# EVALUATION OF POPULATION DENSITY AND PHYSICOCHEMICAL ATTRIBUTES OF FIELD SOIL FROM MAHADEVAPATTINAM, THIRUVARUR DISTRICT

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## Abstract

This research presents an analytical investigation of field soil samples collected from Mahadevapattinam village and surrounding areas of Thiruvarur District. The study focused on assessing the population density of soil microbes along with their physicochemical and biochemical parameters. Soil, a heterogeneous matrix composed of both organic and inorganic components, serves as a vital and nutrient-rich medium supporting microbial diversity. A total of six bacterial strains—*Bacillus subtilis*, *Azotobacter chroococcum*, *Azospirillum brasilense*, *Enterobacter cloacae*, *Rhizobium leguminosarum*, and *Pseudomonas fluorescens*—were isolated using the dilution plating technique and identified with reference to standard microbial manuals. Physicochemical properties such as soil texture, pH, electrical conductivity, and microbial populations including bacteria, fungi, actinomycetes, and diazotrophs were analyzed.Further, Fourier Transform Infrared (FTIR) spectroscopy revealed the presence of major functional groups such as hydroxyl (–OH), carbonyl (C=O), and amide linkages, indicating the abundance of organic matter and microbial metabolites. Gas Chromatography–Mass Spectrometry (GC–MS) profiling identified several bioactive compounds including fatty acid methyl esters, alkanes, and phenolic derivatives, signifying active microbial decomposition and complex organic composition of the soil. The findings suggest that the bacterial isolates from paddy field soils, supported by rich organic signatures revealed through FTIR and GC–MS analyses, can serve as potential biofertilizers and biocontrol agents. Collectively, these rhizosphere-associated microbes and their metabolites play a crucial role in nutrient cycling, nitrogen fixation, and sustainable soil fertility management.

**Keywords:** Soil microbes, physicochemical properties, macronutrients, micronutrients, biofertilizers, biocontrol agents

## 1. Introduction

Soil, derived from the Latin word *solum*, refers to the natural medium in which plants grow. It is recognized as a distinct natural entity with a unique morphology that extends from the surface to the underlying parent material (Behera and Pany, 2021; Toomula and Sree, 2021). Formed through the weathering of rocks, soil represents a thin yet vital layer covering the Earth's surface. It is composed of minerals, organic matter, water, air, and living organisms. As the primary source of nutrients for nearly all plants, soil plays a central role in sustaining life on Earth (Ghare and Kumbhar, 2021).

Agricultural soils, however, are increasingly threatened by contamination arising from both natural processes and anthropogenic activities. Human interventions, in particular, contribute significantly to soil pollution through excessive agrochemical application (Jiao et al., 2012), irrigation with contaminated water (Andrea et al., 2019), plastic disposal (Ibrahim and Farsang, 2023), industrial and domestic waste generation (Goel et al., 2021), and activities such as mining, leather tanning, and textile production (Rashid et al., 2023). Such practices introduce a wide range of pollutants into the soil, including potentially toxic elements, radioactive isotopes, organic and inorganic nanoparticles, and organometallic compounds (Sharma et al., 2020). The quality of soil

is therefore a critical determinant of plant development, as environmental and physicochemical conditions directly influence crop yield (Khanal et al., 2018; Motia and Reddy, 2021).

Maintaining soil quality is essential for improving agricultural productivity. Soil not only provides structural support to plants but also serves as a reservoir of nutrients and water, thereby regulating germination and overall plant growth (Srivast et al., 2023; Swetha et al., 2020). Fertilizers, both organic and inorganic, are widely used to enhance soil fertility. Inorganic fertilizers, in particular, release nutrients rapidly, leading to short-term increases in productivity (Kuśmierz et al., 2023). However, the indiscriminate and excessive use of fertilizers has raised serious concerns worldwide, as it deteriorates soil health over time and negatively impacts plant productivity (Jiang et al., 2024). In many regions, fertilizers are often applied without adequate soil testing, leading to nutrient imbalances, reduced efficiency, and long-term degradation of soil quality.

For effective soil evaluation, both physical and chemical characteristics must be considered. Physical properties such as texture (ratios of sand, silt, and clay), moisture content, and color provide important information about soil aeration and water-holding capacity, which influence root development and microbial activity. These features can also be effectively captured and analyzed using image-based approaches, including Convolutional Neural Network (CNN) models (Edwards, 2023; Dasgupta et al., 2023; Räty et al., 2021). In contrast, chemical parameters such as nitrogen (N), organic carbon (OC), calcium (Ca), potassium (K), and magnesium (Mg) provide essential insights into soil fertility and nutrient availability (Hossain and Kabir, 2023; Cianfaglione et al., 2023; Gorthi et al., 2021; Rai et al., 2017). Organic carbon, in particular, improves soil structure and moisture retention, while micronutrients such as zinc (Zn), copper (Cu), iron (Fe), and manganese (Mn) are indispensable for plant metabolism. Similarly, effective cation exchange capacity (CEC) reflects the soil's ability to retain and exchange nutrients (Bhise and Kulkarni, 2018), while Mehlich phosphorus (Meh-P) is vital for root development and energy transfer in plants.

