

Comparative Analysis of Culturable Microbial Diversity in the Rhizosphere of Hybrid and Traditional Tomato (*Solanum lycopersicum* L.)

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Abstract

Tomato (*Solanum lycopersicum* L.) is one of the most economically important vegetable crops worldwide and supports a diverse rhizosphere microbial community that plays a crucial role in nutrient cycling, soil fertility, plant growth, and disease suppression. Understanding the influence of different tomato varieties on rhizosphere microorganisms is essential for developing sustainable agricultural practices. The present study compared the culturable microbial diversity associated with the rhizospheres of hybrid and traditional tomato varieties using conventional microbiological techniques. Rhizosphere soil samples were collected from healthy plants cultivated under similar environmental conditions. Bacterial and fungal isolates were obtained through serial dilution and culture-based methods, followed by colony characterization, Gram staining, biochemical identification, and microscopic examination. Microbial populations were estimated as colony-forming units (CFU), and representative isolates were identified using standard microbiological procedures.

The results revealed that both tomato varieties supported diverse culturable bacterial and fungal communities. However, the traditional tomato rhizosphere consistently exhibited greater microbial abundance and diversity than the hybrid variety. Beneficial bacterial genera, including *Bacillus*, *Pseudomonas*, and *Azotobacter*, together with fungal genera such as *Aspergillus*, *Penicillium*, and *Rhizopus*, were identified among the isolates. Greater variation in colony morphology and higher CFU counts observed in the traditional tomato rhizosphere suggest that plant genotype may influence the composition and abundance of culturable rhizosphere microorganisms.

Overall, this study demonstrates the usefulness of conventional microbiological techniques for investigating culturable rhizosphere microorganisms and provides valuable baseline information for understanding plant–microbe interactions. The findings contribute to current knowledge of rhizosphere microbial diversity and may support future research aimed at improving soil health, sustainable crop production, and the development of environmentally friendly agricultural practices.

Introduction

Tomato (*Solanum lycopersicum* L.) is one of the most widely cultivated and economically important vegetable crops worldwide. It is valued for its high nutritional content, including vitamins, minerals, dietary fibre, and antioxidants such as lycopene, which contribute significantly to human health and food security. Owing to its broad adaptability, short life cycle, and relatively small genome, tomato has also become an important model crop for studies in plant biology, genetics, and sustainable agriculture. Continuous breeding programmes have led to the development of hybrid varieties with improved yield, fruit quality, disease resistance, and tolerance to various environmental stresses.

The rhizosphere is the narrow zone of soil surrounding plant roots where intense biological and biochemical interactions occur between plants and microorganisms. This dynamic environment supports diverse communities of bacteria, fungi, actinomycetes, and other microorganisms that play essential roles in nutrient cycling, organic matter decomposition, nitrogen fixation, phosphate

solubilisation, phytohormone production, and suppression of soil-borne pathogens. These beneficial microorganisms contribute to improved soil fertility, enhanced plant growth, and increased agricultural productivity. The composition and activity of rhizosphere microbial communities are strongly influenced by root exudates, soil characteristics, environmental conditions, and plant genotype.

Plant genotype is considered an important factor affecting the diversity and abundance of rhizosphere microorganisms. Different tomato varieties release varying quantities and compositions of root exudates, including sugars, amino acids, organic acids, and secondary metabolites, which selectively influence microbial colonisation and community structure. Hybrid tomato varieties developed through conventional breeding may therefore differ from traditional varieties in their interactions with soil microorganisms. Understanding these plant–microbe interactions is important because changes in rhizosphere microbial communities can influence nutrient availability, soil health, and long-term crop productivity.

Although numerous studies have investigated rhizosphere microbial diversity using molecular techniques such as metagenomic sequencing and high-throughput DNA analysis, conventional culture-based methods remain indispensable for isolating viable microorganisms and studying their morphological, physiological, and biochemical characteristics. These techniques facilitate the identification of culturable microorganisms with potential applications in biofertilizer development, biological disease control, and sustainable crop management. Furthermore, culture-dependent approaches provide living microbial isolates that can be preserved for future functional studies and agricultural applications.

The present study was undertaken to compare the culturable microbial diversity associated with the rhizospheres of hybrid and traditional tomato varieties using conventional microbiological techniques. Rhizosphere microorganisms were isolated through serial dilution and cultured on selective media, followed by colony characterisation, Gram staining, biochemical identification, and microscopic examination. The study further compared microbial abundance based on colony-forming unit (CFU) counts and evaluated the diversity of bacterial and fungal isolates associated with each tomato variety. The findings provide valuable insights into the influence of tomato genotype on culturable rhizosphere microbial communities and contribute to a better understanding of plant–microbe interactions, soil microbial ecology, and sustainable agricultural practices.

