

# Population Dynamics of Bacteria and Physiochemical Properties of Soil in Different Agricultural Fields of Tiruvarur District, Rice Bowl of Tamil Nadu

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Received: 25 Sep 2023; Revised accepted: 10 Nov 2023; Published online: 02 Dec 2023

## Abstract

Rice plants are in close contact with the soil through their roots. Microbes inhabited on the root surface (rhizoplane), inside the root (endosphere), and in the soil surrounding the root surface (rhizosphere) play a crucial role in plant immunity and yield. But there is very little information regarding the microbial consortia in the rhizosphere during different seasons of rice cultivation. Therefore, the objective of our study was to assess, contrast and correlate the bacterial population observed during different seasons among various places in Tiruvarur district along with their physiochemical parameters. This study revealed 21 bacterial species that belong to three major phyla, four classes, eight orders, ten families, and fifteen genera. In the Tiruvarur rice fields, bacterial genera such as *Aeromonas*, *Azotobacter*, *Azospirillum*, *Bacillus*, *Bradyrhizobium*, *Enterobacter*, *Escherichia*, *Flavobacterium*, *Pseudomonas*, *Rhizobium*, *Salmonella*, *Serratia*, *Shigella*, *Vibrio*, and *Yersinia* were found. The soil physiochemical characteristics like pH, electrical conductivity, organic carbon, available nitrogen, phosphorus, potassium, zinc, copper, iron, and manganese were studied during the pre-monsoon, monsoon, post-monsoon, and summer seasons in five places in the Tiruvarur rice field. Additionally, the Pearson correlation coefficient analysis was also done on the obtained databases and the level of significance was seen at  $P < 0.05$ . The results of the study demonstrate that a special consortium of bacteria inhabited the rice soil during different seasons which may help to improve crop yield.

**Key words:** Rhizosphere, Rice field, Physiochemical parameters, Bacteria, Monsoon

Rice is the most important crop agriculturally as well as economically feeding over half of the world's population [1]. In Asia and developing nations, rice consumption is very high [2]. Rice is an annual monocot grass that belongs to the family Poaceae. It contains abundant carbohydrates and lot of vitamins, minerals and polyphenols. Only two primary rice species are widely farmed out of the 23 different varieties. They are *Oryza glaberrima*, or African rice, and *Oryza sativa*, or Asian rice. *Oryza sativa* is grown all throughout the world, but *Oryza glaberrima* is only grown in Africa. Indica, which has long grains, and Japonica, which has round grains, are the two primary subspecies of *Oryza sativa*. Indica rice types are extensively farmed in Asia, but Japonica rice is mostly grown and consumed in Australia, China, Taiwan, Korea, Europe, Japan, Russia, Turkey and the United States [3].

Rice is the most important staple food in India which meets around 60% of daily energy requirements or 41% of the nation's total grain production from 35% of the country's grain-producing land. Rice is therefore crucial for ensuring national food security. India is the world's second-largest producer of rice and rice's top exporter. 120 million tonnes of rice would be produced in India in FY 2020–21, up from 53.6 million tonnes

in FY 1980 [4-5]. In India rice is grown under widely varying conditions of altitude and climate. Rice cultivation in India extends from 8 to 35°N latitude and from sea level to as high as 3000 meters. Rice crop needs a hot and humid climate. It is best suited to regions which have high humidity, prolonged sunshine and an assured supply of water. The average temperature required throughout the life period of the crop ranges from 21 to 37 °C. Maximum temp which the crop can tolerate 40 °C to 42 °C.

Soil microbiota play a key role in enhancing the soil's inherent ability to inhibit diseases that affect plants on the soil [6]. In agroecosystems, the dynamics of soil organic matter (SOM) and plant nutrient availability are significantly influenced by microbiota [7-8]. The diversity and activity of bacteria is regulated by various biotic (plants and other organisms) and abiotic (soil pH, moisture, salinity, structure and temperature) factors. This work reports and discusses the most reliable findings in relation to a comprehensive understanding of soil bacteria pertaining to rice crop and their correlation with various physiochemical parameters.

## MATERIALS AND METHODS

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**Citation:** Deepan B, Prakash P, Ambikapathy V, Gomathi S, Panneeselvam A. 2023. Population dynamics of bacteria and physiochemical properties of soil in different agricultural fields of Tiruvarur district, rice bowl of Tamil Nadu. *Res. Jr. Agril. Sci.* **14**(6): 1845-1854.

### Study site and sample collection

The Kaveri delta often known as the "Rice Bowl of Tamil Nadu," is located in the Thiruvavur district of Tamil Nadu, India (Fig 1). The district is located between latitudes 10° 16' and 11° 50' north and longitudes 79° 27' and 79° 50' east. The Thiruvavur district covers a total area of 2377 km<sup>2</sup>. The district is bordered on the east by Nagapattinam district, the north by Mayiladuthurai District, the west by Thanjavur District and the south by Palk Strait. The region experiences hot, tropical weather with daily highs and lows between 26.39 °C and 35.19 °C [9].

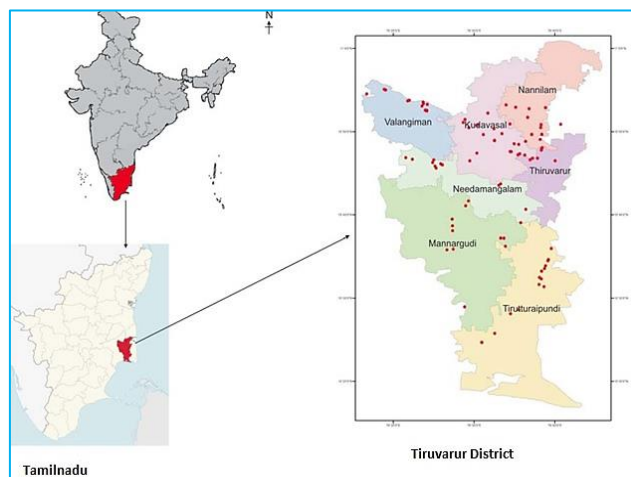


Fig 1 Geographical location of the study area

The soil samples were taken during Pre-monsoon (Aug-Sep, 2022), Monsoon (October- December, 2022) and Post-monsoon (Jan- Feb, 2023) periods in various rice fields of Tiruvavur district i.e., Thiruthuraiipoondi, Tiruvavur, Mannargudi, Needamangalam and Nannilam. Three subsamples of 200-250g soil were collected around the root at a depth of 15cm to form a composite sample (n=45). The samples were placed in Ziplock bags and were stored at -80°C until further analysis.

### Physiochemical analysis

The soil samples were suspended in distilled water and the particles were allowed to settle down. The pH values, electrical conductivity, organic carbon, nitrogen, phosphorous, potassium, iron, manganese, copper and zinc were analyzed. Using a pH meter (Duralab, India), the suspension pH was determined. The electrical conductivity of the soil was measured using a conductivity meter in the water extract filtrate. The macro nutrients such as Nitrogen by Alkaline permanganate method [10], phosphorous by Olsen method [11], potassium (neutral normal ammonium acetate method), organic carbon by Walkley and Block method [12] and micro nutrients such as copper, iron, manganese and zinc were analyzed by DTPA extract method using atomic absorption spectrophotometer [13].

