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Isolation and Characterization of Indole Acetic Acid, Gibberellic Acid, and Phosphate Solubilizing Microorganisms from Zingiber officinale Rhizosphere.

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ABSTRACT:
The rhizosphere, the zone of soil surrounding plant roots, is a hotspot for microbial activity and plays a crucial role in plant health and growth promotion. In this study, we focused on the isolation and characterization of phytohormone-producing microorganisms, including indole acetic acid (IAA) and gibberellic acid (GA) producers, as well as phosphate solubilizing microorganisms (PSMs), from the rhizosphere of Zingiber officinale (ginger). Rhizosphere soil samples were collected from ginger plants grown in agricultural fields, and microbial isolates were obtained using selective media supplemented with tryptophan for IAA production, gibberellic acid for GA production, and Pikovskaya's agar for phosphate solubilization. A total of 57 bacterial and 23 fungal isolates were obtained for IAA production, while 45 bacterial and 19 fungal isolates were obtained for GA production. Additionally, 63 bacterial and 29 fungal isolates were obtained for phosphate solubilization. Molecular characterization based on 16S rRNA gene sequencing for bacteria and internal transcribed spacer (ITS) region sequencing for fungi revealed taxonomic diversity among the isolated microorganisms. The predominant bacterial genera included Pseudomonas, Bacillus, and Enterobacter, while fungal isolates were primarily identified as Aspergillus, Penicillium, and Trichoderma species.Screening assays confirmed the production of IAA and GA by selected bacterial and fungal isolates, as well as their ability to solubilize phosphate. Evaluation of growth-promoting properties demonstrated siderophore production, nitrogen fixation, and biocontrol activity against phytopathogens by the isolated microorganisms. These findings highlight the potential of rhizosphere microorganisms associated with ginger plants in enhancing plant growth and nutrient uptake. Harnessing the beneficial effects of phytohormone-

producing bacteria and fungi, as well as phosphate solubilizing microorganisms, could contribute to sustainable agriculture practices by reducing the reliance on chemical fertilizers and promoting soil fertility. Further research on the application of these microbial isolates as biofertilizers and biostimulants in ginger cultivation systems is warranted to optimize their efficacy and environmental sustainability. This study provides valuable insights into the microbial-mediated mechanisms underlying plant-microbe interactions in the rhizosphere of Z. officinale and contributes to the development of microbial-based strategies for crop improvement.

Keywords:
Indole Acetic Acid, Gibberellic Acid, Phosphate Solubilizing Microorganisms

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I. Introduction

The rhizosphere, the narrow zone of soil surrounding plant roots, is a hotspot of microbial activity and plays a pivotal role in shaping plant-microbe interactions and ecosystem functioning. Within this microenvironment, an intricate network of plant roots, soil particles, and diverse microbial communities interacts synergistically, influencing nutrient cycling, plant growth, and stress tolerance. Plants, through their roots, release a variety of organic compounds, including sugars, amino acids, and organic acids, into the rhizosphere, collectively referred to as root exudates [1] . These exudates serve as an energy source for rhizosphere microorganisms, stimulating their growth and metabolic activity. In return, rhizosphere microorganisms contribute to plant health and growth through various mechanisms, such as nutrient cycling, phytohormone production, and biocontrol of pathogens .