Materials and Methods

Collection of Rhizosphere Soil Samples

Rhizosphere soil samples were collected from healthy **hybrid** and traditional tomato (*Solanum lycopersicum* L.) plants at the fruit-maturity stage. Both varieties were cultivated under similar environmental conditions to minimise variations arising from climatic and soil factors. Before sample

collection, all equipment, including shovels, spatulas, and collection containers, was sterilised with 70% ethanol to prevent contamination.

Plants were carefully uprooted to avoid damage to the root system. Loosely attached soil was gently removed by shaking, whereas the soil firmly adhering to the roots was considered rhizosphere soil. The rhizosphere soil was aseptically transferred into sterile polyethylene bags, appropriately labelled, and transported to the laboratory in an insulated ice box. Samples were stored at 4°C and processed within 24 hours of collection to preserve the native microbial population.

Preparation of Culture Media

Nutrient Agar (NA) was used for the isolation of bacteria, whereas Potato Dextrose Agar (PDA) was used for fungal isolation. Nutrient Agar was prepared by dissolving peptone, beef extract, sodium chloride, and agar in distilled water, and the pH was adjusted to 7.0 before sterilisation. Potato Dextrose Agar was prepared using potato infusion, dextrose, and agar according to standard microbiological procedures.

Both media were sterilised by autoclaving at **121°C under 15 psi pressure for 15 minutes**. After sterilisation, the media were allowed to cool to approximately **45–50°C** before being poured into sterile Petri dishes inside a laminar airflow cabinet. The prepared plates were allowed to solidify and stored under sterile conditions until use.

Sterilisation Procedures

Strict aseptic techniques were maintained throughout the experimental work to minimise contamination. Glassware, culture media, pipettes, conical flasks, Petri dishes, and test tubes were sterilised by autoclaving at **121°C for 15 minutes**. The working surface of the laminar airflow cabinet was disinfected with **70% ethanol** before and after each experiment. Sterile inoculation loops, micropipette tips, gloves, and other laboratory consumables were used throughout all microbiological procedures.

Serial Dilution and Isolation of Microorganisms

One gram of rhizosphere soil was transferred into a sterile test tube containing **9 mL of sterile physiological saline** to obtain the initial suspension (10^{-1} dilution). The suspension was mixed thoroughly using a vortex mixer. Serial ten-fold dilutions were prepared by transferring **1 mL** of the suspension into successive tubes containing **9 mL** of sterile diluent until a final dilution of **10^{-5}** was obtained.

Aliquots from the appropriate dilutions were inoculated onto Nutrient Agar and Potato Dextrose Agar plates using standard microbiological techniques. Separate sterile inoculation loops were used for each sample to avoid cross-contamination. Nutrient Agar plates were incubated at **28–30°C for 24–48 hours**,

whereas Potato Dextrose Agar plates were incubated at approximately **25°C for 3–7 days**. All plates were incubated in an inverted position to prevent condensation on the agar surface.

Isolation and Enumeration of Microorganisms

Following incubation, well-isolated colonies exhibiting distinct morphological characteristics were selected and repeatedly subcultured to obtain pure cultures. Purified bacterial and fungal isolates were maintained on agar slants under refrigerated conditions for further characterisation.

Microbial populations were estimated by counting colonies on plates containing **30–300 colonies**, and the results were expressed as **colony-forming units (CFU) per gram of soil** using the following equation:

$$\text{CFU/g soil} = (\text{Number of colonies} \times \text{Dilution factor}) \div \text{Volume of inoculum plated}$$

Average colony counts from replicate plates were used to improve the reliability of microbial population estimates.

Morphological and Biochemical Characterisation of Bacterial Isolates

Purified bacterial isolates were characterised based on colony morphology, including colony colour, size, shape, elevation, margin, texture, opacity, and consistency. Gram staining was performed to differentiate bacterial isolates into Gram-positive and Gram-negative groups.

Biochemical identification was carried out using standard laboratory tests, including catalase, oxidase, indole, citrate utilisation, and coagulase tests. The biochemical characteristics obtained were compared with descriptions provided in **Bergey's Manual of Determinative Bacteriology** for the tentative identification of bacterial isolates.

Morphological Identification of Fungal Isolates

Fungal isolates were identified based on colony morphology and microscopic characteristics. Colony colour, pigmentation, growth pattern, sporulation, and texture were recorded after incubation.

Microscopic examination was performed using **lactophenol cotton blue staining** to observe hyphae, conidiophores, and spores. Identification was carried out using standard fungal identification manuals.

