and actinomycetes from soil samples of Thiruvarur district, Tamil Nadu (2014-2015)

S.No		Name of t	`	
	Monsoon	Post monsoon	Summer	Pre monsoon
01	Bacillus subtilis	Bacillus polymyxa	Bacillus silvestris	Xymomonas species
02	Bacillus pumilus	Bacillus subtilis	Bacillus mycoides	Corneybacterium species
03	Bacillus licheniformis	Bacillus firmus	Bacillus subtilis	Bacillus subtilis
04	Bacillus thuringiensis	Bacillus silvestris	Escherichia coli	Vibrio species
05	Bacillus firmus	Bacillus cereus	Salmonella species	Thiobacillus species
06	Bacillus polymyxa	Bacillus coagulans	Xymomonas species	Salmonella species
07	Pseudomonas aeruginosa	Bacillus popilliae	Corneybacterium species	Clostridium species
08	Pseudomonas fluorescence	Pseudomonas fluorescence	Rhizobium trifoli	Rhizobium trifoli
09	Escherichia coli	Pseudomonas lini	Rhizobium leguminosorum	Rhizobium leguminosorum
10	Nitrobacter species	Pseudomonas alcaligenes	Proteobacter species	Thiobacillus ferroxidans
11	Nitrosomonas species	Pseudomonas denitrificans	Enterobacter aerogens	Nitrosomomonas species
12	Clostridium species	Pseudomonas aeruginosa	Serratia marsecence	Nitrobacter species
13	Xymomonas species	Pseudomonas putida	Streptococcus species	Serratia marsecence
14	Corneybacterium species	Escherichia coli	Staphylococcus aureus	Proteus vulgaris
15	Rhizobium trifoli	Proteobacter species	Azospirillum species	Proteus mirabilis
16	Rhizobium leguminosorum	Corneybacterium species	Mycobacterium species	Streptococcus species
17	Thiobacillus species	Érwinia species	Actinomyces species	Staphylococcus aureus
18	Enterobacter aerogens	Rhizobium trifoli	Actinoplanes species	Azospirillum species
19	Serratia marsecence	Rhizobium species	Micromonospora species	Mycobacterium species
20	Proteus vulgaris	Enterobacter aerogens	Streptomyces species	Azotobacter species
21	Proteus mirabilis	Serratia marsecence	-	Actinomyces species
22	Streptococcus species	Streptococcus species	-	Actinoplanes species
23	Staphylococcus	Staphylococcus	-	Micromonospora

	aureus	aureus		species
24	Azospirillum species	Azospirillum species	-	Microbispora species
25	Mycobacterium species	Mycobacterium species	-	-
26	Vibrio species	Vibrio species	-	-
27	Actinomyces species	Actinomyces species	-	-
28	Actinoplanes species	Actinoplanes species	-	-
29	Micromonospora species	Micromonospora species	-	-
30	Microbispora species	-	-	-
31	Nocardia species	-	-	-

Table 3.2.2 Bacterial and Actinomycetal species count recorded during four different seasonal soil samples of Thiruvarur district, Tamil Nadu

S.No	Name of the organisms	Mor	soon	Post m	onsoon	Sun	nmer	Pre m	onsoon	Total no. of	% of
		TNS	MD	TNS	MD	TNS	MD	TNS	MD	soils	distribution
01	Bacillus subtilis	08	2.67	08	2.67	08	2.67	-	-	24	3.52
02	Bacillus pumilus	08	2.67	-	-	-	-	-	-	08	1.17
03	Bacillus licheniformis	08	2.67	-	-	-	-	-	-	08	1.17
04	Bacillus thuringiensis	08	2.67	-	1	-	1	-	1	08	1.17
05	Bacillus firmus	06	2.00	06	2.00	-	-	-	-	12	1.76
06	Bacillus polymyxa	08	2.67	08	2.67	-	-	-	-	16	2.35
07	Bacillus silvestris	-	1	07	2.33	07	2.33	-	1	14	2.05
08	Bacillus cereus	-	1	08	2.67	-	ı	-	1	08	1.17
09	Bacillus coagulans	-	1	08	2.67	-	1	-	1	08	1.17
10	Bacillus popilliae	-	-	08	2.67	-	-	-	-	08	1.17
11	Pseudomonas	08	2.67	06	2.00	-	-	-	-	14	2.05
	fluorescence										
12	Pseudomonas lini	-	-	06	2.00	-	-	-	-	06	0.88
13	Pseudomonas	-	-	08	2.67	-	-	-	-	08	1.17
	alcaligenes										
14	Pseudomonas	-	-	08	2.67	-	-	-	-	08	1.17
	denitrificans										
15	Pseudomonas	08	2.67	08	2.67	-	-	-	-	16	2.35
	aeruginosa										
16	Pseudomonas putida	-	-	04	1.33	-	-	-	-	04	0.59
17	Pseudomonas species	-	ı	-	-	-	ı	3	1.00	03	0.44
18	Escherichia coli	08	2.67	06	2.00	08	2.67	-	-	22	3.23
19	Nitrobacter species	06	2.00	-	-	-	1	07	2.33	13	1.91
20	Nitrosomonas species	06	2.00	-	-	-	1	05	1.67	11	1.61
21	Clostridium species	04	1.33	-	-	-	-	06	2.00	10	1.47

Microbial diversity and uses of microorganisms in the soils of Thiruvarur District

22	Xymomonas species	08	2.67	-	-	06	2.00	08	2.67	22	3.23
23	Corneybacterium	06	2.00	06	2.00	06	2.00	07	2.33	25	3.67
	species										
24	Rhizobium trifoli	08	2.67	08	2.67	06	2.00	08	2.67	30	4.40
25	Rhizobium	08	2.67	07	2.33	08	2.67	08	2.67	31	4.55
	leguminosorum										
26	Thiobacillus species	06	2.00	1	-	-	-	05	1.67	11	1.61
27	Enterobacter aerogens	06	2.00	07	2.33	08	2.67	1	-	21	3.08
28	Serratia marsecence	06	2.00	06	2.00	07	2.33	08	2.67	27	3.96
29	Proteus vulgaris	08	2.67	ı	-	-	-	05	1.67	13	1.91
30	Proteus mirabilis	08	2.67	-	-	-	-	07	2.33	15	2.20
31	Streptococcus species	06	2.00	06	2.00	07	2.33	05	1.67	24	3.52
32	Staphylococcus aureus	07	2.33	06	2.00	08	2.67	04	1.33	25	3.66
33	Azospirillum species	08	2.67	07	2.33	06	2.00	06	2.00	27	3.96
34	Mycobacterium species	06	2.00	08	2.67	07	2.33	04	1.33	25	3.66
35	Vibrio species	08	2.67	08	2.67	-	-	04	1.33	22	3.23
36	Salmonella species	-	-	ı	-	05	1.67	07	2.33	12	1.76
37	Proteobacter species	-	-	06	2.00	07	2.33	1	-	13	1.91
38	Klebsiella species	-	-	02	0.66	-	-	ı	-	02	0.30
39	Bacillus mycoides	-	-	-	-	08	2.66	1	-	08	1.18
40	Actinomyces species	06	2.00	08	2.67	04	1.33	05	1.67	23	3.38
41	Actinoplanes species	08	2.67	08	2.67	08	2.67	06	2.00	32	4.70
42	Micromonospora	04	1.33	08	2.67	05	1.67	04	1.33	21	3.08
	species										
43	Microbispora species	06	2.00	-	-	07	2.33	03	1.00	16	2.35
44	Nocardia species	06	2.00	-	-	-	-	-	-	06	0.88
45	Steptomyces species	-	-	-	-	-	-	2	0.66	02	0.30
	Total	215	31.52	200	29.32	136	19.94	131	19.22	682	100.00

TNS – Total number of soil, MD – Mean Deviation

Table 3.2.3 Morphological and biochemical characterization of isolated bacteria and actinomycetes from soil samples of Thiruvarur district

Name of the organisms	Shape	Grams staining	Indole	MR	VP	Citrate	Catalase	TSI	Oxidase	Urease	Motility	Endospore
Bacillus subtilis	Rod	+	-	-	+	+	+	K/A,G	+/-	-	+	+
Bacillus pumilus	Rod	+	-	-	+	-	+	K/A	+	-	+	+
Bacillus licheniformis	Rod	+	-	-	+	+	+	K/A	+	-	+	+
Bacillus thuringiensis	Rod	+	-	-	+	+	+	K/A	+	-	+	+
Bacillus firmus	Rod	+	-	-	+	+	+	K/A	+	-	+	+
Bacillus polymyxa	Rod	+	-	-	+	+	+	K/A	+	-	+	+
Bacillus silvestris	Rod	+	-	-	+	+	+	K/A	+	-	+	+
Bacillus cereus	Rod	+	-	-	+	+	+	K/A	+	-	+	+
Bacillus coagulans	Rod	+	-	-	+	+	+	K/A	+	-	+	+
Bacillus popilliae	Rod	+	-	-	+	+	+	K/A	+	-	+	+
Pseudomonas	Rod	-	-	-	-	+	+	A/A	+	-	+	-
fluorescence												
Pseudomonas lini	Rod	-	-	-	-	+	+	A/A	+	-	+	-
Pseudomonas alcaligenes	Rod	-	-	-	-	+	+	A/A	+	İ	+	-
Pseudomonas	Rod	-	-	-	-	+	+	A/A	+	-	+	-
denitrificans												
Pseudomonas aeruginosa	Rod	-	-	-	-	+	+	A/A	+	İ	+	-
Pseudomonas putida	Rod	-	-	-	-	+	+	A/A	+	İ	+	-
Pseudomonas species	Rod	-	-	-	-	+	+	A/A	+	İ	+	-
Escherichia coli	Rod	-	+	+	-	-	+	A/A	-	İ	+	-
Nitrobacter species	Rod	_	-	-	-	-	+	+/-	+	-	+	+
Nitrosomonas species	Rod	-	-	-	-	-	+	ı	-	-	+	+
Clostridium species	Rod	+	-	+	-	-	-	-	-	+	-	+

Xymomonas species	Rod	-	-	-	+	+	-	-	-	-	-	-
Corneybacterium species	Rod	+	-	+	-	-	+	+/-	-	-	-	-
Rhizobium trifoli	Rod	-	+	+	+	+	+	+	+	+	+	-
Rhizobium leguminosorum	Rod	-	+	+	+	+	+	+	+	+	+	-
Thiobacillus species	Rod	-	-	+	-	+	+	-	-	+	+	-
Enterobacter aerogens	Rod	-	-	-	+	+	+	A/A,G	-	-	+	-
Serratia marsecence	Rod	-	-	-	+	+	+	+/-	-	+	+	-
Proteus vulgaris	Rod	-	-	+	-	+	+	-	-	+	+	-
Proteus mirabilis	Rod	-	-	+	-	+	+	-	-	+	+	-
Streptococcus species	Cocci	+	-	-	-	+	-	-	-	-	-	-
Staphylococcus aureus	Cocci	+	-	+	+	+	+	-	-	+	-	-
Azospirillum species	Rod	-	-	-	-	+	-	-	+	+	+	+
Mycobacterium species	Rod	+	-	-	-	-	-	-	+	+	-	+
Vibrio species	Curved rod	-	+	-	+/-	+	-	-	+	-	+	+
Salmonella species	Rod	-	-	+	-	-	+	A/K	-	-	+	-
Actinomyces species	Rod	+	-	+	-	-	-	-	-	-	-	-
Actinoplanes species	Spherical	+	+/-	+/-	+/-	+/-	+/-	+/-	+/-	+/-	+	+
Micromonospora species	Branched mycelium	+	+/-	+/-	+/-	+/-	+/-	+/-	+/-	+/-	+	+
Microbispora species	Branched mycelium	+	+/-	+/-	+/-	+/-	+/-	+/-	+/-	+/-	-	+
Nocardia species	Rod	+	+/-	+/-	+/-	+/-	+	+/-	+/-	+/-	-	-
Steptomyces species	Filament	+	+/-	+/-	+/-	+/-	+/-	+/-	+/-	+/-	-	+
Proteobacter species	Rod	-	+/-	+/-	+/-	+/-	+/-	+/-	+/-	+/-	+	+
Klebsiella species	Rod	-	-	-	+	+	+	A/A	-	+	-	+
Bacillus mycoides	Rod	+	-	-	+	+	+	K/A	+	-	+	+

MR-Methyl red, VP-Voges-proskauer, TSI- Triple Sugar Iron, A-Acid, K-Alkaline, G-Gas

Plate-3

Isolation of Bacteria from monsoon seasonal soil samples of Thiruvarur District

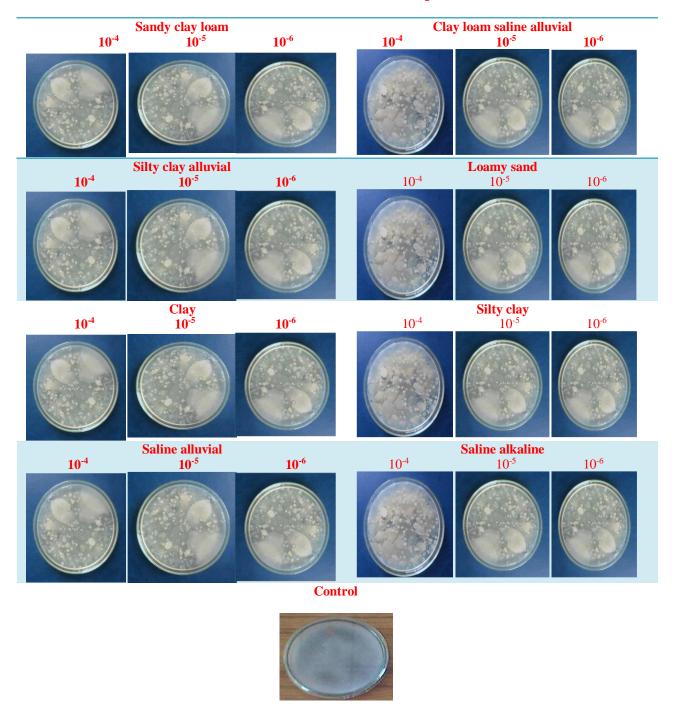


Plate-4

Isolation of Bacteria from post monsoon seasonal soil samples of Thiruvarur District

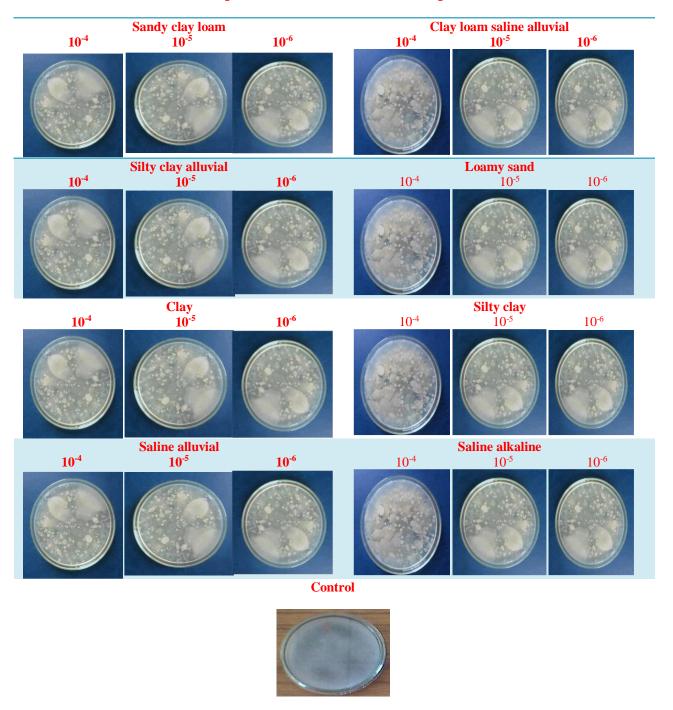


Plate-5
Isolation of Bacteria from summer seasonal soil samples of Thiruvarur district