### Isolation and identification of soil bacteria

One gram of rhizosphere soil sample taken in 9 ml of sterile distilled water. The samples were serially diluted for six-fold and were plated on nutrient agar. Then incubated for 24 hours at 37 °C. After incubation the colonies were purified by the continuous streaking method and characterized on the basis of macroscopic, microscopic and biochemical tests, according to the 9<sup>th</sup> edition, Bergey's Manual of determinative bacteriology 1923 [14]. The bacterial isolates were identified macroscopically by examining colony morphology, surface pigment, size, margin, surface on nutrient agar plates and

microscopic examination including gram's staining behavior, shape and cell arrangement. Motility tests were also performed.

### Gram's staining

Thin smears of bacterial isolates were taken on clean glass slide and heat fixed or air dried. The smear was stained with crystal violet for 2 minutes after washed with running water and air dried. Then flooded with Gram's iodine for 1 minute and decolorized by ethyl alcohol. Finally the smears were added with counter stain safranin for 45 seconds and observed under light microscope. Gram positive bacteria have cell walls that contain thick layers of peptidoglycon. These strains are purple. Gram negative bacteria have thin layer of peptidoglycon so they are in pink in colour [25].

### Indole test

Indole is the product of the breakdown of another amino acid tryptophan by the enzyme tryptophanase. Kovacs reagent was added to the medium containing bacterial isolates. If indole is present in the culture, a red ring appears around the test tube surface.

### Methyl red and Voges Proskauer test

MR-VP TEST was used to determine the ability of a bacterium to oxidize glucose and produce stable acid end products. Methyl red is a pH indicator (red at pH less than 4.4 and yellow at pH greater than 6). MR-VP broth was used. Acid production is positive for methyl red and end product of neutral pH is positive for Voges Proskauer test.

### Citrate utilization test

The citrate agar medium was prepared using sodium citrate, bromothymol blue, sodium chloride, and agar. Citrate agar was used to test an organism's ability to utilize citrate as a source of energy. The medium contains citrate as the sole carbon source and inorganic ammonium salts as the sole nitrogen source. When the bacteria metabolize citrate, the ammonium salts are broken down to ammonia, which increases alkalinity. The shift in pH turns the bromothymol blue indicator in the medium from green to blue above pH 7.6.

### Catalase test

The colony of bacterial isolates was immersed in hydrogen peroxide and tested for rapid elaboration of oxygen bubbles. If the bacterial colony possesses the ability to produce the catalase enzyme, then strong oxygen bubbles will appear, whereas if the bacterial colony cannot produce the catalase enzyme only weak or lack of oxygen bubbles will be observed.

### Carbohydrate fermentation test

The colony of bacterial isolates was inoculated with a purple broth medium that contains peptone with the pH indicator bromocresol purple. Specific carbohydrates are added at a concentration of 0.5–1%. The inoculated media was incubated aerobically at 35–37 °C for 3-5 days to check for yellow colour formation. If the media are inoculated with an organism that is able to ferment the carbohydrate present, acid or gas are produced. The indicator in the media changes from purple to yellow.

### Oxidase test

A Whatman's filter paper soaked in 1% tetramethyl-p-phenylene-diamine dihydrochloride was taken and laid in a Petridis moistened with distilled water. The colony of bacterial isolates is picked up with a platinum loop and smeared over the moist area of filter paper. Organisms that contain cytochrome c as part of their respiratory chain are oxidase-positive and turn

the reagent blue or purple. Organisms lacking cytochrome c as part of their respiratory chain do not oxidize the reagent, leaving it colour less within the limits of the test, and are oxidase-negative. The cytochrome system is usually only present in aerobic organisms which are capable of utilizing oxygen as the final hydrogen receptor.

### Triple sugar iron test

Triple Sugar Iron Agar is designed to differentiate among organisms based on differences in carbohydrate fermentation patterns and hydrogen sulphide production. TSI was a differential medium that contained 1% lactose and sucrose, a small amount of glucose (0.1%), ferrous sulphate, and the PH indicator phenol red. The acid-base indicator phenol red is incorporated for detecting carbohydrate fermentation, which is indicated by the change in colour of the carbohydrate medium from orange red to yellow in the presence of acids. In the case of oxidative decarboxylation of peptone, alkaline products are formed, and the pH rises. This is indicated by the change in colour of the medium from orange red to deep red. Sodium thiosulphate and ferrous ammonium sulphate present in the medium detect the production of hydrogen sulphide, as

indicated by the black colour in the butt of the tube. Red slant or red butt indicates no fermentation; red slant or yellow butt indicates only glucose fermentation; yellow slant or yellow butt indicates lactose and sucrose fermentation; and dark-coloured hydrogen sulphide is produced.

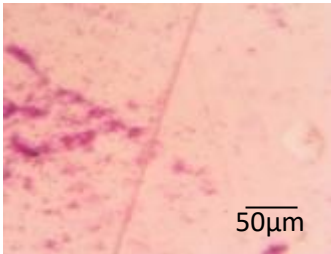
### Statistical analysis

Using SPSS software, the Pearson correlation matrix was generated. For level of significance, correlation coefficients between physicochemical parameters and bacterial populations were recorded.

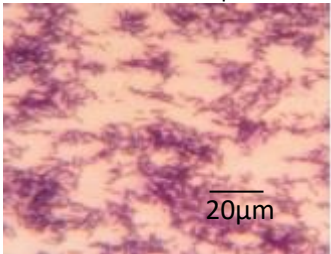
## RESULTS AND DISCUSSION

### Taxonomic analysis of bacterial community abundance on different rice field soils of Tiruvarur district

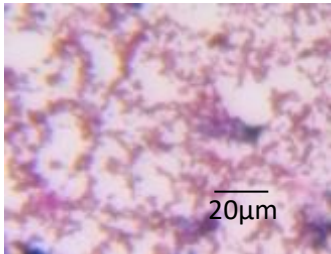
The abundance of bacterial communities was examined in different seasons, including monsoon, pre-monsoon, post-monsoon and summer for all taxonomic levels among different areas of Tiruvarur district. The results were displayed as graphs (Fig 3-7).