Data Analysis

Experimental observations were systematically recorded and organised into tables and figures. Colony counts, microbial abundance, and biochemical characteristics of bacterial and fungal isolates obtained

from the rhizospheres of hybrid and traditional tomato varieties were compared. Mean values were calculated from replicate observations wherever applicable, and microbial populations were expressed as **CFU per gram of soil**. The findings were interpreted through comparative analysis to evaluate differences in culturable microbial diversity between the two tomato varieties.

Results

4.1 Culturable Microbial Population

The rhizosphere soil samples collected from both hybrid and traditional tomato (*Solanum lycopersicum* L.) varieties contained diverse culturable bacterial and fungal populations. Microorganisms were successfully isolated using conventional microbiological techniques, and their abundance was determined by colony-forming unit (CFU) analysis. The results indicated noticeable differences in microbial population between the two tomato varieties, with the traditional tomato rhizosphere generally exhibiting a higher microbial load.

4.1.1 Culturable Bacterial Population

The total culturable bacterial population isolated from the rhizosphere soils of hybrid and traditional tomato varieties is presented in **Table 4.1**. Bacterial colonies were recovered from all serial dilution plates, confirming the presence of viable bacterial communities in both rhizosphere soils.

The hybrid tomato rhizosphere produced **85 colonies** at the 10^{-3} dilution, corresponding to **8.5×10^4 CFU g^{-1} soil**, whereas **35 colonies** were recorded at the 10^{-4} dilution, corresponding to **3.5×10^5 CFU g^{-1} soil**. In comparison, the traditional tomato rhizosphere yielded **125 colonies** at the 10^{-3} dilution and **51 colonies** at the 10^{-4} dilution, indicating a comparatively greater bacterial population than the hybrid variety.

The higher bacterial abundance observed in the traditional tomato rhizosphere suggests that this variety may provide a more favourable environment for bacterial colonisation, possibly because of differences in root exudate composition and rhizosphere interactions.

Table 4.1. Total culturable bacterial population in the rhizosphere soil of hybrid and traditional tomato varieties.

Sample	Inoculum volume (ml)	Dilution Factor	No. of colonies	CFU/g of Soil
Hybrid variety	1ml	10^{-3}	85	8.5×10^4
Hybrid variety	1ml	10^{-4}	35	3.5×10^5
Traditional variety	1ml	10^{-3}	125	1.25×10^5
Traditional variety	1ml	10^{-4}	51	5.1×10^5

4.1.2 Culturable Fungal Population

The total culturable fungal population isolated from the rhizosphere soils of both tomato varieties is presented in **Table 4.2**. Fungal colonies developed successfully on Potato Dextrose Agar (PDA), demonstrating the presence of viable fungal communities in all rhizosphere samples.

The hybrid tomato rhizosphere recorded **45 colonies** at the 10^{-2} dilution, corresponding to **4.5×10^3 CFU g^{-1} soil**, and **20 colonies** at the 10^{-3} dilution, corresponding to **2.0×10^4 CFU g^{-1} soil**. In contrast, the traditional tomato rhizosphere produced **70 colonies** at the 10^{-2} dilution and **31 colonies** at the 10^{-3} dilution, indicating a comparatively higher fungal population than the hybrid variety.

The greater fungal abundance observed in the traditional tomato rhizosphere indicates that it supported a richer culturable fungal community under the experimental conditions employed in this study.

Table 4.2. Total culturable fungal population in the rhizosphere soil of hybrid and traditional tomato varieties.

Sample	Inoculum volume (ml)	Dilution Factor	No. of colonies	CFU/g of soil
Hybrid variety	1ml	10^{-2}	45	4.5×10^3
Hybrid variety	1ml	10^{-3}	20	2.0×10^4
Traditional variety	1ml	10^{-2}	70	7.0×10^3
Traditional variety	1ml	10^{-3}	31	3.1×10^4

4.1.3 Morphological Characterization of Bacterial Isolates

The bacterial isolates obtained from the rhizosphere soils were characterized on the basis of colony morphology, including colony colour, surface characteristics, and colony shape. The morphological characteristics of the representative isolates are presented in **Table 4.3**.

Hybrid bacterial isolate **HB1** formed creamy white, irregular colonies with a rough colony surface, whereas **HB2** produced yellowish colonies with smooth walls and an irregular growth pattern. Traditional

bacterial isolate **TB1** formed milky white, circular colonies with a rough and irregular surface, while **TB2** produced pale brown colonies with smooth walls and a rhizoid colony shape.

The observed variations in colony morphology indicate the presence of morphologically distinct bacterial populations in both hybrid and traditional tomato rhizospheres, reflecting differences in the culturable bacterial community associated with each tomato variety.

Table 4.3. Morphological characteristics of bacterial isolates recovered from hybrid and traditional tomato rhizosphere soils.