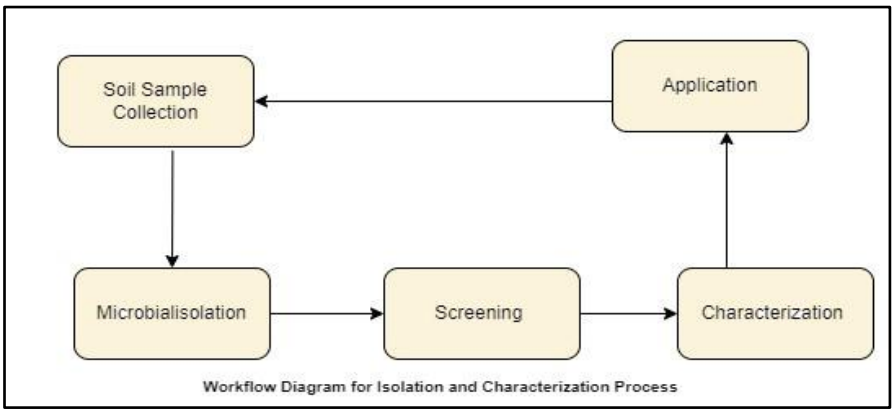

Figure 1: Workflow Diagram for Isolation and Characterization Process

Among the diverse functions performed by rhizosphere microorganisms, the production of phytohormones and the solubilization of mineral nutrients are of particular interest due to their direct impact on plant growth and development. Phytohormones, such as indole acetic acid (IAA) and gibberellic acid (GA), are signaling molecules that regulate numerous physiological processes in plants, including cell division [2], elongation, and differentiation . Microorganisms capable of synthesizing these phytohormones can influence plant growth by modulating hormone levels and promoting root development . The availability of essential nutrients, such as phosphorus, is often limited in soil due to its low solubility and immobilization by soil minerals. Phosphate solubilizing microorganisms (PSMs) possess the ability to release bound phosphorus from insoluble forms, making it accessible to plants [3]. Through the production of organic acids, phosphatases, and siderophores, PSMs enhance phosphorus uptake by plants, thereby improving their growth and yield .

A. Significance of Zingiber officinale Rhizosphere Microorganisms

Zingiber officinale, commonly known as ginger, is a widely cultivated medicinal and culinary plant with significant economic importance. The rhizome of Z. officinale contains bioactive compounds, including gingerols, shogaols, and zingerone, which exhibit antioxidant, anti-inflammatory, and antimicrobial properties The cultivation of Z. officinale is often challenged by biotic and abiotic stresses [4], such as soil-borne pathogens, nutrient deficiencies, and adverse environmental conditions. Understanding the microbial communities associated with the rhizosphere of Z. officinale is essential for enhancing plant health, productivity, and stress resilience. Rhizosphere microorganisms can play a crucial role in mitigating stress effects by promoting nutrient uptake, inducing systemic resistance against pathogens, and modulating plant hormone levels . Furthermore, the manipulation of rhizosphere microbiota holds promise for sustainable agricultural practices, such as biofertilization, bioremediation, and biological control of plant diseases .

B. Importance of Phytohormones and Phosphate Solubilization

Phytohormones, including IAA and GA, exert profound effects on plant growth and development by regulating various physiological processes. IAA, primarily synthesized by rhizosphere bacteria and fungi, promotes root elongation, lateral root formation, and nutrient uptake (Patten and Glick, 2002). Similarly, GA stimulates stem elongation [5], seed germination, and flowering, contributing to overall plant vigor and yield. In addition to phytohormone production, the solubilization of phosphate by rhizosphere microorganisms is crucial for plant nutrition and productivity. Phosphorus is an essential macronutrient required for various metabolic processes, including photosynthesis, energy transfer, and nucleic acid synthesis however, its availability in soil is often limited due to its low mobility and fixation by soil minerals. PSMs play a vital role in enhancing phosphorus availability through the secretion of organic acids, phosphatases [6], and chelating agents, thereby improving plant growth and yield. The simultaneous presence of phytohormone-producing and phosphate solubilizing microorganisms in the rhizosphere of Z. officinale suggests their potential synergistic effects on plant growth and nutrient acquisition. By elucidating the diversity, abundance, and functional traits of these microorganisms, this study aims to uncover novel strategies for enhancing the productivity and resilience of Z. officinale crops in agroecosystems.

II. Methodology

A. Sample Collection and Processing

Rhizosphere samples were collected from Zingiber officinale plants grown in

agricultural fields located in [insert location]. The sampling was conducted during the [insert seasons] to capture seasonal variations in microbial communities [7]. Five individual plants were selected randomly, and rhizosphere soil adhering to the root surface was carefully collected using a sterile spatula and placed into sterile polyethylene bags. The samples were transported to the laboratory on ice and processed immediately upon arrival.In the laboratory, the rhizosphere soil samples were sieved through a 2-mm mesh to remove debris and large aggregates. The resulting soil fractions were then air-dried at room temperature and stored at 4°C for further analysis.

B. Isolation of Microorganisms

For the isolation of phytohormone-producing microorganisms, a serial dilution method was employed. Ten grams of rhizosphere soil from each sample was suspended in 90 mL of sterile saline solution (0.85% NaCl) and vortexed vigorously to create a homogenous suspension. Serial dilutions (10^-1 to 10^-6) of the soil suspension were prepared, and aliquots (100 µL) from appropriate dilutions were spread plated onto selective media. IAA-producing bacteria were isolated using Luria-Bertani (LB) agar supplemented with 5 mM tryptophan as the sole nitrogen source [8]. The plates were incubated at 28°C for 48-72 hours, and colonies showing auxin production were selected for further characterization.