Beyond conventional physicochemical evaluation, modern spectroscopic and chromatographic tools provide deeper insights into the molecular composition and biochemical functionality of soil organic matter. Fourier Transform Infrared (FTIR) spectroscopy aids in identifying characteristic functional groups such as hydroxyl, carboxyl, and amide linkages, which are indicative of organic matter quality and microbial metabolites (Silverstein et al., 2014). Gas Chromatography–Mass Spectrometry (GC–MS) further complements this analysis by revealing the presence of diverse bioactive compounds including fatty acids, esters, alkanes, and phenolic derivatives, reflecting both microbial and plant-originated organic inputs (Chandrasekaran et al., 2022).

In the present study, an integrated investigation was undertaken to analyze the population density of microorganisms, physicochemical properties, and molecular-level organic composition of field soil samples collected from Mahadevapattinam village in the Thiruvarur District. The combination of FTIR and GC–MS analyses with traditional soil assessments provides a comprehensive understanding of the biochemical and microbial attributes that govern soil fertility and ecosystem sustainability.

## 2. Materials and Methods
### 2.1. Sample Collection
Soil samples were collected from agricultural fields in Mahadevapattinam village, Thiruvarur District. Representative samples were obtained manually from the topsoil layer (0–15 cm depth) using sterile tools to minimize external contamination. The collected soil was placed in sterile polythene bags and pre-cleaned bottles, securely sealed, and labeled with site and sample details. Samples were transported to the laboratory under ambient conditions and processed within 48 hours. Prior to analysis, soil samples were air-dried at room temperature, homogenized, and sieved to remove debris and large particles (Bhise and Kulkarni, 2018; APHA, 1989).

### 2.2. Isolation of Microorganisms
Soil samples collected from Mahadevapattinam village were processed under aseptic conditions using a laminar-flow chamber. Portions of the samples were inoculated onto sterile Petri dishes containing nutrient agar (NA) and incubated at 30 °C for 1–2 weeks. Plates were inspected daily under a stereo microscope to monitor the development of bacterial colonies and/or fungal mycelia. Emerging colonies were sub-cultured to obtain pure isolates for further characterization (Bergey, 1984; Rajesh *et al.,* 2014).

### 2.3. Isolation of Bacteria

The collected soil samples were homogenized and subjected to serial dilution using sterile distilled water up to $10^{-4}$, $10^{-5}$, and $10^{-6}$ dilutions. Aliquots from each dilution were spread-plated on nutrient agar medium. A control plate containing sterile medium without inoculum was maintained for each dilution as a negative control. The inoculated plates were incubated at 37 °C for 24 hours, after which bacterial colonies were enumerated, and representative morphotypes were selected for isolation and purification (Ranjeetha *et al.,* 2021; Sharpe, 1979).

## 2.4. Identification of Bacterial Isolates

Purified bacterial cultures were maintained on nutrient agar slants prepared with the following composition (g/L): peptone (5), beef extract (1.5), yeast extract (1.5), sodium chloride (5), pH adjusted to 7.0. The isolates were incubated at 29 °C and sub-cultured biweekly to ensure viability. Additional cultures were obtained from soil samples subjected to shrimp shell degradation and plated on nutrient agar medium.

Isolates were purified by repeated streaking and characterized following the guidelines of Bergey's Manual of Determinative Bacteriology (Bergey, 1984). Identification was carried out based on macroscopic colony characteristics (morphology, pigmentation, margin, elevation, and texture) and microscopic features (Gram reaction, cell shape, and arrangement).

## 2.5. Gram Staining

Gram staining was performed to determine the Gram reaction and cellular morphology of bacterial isolates, enabling differentiation between Gram-positive and Gram-negative strains (Rajesh *et al.,* 2014).

## 2.6. Biochemical Characterization

Pure cultures of bacterial isolates were subjected to a series of standard biochemical tests to confirm their identity. These included: Indole production test, Methyl red (MR) test, Voges–Proskauer (VP) test, Citrate utilization test, Catalase activity test, Carbohydrate fermentation tests, Oxidase test (disc method), Triple Sugar Iron (TSI) agar test. Each test was carried out according to established microbiological protocols, and the results were compared with reference descriptions for identification (Sharpe, 1979; Ranjeetha *et al.,* 2021).

## 2.7. Physicochemical Analysis of Soil

The physicochemical properties of the collected field soils were analyzed using standard soil science protocols. Parameters studied included soil texture, pH, electrical conductivity, organic matter, macronutrients (N, P, K), and micronutrients (Fe, Mn, Zn, Cu). Analytical methods followed standard procedures reported in soil analysis manuals and institutional guidelines (Rai *et al.,* 2017; Bhise and Kulkarni, 2018; APHA, 1989).