Isolates code	Surface	Colour	Surface Texture	Shape
HB1	Irregular	Creamy white	Very rough	Circular
HB2	Smooth walled	Yellowish	Finely smooth	Irregular
TB1	Quietly Spherical	Milky white	Rough and irregular	Circular
TB2	Smooth walled	Pale brown	Smooth	Rhizoid

4.1.4 Biochemical Characterization of Bacterial Isolates

The bacterial isolates recovered from the rhizosphere soils of hybrid and traditional tomato varieties were subjected to Gram staining and standard biochemical tests, including oxidase, catalase, and indole tests. The biochemical characteristics of the isolates are presented in **Table 4.4**.

The results showed considerable variation among the bacterial isolates. Hybrid isolate **HB1** was identified as a Gram-positive bacterium exhibiting positive catalase activity but negative oxidase and indole reactions, and was tentatively identified as *Bacillus* sp. Hybrid isolate **HB2** was Gram-negative and showed positive reactions for oxidase, catalase, and indole tests, indicating characteristics consistent with *Pseudomonas* sp.

Among the traditional tomato isolates, **TB1** was identified as a Gram-positive bacterium showing positive catalase activity and negative oxidase and indole reactions, suggesting its identity as *Staphylococcus* sp. In contrast, **TB2** was Gram-negative, exhibited positive oxidase and catalase reactions with a negative indole reaction, and was tentatively identified as *Azotobacter* sp.

The biochemical characterization confirmed the presence of diverse bacterial communities in both rhizosphere soils. The isolation of beneficial genera such as *Bacillus*, *Pseudomonas*, and *Azotobacter* suggests that both tomato varieties harbour microorganisms that may contribute to nutrient cycling, maintenance of soil fertility, and plant growth promotion.

Table 4.4. Biochemical characteristics and tentative identification of bacterial isolates recovered from hybrid and traditional tomato rhizosphere soils.

Isolates code	Gram staining	Oxidase test	Catalase test	Indole test	Probable organism
HB1	Gram +ve	-	+	-	<i>Bacillus sp.</i>
HB2	Gram -ve	+	+	+	<i>Pseudomonas sp.</i>
TB1	Gram +ve	-	+	-	<i>Staphylococcus sp.</i>
TB2	Gram -ve	+	+	-	<i>Azotobacter sp.</i>

4.1.5 Morphological Characterization of Fungal Isolates

The fungal isolates obtained from the rhizosphere soils were characterized on the basis of colony morphology and microscopic features, including colony texture, pigmentation, spore arrangement, and hyphal characteristics. The observations are presented in **Table 4.5**.

The hybrid tomato rhizosphere yielded two fungal isolates. Isolate **HF1** produced greenish-black powdery colonies with septate hyphae and conidial chains, and was tentatively identified as *Aspergillus* sp. Isolate **HF2** formed white cottony colonies with non-septate hyphae and Sporangiphores, characteristic of *Rhizopus* sp.

Similarly, the traditional tomato rhizosphere yielded two fungal isolates. Isolate **TF1** produced bluish-green velvety colonies with brush-like conidia and septate hyphae, consistent with *Penicillium* sp., whereas **TF2** produced dark green powdery colonies possessing conidial heads and septate hyphae, and was tentatively identified as *Aspergillus* sp.

The occurrence of these fungal genera demonstrates the presence of a diverse culturable fungal community in the rhizosphere soils. The isolation of *Penicillium* sp. and *Aspergillus* sp. from the traditional tomato rhizosphere suggests comparatively greater fungal diversity under the conditions of the present study.

Table 4.5. Morphological characteristics and tentative identification of fungal isolates recovered from hybrid and traditional tomato rhizosphere soils.

Isolates code	Texture	Colour of colony	Spore arrangement	Nature of hyphae	Probable organism
HF1	Powdery	Green black	Conidial chains	Septate	<i>Aspergillus sp.</i>
HF2	Fluffy	White cottony	Sporangiphores	Non-septate	<i>Rhizopus sp.</i>
TF1	Velvet	Bluish green	Brush-like conidia	Septate	<i>Penicillium sp.</i>
TF2	Powdery	Dark green	Conidial heads	septate	<i>Aspergillus sp.</i>

4.1.6 Comparative Microbial Diversity Between Hybrid and Traditional Tomato Rhizospheres

A comparative summary of the culturable microbial diversity observed in the rhizosphere soils of hybrid and traditional tomato varieties is presented in **Table 4.6**.

Both tomato varieties yielded two representative bacterial isolates and two representative fungal isolates following culture-based isolation. However, differences were observed in the overall microbial abundance and dominant microbial groups. The traditional tomato rhizosphere exhibited comparatively higher total bacterial and fungal populations than the hybrid variety, indicating greater culturable microbial abundance under the experimental conditions.