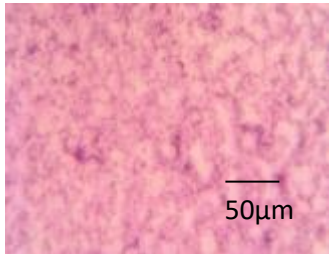
*Aeromonas sp.*



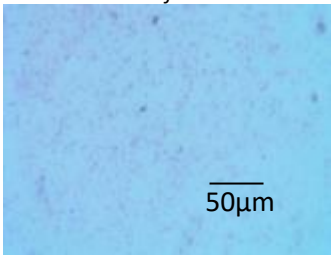
*Flavobacterium odoratum*



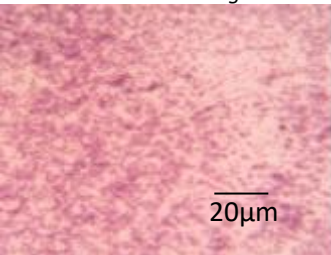
*Bacillus subtilis*



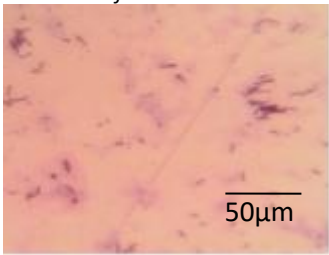
*Serratia fonticola*



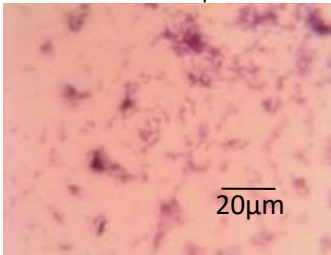
*Pseudomonas aeruginosa*



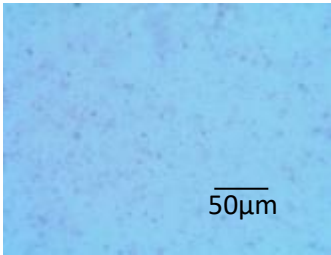
*P.fluorescence*



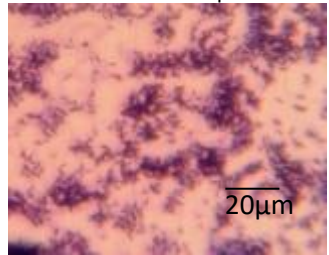
*Bacillus sp.*



*Escherichia coli*



*Rhizobium sp.*



*Vibrio cholerae*

*Bacillus cereus*

*Enterobacter cloacae*



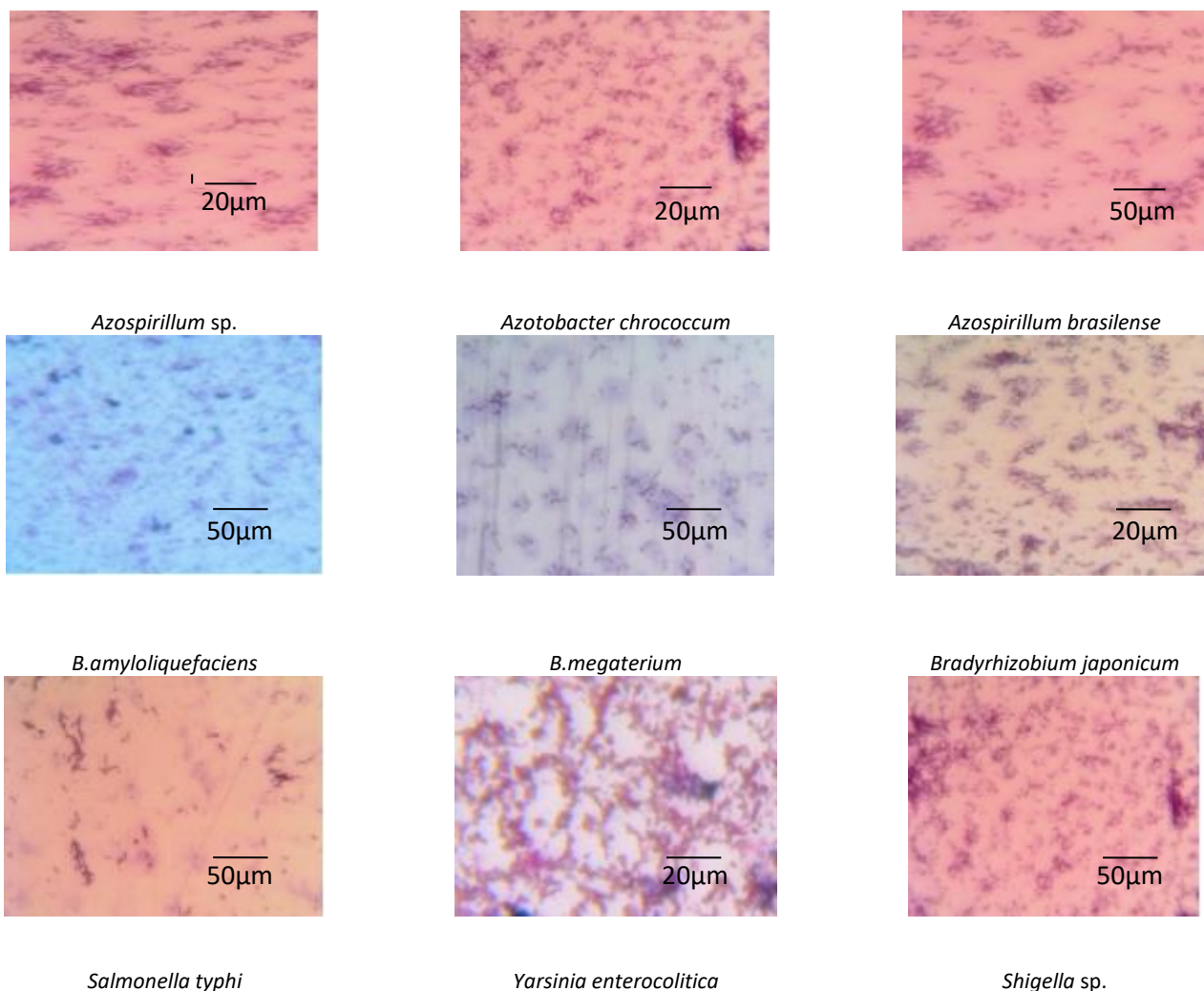


Fig 2 Microphotography of isolated bacteria from paddy fields in different seasons