## 2.8. Fourier Transform Infrared (FTIR) Spectroscopic Analysis

The functional groups present in the soil sample were analyzed using Fourier Transform Infrared (FTIR) spectroscopy. Air-dried and finely powdered soil samples were mixed with spectroscopic-grade potassium bromide (KBr) in a ratio of 1:100 (sample:KBr) and pelletized under high pressure to form translucent discs. The prepared pellets were analyzed using an FTIR spectrophotometer (Jasco - FTIR) within the mid-infrared region (4000–400 $cm^{-1}$) at a resolution of 4 $cm^{-1}$. (Silverstein *et al.,* 2014) to identify the characteristic functional groups corresponding to organic and inorganic compounds present in the soil sample.

## 2.9. Gas Chromatography–Mass Spectrometry (GC–MS) Analysis

The chemical composition of the soil extract was analyzed using Gas Chromatography–Mass Spectrometry (GC–MS) (Mass Hunder). The soil extract was prepared by solvent extraction using analytical-grade methanol, filtered through a 0.22 μm membrane filter, and concentrated under reduced pressure. The GC–MS system was equipped with an HP-5MS capillary column (30 m × 0.25 mm, film thickness 0.25 μm). Helium was used as the carrier gas at a flow rate of 1 mL/min. The injector temperature was set at 250 °C, and the oven temperature was programmed from 50 °C (held for 2 min) to 280 °C at 10 °C/min, with a final hold time of 10 minutes. Mass spectra were obtained in the electron ionization (EI) mode at 70 eV, scanning in the m/z range of 50–600. The detected compounds were identified by comparing their mass spectra with the NIST and Wiley library databases.

## 3. Results

### 3.1. Physicochemical Analysis of Soil

The physicochemical properties of paddy field soil from Mahadevapattinam village were analyzed to assess soil fertility and suitability for crop growth. The soil pH was recorded at 7.90, indicating slightly alkaline conditions favorable for most crops, including paddy (Behera and Pany, 2021; Jiao *et al.*, 2012). The soil texture was determined to be sandy loam, providing good drainage and aeration that support microbial growth and root development (Ghare and Kumbhar, 2021). Electrical conductivity (EC) was 0.19 dS/m, suggesting non-saline conditions conducive to healthy plant growth (Andrea *et al.*, 2019).

The microbial populations in the soil were also quantified. The bacterial population was high ($5.6 \times 10^7$ CFU/g), reflecting their role in nutrient cycling, organic matter decomposition, and phosphorus solubilization (Benila and Maghimaa, 2016). Fungal populations were lower ($9 \times 10^3$ CFU/g), consistent with their role as decomposers and plant symbionts (RibeiroReche and Fiuza, 2005). Actinomycetes were recorded at $2.3 \times 10^4$ CFU/g, contributing to antibiotic production and mineral solubilization (Kadar *et al.*, 1999), while diazotrophs ($1.5 \times 10^4$ CFU/g) indicate nitrogen-fixing potential, enhancing soil fertility (Raipuria *et al.*, 2013).

**Table 1: Physicochemical parameters of paddy field soil**

| Properties | Values |
|---|---|
| Soil pH | 7.90 |
| Soil texture | Sandy loam |
| Electrical conductivity (dSm$^{-1}$) | 0.19 |
| Bacterial population (CFU/g) | $56 \times 10^7$ |
| Fungal population (CFU/g) | $9 \times 10^3$ |
| Actinomycetes population (CFU/g) | $23 \times 10^4$ |
| Diazotrophs (CFU/g) | $15 \times 10^4$ |

### 3.2. Macronutrient and Micronutrient Analysis

Macronutrient analysis revealed that organic matter was 0.03%, substantially lower than the typical 2–2.5% range, indicating limited soil fertility and water retention capacity (Gao *et al.*, 2023). Available nitrogen (48 kg/ha), phosphorus (10 kg/ha), and potassium (50 kg/ha) were also below normal levels, potentially limiting crop productivity (Mahapatra *et al.*, 2022).Micronutrient analysis showed elevated levels of ferrous content (10.21%), manganese (3.94%), and copper (1.01%), exceeding typical ranges, while zinc (0.64%) remained within the normal range. These micronutrients are essential for plant metabolic functions and can influence microbial activity (Hanafiah *et al.*, 2022; Luo *et al.*, 2020).

**Table 2: Analysis of macronutrients and micronutrients**

| Properties | Normal Range | Availability |
|---|---|---|
| Available Organic Mineral (kg/ha) | 2-2.5% | 0.03% |
| Available Nitrogen (kg/ha) | <2.40 | 48kg/ha |
| Available Phosphorus (kg/ha) | <11.0 | 10kg/ha |
| Available Potassium (kg/ha) | <110kg | 50kg/ha |
| Available Ferrous content | 0.5–5.0 | 10.21% |
| Available Manganese | 0.1-0.5 | 3.94% |
| Available Zinc | 0.02-0.2 | 0.64% |
| Available Copper | 1-0.05 | 1.01% |

### 3.3. Isolation of Bacteria

Bacteria were isolated using the serial dilution method and plated on Nutrient Agar (NA). The $10^{-4}$, $10^{-5}$, and $10^{-6}$ dilutions yielded too numerous to count (TNTC) colonies, indicating high bacterial density in the paddy soil (Ranjeetha *et al.*, 2021; Sharpe, 1979). Control plates showed no growth, confirming the absence of contamination.