Among the bacterial isolates, *Bacillus* sp. was predominant in the hybrid tomato rhizosphere, whereas *Azotobacter* sp. was identified as the dominant bacterial isolate in the traditional tomato rhizosphere. Likewise, *Aspergillus* sp. was the dominant fungal genus isolated from the hybrid tomato rhizosphere, while *Penicillium* sp. predominated in the traditional tomato rhizosphere.

Overall, the comparative analysis indicates that the traditional tomato variety supported a comparatively richer culturable microbial community than the hybrid variety. These observations suggest that differences in plant genotype may influence rhizosphere microbial composition and abundance under similar cultivation conditions.

Table 4.6. Comparative microbial diversity between the rhizosphere soils of hybrid and traditional tomato varieties.

Parameters	HYBRID VARIETY	TRADITIONAL VARIETY
No. of fungal isolates	2	2
No. of bacterial isolates	2	2
Total fungal count	Moderate	High
Total bacterial count	Moderate	High
Dominant fungi	<i>Aspergillus</i> sp.	<i>Penicillium</i> sp.
Dominant bacteria	<i>Bacillus</i> sp.	<i>Azotobacter</i> sp.

4.2 Bacterial Growth on Nutrient Agar (NA) Plates – Hybrid Tomato Variety

Bacterial colonies were successfully isolated from the rhizosphere soil of the hybrid tomato variety using Nutrient Agar (NA) medium. Following incubation, moderate bacterial growth was observed on all serial dilution plates. Lower dilution plates exhibited comparatively higher colony density, whereas higher dilution plates produced fewer, well-isolated colonies suitable for purification and characterization.

The bacterial colonies displayed variations in colony morphology, including differences in colour, size, shape, surface texture, and colony margin. These morphological differences indicate the presence of multiple culturable bacterial species within the hybrid tomato rhizosphere. However, the overall bacterial abundance and diversity were comparatively lower than those observed in the traditional tomato rhizosphere.

4.3 Fungal Growth on Potato Dextrose Agar (PDA) Plates – Hybrid Tomato Variety

Fungal isolation on Potato Dextrose Agar (PDA) medium confirmed the presence of culturable fungal communities in the rhizosphere soil of the hybrid tomato variety. Moderate fungal growth was observed following incubation, with fungal colonies developing successfully on all dilution plates.

Lower dilution plates exhibited greater colony density, while higher dilution plates produced well-separated colonies suitable for morphological identification. The fungal colonies differed in pigmentation, colony texture, growth pattern, and sporulation, indicating the presence of different culturable fungal species. Nevertheless, fungal abundance and colony diversity remained comparatively lower than those recorded for the traditional tomato rhizosphere.

4.4 Bacterial Growth on Nutrient Agar (NA) Plates – Traditional Tomato Variety

The rhizosphere soil of the traditional tomato variety exhibited abundant bacterial growth on Nutrient Agar (NA) medium after incubation. Dense bacterial colonies were observed on lower dilution plates, whereas higher dilution plates produced distinct, well-isolated colonies suitable for purification and further characterization.

Considerable variation in colony morphology was observed with respect to colony colour, size, shape, elevation, margin, and surface texture. These characteristics indicate the presence of a diverse culturable bacterial community within the traditional tomato rhizosphere. The comparatively higher colony density observed on the agar plates was consistent with the CFU analysis presented in Table 4.1, demonstrating greater bacterial abundance in the traditional tomato rhizosphere than in the hybrid variety.

4.5 Fungal Growth on Potato Dextrose Agar (PDA) Plates – Traditional Tomato Variety

The rhizosphere soil of the traditional tomato variety supported extensive fungal growth on Potato Dextrose Agar (PDA) medium following incubation. Fungal colonies developed successfully on all serial dilution plates, confirming the presence of a rich culturable fungal community.

Lower dilution plates exhibited dense fungal growth, whereas higher dilution plates produced isolated colonies suitable for morphological characterization and identification. The fungal colonies showed distinct differences in pigmentation, colony texture, growth pattern, and sporulation, indicating the occurrence of multiple fungal species. The higher fungal abundance observed in the traditional tomato rhizosphere was consistent with the CFU values presented in Table 4.2 and further supports the greater culturable microbial diversity associated with the traditional tomato variety under the experimental conditions of this study.

4.6 Summary of Major Findings

The present investigation successfully isolated and characterized culturable bacterial and fungal communities associated with the rhizosphere soils of hybrid and traditional tomato (*Solanum lycopersicum* L.) varieties using conventional microbiological techniques.