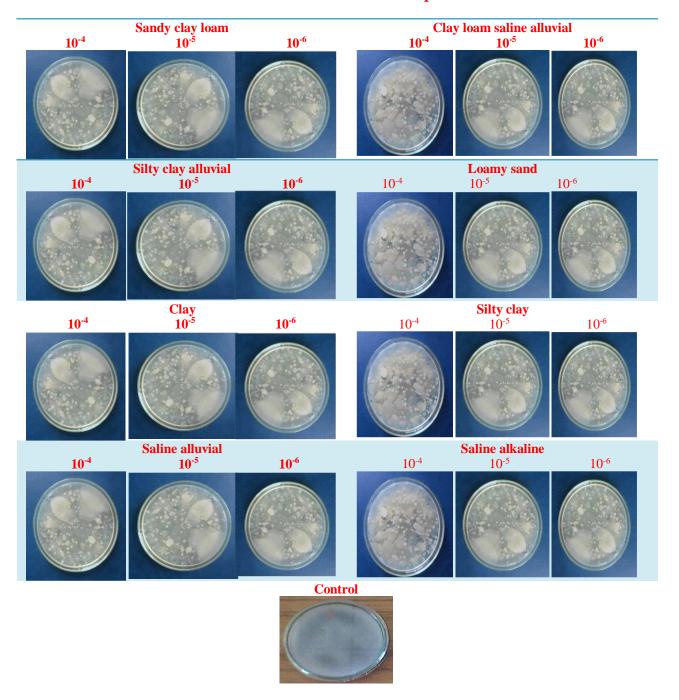
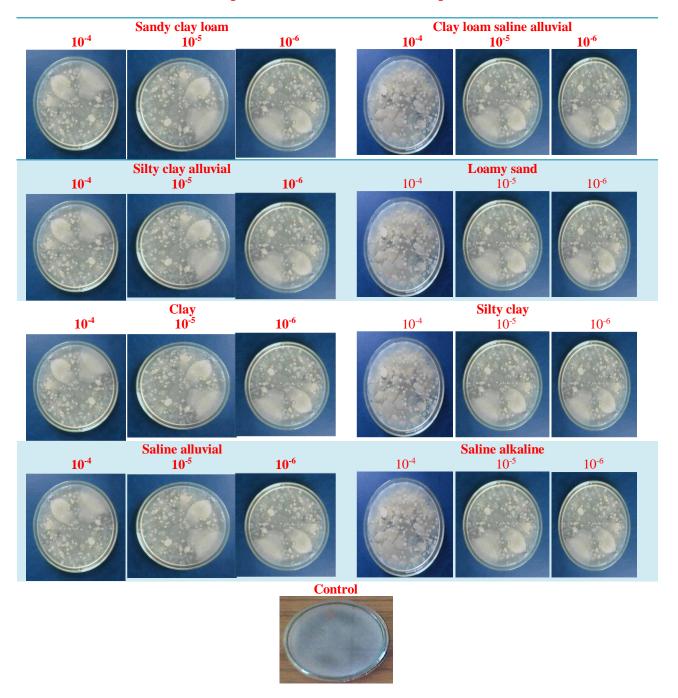
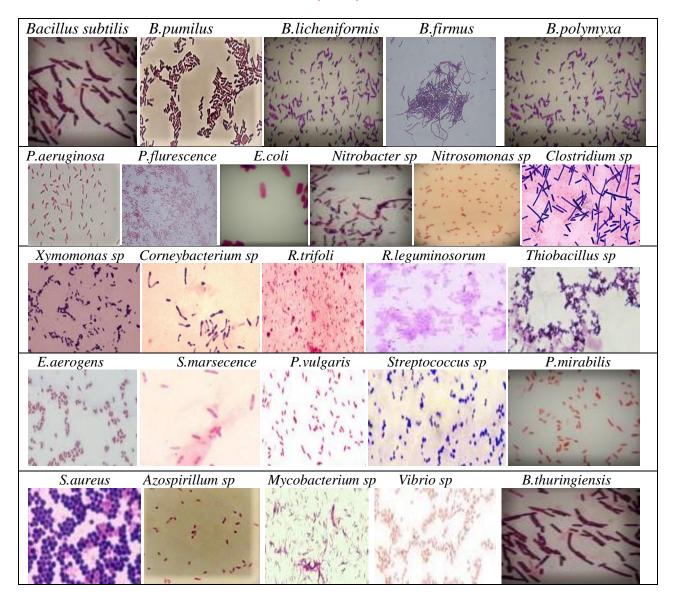


Plate-6
Isolation of Bacteria from pre monsoon seasonal soil samples of Thiruvarur District



 $\label{eq:Plate-7} \mbox{Identification of Bacteria from monsoon seasonal soil samples of Thiruvarur district} \end{math}$

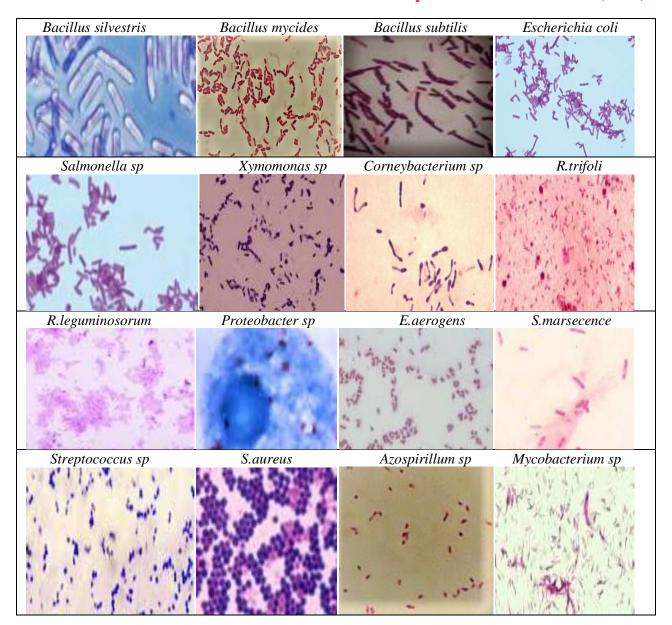


 $\label{eq:Plate-8} \label{eq:Plate-8}$ Identification of Bacteria from post monsoon seasonal soil samples of Thiruvarur district (100X)

B.polymyxa	B.subtilis	B.firmus	B.silvestris	B.cereus
B.coagulans B.po	pilliae P.fluorescenc	e P.lini	P.alcaligenes	P.denitrificans
P.aeruginosa	P.putida	E.coli	Proteobacter sp	Corneybacterium sp
- 1 M - 1 M			0	しし、
Erwinia sp	R.trifoli	Rhizobium sp	E.aerogens	S.marsecence
Streptococcus sp	Staphylococcus sp	Azospirillum sp	Mycobacterium s	o Vibrio species

Plate-9

Identification of Bacteria from summer seasonal soil samples of Thiruvarur district (100X)



 $\label{eq:Plate-10} \label{eq:Plate-10}$ Identification of Bacteria from pre monsoon seasonal soil samples of Thiruvarur district (100X)

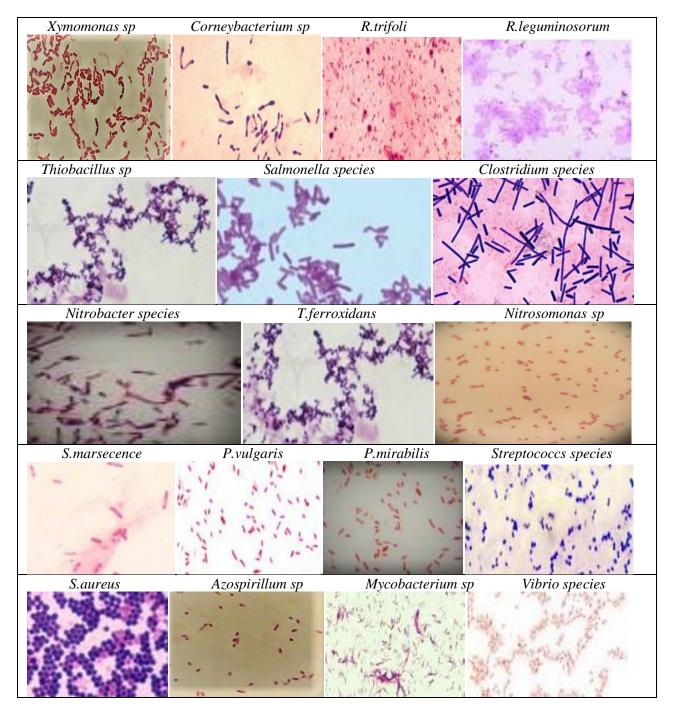


Plate-11

Isolation of Actinomycetes from monsoon seasonal soil samples of Thiruvarur district

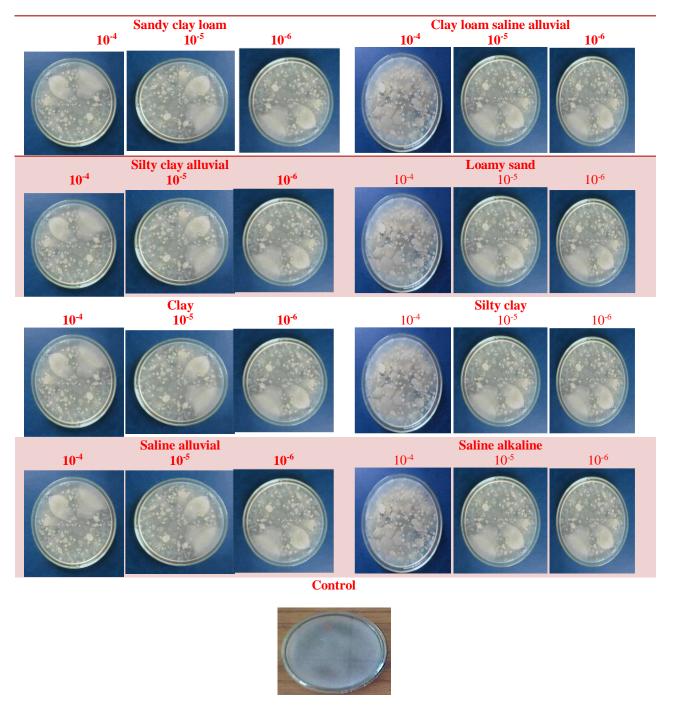


Plate-12

Isolation of Actinomycetes from post monsoon seasonal soil samples of Thiruvarur district

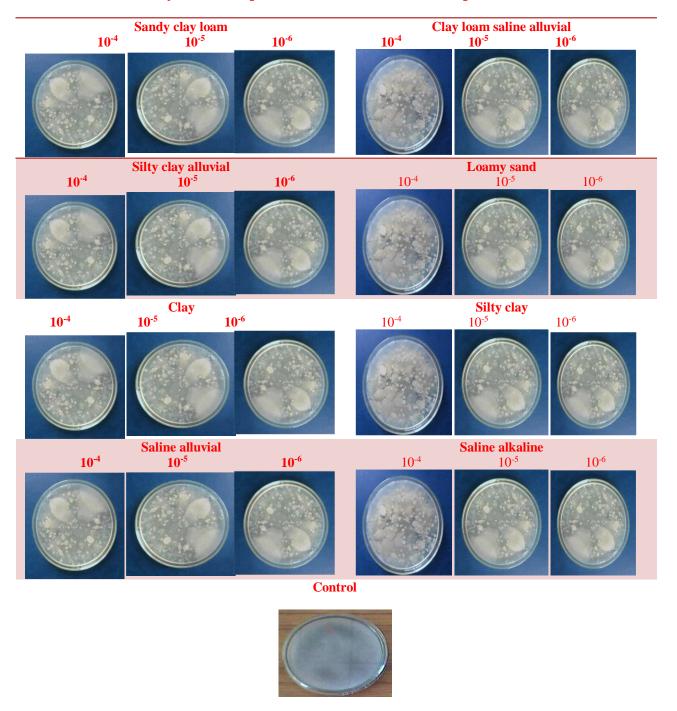


Plate-13

Isolation of Actinomycetes from summer seasonal soil samples of Thiruvarur district

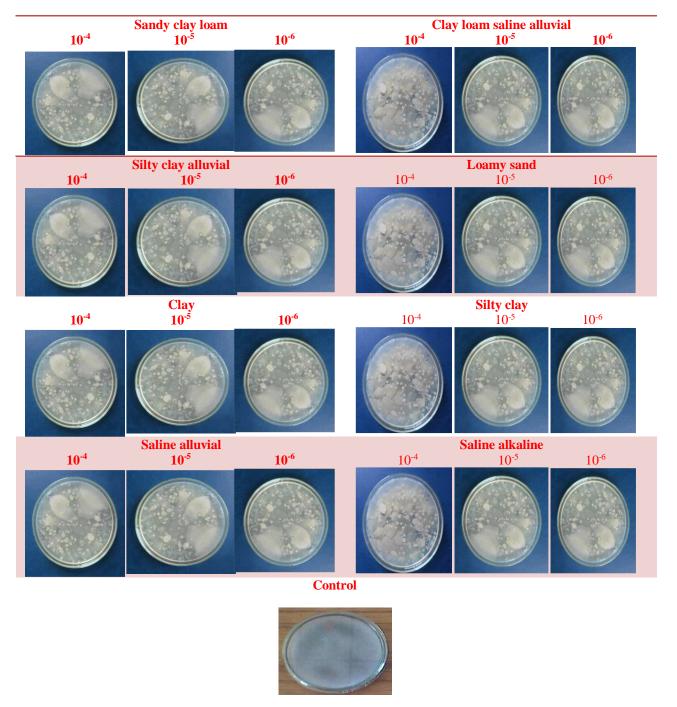


Plate-14

Isolation of Actinomycetes from pre monsoon seasonal soil samples of Thiruvarur district

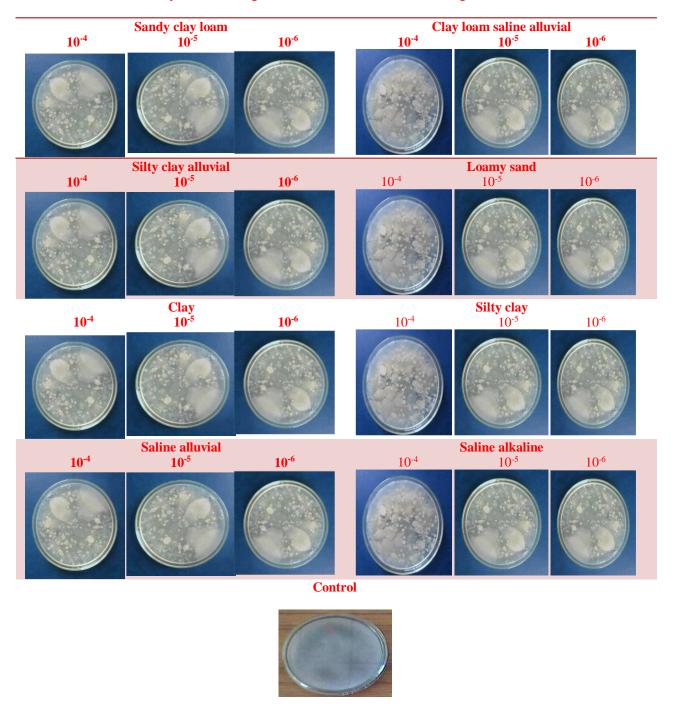


Plate-15

Identification of Actinomycetes from different soil samples of Thiruvarur district (100X)