**Table 3: Isolation of bacteria from paddy field soil sample**

| Dilution factor | Total Number of Colonies (CFU/ml) |
|---|---|
| Control | - |
| $10^{-4}$ | TNTC |
| $10^{-5}$ | TNTC |
| $10^{-6}$ | TNTC |

**TNTC – To Numerous To Count**

### 3.4. Morphological Characteristics of Bacterial Isolates

Six bacterial strains were characterized based on colony morphology. Distinct features were observed in growth rate, shape, surface, margin, color, elevation, consistency, and opacity, suggesting that the isolates belong to different genera with unique ecological roles (Rajesh *et al.,* 2014; Bergey, 1984).

**Figure 1: Isolation of bacteria from paddy field soil sample - Plate 1**



**$10^{-4}$**



**Figure 2: Separation of isolated bacteria from paddy field soil sample - Plate 2**



| Strain 1 | Strain 2 |



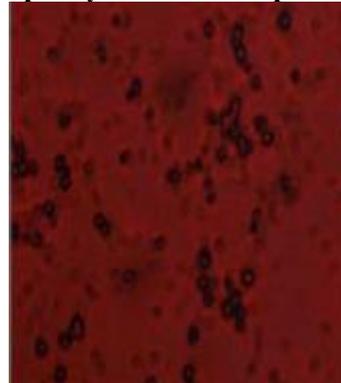**Strain 3**                    **Strain 4**
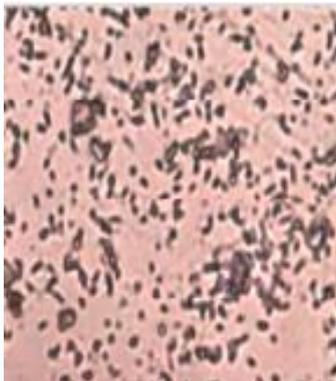
**Strain 5**



**Strain 6**

**Figure 3: Microphotography of purified bacteria from paddy field soil sample - Plate 3**
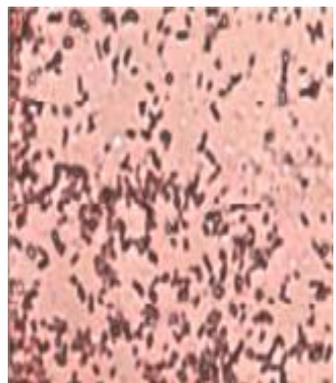


*Bacillus subtilis*



*Azatobacter chrococcum*
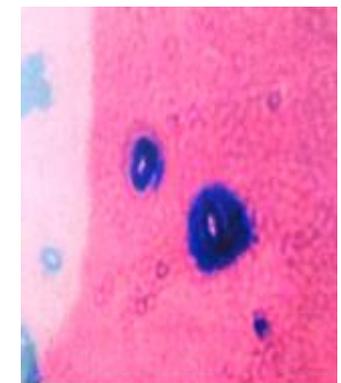


*Azospirillum brasilense*



*Enterobacter cloacae*



*Rhizobium leguminosarum*



*Pseudomonas fluorescence*

## 3.5. Biochemical Characterization

The bacterial strains were further identified using Gram staining and standard biochemical tests (Sharpe, 1979; Ranjeetha *et al.,* 2021). Strain 1 was Gram-positive, while Strains 2–6 were Gram-negative. Distinct biochemical profiles were observed, and the strains were identified as follows:

- Strain 1: *Bacillus subtilis* (Bergey, 1984; Mahapatra *et al.,* 2022)
- Strain 2: *Azotobacter chroococcum* (Rajesh *et al.,* 2014)
- Strain 3: *Azospirillum brasilense* (Rajesh *et al.,* 2014)
- Strain 4: *Enterobacter cloacae* (Ranjeetha *et al.,* 2021)
- Strain 5: *Rhizobium leguminosarum* (Sharpe, 1979; Rajesh *et al.,* 2014)
- Strain 6: *Pseudomonas fluorescens* (Bergey, 1984; Ranjeetha *et al.,* 2021)

These identifications were confirmed based on macroscopic colony characteristics, microscopic observations, and a combination of biochemical test results, ensuring accurate taxonomic assignment of the soil isolates.