The traditional tomato rhizosphere exhibited comparatively higher bacterial and fungal populations than the hybrid tomato rhizosphere, as indicated by colony-forming unit (CFU) analysis. Morphological and biochemical characterization identified agriculturally important bacterial genera, including *Bacillus*, *Pseudomonas*, *Staphylococcus*, and *Azotobacter*, together with fungal genera such as *Aspergillus*, *Penicillium*, and *Rhizopus*.

The higher microbial abundance observed in the traditional tomato rhizosphere suggests that differences between the two tomato varieties may influence the composition of culturable rhizosphere microorganisms under similar cultivation conditions. The isolation of beneficial microorganisms known to participate in nutrient cycling and plant growth promotion highlights the ecological importance of rhizosphere microbial communities in sustainable tomato cultivation.

Discussion

The present study investigated the culturable microbial diversity associated with the rhizosphere soils of hybrid and traditional tomato (*Solanum lycopersicum* L.) varieties using conventional microbiological techniques. The findings demonstrated that both tomato varieties supported diverse culturable bacterial and fungal communities; however, the traditional tomato rhizosphere consistently exhibited a comparatively higher microbial population than the hybrid variety. This observation suggests that plant variety may influence the composition and abundance of culturable rhizosphere microorganisms under similar cultivation conditions.

The comparatively higher bacterial and fungal populations observed in the traditional tomato rhizosphere may be associated with differences in root exudate composition, which is one of the major factors influencing microbial colonization in the rhizosphere. Root exudates, including sugars, amino acids, organic acids, and phenolic compounds, provide essential nutrients for soil microorganisms and contribute to the establishment of beneficial microbial communities. Variations in the quantity and

composition of these compounds among tomato varieties may therefore influence the abundance of culturable microorganisms recovered from the rhizosphere.

Culture-based analysis revealed the presence of several agriculturally important bacterial genera, including *Bacillus*, *Pseudomonas*, *Staphylococcus*, and *Azotobacter*. Members of the genus *Bacillus* are widely recognized for their ability to produce extracellular enzymes, suppress soil-borne pathogens, and promote plant growth through the production of phytohormones. Similarly, *Pseudomonas* species are known for phosphate solubilization, siderophore production, and biological control of plant diseases. The identification of *Azotobacter* is particularly significant because of its ability to fix atmospheric nitrogen and improve soil fertility, thereby contributing to sustainable crop production.

The fungal isolates identified during the present investigation included *Aspergillus*, *Penicillium*, and *Rhizopus*. These fungal genera are commonly reported from agricultural soils and participate in the decomposition of organic matter, nutrient recycling, and maintenance of soil biological activity. The comparatively higher occurrence of *Penicillium* species in the traditional tomato rhizosphere may indicate favourable environmental conditions for fungal growth and nutrient transformation within the rhizosphere.

The present findings are consistent with previous studies reporting that plant genotype influences rhizosphere microbial communities by altering root exudation patterns and root–microbe interactions. Although the present study relied on conventional microbiological techniques and therefore represents only the culturable fraction of the microbial community, these methods remain valuable for isolating viable microorganisms that can be further characterized and evaluated for potential agricultural applications.

One limitation of the present study is that only culturable microorganisms were investigated. Many rhizosphere microorganisms cannot be cultured using routine laboratory media and therefore remain undetected by conventional microbiological techniques. Future studies employing molecular approaches, such as 16S rRNA gene sequencing for bacteria and ITS sequencing for fungi, together with metagenomic analyses, could provide a more comprehensive understanding of rhizosphere microbial diversity and functional potential.

Despite this limitation, the present investigation provides valuable baseline information on the culturable microbial diversity associated with hybrid and traditional tomato rhizospheres. The isolation of beneficial bacterial and fungal genera highlights their potential role in improving soil fertility, nutrient cycling, and sustainable tomato cultivation. These findings may contribute to the future development of biofertilizers and other environmentally friendly microbial technologies for crop improvement.

Conclusion

The present study demonstrated that both hybrid and traditional tomato (*Solanum lycopersicum* L.) varieties support diverse culturable bacterial and fungal communities within their rhizosphere soils.

However, the traditional tomato rhizosphere exhibited comparatively higher culturable microbial abundance than the hybrid variety under the conditions investigated.

Conventional microbiological techniques successfully isolated and characterized several agriculturally important microorganisms, including *Bacillus*, *Pseudomonas*, *Azotobacter*, *Aspergillus*, *Penicillium*, and *Rhizopus*. The presence of these microorganisms indicates the ecological importance of the tomato rhizosphere in maintaining soil biological activity and supporting plant growth.