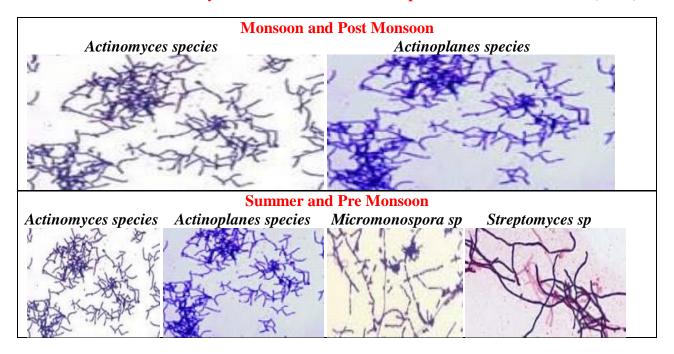
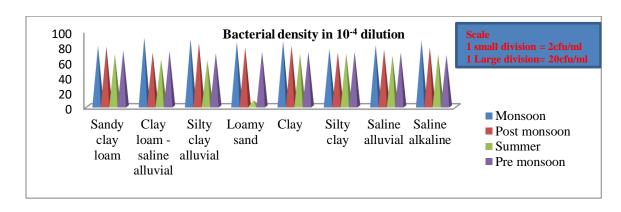
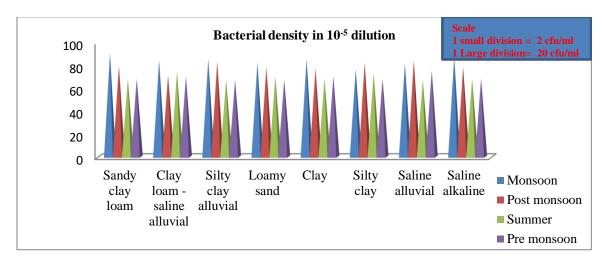


Fig 4.1: Bacterial density of different seasonal soil types of Thruvarur district





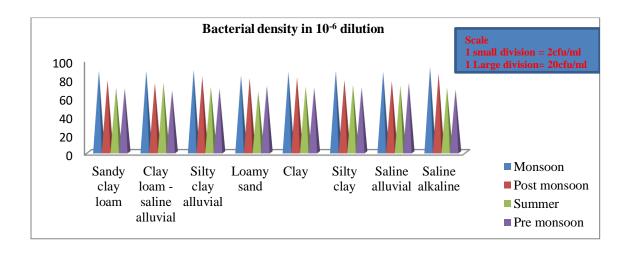
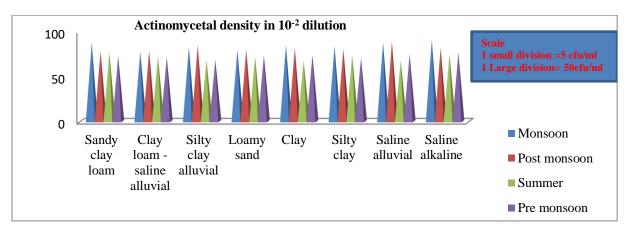
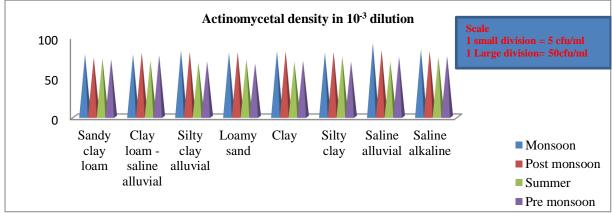
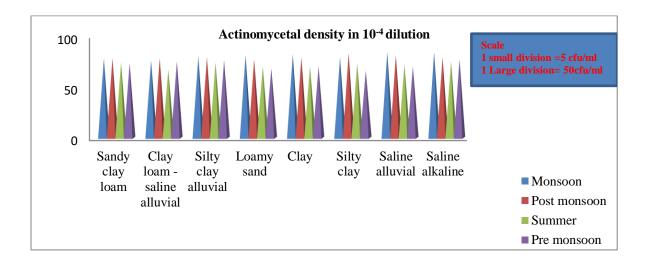


Fig 4.2: Actinomycetal density of different seasonal soil types of Thruvarur district







4.4.1 Isolation and identification of fungal species

Thiruvarur district has eight different soil types, according to the study. Verticillium, Phythium, Rhizoctonia, Phytophthora, Penicillium, Aspergillus, Rhizopus, Trichoderma, Saccharomyces, Absidia, Mortierella, Mucor, Fusarium, Agaricus, Phoma, Alternaria, and Cephalosporium were among the fungal genus found. Above three fungus were detected in all soil types during the monsoon season. Except for saline-alkaline soil, Penicillium notatum and Aspergillus fumigates were found in seven soil types. Except for loamy sand and saline alkaline soil, two fungal species were found in six soil types.

Penicillium chrysogenum, Rhizopus oryzae, Saccharomyces cerevisiae, Fusarium solani, and Agaricus campestris were found in sandy clay loam, clay, silty clay, saline alkaline, and silty clay alluvial soil, among others. In four soil types, Phytophthora species, Penicillium glaucum, Aspergillus niger, Aspergillus clavatus, Aspergillus nidulans, Rhizopus stolonifer, Trichoderma harzianum, Trichoderma koningii, Mucor species, Candida species, Fusarium oxysporum, Alternaria solani, Cephalosporium species and Trichoderma virens. In total, eight fungal isolates were discovered in three different soil types. (Table 3.1.1, 3.1.2, 3.1.3, 3.1.4, 3.3.1 and 3.3.2; Plate – 16, 17, 18, 19, 20, 21, 22 and 23; Fig- 4.3).

Verticillium fusisporum was found in all soil types during the post-monsoon season. Except for clay and saline alkaline soils, two fungal species were found in all six soil types. In clay, silty clay, sandy clay loam, and saline alkaline soil types, fifteen fungal species were discovered. Alternaria species, Trichoderma harzianum, Trichoderma viride, Rhizopus oryzae, Rhizopus stolonifer, Aspergillus oryzae and Aspergillus niger were discovered in three different

soil types: silty clay, clay, and saline alkaline soil. Clay and silty clay contained *Saccharomyces* species, *Absidia species, Fusarium species, Agaricus species* and *Alternaria alternata*.

Only two fungal species were found in five summer seasonal soil types: sandy clay loam, clay, silty clay, and saline alluvial. In three soil types, namely clay, clay loam-saline alluvial, and saline alkaline, *Rhizopus species*, *Aspergillus clavatus*, *Aspergillus niger*, *Aspergillus fumigatus*, and *Phytophthora* were found. *Rhizopus stolonifer* was found in seven soil types except saline alkaline in the pre-monsoon season. In sandy clay loam, clay, silty clay, loamy sand, saline alkaline, and salty alluvium, *Fusarium solani*, *Fusarium oxysporum*, *Rhizopus species*, *Aspergillus oryzae*, *Aspergillus nidulans*, *Aspergillus flavus*, *Aspergillus fumigatus* and *Rhizoctonia solani* were found. *Phytophthora species*, *Verticillium fusisporum*, *Penicillium glaucum*, *Penicillium chrysogenum*, *Penicillium notatum*, *Aspergillus clavatus*, *Rhizopus oryzae*, *Trichoderma viride*, *Trichoderma harzianum*, *Trichoderma koningii*, *Saccharomyces cerevisiae* and *Mortierella* species were found (Table 3.3.1 and 3.3.2 Plate – 16, 17, 18, 19, 20, 21, 22 and 23; Fig- 4.3).

Table 3.3.1: Identification of fungi soil samples of Thiruvarur district, Tamil Nadu

S.No	Name of the season								
	Monsoon	Post monsoon	Summer	Pre monsoon					
01	Verticillium fusisporum	Verticillium fusisporum	Phythium species	Verticillium fusisporum					
02	Veticillium affinae	Phythium species	Rhizoctonia solani	Rhizoctonia solani					
03	Phythium species	Rhizoctonia solani	Phytophthora species	Phytophthora species					
04	Rhizoctonia solani	Phytophthora species Penicillium glaucum		Penicillium glaucum					
05	Phytophthora species	Penicillium glaucum	Penicillium chrysogenum	Penicillium chrysogenum					
06	Penicillium candidum	Penicillium chrysogenum	Penicillium notatum	Penicillium notatum					
07	Penicillium glaucum	Penicillium notatum	Aspergillus fumigates	Aspergillus fumigates					
08	Penicillium chrysogenum	Aspergillus fumigates	Aspergillus flavus	Aspergillus flavus					
09	Penicillium notatum	Aspergillus flavus	Aspergillus clavatus	Aspergillus clavatus					
10	Aspergillus fumigates	Aspergillus clavatus	Aspergillus nidulans	Aspergillus nidulans					
11	Aspergillus flavus	Aspergillus nidulans	Aspergillus niger						
12	Aspergillus niger	Aspergillus niger	Aspergillus oryzae	Aspergillus oryzae					
13	Aspergillus clavatus	Aspergillus oryzae	Rhizopus oryzae	Aspergillus terreus					
14	Aspergillus nidulans	Aspergillus terreus	Rhizopus species	Rhizopus stolonifer					
15	Aspergillus oryzae	Rhizopus stolonifer	Trichoderma harzianum	Rhizopus oryzae					
16	Aspergillus terreus	Rhizopus oryzae	Trichoderma koningii	Rhizopus species					
17	Aspergillus species	Rhizopus species	Cephalosporium species	Trichoderma viride					
18	Rhizopus stolonifer	Trichoderma viride	Trichoderma virens	Trichoderma harzianum					
19	Rhizopus oryzae	Trichoderma harzianum	-	Trichoderma koningii					
20	Rhizopus species	Trichoderma koningii	-	Trichoderma species					
21	Trichoderma viride	Trichoderma species	-	Fusarium oxysporum					
22	Trichoderma harzianum	Saccharomyces cerevisiae	-	Fusarium solani					
23	Trichoderma koningii	Saccharomyces species	-	Cephalosporium species					
24	Trichoderma species	Absidia species	-	Trichoderma virens					
25	Saccharomyces cerevisiae	Fusarium solani	-	Saccharomyces cerevisiae					
26	Saccharomyces species	Fusarium species	-	Saccharomyces species					
27	Absidia species	Agaricus campestris	-	Absidia species					

28	Mortierella species	Agaricus bisporus	-	Mortierella species
29	Mucor species	Agaricus species	-	Mucor species
30	Candida species	Phoma species	-	-
31	Fusarium oxysporum	Alternaria alternate	-	-
32	Fusarium solani	Alternaria species	-	-
33	Fusarium species	-	-	-
34	Agaricus campestris	-	-	-
35	Agaricus bisporus	-	-	-
36	Agaricus species	-	-	1
37	Phoma species	-	-	1
38	Alternaria alternate	-	-	1
39	Alternaria species	-	-	-
40	Alternaria solani	-	-	-
41	Cephalosporium species	-	-	-
42	Trichoderma virens	-	-	-

Table 3.3.2: Fungal species count recorded during four different seasonal soil samples of Thiruvarur districts, Tamil Nadu

S.No Name of the fungi		Monsoon		Post monsoon		Summer		Pre monsoon		Total no. of	% of
		TNS	MD	TNS	MD	TNS	MD	TNS	MD	soils	distribution
01	Verticillium fusisporum	08	2.67	08	2.67	-	ı	04	1.33	20	4.00
02	Veticillium affinae	08	2.67	1	ı	-	ı	-	1	08	1.00
03	Phythium species	08	2.67	04	1.33	05	1.67	-	1	17	3.00
04	Rhizoctonia solani	06	2.00	06	2.00	04	1.33	05	1.67	21	4.00
05	Phytophthora species	04	1.33	04	1.33	03	1.00	04	1.33	15	3.00
06	Penicillium candidum	04	1.33	-	-	-	-	-	-	04	1.00
07	Penicillium glaucum	03	1.00	04	1.33	04	1.33	04	1.33	15	3.00
08	Penicillium	05	1.67	05	1.67	04	1.33	04	1.33	18	4.00
	chrysogenum										
09	Penicillium notatum	07	2.33	05	1.67	04	1.33	04	1.33	20	4.00
10	Aspergillus fumigates	07	2.33	04	1.33	03	1.00	05	1.67	19	4.00
11	Aspergillus flavus	08	2.67	04	1.33	04	1.33	05	1.67	21	4.00
12	Aspergillus niger	04	1.33	03	1.00	03	1.00	-	-	10	2.00
13	Aspergillus clavatus	04	1.33	04	1.33	03	1.00	04	1.33	15	3.00
14	Aspergillus nidulans	04	1.33	04	1.33	04	1.33	05	1.67	17	3.00
15	Aspergillus species	03	1.00	04	1.33	04	1.33	06	2.00	17	3.00
16	Aspergillus oryzae	06	2.00	03	1.00	-	-	05	1.67	14	3.00
17	Aspergillus terreus	03	1.00	04	1.33	-	-	06	2.00	13	3.00
18	Rhizopus stolonifer	04	1.33	03	1.00	-	-	07	2.33	14	3.00
19	Rhizopus oryzae	05	1.67	03	1.00	04	1.33	04	1.33	16	3.00
20	Rhizopus species	02	0.66	06	2.00	03	1.00	05	1.67	16	3.00
21	Trichoderma viride	03	1.00	03	1.00	-	-	04	1.33	10	2.00
22	Trichoderma harzianum	04	1.33	03	1.00	04	1.33	04	1.33	15	3.00
23	Trichoderma koningii	04	1.33	03	1.00	04	1.33	04	1.33	15	3.00

24	Trichoderma species	02	0.66	04	1.33	-	-	06	2.00	12	2.00
25	Saccharomyces	05	1.67	04	1.33	-	-	04	1.33	13	3.00
	cerevisiae										
26	Saccharomyces species	02	0.66	02	0.66	-	-	ı	-	04	1.00
27	Absidia species	02	0.66	02	0.66	-	-	02	0.66	06	1.00
28	Mortierella species	03	1.00	-	-	-	-	04	1.33	07	1.00
29	Mucor species	04	1.33	-	-	-	-	04	1.33	08	1.00
30	Candida species	04	1.33	-	-	-	-	-	-	04	1.00
31	Fusarium oxysporum	04	1.33	-	-	-	-	05	1.67	09	1.00
32	Fusarium solani	05	1.67	04	1.33	-	-	05	1.67	14	3.00
33	Fusarium species	04	1.33	02	0.66	-	-	-	-	06	1.00
34	Agaricus campestris	05	1.67	04	1.33	-	-	-	-	09	2.00
35	Agaricus bisporus	03	1.00	04	1.33	-	-	-	-	07	1.00
36	Agaricus species	03	1.00	02	0.66	-	-	-	-	05	1.00
37	Phoma species	03	1.00	04	1.33	-	-	-	-	07	1.00
38	Alternaria alternate	03	1.00	02	0.66	-	-	-	-	05	1.00
39	Alternaria species	03	1.00	03	1.00	-	-	-	-	06	1.00
40	Alternaria solani	04	1.33	-	-	-	-	-	-	04	1.00
41	Cephalosporium species	04	1.33	-	-	05	1.67	04	1.33	13	3.00
42	Trichoderma virens	04	1.33	-	-	04	1.33	04	1.33	12	2.00
	Total	182	36.47	121	24.25	69	13.83	127	25.45	499	100.00