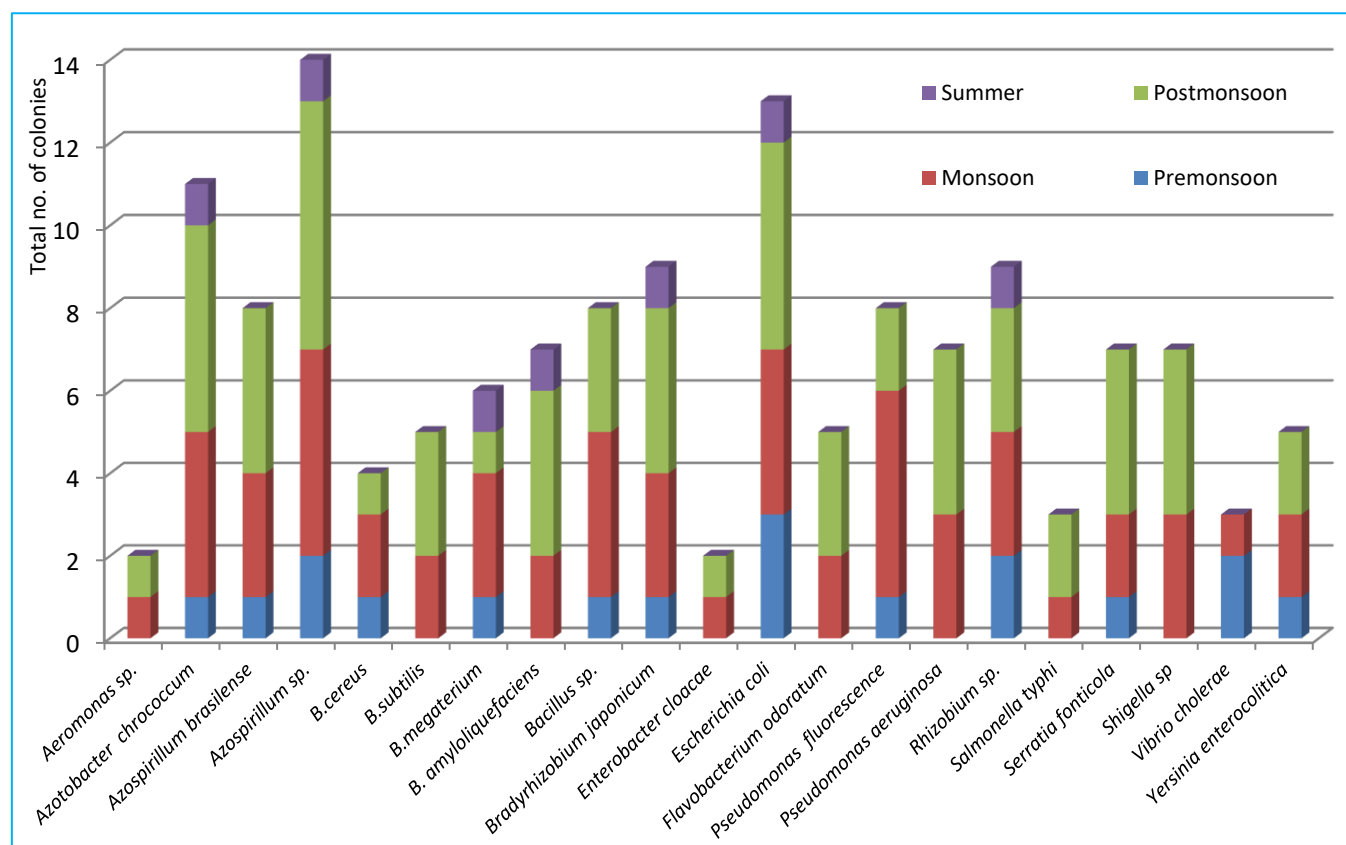


Fig 3 Bacteria of paddy fields in Thiruthuraipoondi region of Tiruvarur district during different seasons

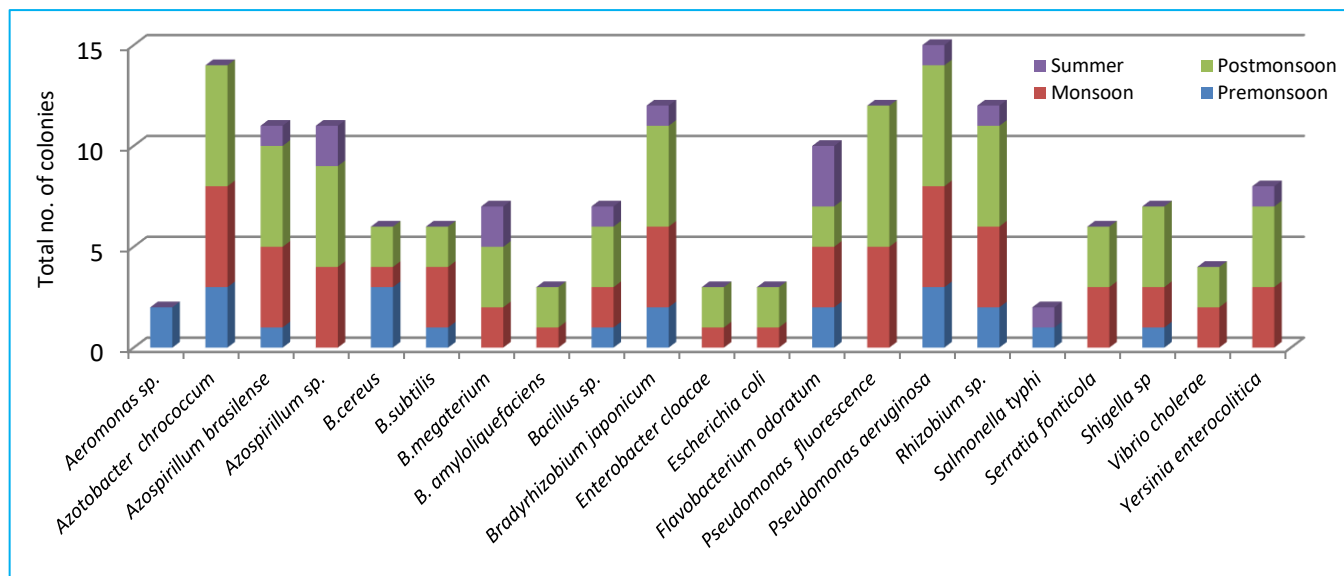


Fig 4 Bacteria of paddy fields in Mannargudi region of Tiruvallur district during different seasons

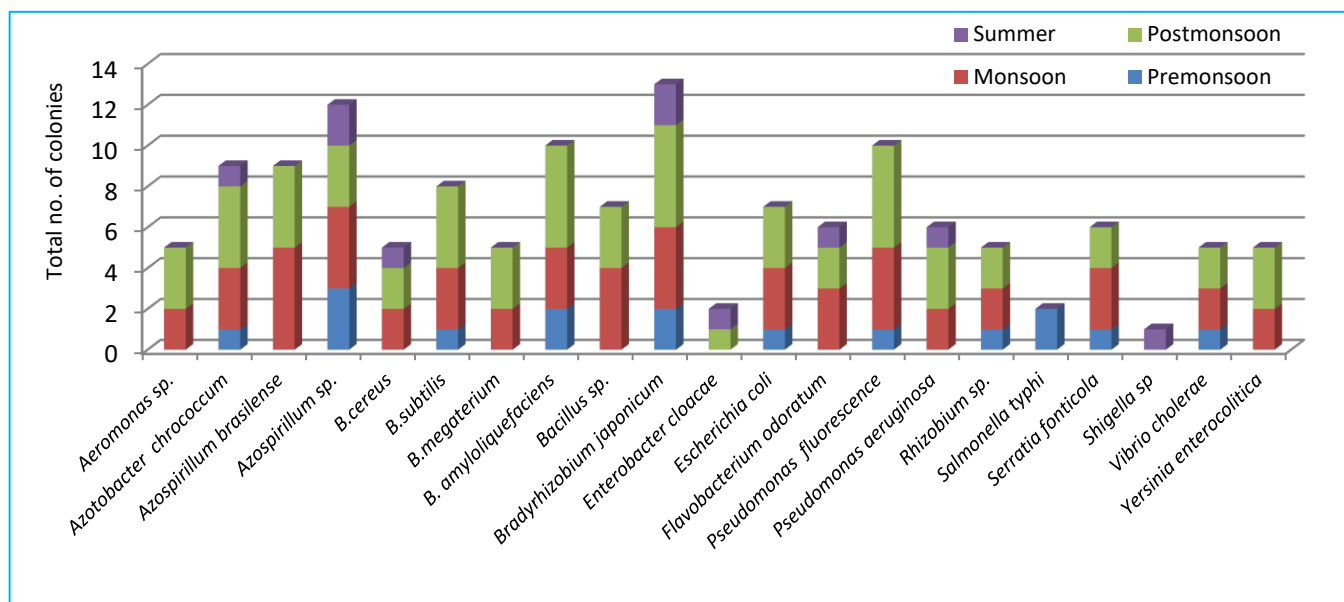


Fig 5 Bacteria of paddy fields in Tiruvallur region of Tiruvallur district during different seasons