Overall, the study provides useful baseline information on culturable rhizosphere microorganisms associated with hybrid and traditional tomato varieties. The findings contribute to a better understanding of plant–microbe interactions and may support future research focused on sustainable agriculture, biofertilizer development, and environmentally friendly crop management practices. Further investigations using molecular approaches are recommended to obtain a more comprehensive understanding of rhizosphere microbial diversity and its functional significance.

Declarations

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Author Contributions

All authors contributed to the conception and design of the study. Material preparation, sample collection, laboratory experimentation, data analysis, and interpretation were performed by the authors. The first draft of the manuscript was prepared by the first author, and all authors critically reviewed, revised, and approved the final manuscript.

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Data Availability

The datasets generated or analysed during the current study are available from the corresponding author upon reasonable request.

Code Availability

Not applicable.

Ethics Approval

Ethical approval was not required for this study because it involved the microbiological analysis of rhizosphere soil collected from cultivated tomato (*Solanum lycopersicum* L.) plants. Plant materials were collected in accordance with applicable institutional and local guidelines. No protected or endangered plant species were used, and no specific permits or licences were required for sample collection.

Consent to Participate

Not applicable.

Consent for Publication

Not applicable.

Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Figures

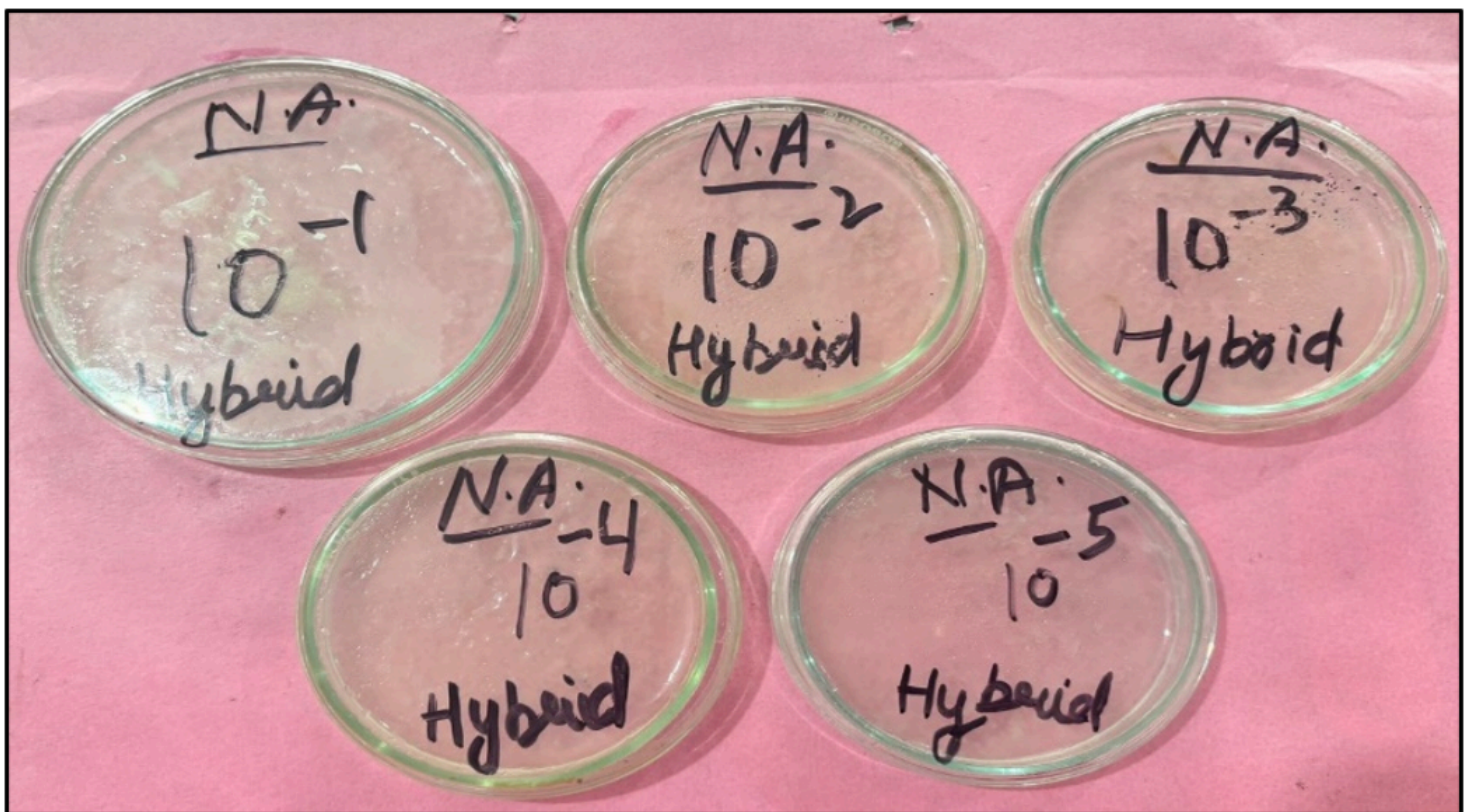


Figure 1

Figure 4.1 presents representative bacterial colonies isolated from the rhizosphere soil of the hybrid tomato variety at different serial dilutions.