TNS – Total number of soil, MD – Mean Deviation

Plate-16

Isolation of fungi from Monsoon seasonal soil types

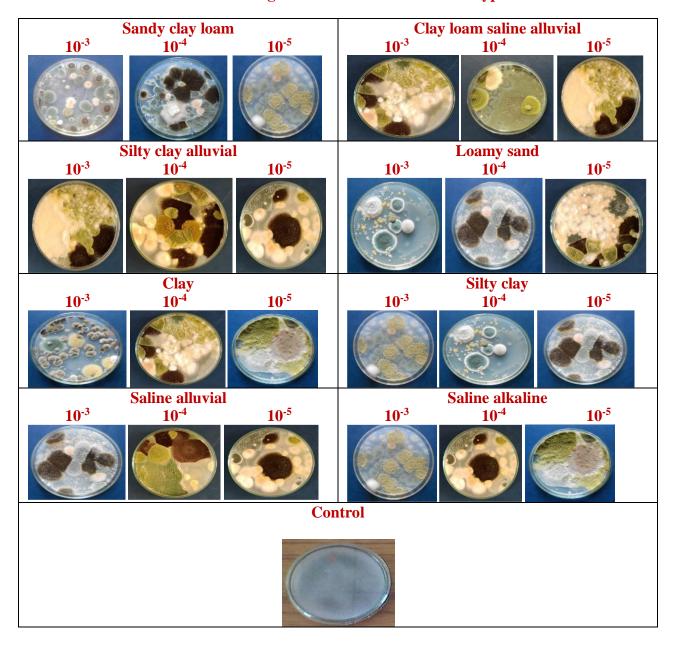


Plate-17

Isolation of fungi from Post Monsoon seasonal soil types

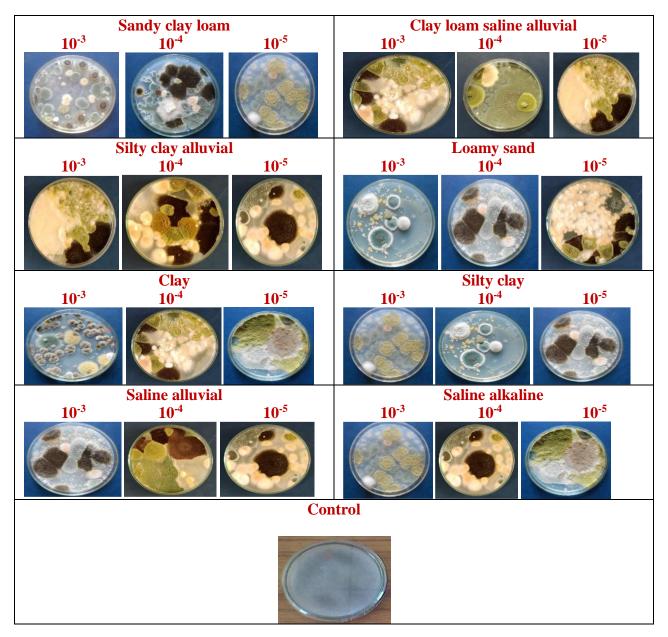


Plate-18

Isolation of Fungi from Summer Seasonal Soil Types

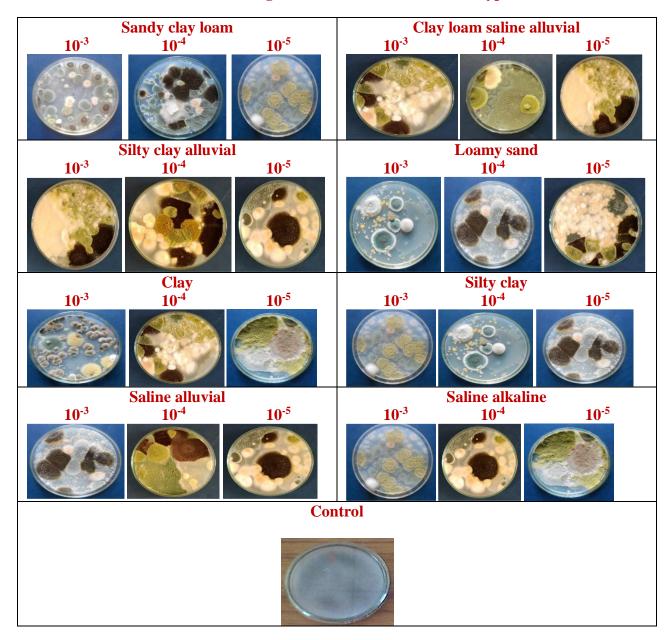
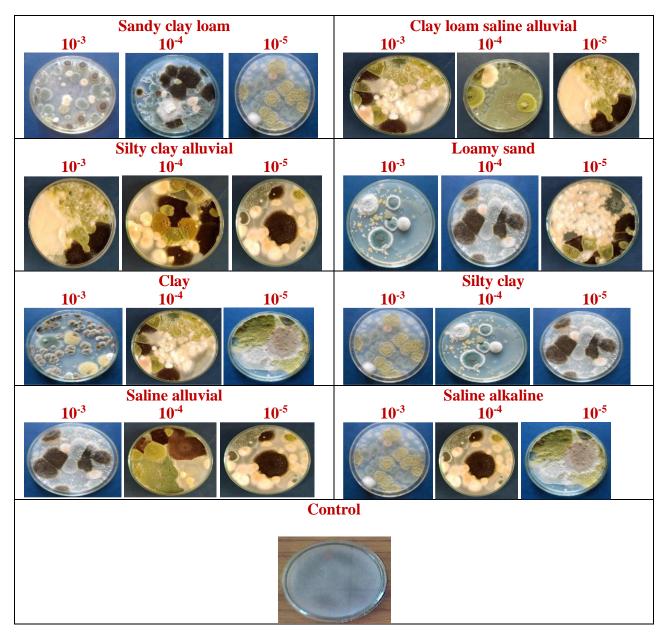


Plate-19
Isolation of fungi from Pre Monsoon seasonal soil types



 $\label{eq:Plate-20} Plate-20$ Identification of fungi from Monsoon seasonal soil types (40X)

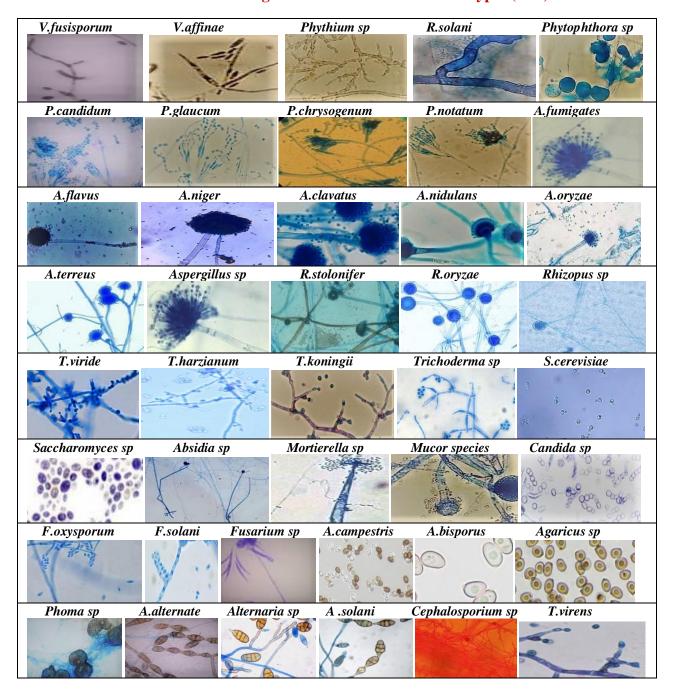
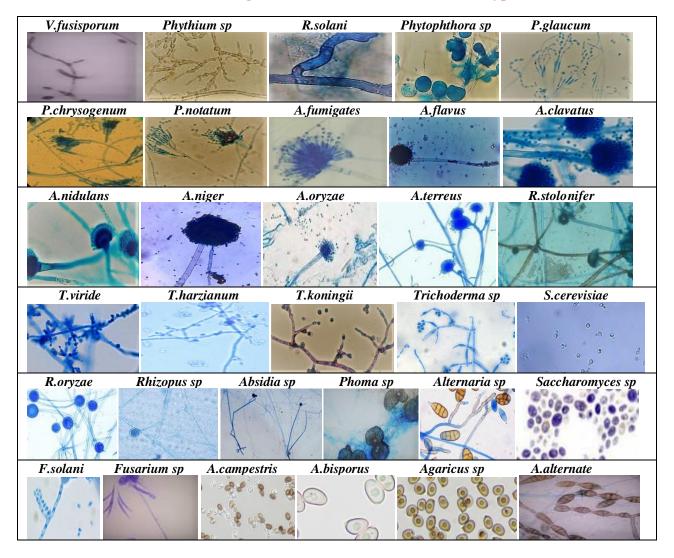
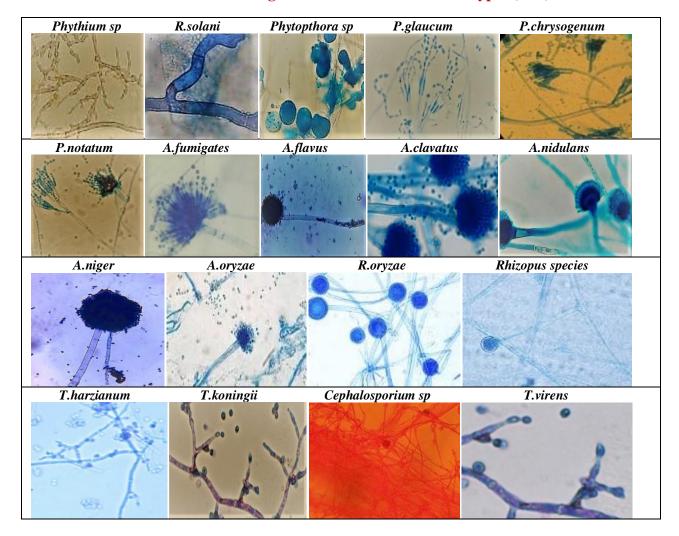


Plate-21

Identification of fungi from Post Monsoon seasonal soil types (40X)



 $\label{eq:Plate-22} \mbox{Identification of fungi from Summer seasonal soil types (40X)}$



 $\label{eq:Plate-23}$ Identification of fungi from Pre Monsoon seasonal soil types (40X)

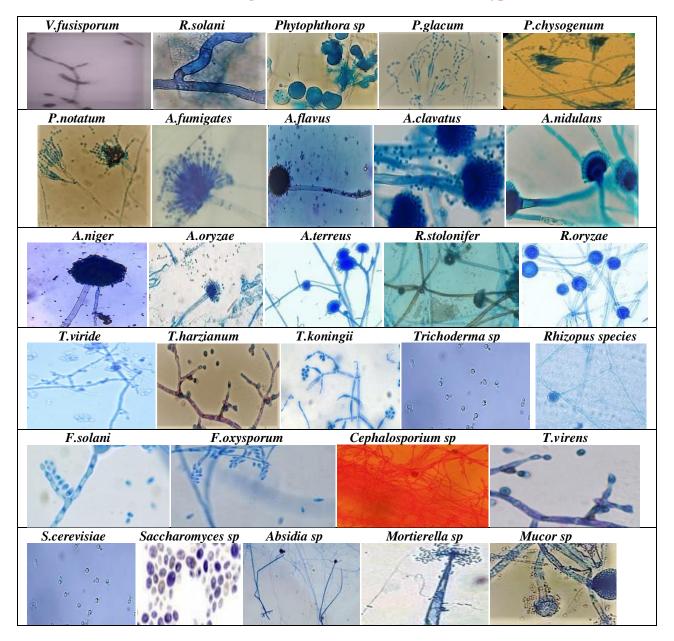
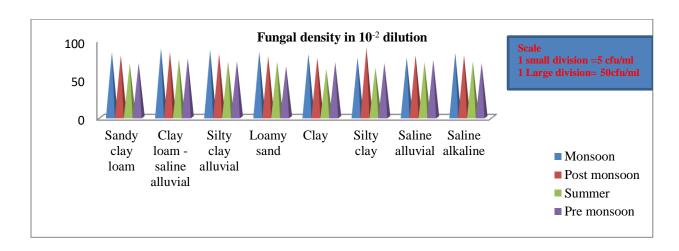
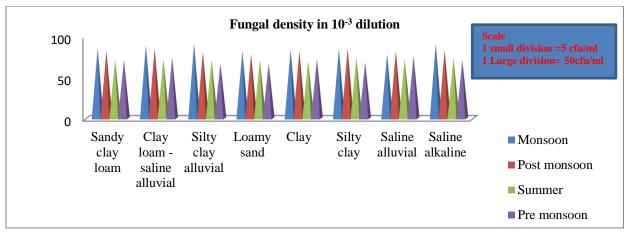
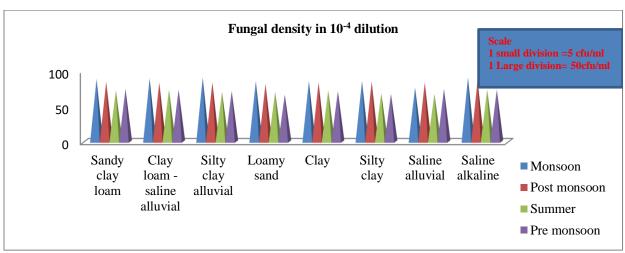


Fig 4.3: Fungal density of different seasonal soil types of Thruvarur district







4.5.1 Synthesis of silver nanoparticles

Filtrate without cells of *E.coli*, *Klebsiella sp.*, *Enterobacter sp.*, *Proteus sp.*, *Pseudomonas sp.*, and *Bacillus sp.* were mixed with silver nitrate solution and cultured in the dark for 72 hours in a rotary shaker. The colour of the samples changed from practically colourless to brown, indicating the creation of silver nanoparticles in the reaction mixture. During the incubation period, the colour intensity was raised. The activation of surface Plasmon vibrations caused the brown colour to develop. When incubated in the same conditions, the control revealed no change in the colour of the combination (Plate-24).

4.5.2 UV-VIS Spectrophotometric analysis

UV-Visible Spectroscopic analysis was used to create colloidal silver nanoparticles at first. A high peak was identified in the UV-Visible spectrum between 420 nm, confirming the presence of silver nanoparticles and the reading was indicated as the concentration of silver nanoparticle synthesis (Table-4:1).

Table 4:1: OD values of UV-VIS Spectrophotometric analysis for production of silver nanoparticles

Anal	lysed sample	Time (hours)							
		0	24	42	72				
	Blank	0.0	0.0	0.0	0.0				
	E.coli	0.14	0.23	0.34	0.38				
	Klebsiella sp	0.16	0.20	0.31	0.42				
Test	Enterobacter sp	0.19	0.38	0.53	0.85				
organisms	Proteus sp	0.26	0.31	0.43	0.63				
	Pseudomonas sp	0.31	0.42	0.47	0.54				
	Bacillus sp	0.34	0.36	0.42	0.52				

4.5.3 Nitrate reductase assay

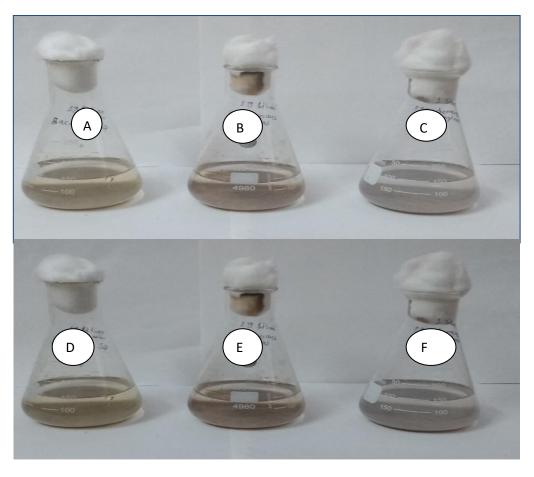
The nitrate reductase activity and presence of nitrate reductase enzyme in the culture filtrate of *E.coli, Klebsiella sp, Enterobacter sp, Proteus sp, Pseudomonas sp,* and *Bacillus*. As a result, the activity of nitrate reductase and the presence of nitrate reductase enzyme in the isolate indicate that silver nitrate is reduced to silver nanoparticles (Table - 4.2).

Table 4.2: OD values of UV-VIS Spectrophotometric analysis for nitrate reductase assay

Anal	lysed sample	Time (hours)							
		0	24	42	72				
	Blank	0.0	0.0	0.0	0.0				
	E.coli	0.28	0.35	0.41	0.48				
	Klebsiella sp	0.35	0.51	0.66	0.70				
Test	Enterobacter sp	0.35	0.47	0.54	0.68				
organisms	Proteus sp	0.37	0.42	0.50	0.54				
	Pseudomonas sp	0.36	0.42	0.46	0.53				
	Bacillus sp	0.26	0.34	0.38	0.46				

Plate-24

Synthesis of silver nano particle from certain isolated bacterium



Note: A-Escherichia coli, B-Klebsiella species, C-Enterobacter species, D-Proteus species, E-Pseudomonas species, F-Bacillus species

4.6.1 Soil nutrients influence the growth of traditional plant in Thiruvarur district

Plants such as *Oryza sativa* (paddy), *Vigna mungo* (black gram), and *Vigna radiata* have a high prevalence of bacterial, fungal, and actinomycetal isolates that assist the breakdown of organic substances, consequently impacting plant growth (green gram). The water content of the soil was changed to 50% water holding capacity; plants grew well at this water content as opposed to below 50% water holding capacity (Tables 5.1 and 5.2; Plate – 25 and 26).