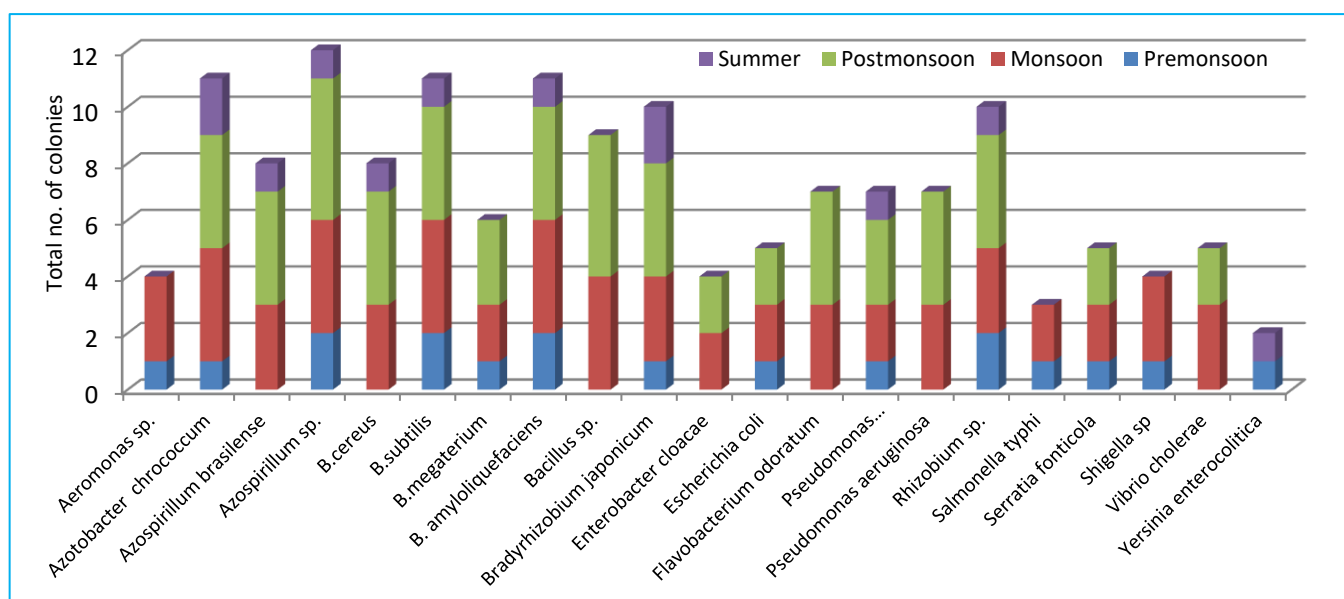


Fig 6 Bacteria of paddy fields in Nannilam region of Tiruvallur district during different seasons

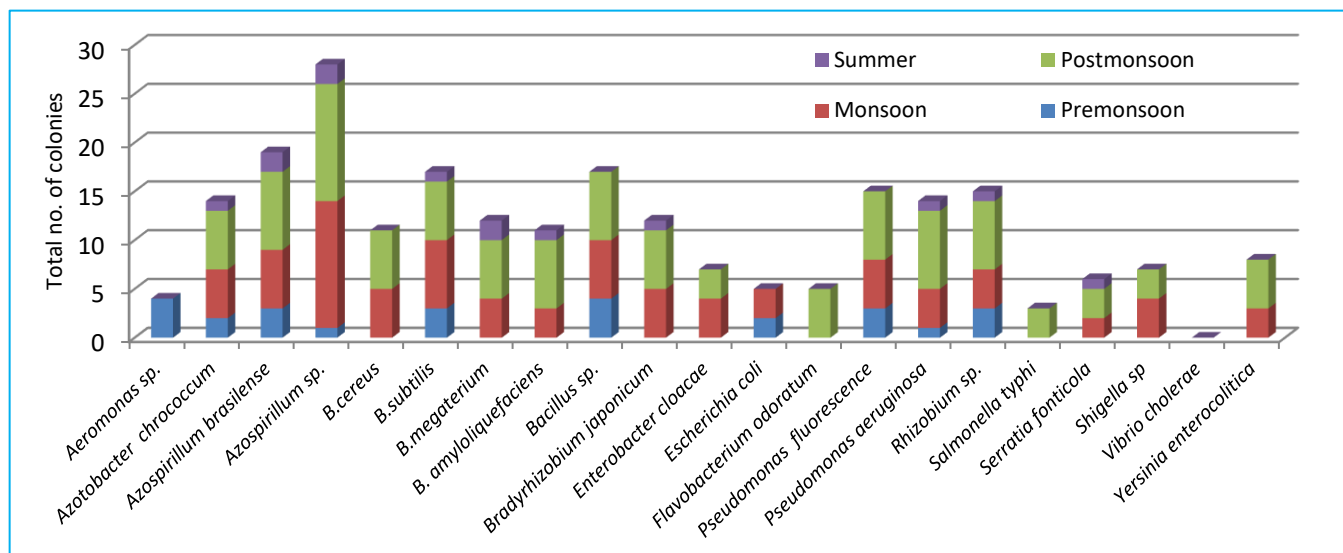


Fig 7 Bacteria of paddy fields in Needamangalam region of Tiruvur district during different seasons

#### Phyla and class analysis

A total of three bacterial phyla were discovered in different seasons such as pre-monsoon, monsoon, post monsoon and summer. Proteobacteria (96.45%) is the most abundant phylum found in all five sites of Tiruvur district. Bacillota (2.2%), and Bacteroidetes (1.3%) are the next two abundant phyla found in the rice field soil. A total of four bacterial classes were observed in rice field soil. They are Gammaproteobacteria, Alphaproteobacteria, Bacilli and Flavobacteriia. Gammaproteobacteria (82.5%) was the most abundant class, while Flavobacteria (1.66%) was the least abundant in all seasons of Tiruvur rice field soil. Next to Gammaproteobacteria, Alphaproteobacteria (13.25%) and Bacilli (4.24%) ranked as the second and third most abundant classes in rice field soil, respectively.

#### Order and family analysis

There are eight orders found in Tiruvur rice field soil observed in all seasons. They are Aeromonadales, Pseudomonadales, Rhodospirillales, Bacillales, Hyphomicrobiales, Enterobacterales, Flavobacteriales, Vibrionales. Among them, Pseudomonadales (43.9%) was the most abundant order whereas Flavobacteriales (1.69%) was the least abundant in all seasons of Tiruvur rice field soil. Next to Pseudomonadales, Bacillales (28.3%), Rhodospirillales (4.6%) and Hyphomicrobiales (4.39%) ranked as the second, third and fourth most abundant orders in rice field soil, respectively. In total, ten different bacterial families were found in the Tiruvur

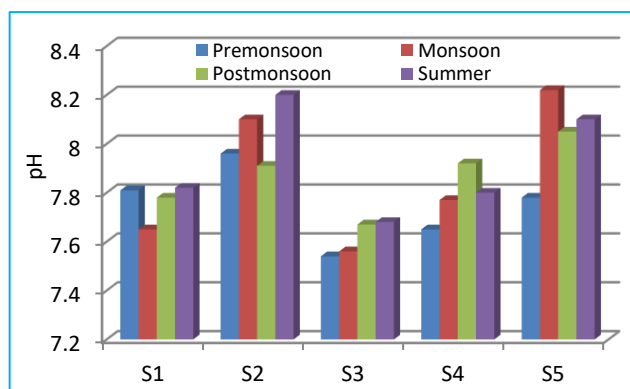
rice field during the year. Aeromonadaceae, Azospirillaceae, Bacillaceae, Nitrobacteraceae, Enterobacteriaceae, Pseudomonadaceae, Flavobacteriaceae, Rhizobiaceae, Vibrionaceae and Yersiniaceae were the eight abundant families found in the rice fields of Tiruvur. Pseudomonadaceae (42.3% of the total) was the most abundant family while Yersiniaceae (1.33%) was the least abundant in all seasons of Tiruvur rice field soil.