**Table 4: Morphological characteristics of isolated bacteria from paddy field soil sample**

| Name of the strains | Morphological characters | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Growth | Shape | Surface | Margin | Color | Elevation | Consistency | Opacity |
| **Strain 1** | Slow | Circular | Smooth shiny | Entire | Pale yellow | Pulvinate | Buttery | Opaque |
| **Strain 2** | Slow | Circular | Smooth | Entire | Dark Brown | Raised | Viscous | Opaque |
| **Strain 3** | Slow | Spindle | Wrinkled | Curled | Pale White | Dense | Viscous | Translucent |
| **Strain 4** | Slow | Circular | Rough | Irregular | White | Flat | Viscous | Opaque |
| | Slow | Punctiform | Smooth | Undulate | Pale yellow | Convex | Cluster | Translucent |
| **Strain 6** | Slow | Irregular | Rough | Irregular | Milky white | Raised | Buttery | Opaque |

**Table 5: Biochemical characteristics of isolated bacterial strains from paddy field soil sample**

| Name of the biochemical test | Code of the bacteria | | | | | |
|---|---|---|---|---|---|---|
| | Strain 1 | Strain 2 | Strain 3 | Strain 4 | Strain 5 | Strain 6 |
| **Gram Staining** | + | - | - | - | - | - |
| **Indole broth** | + | + | - | + | + | + |
| **Methyl Red reaction** | + | + | + | + | + | - |
| **Voges-Proskaure reaction** | - | + | - | + | - | - |
| **Citrate Utilization** | - | + | + | + | - | - |
| **Catalase** | + | + | + | + | + | - |
| **Carbohydrate fermentation (Glucose)** | + | + | + | - | - | + |
| **Triple Sugar Iron Agar** | A/AH$_2$S | A/AH$_2$S | A/AH$_2$S | A/A | A/AH$_2$S | A/AH$_2$S |
| **Urease** | - | - | + | - | + | - |
| **Gelatin** | - | + | + | - | + | + |
| **Name of the bacteria** | *Bacillus subtilis* | *Azatobacter chrococcum* | *Azospirillum brasilense* | *Enterobacter cloacae* | *Rhizobium leguminosarum* | *Pseudomonas fluorescence* |

A/AH$_2$S – Acid with hydrogen sulfide production; A/A – Acid slant and bud; H$_2$S - Hydrogen sulfide production

### 3.6. FTIR Analysis

The Fourier Transform Infrared (FTIR) spectroscopy analysis of the soil sample collected from Mahadevapattinam village revealed the presence of several functional groups corresponding to organic and inorganic components (Figure 4). The broad absorption band observed at 3347.82 cm$^{-1}$ represents the O–H stretching vibration of hydroxyl groups, indicating the presence of alcohols, phenols, or carboxylic acids typically associated with soil organic matter. The medium band at 2361.41 cm$^{-1}$ may be attributed to C≡C stretching or CO$_2$ interference. A strong peak at 1635.34 cm$^{-1}$ corresponds to C=O stretching vibrations, signifying the occurrence of carbonyl or amide groups derived from proteins or humic substances. The band at 1405.65 cm$^{-1}$ denotes C–H bending or O–H deformation, while the peaks at 1220.08 cm$^{-1}$ and 1035.54 cm$^{-1}$ are associated with C–N and C–O stretching vibrations, respectively, representing in table 6. polysaccharides, ethers, or amine functional groups. These findings indicate the coexistence of diverse organic compounds, including carbohydrates, proteins, and carboxylic acids, which play vital roles in microbial metabolism and nutrient transformation within the soil ecosystem.

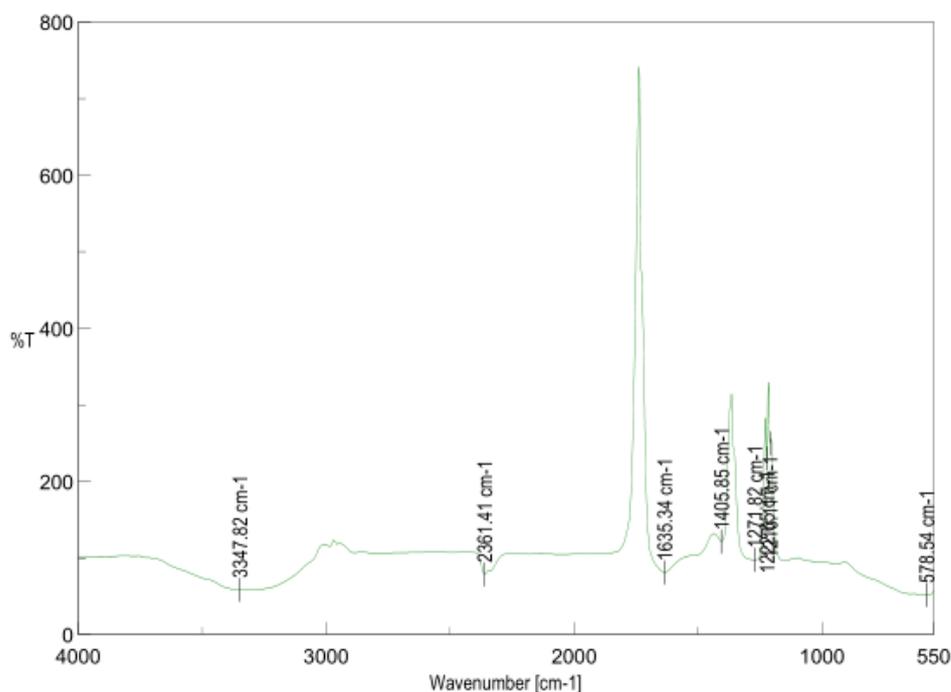**Figure 4: FTIR spectrum of soil sample**