Table 5.1: Frequent distribution of microbial communities influence the plant growth (soil water content adjusted 50%)

S.No	Name of the	S1	S2	S3	S4	S5	S6	S7	S8
	parameter								
		Vigna	mungo	(Black	gram)	•	•	•	
01	Germination Percentage	93	94	92	93	98	98	92	93
02	Seedling length (cm/seedling)	14	13	12	12	12	12	13	12
03	Fresh weight of seedling (g/seedling)	5.00	3.50	3.82	4.21	4.81	3.81	3.60	3.41
04	Dry weight of seedling (g/seedling)	3.50	2.01	2.12	2.80	2.92	2.08	1.76	2.50
05	Shoot length (cm)	4.26	3.60	3.60	3.78	4.02	3.96	3.00	3.45
06	Root length (cm)	6.00	5.74	5.46	5.07	5.04	4.80	5.00	3.00
		0	ryza sat	iva (Rice	e)				
01	Germination Percentage	93	94	92	93	98	98	92	93
02	Seedling length (cm/seedling)	22	20	19	17	15	15	13	12
03	Fresh weight of seedling (g/seedling)	4.23	3.80	4.09	3.89	3.56	3.52	3.45	4.31
04	Dry weight of seedling (g/seedling)	3.02	2.01	2.46	2.24	2.18	2.02	2.20	2.42
05	Shoot length (cm)	3.42	3.00	2.86	2.94	2.56	2.85	2.67	2.65
06	Root length (cm)	3.00	2.89	3.02	2.45	2.83	3.00	2.98	2.95
		Vigna	radiata	(Green	gram)				
01	Germination Percentage	94	93	94	90	92	92	92	92
02	Seedling length (cm/seedling)	12	11	10	11	10	09	12	10
03	Fresh weight of seedling (g/seedling)	4.56	4.00	4.02	3.89	4.00	3.98	4.02	4.02
04	Dry weight of seedling (g/seedling)	3.00	2.89	2.86	2.04	2.78	1.92	2.70	2.02
05	Shoot length (cm)	4.22	3.24	3.03	3.02	2.89	2.94	2.56	2.59
06	Root length (cm)	3.45	3.67	2.63	2.84	2.56	2.73	2.94	2.63

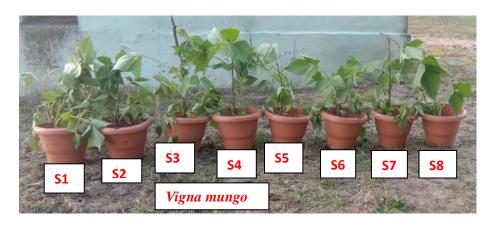
Note: S1- Sandy clay loam, S2- Clay loam saline alluvial, S3- Silty clay alluvial, S4- Loamy sand, S5- Clay, S6- Silty clay, S7- Saline alluvial and S8- Saline alkaline

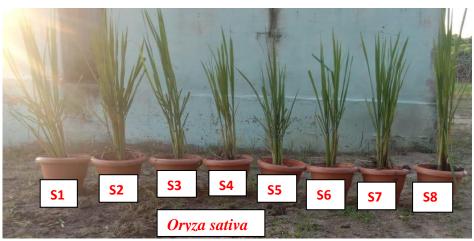
Table 5.2: Frequent distribution of microbial communities influence the plant growth (soil water content adjusted below 50%)

S.No	Name of the	S1	S2	S3	S4	S5	S6	S7	S8
	parameter								
Vigna mungo (Black gram)									
01	Germination Percentage	72	68	59	63	58	68	52	53
02	Seedling length (cm/seedling)	08	06	08	07	08	08	07	06
03	Fresh weight of seedling (g/seedling)	4.00	3.23	3.24	3.58	3.82	3.43	3.02	3.31
04	Dry weight of seedling (g/seedling)	3.20	2.08	2.05	2.50	2.42	2.38	1.46	2.00
05	Shoot length (cm)	3.26	3.10	3.10	3.18	3.02	3.26	2.00	3.25
06	Root length (cm)	3.00	3.74	3.46	3.07	3.04	3.20	3.02	2.80
		O	ryza sati	va (Rice	e)				
01	Germination Percentage	73	64	72	43	58	68	52	63
02	Seedling length (cm/seedling)	162	10	12	12	11	10	08	10
03	Fresh weight of seedling (g/seedling)	3.23	2.80	3.09	2.89	2.56	3.02	3.15	3.31
04	Dry weight of seedling (g/seedling)	3.12	2.11	2.16	2.00	2.00	2.22	2.12	2.02
05	Shoot length (cm)	3.22	3.10	2.16	2.94	2.16	1.85	2.17	2.05
06	Root length (cm)	2.00	2.29	3.12	2.25	2.13	2.00	2.08	2.05
		Vigna	radiata	(Green	gram)				
01	Germination Percentage	67	63	64	58	52	52	58	50
02	Seedling length (cm/seedling)	07	05	06	06	08	06	06	07
03	Fresh weight of seedling (g/seedling)	3.56	3.00	3.02	2.89	3.00	2.98	3.02	3.02
04	Dry weight of seedling (g/seedling)	2.00	1.72	1.60	1.65	1.24	1.34	1.70	1.02
05	Shoot length (cm)	3.22	2.24	2.03	2.02	2.00	2.04	2.06	2.29
06	Root length (cm)	2.05	2.67	2.33	2.34	2.56	2.43	2.34	2.13

Note: S1- Sandy clay loam, S2- Clay loam saline alluvial, S3- Silty clay alluvial, S4- Loamy sand, S5- Clay, S6- Silty clay, S7- Saline alluvial and S8- Saline alkaline

Plate - 25
Frequent distribution of microbial communities influence the plant growth (soil water content adjusted 50%)

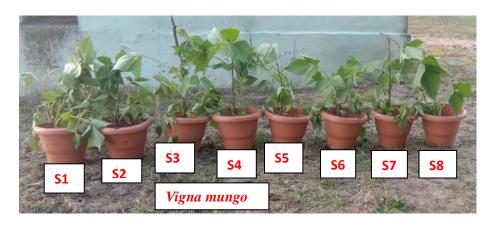


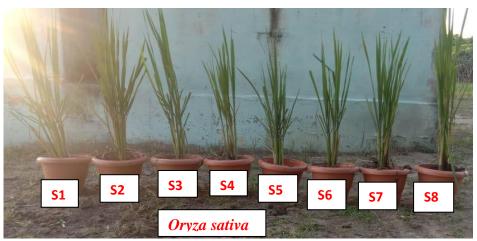




Note: S1- Sandy clay loam, S2- Clay loam saline alluvial, S3- Silty clay alluvial, S4-Loamy sand, S5- Clay, S6- Silty clay, S7- Saline alluvial and S8- Saline alkaline

Plate - 26
Frequent distribution of microbial communities influence the plant growth (soil water content adjusted below 50%)







Note: S1- Sandy clay loam, S2- Clay loam saline alluvial, S3- Silty clay alluvial, S4- Loamy sand, S5- Clay, S6- Silty clay, S7- Saline alluvial and S8- Saline alkaline

4.7.1 Molecular characterization of Predominant organism

Using agarose gel electrophoresis, the molecular characterisation of primarily exhibiting microbial species detected by total microbial community DNA was isolated and segregated. The date of submission of the isolated bacteria by GenBank (05-Apr-2021) and their Accession number – MW858250, Version – MW858250.1. The purpose of this work is to use 16S rRNA gene partial sequencing to characterise the gene sequence of primarily presenting isolates from key soil types in Thiruvarur district, as well as to identify and analyse the phylogenetic connection of this bacteria. The 16S rRNA gene sequence is approximately 850bp long, with both linear and conserved sections (Plate-27, 28 and 29).

Plate-27

16S rRNA gene sequencing of predominant bacteria isolated from major soil types of Thiruvarur district

4/15/2021	Bacillus subfilis strain RA 16S ribosomal RNA gene, partial sequence - Nucleofide - NCBI
Nucleotide	v
GenBank ▼	
Bacillus GenBank: M	s subtilis strain RA 16\$ ribosomal RNA gene, partial sequence
FASTA GR	
LOCUS	MW858259 850 bp DNA linear BCT 11-APR-2021
DEFINITION	Bacillus subtilis strain RA 165 ribosomal RNA gene, partial sequence.
VERSION KEYWORDS	MW858250 MW858250.1
	Bacillus subtilis Bacillus subtilis
	Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus.
	1 (bases 1 to 850) Arulmozhi,R., Kannahi,M., Shijila Rani,A.S. and Ambikapathy,V.
TITLE	characterization of Bacillus substilis from soil sample
	Unpublished 2 (bases 1 to 850)
AUTHORS	Arulmozhi,R., Kannahi,M., Shijila Rani,A.S. and Ambikapathy,V.
TITLE JOURNAL	Direct Submission Submitted (05-APR-2021) MICROBIOLOGY, INDIAN BIOTRACK RESEARCH
COMMENT	INSTITUTE, KARPAGAM NAGAR, THANJAVUR, TAMILNADU 613005, India ##Assembly-Data-START##
COPPLEM	Sequencing Technology :: Sanger dideoxy sequencing
FEATURES	##Assembly-Data-END## Location/Qualifiers
source	1850
	/organism-"Bacillus subtilis" /mol_type-"genomic DNA" /strain-"RA"
	/isolation_source="soil"
	/host="soil" /db xref="taxon:1423"
rRNA	<1>850
ORIGIN	/product="165 ribosomal RNA"
	togtaacaa ggtaacogag tggtagtttg atcatggoto aagggaatao gtaaactggg
	accttgagt gcagaagagg agagtggaat tagagtggaa ttccacgtgt agcggtgaaa gcgtagaga tgtggaggaa caccagtggc gaaggcgact ctctggtctg taactgacgc
	gaggagcga aagcgtgggg agcgaacagg attagatacc cctggtagtc cacgccgtaa
	cgatgagtg ctaagtgtta gggggtttcc gccccttagt gctgcagcta acgcattaag actccgcct ggggagtacg gtcgcaagac tgaaactcaa aggaattgac gggggcccgc
	caagoggtg gagoatgtgg tttaattoga agoaaogoga agaaoottao caggtottga atoototga caatootaga gataggaogt cocottoggg ggoagagtga caggtggtgo
	antititya taantitaga garaggargi titititggg ggragagiga taggitggig taggitgtig tragetigtig tigtgagatg tigggitaag ticcgicaacci
541 t	tgatcttag ttgccagcat tcagttgggc actctaaggt gactgccggt gacaaaccgg
	ggaaggtgg ggatgacgtc aaatcatcat gccccttatg acctgggcta cacacgtgct caatggaca gaacaaaggg cagcgaaacc gcgaggttaa gccaatccca caaatctgtt
	tragttrgg atrgragtrt graactrgar tgrgtgaagr tggaatrget agtaatrgrg
841 g	atcagcatg ccgcggtgaa tacgttcccg ggccttgtac acaccgcccg tcactcacga agagagttt
//	

https://www.ncbl.nlm.nlh.gov/nuccore/MW858250

Plate-28

16S rRNA gene sequencing of predominant bacteria *Bacillus subtilis* isolated from major soil types of Thiruvarur district

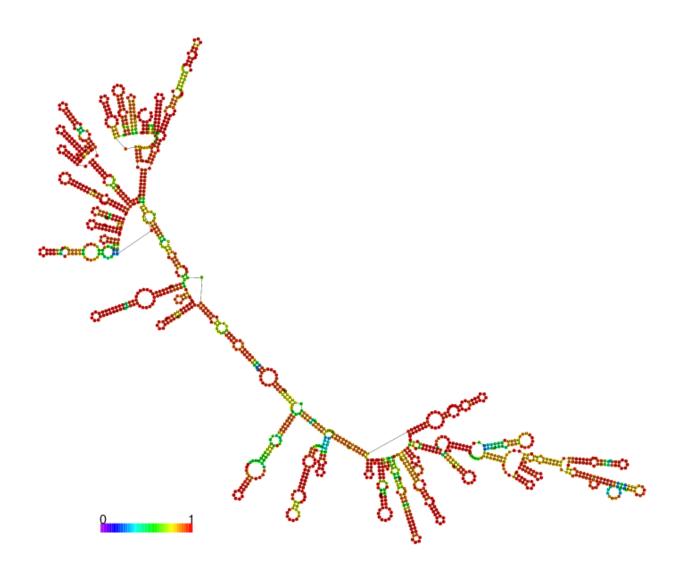
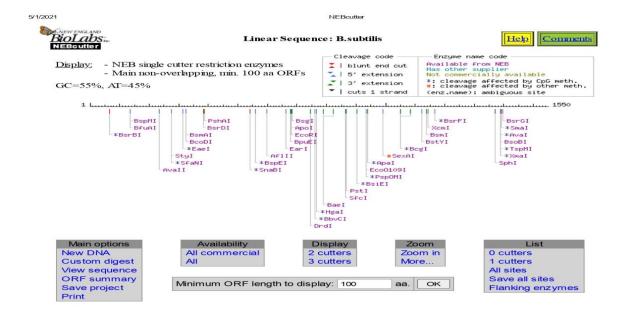


Plate-29

16S rRNA gene sequencing of predominant bacteria (*Bacillus subtilis*) linear sequence isolated from major soil types of Thiruvarur District



nc2.neb.com/NEBcutter2/cutshow.php?name=acf2e248-B.subtilis

4.8.1 Biocontrol activity

The pathogen's of rice bacterial blight was isolated and identified. *Trichoderma* viride, *Pseudomonas fluorescence*, and *Bacillus subtilis* were used to test the *Rhizoctonia* solani isolate against 25, 50, 75, and 100 μl concentrations of the three bacteria. The biocontrol measurements of *Trichoderma viride*, *Pseudomonas fluorescence*, and *Bacillus* subtilis against *R.solani* were 29 mm, 25 mm, and 23 mm, respectively, at a concentration of 25μl. The biocontrol measurements of *Trichoderma viride*, *Pseudomonas fluorescence*, and *Bacillus subtilis* against *R.solani* were 36mm, 30mm, and 25mm, respectively, at a concentration of 50 μl.

The biocontrol measurement of *Trichoderma viride*, *Pseudomonas fluorescence*, and *Bacillus subtilis* against *R.solani* at 75 μl concentration was 42mm, 38mm, and 32mm, respectively, for *Trichoderma viride*, *Pseudomonas fluorescence*, and *Bacillus subtilis*. The biocontrol measurements of *Trichoderma viride*, *Pseudomonas fluorescence*, and *Bacillus subtilis* against *R.solani* were 57mm, 45mm, and 40mm, respectively, at a concentration of 100 μl (Fig-5.1; Plate-30).