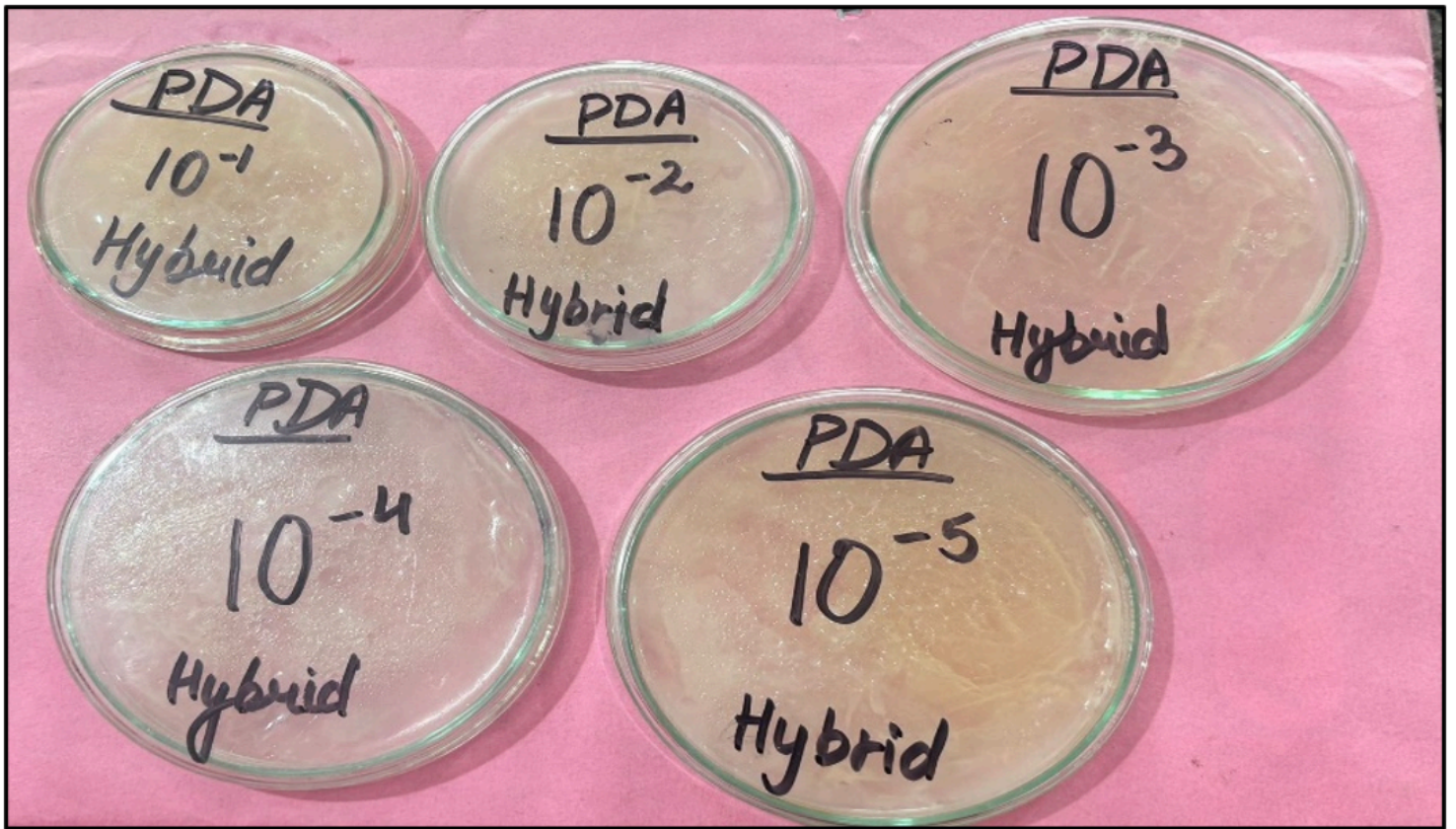


Figure 2

Figure 4.2 illustrates representative fungal colonies isolated from the hybrid tomato rhizosphere.



Figure 3

Figure 4.3 shows representative bacterial colonies isolated from the rhizosphere soil of the traditional tomato variety.



Figure 4

Figure 4.4 illustrates representative fungal colonies isolated from the rhizosphere soil of the traditional tomato variety.