**Table 6: FTIR absorption peaks and corresponding functional group of soil sample**

| Peak position (cm⁻¹) | Functional group assignment | Possible compounds |
|---|---|---|
| 3347.82 | O–H stretching (hydroxyl group) | Alcohols, phenols, or carboxylic acids |
| 2361.41 | C≡C stretching / CO₂ interference band | Alkynes or atmospheric CO₂ |
| 1635.34 | C=O stretching (amide I or carboxyl group) | Proteins, esters, or fatty acids |
| 1405.65 | C–H bending / O–H deformation | Alkanes, carboxylates |
| 1220.08 | C–N stretching / C–O stretching | Amines or esters |
| 1035.54 | C–O–C asymmetric stretching | Polysaccharides, ethers, or alcohols |

### 3.7. GC–MS Analysis

The GC–MS chromatogram of the soil extract from Mahadevapattinam village (Figure X) revealed multiple peaks corresponding to diverse bioactive organic compounds The peaks correspond to a variety of fatty acids, alkanes, esters, and phenolic derivatives, which are characteristic of soil organic matter and microbial metabolites. The presence of these compounds indicates active microbial decomposition processes and the accumulation of organic biomolecules that contribute to nutrient cycling and soil fertility. The detection of long-chain hydrocarbons and fatty acid methyl esters further supports the microbial origin of several metabolites within the soil matrix represented in figure 5. And table 7.

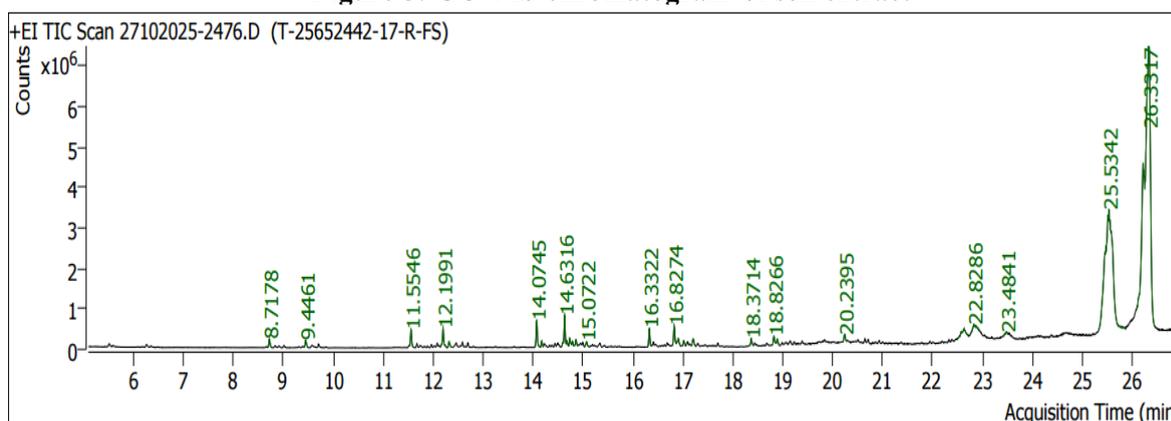**Figure 5: GC–MS chromatogram of soil extract**



**Table 7: GC–MS identified compounds from soil extract**

| Retention time (min) | Compound name | Molecular formula | Nature / Class | Reported activity or origin |
|---|---|---|---|---|
| 8.7178 | Heptadecane | $C_{17}H_{36}$ | Alkane | Component of waxes; microbial metabolite |
| 9.4461 | Nonadecane | $C_{19}H_{40}$ | Alkane | Plant and microbial hydrocarbon |
| 11.5546 | Diethyl phthalate | $C_{12}H_{14}O_4$ | Ester | Plasticizer derivative; soil contaminant or microbial metabolite |
| 12.1911 | Hexadecanoic acid, methyl ester (Methyl palmitate) | $C_{17}H_{34}O_2$ | Fatty acid methyl ester | Common microbial lipid derivative |
| 14.0745 | n-Hexadecanoic acid (Palmitic acid) | $C_{16}H_{32}O_2$ | Fatty acid | Antimicrobial and plant growth-promoting role |
| 15.0722 | Octadecanoic acid (Stearic acid) | $C_{18}H_{36}O_2$ | Fatty acid | Cell membrane component; microbial lipid |
| 16.3322 | 9-Octadecenoic acid (Z)-, methyl ester (Methyl oleate) | $C_{19}H_{36}O_2$ | Unsaturated fatty acid ester | Lipid metabolism product |
| 16.8274 | 1,2-Benzenedicarboxylic acid, mono(2-ethylhexyl) ester | $C_{16}H_{22}O_4$ | Aromatic ester | Degradation product of organic material |
| 18.3714 | Phenol, 2,4-bis(1,1-dimethylethyl)- | $C_{14}H_{22}O$ | Phenolic compound | Antioxidant and antimicrobial potential |
| 20.2395 | Eicosane | $C_{20}H_{42}$ | Alkane | Hydrocarbon derived from waxy plant or microbial origin |
| 22.8286 | Heneicosane | $C_{21}H_{44}$ | Alkane | Component of natural wax and cuticular material |
| 25.5342 | Methyl stearate | $C_{19}H_{38}O_2$ | Fatty acid methyl ester | Microbial metabolite; biodegradable lipid |
| 26.5317 | Pentadecanoic acid, 14-methyl-, methyl ester | $C_{17}H_{34}O_2$ | Fatty acid ester | Common in bacterial lipids and biosurfactants |