Figure 5.1: Determination of biocontrol activity of different microorganisms against *Rhizoctonia solani*

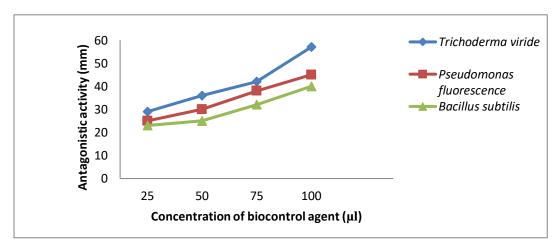
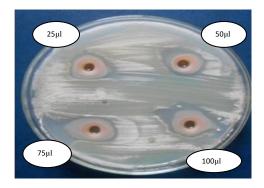
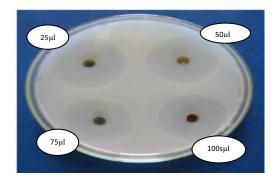


Plate-30

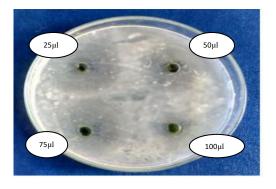
Biocontrol activity of certain microorganisms isolated from different soil types of Thiruvarur district



Pseudomonas fluorescens



Trichoderma viride



Bacillus subtilis

4.9.1 Formulation of Microbial fertilizer

Biofertilizers are usually prepared as carrier based inoculants containing effective organisms. These identified effective species were used for the preparation of bioformulation using organic manure as carrier material and evaluated for their viable count during storage period of 150 days in laboratory conditions. The use of organic manure in soil as bioformulation is useful because it increases the soil pH, converts the nutrients in the available form and supplies nutrients to soil. The use of these native organisms as biocontrol agent and biofertilizers helps in reducing the use of chemical pesticides and fertilizers and also effective in reducing the cost of cultivation and maintaining the natural fertility of soil (Plate-29 and 30).

4.9.2 Morphometric analysis of Vigna mungo

After 15th days in cultivation of *Vigna mungo*, seed germination observed by T1 (*Azospirillum* only), T2 (*Rhizobium* only), T3 (*Azospirillum* + *Rhizobium*) and C (control). The maximum morphometric analysis i.e., seedling length (cm), weight of seedlings (fresh and dry), vigour index, shoot length and root length were 9.3(cm), 5.3 (mg), 4.5 (mg), 892.8, 1.91, 7.0 (cm) and 4.2 (cm) respectively. In 30 and 45th days of cultivation, the maximum morphometric parameters were observed in combined inoculation of *Rhizobium* and *Azotobacter* denoted in the table – 6.1.

4.9.3 Phytochemical analysis of Vigna mungo

Biometric analysis of different treatment of *biofertilizer* soaked *V.mungo* seeds were studied after 15th and 30th days of experiment and the results were predicted in the Table 6.2. The carbohydrates were 2.5, 3.0 and 3.1 mg/ml; protein was 18.01 18.9 and 20.01 mg/ml and chlorophyll content was 0.05, 0.09 and 0.13 µg/ml respectively recorded in different treatmet of biofertilizer on15th day of growing plants. Other hand 30th day of

growing plant analysed in carbohydrates, protein, chlorophyll content was 0.6, 2.9, 4.12 mg/ml; 14.25, 19.36, 20.03 mg/ml and 0.01, 0.09 and 0.2 µg/ml recorded respectively *Rhizobium* sp. treated *V.mungo* plant (Table-6.2)

Table-6.1 Morphometric analysis of formulated biofertilizer in Vigna mungo growth

S.No	Name of the parameter	(C)	(T1)	(T2)	(T3)
		15 th day			
01	Germination Percentage	78	84	85	96
02	Seedling length (cm/seedling)	7.3	8.5	8.4	9.3
03	Fresh weight of seedling(mg/seedling)	3.4	4.8	4.6	5.4
04	Dry weight of seedling (mg/seedling)	2.2	3.4	3.5	4.5
05	Vigour Index	569.4	714	714	892.8
06	Tolerance index	-	1.55	1.50	1.91
07	Shoot length (cm)	5.3	6.4	6.2	7.0
08	Root length (cm)	2.2	3.4	3.2	4.2
	30 th da	y			
09	Seedling length (cm/seedling)	11.7	14.6	14.5	15.8
10	Fresh weight of seedling (mg/seedling)	7.4	8.9	8.5	9.6
11	Dry weight of seedling (mg/seedling)	6.2	7.2	7.5	8.2
12	Shoot length (cm)	11.2	13.4	13.5	14.8
13	Root length (cm)	5.11	7.3	7.8	9.2
14	Number of root nodule	7	9	10	15
15	Total leaf area (cm ²)	2.06	3.34	3.72	4.2
16	Fresh weight of plant (mg)	13.00	15.03	15.90	17.56
17	Dry weight of plant (mg)	10.20	13.67	13.92	15.62
	45 th da	y			
18	Total leaf area (cm ²)	3.00	4.78	4.62	5.04
19	Fresh weight of plant (mg)	17.46	20.43	19.24	23.54
20	Dry weight of plant (mg)	14.32	16.56	15.45	20.32
21	Number of pod/plants	12	17	18	25
22	Number of seeds/pod	04	05	06	07
23	Dry weight of pod/plant (mg)	3.46	4.73	4.23	5.67
24	Seed yield	33	52	46	62

Note: T1- Azospirillum only, T2- Rhizobium only, T3- Azospirillum + Rhizobium, C - Control

 ${\bf Table \hbox{-} 6.2\ Phytochemical\ analysis\ of\ formulated\ biofertilizer\ in\ \it Vigna\ mungo\ growth}$

S.No	Name of the parameter	15 th day					
		C	T1	T2	T3		
01	Carbohydrate (mg/ml)	1.8	2.5	3.0	3.1		
02	Protein (mg/ml)	15.02	18.01	18.91	20.01		
03	Chlorophyll (µg/ml)	0.03	0.05	0.09	0.13		
		30 th day					
04	Carbohydrate (mg/ml)	1.2	2.6	2.9	4.12		
05	Protein (mg/ml)	14.02	14.25	19.36	20.03		
06	Chlorophyll (µg/ml)	0.02	0.01	0.09	0.2		

Note: T1- Azospirillum only, T2- Rhizobium only, T3- Azospirillum + Rhizobium, C - Control

Effect of formulated biofertilizer on Vigna mungo

Plate-31



T 1- Azospirillum only

T 2- Rhizobium only

T 3- Azospirillum + Rhizobium

C - Control

CHAPTER V

DISCUSSION

5.1 Physico-chemical parameter analysis of soil

The soil type was discovered after physico-chemical examination of the soil near the microbiology laboratory at the University of Ilorin's main campus. All of the samples had a pH ranging from 7.10 to 7.81. According to the soil texture analysis, the soil is loamy sand, with a mean composition of 89 percent sand, 7% silt, and 4% clay, respectively. The water holding capacity ranged from 0.28 to 0.53 ml per gram. The moisture level varied between 2.10 and 5.23 percent. Loamy sand was discovered to be the soil type. According to Brown's work from 2003, this is correct.

The moisture content of a soil, according to Molin and Molin, 1997, is one of the most critical elements that impact the survival of soil microflora. Many additional physical and chemical aspects of the soil can be affected by textural changes. In the creation of soil, the texture of the soil is very important. Soils with a high proportion of big particles drain quickly and are less fertile. Soils with a very fine texture might be poorly drained and waterlogged, making them unsuitable for cultivation (Wayne *et al.*, 2007).

Joshi and Negi (2015) investigated the physicochemical features of two prominent forest types in the Western Himalaya (Uttarkhand's Chamoli and Champawat districts), namely oak and pine soils. The pH of oak soil (range 4.2-6.2) was found to be comparable to that of pine soil (range 4.3-6.3). The soils were determined to be mildly acidic in both cases. The pH of forest soils was found to be lower than that of cultivated soils, according to our findings. The dissolved material in an aqueous solution is measured by the soil EC, which is related to the material's

ability to conduct electric current. The EC values were found to be in the range of 0.2 to 0.7 dS m-1, which is quite low.

According to Tiwari *et al.*, 2016, the EC of the soils from B1 and B2 sites were 0.199 and 0.198 dS m-1, respectively. The experimental values of EC in agricultural areas were 0.2 and 0.7 dS m⁻¹, which were higher than the results recorded in 2013. The samples taken from olericulture land in the Bajpur region had the highest percentages of organic carbon and organic matter, at 1.64 percent and 2.85 percent, respectively.

Tewari and Pande (2013) reported comparable findings. The organic carbon content of the B1 site (sugar mill), which was 1.76 percent, was similar to that of the vegetable field soil, which was 1.64 percent. The amount of organic matter in the soils was found to be low, implying that they are low-level organic soils (3 to 19 percent OM content). The number of exchangeable cations per dry weight that soil can contain is known as cation exchange capacity. It's a critical soil feature that affects soil structure, stability, nutrient availability, pH, and the soil's response to fertilizers and other additions (Hazelton and Murphy, 2007).

The selected soil's high cation exchange capacity (31.24 to 51.75 meq/100 g soil) suggested that they included more clay and organic matter, as well as a high water retention capacity (50.00 % to 94.28 %). The WHC rises when organic carbon levels rise and the percentage of silt and clay particles in the soil rises, because clay and silt particles have a considerably larger surface area and can hold more water. When compared to pine soil, oak soil had a higher water retention capacity (64.6-65.5%) (range 52.3-45.0 %) Joshi and Negi (2015).

The basic macronutrients of soil are nitrogen, phosphorus, and potassium, which are the most crucial for plant health and performance. The amount of nitrogen in the soil ranged from 0.217 percent to 0.661 percent (agricultural soil from Khatima) (oak soil). Organic carbon (0.46-

1.64 percent) in pine soils was much lower than in oak soils, according to Joshi and Negi (2015). (0.85-3.28 %). Our research into forest soils yielded similar results. The vegetable fields were rich in accessible phosphorus due to the decomposition and recycling of old leaves or branches of mature plants (0.0105 %; oak soil and 0.0183 %; olericulture soil from Bajpur).

According to Tisdale *et al.* (1997), approximately 50% of phosphorus is present in organic form, and humus found in organic matter forms complexes with Al and Fe, protecting phosphorus fixation. The accessible potassium level in the soils ranged from 0.0181 percent (agriculture soil of Khatima) to 0.0463 percent (non-agricultural soil of Khatima) (oak soil). The presence of most of the mica (biotite and muscovite) in finer fractions may explain the significant positive association between accessible potassium and clay content (Chauhan, 2001). In comparison to agriculture and olericulure land use systems, soil characteristics such as WHC, percent OC, CEC, available nitrogen, and available potassium had a greater value in the forest land use system. There are some papers on soil property analysis from either agricultural areas or forest areas (Deb *et al.*, 2017), (Gairola Sumeet *et al.*, 2012).

The assessment of physicochemical qualities of soil under various land use types is the subject of one Ethiopian report. Muche *et al.*, (2015) found that the value of CEC and accessible potassium in natural forest soils (31.9 cmol+ /kg; 120 mg/kg) was higher than in cultivated field soil (14.4 cmol+ /kg; 10 mg/kg). The higher accessible potassium value in the natural forest could be attributed to the higher CEC of the forest soil.

The geomorphology and vegetation type of the area have complex interrelationships with soil and vegetation. The vegetation influences the soil properties, and the soil properties influence the vegetation. Changes in soil properties are caused by different tree species' selective absorption of nutrient elements and their capacity to return nutrients to the soil (Singh *et al.*,

1990). The relationship between the plant and the soil was also highlighted in this study. In addition, the study looked at the soil physico-chemical properties of growing areas and compared them to non-growing areas at nearly the same altitude to see how this plan improved soil fertility.

5.2 Microbial diversity

Furthermore, an uncultureable study of Gangotri soil reveals that it is rich in bacterial diversity, as evidenced by the presence of a large number of different bacterial taxa. Furthermore, the presence of many unclassified taxonomic sequences indicates the presence of novel bacterial diversity. Furthermore, Proteobacteria, Acidobacteria, and Actinobacteria were found in abundance in Gangotri soil, whereas Bacteroides and Firmicutes were found in greater abundance in Kandakhal soil. Firmicutes were the third most abundant phylum in Kandakhal, but their abundance was very low in Gangotri, indicating that high altitude has a negative impact on gram positive bacteria diversity (Demergasso *et al.*, 2004).

Due to a selective increase in proteobacterial diversity and a decrease in Firmicutes diversity, Gangotri soil has a high ratio of Gram-negative to Gram-positive bacteria. As a result, in high-altitude ecosystems, altitude has a significant impact on the ratio of Gram negative to Gram positive bacteria. Bacteroides, Gemmatimonadetes, Nitrospirae, Verrucomicrobia, Armatimonadetes, Cyanobacteria, Planctomycets, and Chloroflexi were among the bacterial phyla found in both soils. High altitude was found to be positively correlated with the abundance of Cytophaga, Flavobacterium, and Bacteroides (CFB). Many studies have reported the presence of these phyla in cold deserts (Yang *et al.*, 2006).

In both soils, the community composition of bacteria within the phyla mentioned above was significantly different. Alpha proteobacteria (16.88%) were the most abundant bacterial class of Proteobacteria in Gangotri, followed by Beta proteobacteria (9.44%). Delta and Gamma

proteobacteria (6.17 percent and 6.17 percent, respectively) (5.9 percent). However, in Kandakhal soil, all of the above-mentioned proteobacteria classes were evenly distributed, with each having an abundance of 8%. In cold deserts, the distribution of proteobacterial classes is sensitive to seasonal variation, with Beta proteobacteria dominating in the summer and Alpha proteobacteria showing equal abundance throughout the year. Despite the fact that Beta proteobacteria is the most abundant proteobacterial class at high altitudes, little is known about Proteobacteria distribution in glacier ecosystems (Skidmore *et al.*, 2005).

In previous studies of permafrost glaciers, the Alpha proteobacteria was found to be the most prevalent proteobacteria in glacier soil. Thus, glacier conditions at Gangotri could be a factor in determining Alpha proteobacteria dominance in Gangotri soil. Incubation in an indigenous diffusion chamber resulted in the isolation of bacteria that had not been previously identified and were thought to be novel. This was the first time culturable bacteria were isolated from high altitude cold desert soil using a diffusion chamber based on microbial diversity and higher altitude soil characteristics. Paenarthrobacter nitroguajacolicus, Dyadobacter endophyticus, Arthrobacter pascens, Paenarthrobacter siccitolerans, Pseudomonas mandelii, Acidovorax facilis, Pantoea gaviniae, Pseudomonas baetica, Pseudomonas frederiksbergensi, and Arthrobacter equi. When culturable isolates were compared to unculturable isolates, it was discovered that these isolates belonged to the phyla Proteobacteria, Actinobacteria, and Bacteroides, which were the most dominant bacterial phylum in Gangotri soil. The majority of these isolates had never been found in the Gangotri and other WIH regions. As a result, these findings show that the "Indigenous Diffusion Chamber" is effective in isolating rare bacterial species. Furthermore, full-length sequencing and phylogenetic analysis of one isolate revealed that it belongs to the Dyadobacter genus, with 97.6% similarity to Dyadobacter endophyticus 65.

(T). Although previous research has shown that *Dyadobacter endophyticus* 65 (T) is an endophyte of the maize plant, no such cropping was done at Gangotri's high altitude (Goa *et al.*, 2016).

Psychrophilic nitrogen-fixing bacteria from Gangotri soil were isolated due to the high altitude and constant cold stress. *Pseudomonas helmanticensis*, *Arthrobacter humicola*, *Brevibacillus invocatus*, and *Pseudomonas mandelii* were identified as psychrophilic diazotrophs after molecular characterization. To the best of our knowledge, these isolates have been described as cold adapted but without the ability to fix nitrogen. Furthermore, nitrogen fixation is an enzymatic process that is negatively influenced by temperatures other than the nitrogenase optimal temperature (Stal, 2017).

Each season's fungal population was significantly different, demonstrating the impact of varying climatic conditions on fungal diversity. Increased soil moisture and optimum temperature can be attributed to higher fungal density and diversity during rainy and summer seasons. Low fungal population and thus low rate of nutrient release in soil, as indicated by lower values of C, N, and organic matter in winter, can be attributed to comparatively low temperature, moisture, and total N availability of the soil. Seasonal variations in fungal population have also been reported (Dwivedi, 1966; Persiani *et al.*, 1998; Rama Rao, 1969).

They also discovered significant seasonal variations in the population of soil microfungi. Seasonal variation of fungal population in some soil types was discussed by Dkhar and Mishra (1987), who concluded that changes in soil organic content, water holding capacity, temperature, and pH of the respective season were likely factors associated with increases and decreases in fungal population. The current study also came up with similar results. During these three seasons, however, there was a lot of overlap in fungal species. Furthermore, some fungal species

only appeared after distinct seasonal intermissions, whereas others were prevalent throughout the year. These species were isolated repeatedly throughout the year; some species were restricted to a single season due to unsuitable conditions in other seasons.