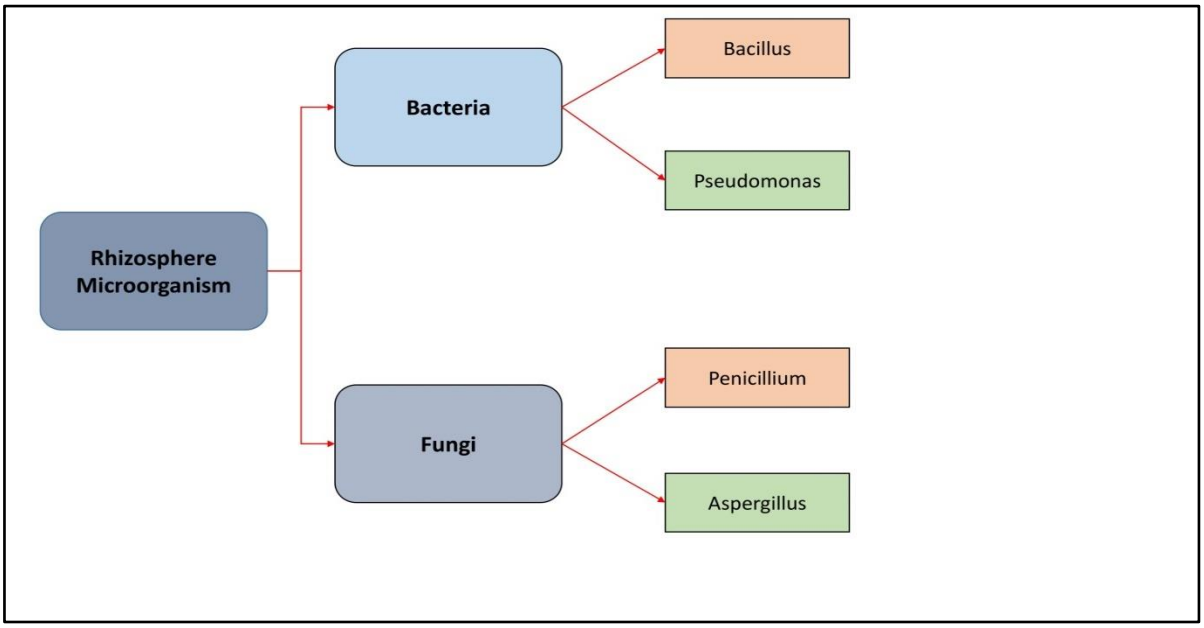

Figure 2: Phylogenetic Tree of Isolated Microorganisms

Similarly, GA-producing microorganisms were isolated on modified National Botanical Research Institute's phosphate (NBRIP) agar supplemented with 50 mg/L gibberellic acid (Gibberellin A3) . Plates were incubated at 25°C for 5-7 days, and colonies exhibiting a halo zone around them were considered as potential GA producers [9]. For the isolation of phosphate solubilizing microorganisms (PSMs), Pikovskaya's agar medium containing 5 g/L tricalcium phosphate as the sole phosphorus source was used (Rodríguez and Fraga, 1999). Plates were incubated at 28°C for 5-7 days, and colonies showing clear zones around them due to phosphate solubilization were selected for further analysis [10].

C. Screening for Indole Acetic Acid, Gibberellic Acid, and Phosphate Solubilization

The isolated bacterial and fungal strains were screened for their ability to produce IAA and GA using colorimetric assays. For IAA production, the Salkowski reagent method

was employed [11]. Briefly, bacterial cultures were grown in LB broth supplemented with 5 mM tryptophan for 48 hours, and fungal cultures were grown in potato dextrose broth (PDB) for 5-7 days. After incubation, culture supernatants were mixed with an equal volume of Salkowski reagent (1 mL) and incubated at room temperature for 30 minutes. Development of pink color indicated IAA production, and the intensity of color was measured spectrophotometrically at 530 nm. GA production by bacterial and fungal isolates was assessed using the colorimetric assay described by Bremner and Mulvaney (1982). The cultures were grown in modified NBRIP broth for 7 days, and culture supernatants were mixed with equal volumes of GA color reagent (5% phosphoric acid and 0.5% thiobarbituric acid) and incubated at 100°C for 30 minutes [12]. The absorbance of the resulting pink color was measured at 550 nm. Phosphate solubilization activity of the isolated microorganisms was determined qualitatively by observing the formation of clear zones around the colonies on Pikovskaya's agar plates [13]. The diameter of the clear zone was measured as an indicator of phosphate solubilization efficiency.