#### Genera analysis

There are about 15 genus-level taxa found in various sites of the Tiruvur rice field. Among the genera, *Pseudomonas* (27%), *Azotobacter* (15.6%), and *Azospirillum* (12.5%) appear to be the most abundant during all seasons of rice growth. The other abundant genera are in descending order as follows: *Bacillus* (10.8%), *Aeromonas* (5.2%), *Bradyrhizobium* (5.5%), *Flavobacterium* (4.5%), *Escheichia* (3.88%), *Rhizobium* (3.66%), shigella (2.8%), *Enterobacter* (2.66%), *vibrio* (2.4%), *Serratia* (1.32%), *salmonella* (0.9%) and *Yersinia* (0.33%).

#### Physiochemical parameters

The present study includes the observation of physiochemical factors with respect to the monsoon, pre-monsoon, post-monsoon and summer seasons. Physiochemical parameters such as pH, electrical conductivity, organic carbon, nitrogen, phosphorus, potassium, iron, manganese, zinc, and copper are shown as graphs (Fig 8-17).



S<sub>1</sub>- Thiruthuraipoondi site, S<sub>2</sub>- Mannargudi site, S<sub>3</sub>- Tiruvur site, S<sub>4</sub>- Nannilam site, S<sub>5</sub>- Needamangalam site

Fig 8 pH value of different regions of Tiruvur with respect to monsoon periods

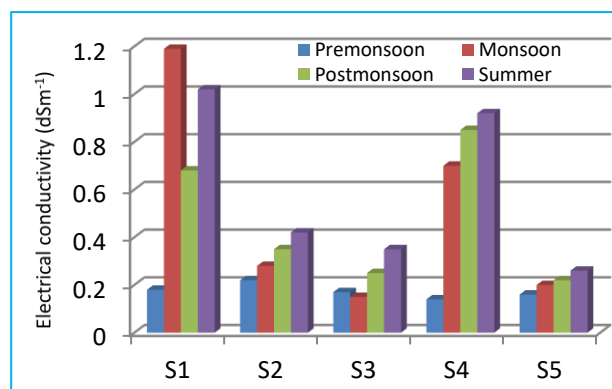
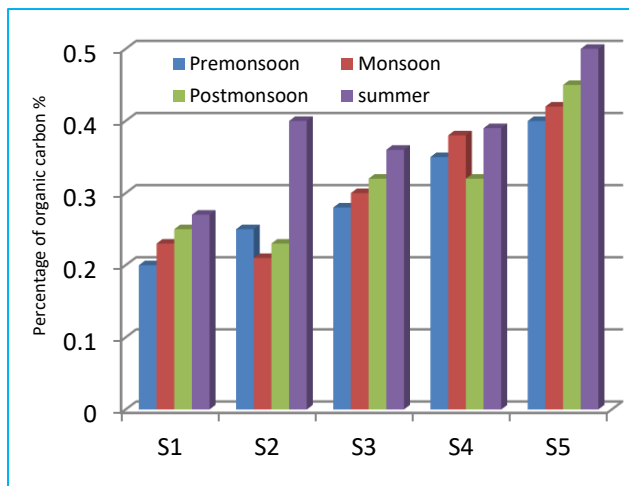


Fig 9 Electrical conductivity (dSm<sup>-1</sup>)Value of different regions of Tiruvur with respect to monsoon periods



S<sub>1</sub>- Thiruthuraipoondi site, S<sub>2</sub>- Mannargudi site, S<sub>3</sub>- Tiruvarur site, S<sub>4</sub>- Nannilam site, S<sub>5</sub>- Needamangalam site

Fig 10 Percentage of organic carbon in soil during different seasons in Tiruvarur district

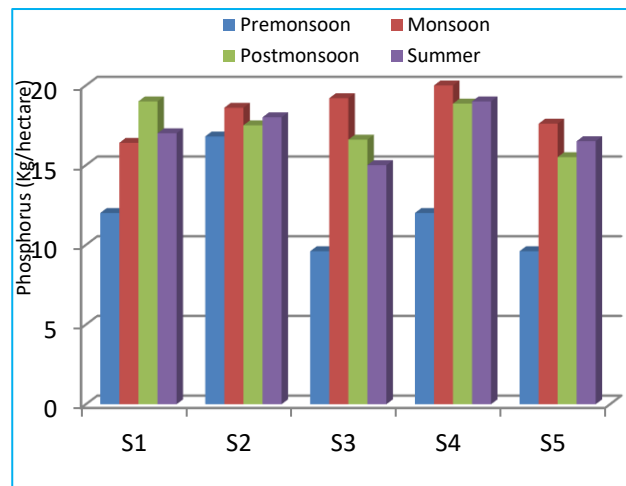
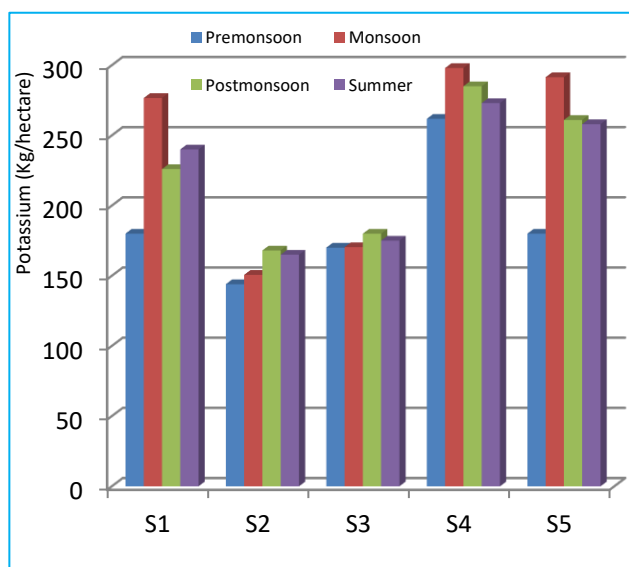


Fig 11 Phosphorus (Kg/hectare) in soil during different seasons in Tiruvarur district



S<sub>1</sub>- Thiruthuraipoondi site, S<sub>2</sub>- Mannargudi site, S<sub>3</sub>- Tiruvarur site, S<sub>4</sub>- Nannilam site, S<sub>5</sub>- Needamangalam site

Fig 12 Potassium (Kg/hectare) in soil during different seasons in Tiruvarur district