The presence of certain fungal species in a given area is influenced by the type of vegetation that grows there (Entry and Emmingham, 1996), as well as topography (Tsai *et al.*, 2007). Only a few species predominate in an area due to the strong effect of environmental conditions on the other species, according to Jha *et al.*, (1992). The dominant species in this study were *Aspergillus, Penicillium* and *Trichoderma*. Fungal species with a high rate of sporulation and dispersion were found to be dominant, according to Schimel (1995). Different soil parameters influence changes in population and relative abundance of fungal species. Variation in soil physico-chemical properties has a significant impact on fungal population (Schimel, 1995). The relationship between fungal population and soil pH, C, moisture content, N, and available K demonstrates the importance of these physico-chemical factors on fungal species. The impact of soil moisture on fungal activity by increasing C availability has also been well demonstrated (Kennedy *et al.*, 2005; Schreven, 1967).

5.3 Biosynthesis of silver nano particle

Bacteria were isolated using a nutrient agar medium supplemented with various concentrations of AgNO₃. Bacteria that could tolerate high concentrations of AgNO₃ were isolated as the concentration of AgNO₃ in the nutrient agar medium was gradually increased. The color of all bacterial cultures changed from creamy to brown. This could be because silver has accumulated inside the bacterial cells. *Staphylococcus aureus, Pseudomonas aeruginosa*, and *E.coli* were grown on AgNO supplemented media, and a similar observation was made. According to Lara *et al.* (2010), this color change indicates silver resistance. This study used a

higher concentration of 30 mM AgNO₃ than a previous study in which multidrug-resistant *Pseudomonas aeuruginosa* tolerated 25 mM AgNO₃.

Between the outer membrane and the plasma membrane, the majority of the accumulated silver was deposited as seed-like particles. Our deposits are very small (5-15 nm) compared to previous studies using *P.stutzeri* Ag259 (35-46 nm), which could be due to differences in cell growth and metal incubation conditions (Haefeli *et al.*, 1984).

Only sonicated cell lysate supernatant produced *E.cloacae* Ism26 AgNPs, but neither culture free supernatant nor bacterial pellets produced AgNPs. The lack of extracellular enzymes required for AgNO₃ reduction could explain this. Previously, it was reported that gram-negative bacteria, such as *K.pneumoniae* and *E.coli*, as well as gram-positive bacteria, such as *Bacillus indicus* and *Bacillus cecembensis*, could synthesise AgNPs in cell-free supernatants (Natarajan *et al.*, 2010). Another study found that whole bacterial cells were capable of producing AgNPs (Seshadri *et al.*, 2012).

The current findings revealed that AgNP synthesis was successful only when incubated in light, implying that light may be a critical factor in the AgNP biosynthesis process. This corresponds to previous research on both gram negative and gram positive bacteria (Shivaji *et al.*, 2011). The synthesis of AgNP by *Klebsiella pneumoniae* was found to be aided by light, and the reaction did not change color when conducted in the dark. These findings highlight the importance of light in the production of AgNPs by certain bacterial species. Nonetheless, *Streptomyces platensis* has been shown to synthesise AgNPs under dark conditions in a recent study (Morsy, 2015).

The ability of bacteria to synthesise AgNPs is thought to be dependent on two major factors. The first is the presence of the appropriate enzymatic machinery, which can be found on

the bacterial wall or inside the cell. The presence of light, on the other hand, facilitates the synthesis process (Nam *et al.*, 2008). The effect of light could be due to the activation of reducing agents in the culture supernatant, resulting in the release of electrons for the reduction of Ag^+ to Ag^0 nanoparticles (Wei *et al.*, 2012).

5.4 Pot culture experiment

Because the assessed plant and soil parameters differed little between the constantly moist treatment and the one dry week followed by three wet weeks, the hypothesis (plant growth and microbial biomass will lengthen the dry period with a greater effect if the dry period is in the early stages of plant growth) cannot be categorically accepted or rejected. However, when compared to CW, two or more dry weeks reduced shoot and root biomass and MBC while increasing available N. In agreement with previous studies (Matsui and Singh, 2003; Wang *et al.*, 2014), the effect of low water content was greater for shoots than roots because plants invest relatively more carbon into roots than shoots when water availability is low to access the remaining water.

Cumulative respiration in planted and unplanted soil decreased with water content, which can be explained by the thinning of water films around soil particles as soil dries, reducing substrate diffusion to cells. Water may also be drawn out of the cells when the water content is very low (Asch *et al.*, 2005). As a result, on day 25, the ratio of cumulative respiration to MBC was twofold higher at 50% than at 10% WHC. Due to greater substrate availability, the relative reduction of cumulative respiration with water content was slightly lower in planted soil than unplanted soil (at 10% WHC compared to 50% WHC, cumulative respiration was 49 and 42 percent in planted and unplanted soil, respectively). Microbes may have access to substrates even when the water film is thin at higher substrate concentrations in the soil solution. This is

supported by a two-fold higher ratio of cumulative respiration to MBC on day 25 in planted soil compared to unplanted soil at 10% WHC.

5.5 Molecular characterization

The 16S rRNA sequence of bacteria was compared using a preferred genetic technique. The 16S rRNA sequence was widely used as a molecular clock to estimate the relationship between bacteria (phylogeny), but it became more important as a means to identify an unknown genus or species according to (Sacchi *et al.*, 2002). For several reasons, 16S rRNA gene sequencing was used to study bacterial phylogeny (Amann *et al.*, 1995) and taxonomy, as well as the most common genetic marker used in housekeeping.

Among the reasons are the following: When the 16S rRNA gene is present in almost all bacteria, multi-gene families or operons are common. (ii) While it has been suggested that changes in random sequence provide a more accurate measure of time, the function of 16S rRNA has remained constant over time. (iii) The gene's size (1500 bp) is adequate for information (Patel, 2001). It is a crucial microbiological method based on rRNA analysis that is used to not only explore microbial diversity but also to identify new strains. This study used a commercial source of bacterial sample to determine the bacterial strain isolation. Two hundred and sixty-four isolates were obtained for further investigation. Colonies were isolated from mixed populations and sub-cultured on nutrient agar plates to identify isolated bacteria based on biochemically analysed activities in order to obtain pure culture. *Clostridium butyricum, Thiobacillus denitrificans*, and *Thiobacillus thioparus* were identified using a molecular approach for the activities of catalase, oxidase, MR-VP test, citrate test, starch hydrolysis, gelatin test. The standard protocol was used to isolate bacterial genomic DNA (Hoffman and Winston, 1987).

The presence of the isolated bacterial genome was confirmed using an ethidium bromide-stained 0.8 percent agarose gel. Along with the DNA marker, an intense band was visible. The extracted DNA was used to amplify the 16S rRNA gene as a tempelate. The 16S rRNA gene fragments were sequenced and amplified using the universal primers 27F/1429R for *Clostridium butyricum*, Bac967Fd/Bac967Rd for *Thiobacillus denitrificans*, and Bact363F/Bact363R for *Thiobacillus thioparus*. The ideal temperature for annealing has been determined to be 55°C.

The percentage of sequencing matching for all closely related data was calculated, and a homology search was conducted using BLAST, which revealed that *Clostridium butyricum* strain CDC 51208 has a 100% identity and the NCBI Gene Bank accession number is M59085.1, with an E-value of 0. Similarly, the E-value for *Thiobacillus denitrificans* strain ATCC 25259 is 0 and the NCBI Gene Bank accession number is CP000116.1. NCBI Gene accession no: HM173633.1, E - value equal to 0 for all closely related data, *Thiobacillus thioparus* strain Pankhurst T4 showed 99-100 percent identity. For the sequences of the bacterial isolates, a phylogenic tree has been constructed to show the genetic relationship between them. With the help of a phylogenic tree, all closely related homologous data shows the origin of evolutionary identified bacteria. *Thiobacillus denitrificans* strain ATCC 25259, *Clostridium butyricum* strain CDC 51208, and *Thiobacillus thioparus* strain.

5.6 Formulation of biocontrol agent

In comparison to other pathogens, the results of dual culture revealed that *Trichoderma* isolates used against *Sclerotium rolfsii* grew quickly and effectively (*Sclerotionia sclerotiorum*, *Fusarium solani* and *Rhizoctonia solani*). The dual culture technique was used to investigate the *in vitro* efficacy of a biocontrol agent against a soil-borne pathogen. For a reliable result, three replications of *Trichoderma* species were used in this technique to calculate average diameter

growth of respective pathogens. On the fourth day of incubation, the colony growth of *Sclerotium rolfsii* was found to be covered by the growth of the test fungal pathogen, which was found to be highly inhibited. *Sclerotium rolfsii*, which causes wilt and rot diseases in plants, showed excellent antimicrobial activity against *Trichoderma* species isolate TS 215. In another study, the damping off disease caused by *Sclerotium rolfsii*, an important disease of tomato (*Lycopersicon esculentum*) and other vegetable crops, was reduced by 52-62 percent when treated with the biocontrol agent *Trichoderma harzianum* (Okereke and Wokocha, 2006).

Similarly, isolates of *Trichoderma* inhibited *Rhizoctonia solani* mycelium growth by 66.08-29.07 percent in this study, whereas three different isolates of *Trichoderma* inhibited *Rhizoctonia solani* mycelium growth by 74.4-67.8 percent in another study (Asad *et al.*, 2004).

Some of the antagonist's tests were not found to be very effective against test pathogens in vitro, but they may perform better in the field because their activities are dependent on the physico-chemical characteristics of the environment (Burgess and Griffin, 1967). Radial growth was also observed on a dual culture plate with *Trichoderma* species placed in the same plate. When pathogen colony growth and biocontrol agent colony growth collided, both showed their effects on each other, but *Trichoderma* isolates had fewer efficacies against pathogen growth. The biocontrol activity of *Trichoderma* isolate TS 215 was also demonstrated in this study against the soil-borne pathogen *Fusarium solani*, with an inhibition percentage of more than 60%. *Trichoderma harzianum*, isolates N-8, was found to effectively inhibit the pathogen's radial mycelia growth by 68.22 percent under *in vitro* conditions, similar to the results of other experiments (Barari and Foroutan, 2013).

The antagonists' inhibition may be due to the release of antibiotics or antibiotic-like substances, or hyphal parasitism, which causes the pathogen's growth to be directly inhibited by

dissolving the hyphal wall, resulting in mycelium penetration, absorption, and lysis. Biological control is a promising tool for maintaining current levels of agricultural production by reducing the release of polluting chemical pesticides into the environment and freeing plants from soilborne pathogens, resulting in higher crop yields. It's a complicated process with several steps, but the main point of contact is between the fungal antagonist and the host (pathogen) surface. Plant pathogenic fungi and nematodes are a common problem, and chemical treatments are rarely effective. Biological control, according to this study, is a better option and may be beneficial, particularly against the soil-borne fungal pathogens Sclerotium rolfsii, Fusarium solani, Rhizoctonia solani and Sclerotionia sclerotiorum. One of the main benefits of biocontrol agents is that they are inexpensive and do not harm the crop. For biological control of fungal pathogens, Bacillus, Pseudomonas, and Trichoderma species are most commonly used. Trichoderma species is one of the fungal biocontrol agents used in this study. They're saprophytic fungi that can be found in almost any soil or rhizospheric microflora. Because of their ability to reduce the incidence of disease caused by plant pathogenic fungi, Trichoderma species have been chosen as potential biocontrol agents (Dubey et al., 2007).

Biocontrol active agents must be discovered in order to develop natural resources for controlling plant pathogens. This research is carried out by isolating and identifying *Trichoderma*. It is not only fungal pathogens that produce antibiotics, but also bacteria. Meanwhile, many fungi have beneficial effects on plant growth, such as increased agricultural product yield, increased soil nutrient yield, increased plant nitrogen fixing capacity, increased plant and soil nutrient uptake capacity, increased fertiliser utilisation efficiency, increased seed germination rate, and increased systemic resistance to plant diseases (Baker, 1987).

The current study focused on identifying and isolating fungus from various locations, which is crucial for the biocontrol agent's ability to protect plants from pathogens. The microorganism's role in waste management is important because it neutralises pollutants in contaminated waste. So, in this study, soil samples were collected from various locations and serial dilution was performed. Then, pour the nutrient agar plate and PDA broth on top of it. In addition, the same sample is transferred to PDA agar. The isolated fungal colonies were then after 2 to 3 days poured into PDA broth before being incubated for culture filtrate.

5.7 Formulation of biofertilizer

Molasses is a type of carrier medium that, when compared to rice water and sucrose, provides the best response to mustard growth and productivity in terms of leaf area and dry weight. Molasses is a sugar industry by-product that contains nitrogen compounds, trace elements, 34% sucrose, and a total carbon content of about 37%. Biotin, pantentonic acid, phosphorus, and sulphur are all abundant in molasses. Sulfur is a component of the amino acids cysteine, biotin, and thiamin, and plays a role in protein synthesis. Sulfur aids in the stabilisation of protein structure, oil synthesis, and chlorophyll formation, as well as reducing disease attacks on the plant body. Phosphorus, which is found in amino acids and the coenzymes NAD, NADP, and ATP, all of which are involved in cell division, promotes seed growth and flowering. Magnesium and calcium are also found in molasses. Magnesium, a component of chlorophyll, functions as a cofactor in most enzymes that activate the phosphorylation process, acting as a link between the pyrophosphate structure of ATP and ADP and enzyme molecules, as well as stabilising the particles in the protein synthesis configuration. Calcium, a component of cell walls, is important for cell integrity and membrane permeability (Wulandari *et al.*, 2011).

Positive interactions allow the bacterial population to thrive in an environment where they could not survive alone. Positive nitrogen-fixing bacteria interactions, such as exudates produced by plant roots, are sufficient for bacteria to grow. Plants will receive nutrients in the form of N nutrients provided by bacteria via the N fixation process. In addition, the formulation has a positive interaction with decomposer bacteria. N-fixing bacteria require C for nutrition growth in order to complete the fixation process, whereas decomposer bacteria are unaffected (Madigan *et al.*, 2000).

Organic fertilizer had a significant individual effect, as well as improving the vegetative characteristics of summer squash plants (Tomar *et al.*, 1995). Similarly, *Azotobacter* has an indirect impact primarily through improved soil structure (Hamdi, 1982) and the release of compounds such as polysaccharides that help keep soil particles together (Brown and Burlingham, 1968).

The development of vegetative growth may be due to the role of organic fertilizer in increasing soil ventilation by increasing porosity, and this animal fertilizer is considered a significant source of nutrient elements, particularly nitrogen and phosphorus, because it is an organic matter in the ground. These findings were in line with the current study's findings for improved plant growth. The ability of *Azotobacter* to fix atmospheric nitrogen, which may play a role in increasing the amount of mineral nutrient in the soil, could explain the improvement in plant vegetative attributes (Farida *et al.*, 2003). It also increases the surface area of root hairs, which leads to an increase in average mineral nutrient absorption (Abou-Hssein *et al.*, 2002, Mostafa, 2002). Similarly, Azotobacter could release specific chemical compounds that could affect plant growth enhancement (Arteca, 1996).

The release of growth-promoting phytohormones like indole acetic acid (Marha *et al.*, 2000), cytokinin (Tomar *et al.*, 1995), and gibberellins may be a significant effect of both bio and organic fertilizers on plant yield and quality (Forlain *et al.*, 1995). The physicochemical properties of soil, macro and micronutrient uptake, nitrogen transformation, and nutritional composition are all affected by these substances (Yadav and Lourduraj, 2005).

Excessive and continuous use of chemical fertilizers over a longer period of time has deteriorated soil character and reduced productivity. Vermicompost application increased leaf gas exchange and photosynthetic pigments in red chillies. The ratio of chlorophyll in beans determines the significant increase in photosynthetic pigments (Fernandez-Luqueno *et al.*, 2010).