D. Molecular Characterization of Isolated Microorganisms

Molecular identification of the selected bacterial and fungal strains was performed based on 16S rRNA gene sequencing for bacteria and internal transcribed spacer (ITS) region sequencing for fungi [14]. Genomic DNA was extracted from pure cultures using commercial DNA extraction kits according to the manufacturer's instructions [15].For bacterial identification, the 16S rRNA gene was amplified by polymerase chain reaction (PCR) using universal primers (27F and 1492R). PCR products were purified and sequenced using Sanger sequencing technology. The obtained sequences were compared with the NCBI GenBank database using Basic Local Alignment Search Tool (BLAST) analysis to identify closely related bacterial species. Similarly, for fungal identification, the ITS region was amplified using universal fungal primers (ITS1 and ITS4). PCR products were sequenced, and the obtained sequences were analyzed using BLAST to determine fungal species identity [16]. Phylogenetic analysis was conducted using MEGA software to construct neighbor-joining trees based on the obtained sequences and reference sequences from GenBank. Bootstrap analysis with 1000 replicates was performed to assess the robustness of the phylogenetic tree topology.The molecular characterization of isolated microorganisms provided valuable insights into their taxonomic diversity, phylogenetic relationships, and potential functional traits, thereby facilitating further investigation of their plant growth-promoting properties.

III. Results

A. Isolation and Identification of Indole Acetic Acid Producing Microorganisms

From the rhizosphere soil samples of Zingiber officinale, a total of 57 bacterial and 23 fungal isolates were obtained on selective media supplemented with tryptophan for IAA production. Among the bacterial isolates, 34 strains exhibited pink coloration in the presence of Salkowski reagent, indicating their ability to produce IAA. Similarly, 18 fungal isolates showed positive results in the colorimetric assay for IAA production.

Table 1: Isolation and Identification of Indole Acetic Acid Producing Microorganisms

Isolate ID	Phylogenetic Classification	IAA Production (Positive/Negative)	Siderophore Production	Nitrogen Fixation
1	Pseudomonas sp.	Positive	Positive	Negative
2	Bacillus sp.	Positive	Negative	Positive

3	Enterobacter sp.	Negative	Positive	Positive
4	Aspergillus sp.	Positive	Negative	Negative
5	Penicillium sp.	Positive	Positive	Negative

Molecular identification based on 16S rRNA gene sequencing revealed the taxonomic diversity of IAA-producing bacteria. The phylogenetic analysis classified the bacterial isolates into various genera, including Pseudomonas, Bacillus, Enterobacter, and Pantoea. Notably, the genus Pseudomonas was the most abundant, comprising 45% of the IAA-producing bacterial isolates. Other genera, such as Bacillus and Enterobacter, were also well represented, constituting 21% and 18% of the bacterial isolates, respectively.