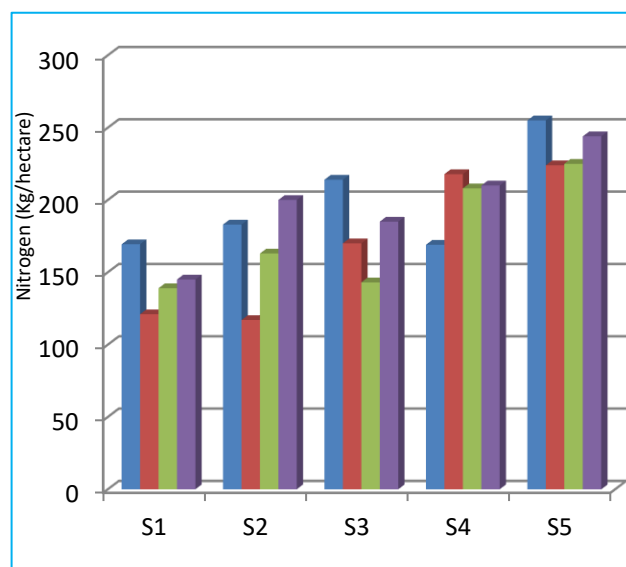
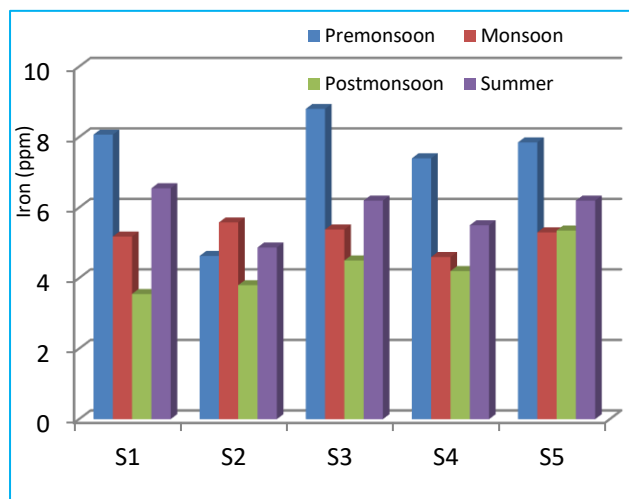


Fig 13 Nitrogen (Kg/hectare) in soil during different seasons in Tiruvarur district



S<sub>1</sub>- Thiruthuraipoondi site, S<sub>2</sub>- Mannargudi site, S<sub>3</sub>- Tiruvarur site, S<sub>4</sub>- Nannilam site, S<sub>5</sub>- Needamangalam site

Fig 14 Iron (ppm) in soil during different seasons in Tiruvarur district

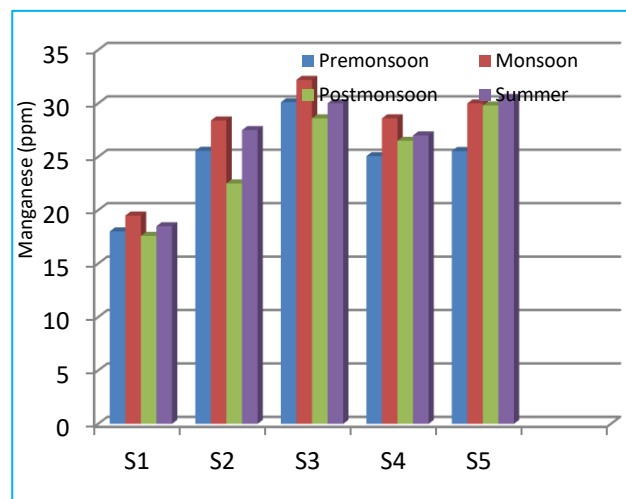
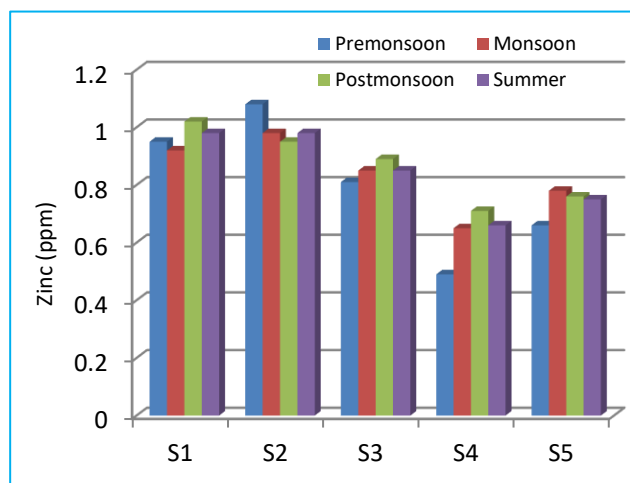


Fig 15 Manganese (ppm) in soil during different seasons in Tiruvarur district



S<sub>1</sub>- Thiruthuraipoondi site, S<sub>2</sub>- Mannargudi site, S<sub>3</sub>- Tiruvarur site, S<sub>4</sub>- Nannilam site, S<sub>5</sub>- Needamangalam site

Fig 16 Zinc (ppm) in soil during different seasons in Tiruvarur district

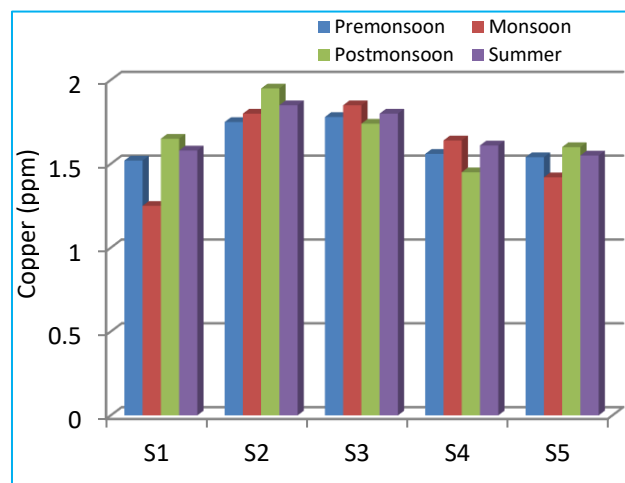


Fig 17 Copper (ppm) in soil during different seasons in Tiruvarur district

Table 1 Pearson correlation coefficient of physiochemical parameters and bacterial population density of five different soil samples in Tiruvarur district

Correlation	pH	EC	OC	AP	AK	AN	AI	AM	AZ	AC	PD
pH	1										
EC	-0.3	1									
OC	0.28	-0.48	1								
AP	0.22	0.44	-0.44	1							
AK	-0.03*	0.51	0.5	-0.02*	1						
AN	0.37	-0.5	0.99	-0.36	0.47	1					
AI	-0.46	-0.19	0.44	-0.93	0.27	0.35	1				
AM	0.04*	-0.82	0.68	-0.28	-0.15	0.68	0.23	1			
AZ	0.11	-0.06	-0.78	0.09	-0.76	-0.76	-0.32	-0.48	1		
AC	-0.001	-0.56	-0.3	0.25	-0.87	-0.26	-0.41	0.45	0.42	1	
PD	0.77	-0.51	0.74	-0.38	0.22	0.77	0.18	0.33	-0.25	-0.28	1

OC-Organic Carbon, AP- Available Phosphorus, AK- Available Potassium, AN – Available Nitrogen, AI- Available iron, AM – Available Manganese, AZ- Available Zinc, AC- Available Copper, PD- Population Density