The availability of chlorophyll in plants has a significant impact on the production of secondary metabolites and other important plant constituents. The amount of chlorophyll in the vermicompost and phosphobacteria-treated paddy plant increased in this experiment, which is related to an earlier report on marigold growth (Subler *et al.*, 1996).

CHAPTER – VI

SUMMARY

The current research focused on the microbial diversity and usage of several natural microorganisms in Thiruvarur's primary soil types.

- Monsoon, post-monsoon, summer, and pre-monsoon seasonal soil samples were collected in Thiruvarur district, Tamil Nadu. Among the eight types of soil found in this district were sandy clay loam saline alluvial, clay loam saline alluvial, silty clay alluvial, loamy sand, clay, silty clay, saline alluvial, and saline alkaline soil.
- > pH, temperature, moisture, loss of ignition, electrical conductivity, nitrogen, nitrate, ammonium, phosphorus, potassium, sulphur, and hydrogen sources were investigated in the soil samples.
- The sandy clay loam soil has high content of copper and available iron content. Clay loam soil has high content of calcium and potassium. Silty clay alluvial soil has rich nitrogen, phosphorus, calcium, potassium, manganese and zinc sources.
- > The largest size of soil particle 596.80 μm (monsoon) was found in Rhishiyur's (SENS2) loamy sand soil, while the smallest size of soil particle 321.67 μm (summer) was found in Parappanamedu's (SANS3) sandy clay loam soil.
- ➤ The salty alkaline soil of Bhagavathamangalam (SDNS2) and the silty clay soil of Pamani (SATpS1) had the highest soil pH of 8.3 (summer and premonsoon). Pandaravadai's (SANaS1) sandy clay loam had the lowest soil pH of 6.2 (post monsoon). The highest soil temperature was 41.9°C (Summer) in the Sandy clay loam soil of

- Nalamsethi (SAMS2), while the lowest soil temperature was 23°C (Monsoon) in the Loamy sand soil of Paruthiyur (SEKS1) and Kurungulam (SENaS2).
- The maximum soil moisture content of 70.67% (Monsoon) was measured in Vilamal's silty clay alluvial soil (SFTS1), while the lowest soil moisture content of 21.67 % (Summer) was measured in Vengatesapuram's saline alkaline soil (SHTS2).
- The largest loss of ignition 46.78% (Pre Monsoon) was observed in Muthalsethi's sandy clay loam soil (SAMS1), while the least loss of ignition 23.41% (Post Monsoon) was measured in Munnavalkottai's saline alkaline soil (SDNS3).
- The sandy clay loam soil at Serankulam (SAMS3) had the highest electrical conductivity 0.56 dsm⁻¹ (Pre Monsoon), while Muthalsethi (SAMS1) had the lowest electrical conductivity 0.18 dsm⁻¹ (Monsoon).
- The highest nitrogen concentration of 98 kg/ac (Monsoon) was found in Mangudi's sandy clay loam soil (SAKS2), while the lowest nitrogen concentration of 73.41 percent kg/ac (Summer) was found in Thinaichur's sandy clay loam soil (SANaS3).
- The sandy clay loam soil of Mangudi (SAKS2) had the maximum nitrates of 97 kg/ac (Monsoon), whereas the loamy sand soil of Laxmangudi had the lowest nitrates of 71.89 kg/ac (Post Monsoon) (SENS3).
- The highest concentration of ammonium, 97.67 kg/ac (Monsoon), was found in the saline alkaline soil of Chettichathram (SDNS1), while the lowest concentration, 73 kg/ac (Monsoon) was found in the clay loam soil of Laxmangudi (SENS3).
- The saline alkaline soil of Thappalampulliyur (SHTS1) had the highest phosphorus content of 72 kg/ac (Post Monsoon), while the lowest concentration, 31.89 kg/ac (Pre Monsoon) was found in the silty clay soil of Pamani (SCTpS1).

- The silty clay soil of Pamani (SCTpS1) had the maximum soil potassium of 58.34 kg/ac (Post Monsoon), whereas the loamy sand soil of Vengathangudi (SEMS2) had the lowest potassium of 31.23 kg/ac (Pre Monsoon).
- The highest sulphur concentration of 57.65 kg/ac (Post Monsoon) was found in Karrappur's salty alkaline soil (SHTS3), while the lowest sulphur content of 31.67 kg/ac (Pre Monsoon) was found in Vengathangudi's loamy sand soil (SEMS2).
- The highest hydrogen concentration (Monsoon) was found in the sandy clay loam soil of Nagar (SANS2), while the lowest hydrogen content 31.45 kg/ac (Summer) was found in the sandy clay loam soil of Valangaiman (SAVS1).
- The clay soil of Keerakkolore (SBTpS3) and saline alkaline soil of Pinnathore (SDTpS1) had the greatest content of iron 7.53 μg/kg (Monsoon). The lowest concentration of 2.76 μg/kg (Summer) was found in Vijayapuram's silty clay alluvial soil (SFTS2).
- The maximum content of cobalt 5.21 μg/kg (Pre Monsoon) was found in saline alkaline soil of Karrappur (SHTS3) while the lowest concentration 1.06 μg/kg (Monsoon) was found in clay soil of Manali (SBTpS2).
- The highest concentration of chromium 5.53 μg/kg (Monsoon) was found in Valangaiman's sandy clay loam soil (SAVS1), while the lowest concentration 2.46 μg/kg (Pre Monsoon) was found in Kurungulam's loamy sand soil (SENaS2).
- Fig. The maximum concentration of Iodine 7.60 μg/kg (Monsoon) was found in Vengathangudi's loamy sand soil (SEMS2), while the lowest concentration 1.89 μg/kg (Summer) was found in Nagar's sandy clay loam soil (SANS2).

- Fig. The highest manganese concentration was 8.37 μg/kg (Monsoon) in Parappanamedu (SANS3) sandy clay loam soil, while the lowest was 2.45 μg/kg (Summer) in Sanganthi saline alkaline soil (SDTpS3).
- The maximum concentration of zinc 7.40 μg/kg (Monsoon) was found in Pandaravodai's sandy clay loam soil (SANaS1), while the lowest concentration 2.04 μg/kg (Pre Monsoon) was found in Pandaravodai's sandy clay loam soil (SANaS1).
- The highest concentration of Molybdenum 7.37 μg/kg (Monsoon) was found in the sandy clay loam soil of Chettiyamolai (SATpS3), while the lowest concentration 2.18 μg/kg (Summer) was found in the sandy clay loam soil of Rayanallore.
- The highest concentration of selenium 7.43 μg/kg (Monsoon) was found in Bhagavathamangalam's saline alkaline soil (SDNS2), while the lowest concentration 1.78 μg/kg (Summer) was found in Bhagavathamangalam's saline alkaline soil (SDNS2).
- ➤ The soil samples were subjected to microbiological analysis, which included bacteria, fungus, and actinomycetes isolation and enumeration. A large number of microorganisms can be found in a soil sample taken during the monsoon season.
- In a monsoon seasonal soil sample, there are eleven *Bacillus* species, seven *Pseudomonas* species, *Escherichia coli, Nitrobacter, Nitrosomonas, Clostridium, Xymomonas, Corneybacterium,* two *Rhizobium* species, two *Proteus* species, *Thiobacillus* species, *Enterobacter aerogens, Staphylococcus aureus, Streptococcus, Vibrio, Azospirillum* and actinobacteria includes *Actinomycetes, Actinoplanes, Microbispora* and *Nocardia* species.
- In a post monsoon seasonal soil sample, there are seven *Bacillus* species, six *Pseudomonas* species, two *Rhizobium* species, *Escherichia coli*, *Proteobacter*,

- Corneybacterium, Erwinia, Enterobacter aerogens, Serratia marsecence, Streptococcus, Staphylococcus aureus, Azospirullum, Mycobacterium, Vibrio and actinobacteria includes Actinomyces, Actinoplanes and Micromonospora.
- In summer seasonal soil sample, there are three *Bacillus* species, two *Rhizobium* species, *Escherichia coli, Salmonella, Xymomonas, Corneybacterium, Proteobacter, Enterobacter aerogens, Sarratia marsecence, Streptococcus, Staphylococcus aureus, Azospirillum, Mycobacterium* and actinobacteria includes *Actinomyces, Actinoplanes, Streptomyces* and *Micromonospora*.
- In pre monsoon seasonal soil sample, there are two *Rhizobium* species, two *Proteus* species, *Xymomonas, Corneybacterium, Thiobacillus, Salmonella, Clostridium, Nitrosomonas, Nitrobacter, Sarratia marsecence, Streptococcus, Staphylococcus aureus, Azospirillum, Mycobacterium, Vibrio* and actinobacteria includes *Actinomyces, Actinoplanes, Micromonospora* and *Microbispora*.
- Throughout the season, the bacteria *Rhizobium trifoli*, *Rhizobium leuminosporum*, Serratia marsecnce, Azospirillum species and Mycobacterium species were discovered. Pseudomonas denitrificans, Pseudomonas putida and Klebsiella species were only found during the post monsoon season. Bacillus mycoides was only found during the summer months.
- Actinoplane species, Actinomyces species and Micromonospora species were found throughout the year. Only during the monsoon season was the Nocardia species present.
- In monsoon seasonal soil sample, there are eight *Aspergillus* species, five *Trichoderma* species, four *Penicillium* species, three species of *Rhizopus*, *Fusarium*, *Agaricus* and *Alternaria*, two species of *Verticillium* and *Saccharomyces*, a species of *Phythium*,

- Rhizoctonia, Phytophthora, Absidia, Mortierella, Mucor, Candida, Phoma and Cephalosporium.
- In post monsoon seasonal soil sample, there are seven *Aspergillus* species, four *Trichoderma* species, three species of *Penicillium* and *Agaricus*, two species of *Saccharomyces, Fusarium* and *Alternaria*, a species of *Verticillium, Phythium, Rhizoctonia, Phytophthora* and *Phoma*.
- In summer seasonal soil sample, there are six *Aspergillus* species, three species of *Penicillium* and *Trichoderma*, two *Rhizopus*, *Phythium*, *Rhizoctonia*, *Phytophthora* and *Cephalosporium*.
- In pre monsoon seasonal soil sample, there are seven *Aspergillus* species, four *Trichoderma* species, three species of *Penicillium, Rhizopus* and *Fusarium*, two *Saccharomyces, Verticillium, Rhizoctonia, Phytophthora, Cephalosporium, Absidia, Mortierella* and *Mucor*.
- In all seasons, the fungi *Rhizoctonia solani*, *Phytopthora* species, *Penicillium glaucum*, *Penicillium notatum*, *Penicillium chrysogenum*, *Aspergillus fumigates*, *Aspergillus flavus*, *Aspergillus clavatus*, *Aspergillus nidulans*, *Rhizopus oryzae*, *Trichoderma harzianum*, and *Trichoderma koningii*. Only during the monsoon season were *Penicillium candidum*, *Verticillium affinae*, *Candida* species and *Alternaria solani* discovered.
- For the examination of silver nanoparticle production, *E.coli, Klebsiella* species, *Enterobacter* species, *Proteus* species, *Pseudomonas* species, and *Bacillus* species were isolated and identified.

- ➤ Silver nanoparticle was analyzed by UV-Visible spectronic analysis was employed. The existence of silver nanoparticles was confirmed by a prominent peak in the UV-Visible spectrum at 420nm.
- Each of the eight treatments (sandy clay loam, clay loam, saline alluvial, silty clay allvial, loamy sand, clay, silty clay, saline alluvial and saline alkaline) had three duplicates and a distinct watering schedule.
- The soil was sprayed with water (50 percent WHC and below 50 percent soil water content) Pre-germinated black gram (*Vigna mungo*), green gram (*Vigna radiata*), and rice (*Oryza sativa*) seeds were sown in 400g of soil per pot. Roots and shoots were removed after four weeks of sowing and evaluated for seedling length, fresh weight of seedling, dried weight of seedling, vigour index, tolerance index, shoot length, and root length.
- Numerous microorganisms have been found in monsoon, pre monsoon, summer, and post monsoon seasonal soil samples in Thiruvarur districts. *Bacillus subtilis* was abundant in all soil types studied. 16S rRNA sequencing was performed on fresh *Bacillus subtilis*. The sequence was then run through the NCBI FASTA search tool to look for 16S rRNA sequences.
- The biocontrol efficiency of all the isolates found from the soil samples (*Trichoderma viride, Pseudomonas fluorescence* and *Bacillus subtilis*) was tested *in vitro* against the fungal pathogen *Rhizoctonia solani* using the minimum inhibitory concentration method. The pathogen *Rhizoctonia solani* was efficiently controlled by *Trichoderma viride*.
- The *Azotobacter* and *Rhizobium* bacterial strains that had been isolated and identified were then produced as a starting culture.

- ➤ In the fermentor, the culture was transferred to liquid broth of the selective as well as optimal medium for 4 days. When the cell count reached 10⁻⁸ to 10⁻⁹ cells/ml, the broth was combined with an inert carrier substance and used as inoculants.
- After proper mixing, the carrier containing inoculants was left for 7 days, and the above created microbial inoculants were used as biofertilizer.
- ➤ The *Vigna mungo* plant was grown using the biofertilizers that had been generated. The morphological and phytochemical parameters were also examined after the plants were planted.
- ➤ Vigna mungo growth was improved by a combination of Azospirillum and Rhizobium inoculation.

CHAPTER – VII

CONCLUSION

- A soil test can reveal nutrient deficiencies, potential toxicities from excessive fertility, and inhibitions from the presence of non-essential trace minerals, as well as indicate nutrient deficiencies, potential toxicities from excessive fertility, and inhibitions from the presence of non-essential trace minerals. The test is designed to imitate the function of roots in mineral absorption.
- Microbial diversity refers to the range of variation among all types of microorganisms found in nature and as influenced by human activity. Microorganisms have an important function on land and in water, including serving as the initial colonizer, which helps to alleviate the consequences of both naturally occurring and man-made distributed habitats.
- Microbial diversity in the soil is always important for any ecosystem since it helps to improve soil health, plant growth, yield, and ecosystem sustainability while also minimizing the usage of artificial fertilizers.
- > Soil microbial diversity and biomass are key regulators of essential ecosystem processes such as organic matter break down, nitrogen cycling and gaseous exchange.
- The present study revealed the microbial diversity of Thiruvarur district primary soil types has thirty nine bacteria, six actinomycetes and forty two fungal species.
- The present study suggested the Thiruvarur district primary soil types native microorganisms used for the production of silver nanoparticle and formulation of biofertilizer and biopesticide that would be helpful to support and uplift the sustainable agriculture globally.

- ➤ Due to their distinctive physical and chemical features, silver nonoparticles (AgNPs) are increasingly used in a variety of industries, including medical, food, healthcare, consumer, and industrial applications. Optical, electrical, thermal, high electrical conductivity and biological qualities are some of them.
- The microbial manufacture of silver nanoparticles is a straightforward technique with low toxicity and ease of application.
- ➤ Biocontrol agent formulation can be used to stabilise organisms during production, distribution, and storage; assist in product handling and application; protect the agent from harmful environmental factors; and boost organism activity.
- ➤ Biofertilizers are biological preparations of effective microorganisms that improve nutrient uptake and stimulate plant development. They improve soil productivity by fixing nitrogen from the atmosphere, solubilizing phosphorus in the soil, and encouraging plant development.
- ➤ In future the research may focus on tools in the genetic engineering and nanotechnology needed to improve the current status of biofertilizer and biopesticide.
- Microbes and microbial products appear to have an almost limitless number of applications. However, despite the loss of many microbial species, there is one intangible benefit that would be gone forever. There will be no way to understand the evolutionary richness of life until we find ways to continue screening and researching microbes and maintaining their habitats inside their natural settings. Microorganisms are critical for the continuous existence of human populations on Earth, as per a major duty of public education.

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