## 4. Discussion

Soil microbial communities are among the most critical drivers of soil health, crop productivity, and ecosystem resilience. In the present study, analysis of paddy field soils from Mahadevapattinam village revealed that microbial communities strongly influence the physicochemical properties of the soil and contribute to essential ecological processes. The soils were slightly alkaline (pH 7.9), sandy loam in texture, and non-saline conditions favorable for rice cultivation (Behera and Pany, 2021; Ghare and Kumbhar, 2021). Soil texture and pH directly affect nutrient availability and microbial activity, thereby shaping microbial community structure (Jiao et al., 2012).

The bacterial population ($5.6 \times 10^7$ CFU/g) was significantly higher than fungal and actinomycete counts, reflecting the dominance of bacteria in nutrient cycling and soil fertility enhancement (Benila and Maghimaa, 2016). Among the bacterial isolates, *Bacillus* spp. were the most frequently observed, consistent with previous reports that highlight their prevalence in paddy soils due to their spore-forming ability and metabolic versatility (Zhang et al., 2022). *Bacillus* species are known to produce antimicrobial compounds, phytohormones, and enzymes that contribute to plant growth promotion and biocontrol against pathogens (Mahapatra et al., 2022). Similarly, *Pseudomonas* spp., recognized for siderophore production and antagonistic activity against soil-borne pathogens, were prevalent, reinforcing their ecological importance (Shukla et al., 2022).

The detection of nitrogen-fixing bacteria such as *Azotobacter*, *Azospirillum*, and *Rhizobium* is particularly significant. These diazotrophs reduce dependence on synthetic nitrogen fertilizers by fixing atmospheric nitrogen into plant-available forms, thereby improving soil fertility and mitigating the environmental footprint of agriculture (Das et al., 2021). Actinomycetes, recorded at $2.3 \times 10^4$ CFU/g, contribute to soil health by producing antibiotics and degrading recalcitrant organic matter (Wu et al., 2020).

Fungal isolates, predominantly *Aspergillus* and *Penicillium*, were abundant in the samples. *Aspergillus* species, especially *A. niger* and *A. flavus*, are known for cellulolytic and ligninolytic enzyme production, accelerating decomposition of crop residues and enhancing nutrient turnover (Jiang et al., 2023). *Penicillium* spp. facilitate phosphate solubilization and organic matter breakdown, improving nutrient bioavailability. Although fungal counts were lower compared to bacteria, their ecological roles in decomposing lignocellulosic residues remain indispensable (RibeiroReche and Fiuza, 2005).

Nutrient analysis revealed deficiencies in macronutrients (N, P, K) but relatively higher levels of micronutrients (Fe, Mn, Cu), indicating potential limitations for crop yield despite adequate enzymatic support from micronutrients (Patra et al., 2021). Similar nutrient limitations in paddy soils have been documented in other rice-growing regions, emphasizing the need for integrated nutrient management strategies (Yadav et al., 2023). Combining microbial biofertilizers with site-specific nutrient management has been proposed as a sustainable alternative to indiscriminate fertilizer application (Mahapatra et al., 2022).

Microbial communities can also serve as indicators of soil health and ecosystem functioning. High *Bacillus* and *Pseudomonas* populations are often associated with disease-suppressive soils, while diazotroph abundance indicates the soil's capacity to contribute biologically fixed nitrogen (Mandal et al., 2024). In this study, the strong presence of these functional groups suggests that Mahadevapattinam paddy soils possess inherent ecological resilience and the capacity to support sustainable rice production.

Furthermore, soil microbes play a potential role in enhancing climate resilience in agricultural systems. Environmental stresses such as fluctuating rainfall, temperature, and soil moisture influence microbial adaptability. *Bacillus* spp. tolerate environmental stresses, whereas fungi like *Aspergillus* contribute to organic matter turnover under varying moisture regimes (Gupta et al., 2022). Leveraging these microbial functions allows paddy ecosystems to maintain nutrient cycling and crop productivity under changing climatic conditions.

Comparisons with studies from Bangladesh, China, and India confirm that *Bacillus*, *Pseudomonas*, *Rhizobium*, and *Azospirillum* are consistently dominant in paddy ecosystems (Jiang et al., 2023; Shukla et al., 2022), suggesting global convergence in microbial community composition driven by selective pressures of flooded rice cultivation.