\*Strongly presented correlation significance at the level ( $p < 0.05\%$ )

All our sampling sites in Tiruvarur, such as Thiruthuraipoondi, Mannargudi, Tiruvarur, Nannilam, and Needamangalam, showed a pH value above 7. Among them, the Nannilam and Mannargudi sites possess a high pH value above 7.2 comparable to all other sites in Tiruvarur district (Fig 8). The electrical conductivity in the Thiruthuraipoondi and Nannilam sites was high ( $0.8\text{--}1.2 \text{ dsm}^{-1}$ ), but it was low at the Tiruvarur site ( $0.15 \text{ dsm}^{-1}$ ). In every season examined, Nannilam and Needamangalam sites have a higher percentage of organic carbon, while Mannargudi and Thiruthuraipoondi sites have a lower percentage. Tiruvarur and Needamangalam have the lowest mass of phosphorus during the premonsoon season, whereas Nannilam has the highest mass during the monsoon season. Nannilam and Needamangalam sites have high potassium levels during the monsoon but Mannargudi sites have lower levels during the premonsoon season. Nannilam and Needamangalam sites have high potassium levels during the monsoon, but Mannargudi and tiruvarur sites have lower levels during the premonsoon season. Needamangalam has a higher mass of nitrogen than Thiruthuraipoondi which has a lower mass of nitrogen throughout the seasons studied. The levels of iron and manganese are higher in the Tiruvarur rice field during the monsoon season and lower in Mannargudi and Thiruthuraipoondi during the post-monsoon season. In a similar way, copper and zinc concentrations are higher in the

mannargudi rice field in almost all seasons studied. Further the Pearson correlation coefficient of physiochemical parameters and population density of bacterial isolates are performed as shown in (Table 1) [15].

Although rice soil microbiota was well studied already but only limited studies reported the bacterial community present in rice rhizosphere. Especially, no reports were found in rice bowl of Tamil Nadu, Tiruvarur. The distribution of bacteria is greatly influenced by environmental parameters such as soil pH, moisture, temperature, organic carbon, and nitrogen [16]. In this study, we have collected soil samples of rice and their bacterial profile was recorded through classical culturing technique. Our studies showed the abundances of Phylum Proteobacteria followed by Bacillota and Bacteroidetes in rice soil microbiota and are consistent with previous reports [17]. Proteobacteria are a phylum of Gram-negative bacteria and are related to a wide range of functions involved in carbon, nitrogen, and sulphur cycling [18]. Their relative richness increases with high organic carbon availability in soils as aligned with findings of Fierer *et al.* [19], Eilers *et al.* [20]. Bacteroidetes phylum have been found to function as degraders of polymeric organic matter.

In the present study, the bacterial population isolated from five different sites of rice field in Tiruvarur district with respect to four different seasons (Pre-monsoon, Monsoon, Post-



monsoon and Summer) were recorded. The isolated bacterial species in rice field soil include *Aeromonas* sp., *Flavobacterium odoratum*, *Bacillus subtilis*, *Serratia fonticola*, *Pseudomonas fluorescence*, *Bacillus* sp., *Escherichia coli*, *Rhizobium* sp., *Vibrio cholera*, *Bacillus cereus*, *Enterobacter cloacae*, *Azospirillum* sp., *Azotobacter chroococcum*, *Azospirillum brasilense*, *B. amyloliquefaciens*, *B. megaterium*, *Bradyrhizobium japonicum*, *Salmonella typhi*, *Yersinia enterocolitica*, *Shigella* sp. The maximum bacterial colonies were screened (230) from needamangalam rice field clay soil whereas minimum colonies were observed (138) from tiruvarur rice field soil. In the rice rhizosphere, *Azotobacter* species, free-living nitrogen-fixing bacteria, have been used as biofertilizers to improve the productivity of non-leguminous crops including rice, due to their various plant growth-promoting traits. *Azospirillum* belong to rhodospirillales possess the ability to synthesize phytohormones, especially indole-3-acetic acid and gibberellins, and helps to promote proliferation of roots [21].

The Pearson correlation coefficient of physicochemical parameters (temperature, pH, organic carbon, organic matter, salinity, available nitrogen, phosphorus, potassium, zinc, copper, iron, manganese and sodium, calcium, magnesium, potassium) and population density of bacteria were analyzed using SPSS Software. The sign put in front of the coefficient value indicates the direction of the relationship. Relationship values can be between -1 and +1, with +1 signifying an absolutely perfect linear relationship, 0 signifying no linear relationship, and -1 signifying an entirely inverse relationship between the coordinates. The physicochemical parameters were positively correlated at the p 0.05% level of significance whereas the bacteria population density was negatively correlated with some physicochemical characteristics. It clearly indicates that the soil collected at monsoon and post-monsoon seasons showed maximum bacterial propagules compared to pre-monsoon and summer with few exceptions as studied by Kalaivani *et al.* [24]. In addition, more number of bacterial colonies observed during post monsoon season when compared to monsoon and pre-monsoon seasons. Different agricultural plants have responded favourably to co-inoculation with *Azotobacter* and *Rhizobium* in laboratory, greenhouse, and outdoor environments. *Azotobacter* is able to produce growth hormones like auxins and gibberellins and thus enhancing root growth, it in turn could make available more root area to rhizobia for infection. This would result in increased

nodulation, nitrogen fixation and ultimately crop yield improvement [21-23]. Here in our study both *Azotobacter* and *Rhizobia* naturally present in rhizospheric soil, Tiruvarur district.

## CONCLUSION

Soil microbiota study of rice illustrates a total of 827 bacterial colonies observed among 21 species in all seasons of Tiruvarur district. Among them, the Needamangalam clay soil possessed the highest number of colonies (230), and the lowest (138) was observed in the Tiruvarur soil. These distinct colonies may correspond to specific functional roles to be performed under various physiochemical conditions. The taxonomic analysis of the rice soil fungal community reported the abundance of Proteobacteria, Bacillota, Bacteroidetes at the phylum level; Gammaproteobacteria, Alphaproteobacteria and Bacilli at the class level; Pseudomonadales, Rhodospirillales and Hyphomicrobiales at the order level; and Azospirillaceae, Pseudomonadaceae, and Bacillaceae at the family level taxon. Moreover, the microbiota of rice soil is largely populated by bacteria belonged to genera such as *Pseudomonas*, *Azotobacter*, *Azospirillum* and *Bacillus*. This study also addressed the physiochemical parameters such as pH, electrical conductivity, organic carbon, nitrogen, phosphorus, potassium, iron, manganese, zinc, and copper in the seasons such as pre-monsoon, monsoon, post-monsoon and summer across all sites of the Tiruvarur district. In addition to being useful in improving plant growth and yield attributes, co-inoculation of *Azotobacter* and *Azospirillum* have also been found to alleviate the adverse effect of salinity stress on some plants. The discovery of different bacterial taxa during different seasons of the year in rice-growing regions may stimulate the development of novel strategies such as incorporating populations of useful bacteria into agroecosystems, which could be used to improve plant growth and development.

## Acknowledgement

The authors greatly thank Principal, Secretary and Correspondent, A.V.V.M. Sri Pushpam College (Autonomous), Poondi, Thanjavur and The Director, Indian Biotrack Research Institute, Thanjavur for providing necessary laboratory facilities.

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