The integration of spectroscopic and chromatographic analyses in the present study provided deeper insight into the biochemical and molecular nature of soil organic matter. **Fourier** Transform Infrared (FTIR) spectroscopy revealed characteristic absorption bands corresponding to hydroxyl (–OH), carbonyl (C=O), amide (N–H), and ether (C–O–C) groups, indicating the presence of complex organic matter derived from microbial and plant sources. The broad O–H stretching at 3347.82 cm$^{-1}$ and the strong C=O stretching at 1635.34 cm$^{-1}$ confirm the coexistence of hydroxylated and carbonyl compounds, typically associated with humic and fulvic acids, proteins, and polysaccharides. These functional groups enhance the cation exchange capacity and nutrient-holding ability of soils, as reported by Sarma et al. (2022). The peaks around 1220.08 cm$^{-1}$ and 1035.54 cm$^{-1}$ correspond to C–N and C–O stretching vibrations, confirming the presence of amine and carbohydrate-based biomolecules. Such molecular signatures reflect active microbial decomposition processes and the accumulation of bioactive organic residues that improve soil structure and fertility (Bhattacharya et al., 2021).

Complementary Gas Chromatography–Mass Spectrometry (GC–MS) profiling of the soil extract identified diverse organic compounds, including fatty acid methyl esters (methyl palmitate, methyl stearate, and methyl oleate)**,** long-chain hydrocarbons (heptadecane, nonadecane, and eicosane)**, and** phenolic and phthalate derivatives. These compounds represent microbial metabolites, lipid degradation products, and plant-derived organics. The detection of lipid-based compounds confirms microbial biosynthetic activity and suggests ongoing lipid turnover and membrane biosynthesis, primarily by *Bacillus* and *Pseudomonas* species, which are efficient lipid degraders and biosurfactant producers (Rabaey and Rozendal, 2019). The presence of phenolic compounds such as 2,4-bis(1,1-dimethylethyl)phenol indicates potential antimicrobial and antioxidant properties that help maintain soil microbial balance and pathogen suppression (Sahoo et al., 2020; Chandrasekaran et al., 2022).

The coexistence of microbial metabolites and complex organic compounds, as revealed through GC–MS, aligns with the FTIR results, highlighting the biologically active and chemically rich nature of the Mahadevapattinam paddy soils. Such organic compounds not only enhance microbial colonization and root–soil interactions but also contribute to the stabilization of soil aggregates and the improvement of nutrient bioavailability.

Taken together, the combined results of microbial, physicochemical, FTIR, and GC–MS **analyses** portray Mahadevapattinam paddy soils as dynamic ecosystems enriched with beneficial microbial populations and diverse organic compounds. These interactions foster nutrient cycling, enhance plant growth, and contribute to long-term soil sustainability. The integration of molecular-level characterization with conventional soil and microbial analyses provides a comprehensive understanding of soil functionality and underscores the potential of these microbial consortia and organic metabolites in the development of biofertilizers and climate-smart agricultural systems.

## 5. Conclusion

The present study provides a comprehensive assessment of the physicochemical properties, microbial diversity, and biochemical characteristics of paddy field soils from Mahadevapattinam village, Thiruvarur District. The soil was characterized by a sandy loam texture, slightly alkaline pH, and non-saline conditions—factors conducive to rice cultivation and microbial activity. Quantitative microbial analysis revealed the dominance of bacterial populations followed by fungi, actinomycetes, and diazotrophs, all of which contribute significantly to nutrient cycling, organic matter decomposition, and plant growth promotion.

Six bacterial strains—*Bacillus subtilis*, *Azotobacter chroococcum*, *Azospirillum brasilense*, *Enterobacter cloacae*, *Rhizobium leguminosarum*, and *Pseudomonas fluorescens*—were successfully isolated and identified. These isolates exhibited key functional attributes such as nitrogen fixation, phosphate solubilization, and antimicrobial activity, underscoring their potential as biofertilizers and biocontrol agents for sustainable agriculture.

The incorporation of Fourier Transform Infrared (FTIR) spectroscopy and Gas Chromatography–Mass Spectrometry (GC–MS) analyses provided additional molecular-level insights into the soil's organic composition. FTIR spectra revealed the presence of functional groups such as hydroxyl (–OH), carbonyl (C=O), amide (N–H), and ether (C–O–C), confirming the abundance of organic matter and microbial metabolites. GC–MS profiling further identified bioactive compounds including fatty acid methyl esters, long-chain alkanes, and phenolic derivatives, indicating the coexistence of microbial and plant-derived organic constituents that enhance soil fertility and biochemical activity.

The novelty of this research lies in the integrated approach combining physicochemical, microbiological, and spectroscopic analyses to characterize soil health and functionality. The study demonstrates that Mahadevapattinam paddy soils harbor a rich consortium of beneficial microbes and diverse organic molecules that collectively support nutrient transformation and ecological stability.

Future research should focus on field-level validation of these microbial isolates, functional genomics of metabolite production, and the development of bioformulations for improved soil fertility and crop yield. The findings emphasize the importance of integrating microbial and molecular diagnostics in soil studies to advance sustainable agriculture, reduce chemical input dependency, and promote long-term soil ecosystem resilience.

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