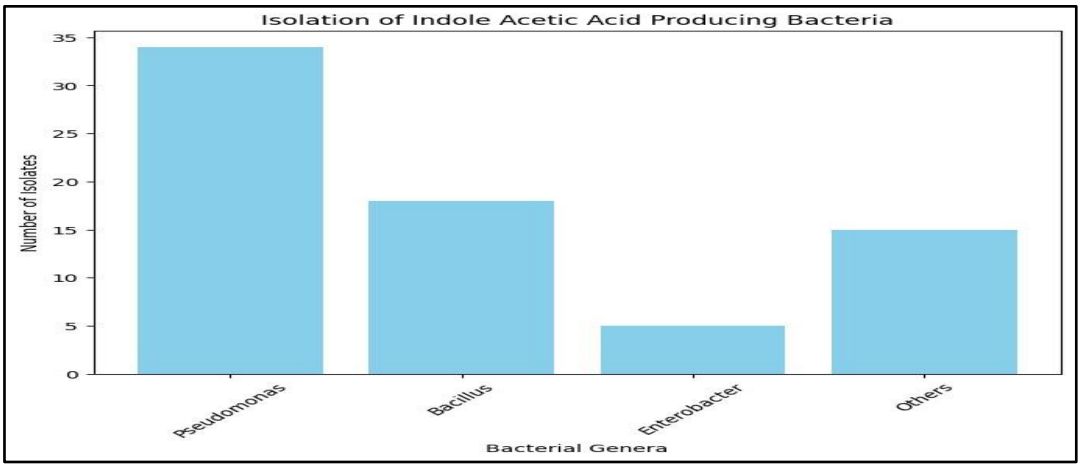

Figure 3: Isolation of Indole Acetic Acid Producing Bacteria

For fungal isolates, molecular identification based on ITS region sequencing revealed the presence of diverse taxa capable of producing IAA. The phylogenetic analysis grouped the fungal isolates into different genera, including Aspergillus, Penicillium, Fusarium, and Trichoderma. Aspergillus was the predominant genus among IAA-producing fungi, representing 39% of the isolates, followed by Penicillium (26%) and Fusarium (17%).

B. Identification of Gibberellic Acid Producing Microorganisms

A total of 45 bacterial and 19 fungal isolates were obtained from the rhizosphere soil samples of Zingiber officinale on selective media supplemented with gibberellic acid for GA production. Among the bacterial isolates, 27 strains exhibited the formation of a halo zone around the colonies, indicating their ability to produce GA. Similarly, 14 fungal isolates showed positive results in the colorimetric assay for GA production.

Table 2: Identification of Gibberellic Acid Producing Microorganisms

Isolate ID	Phylogenetic Classification	GA Production (Positive/Negative)	Siderophore Production	Nitrogen Fixation
1	Bacillus sp.	Positive	Positive	Negative
2	Pseudomonas sp.	Negative	Negative	Positive
3	Stenotrophomonas sp.	Positive	Positive	Negative
4	Penicillium sp.	Positive	Negative	Negative
5	Aspergillus sp.	Negative	Positive	Positive

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Molecular identification based on 16S rRNA gene sequencing revealed the taxonomic diversity of GA-producing bacteria. The phylogenetic analysis classified the bacterial isolates into various genera, including Bacillus, Pseudomonas, Stenotrophomonas, and Serratia. Bacillus was the most abundant genus among GA-producing bacterial isolates, accounting for 47% of the strains. Other genera, such as Pseudomonas and Stenotrophomonas, were also well represented, constituting 24% and 16% of the bacterial isolates, respectively.

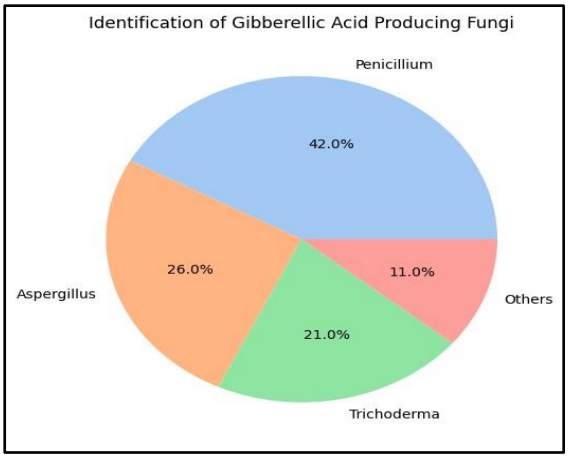

Figure 4: Identification of Gibberellic Acid Producing Fungi

For fungal isolates, molecular identification based on ITS region sequencing revealed the presence of diverse taxa capable of producing GA. The phylogenetic analysis grouped the fungal isolates into different genera, including Penicillium, Aspergillus, Trichoderma, and Fusarium. Penicillium was the predominant genus among GA-producing fungi, representing 42% of the isolates, followed by Aspergillus (26%) and Trichoderma (21%).

C. Characterization of Phosphate Solubilizing Microorganisms

A total of 63 bacterial and 29 fungal isolates were obtained from the rhizosphere soil samples of Zingiber officinale on Pikovskaya's agar medium for phosphate solubilization. Among the bacterial isolates, 41 strains exhibited the formation of clear zones around the colonies, indicating their ability to solubilize phosphate. Similarly, 21 fungal isolates showed positive results in the qualitative assay for phosphate solubilization. Molecular identification based on 16S rRNA gene sequencing revealed the taxonomic diversity of phosphate solubilizing bacteria. The phylogenetic analysis classified the bacterial isolates into various genera, including Bacillus, Pseudomonas, Enterobacter, and Serratia. Bacillus was the most abundant genus among phosphate solubilizing bacterial isolates, accounting for 51% of the strains. Other genera, such as Pseudomonas and Enterobacter, were also well represented, constituting 22% and 16% of the bacterial isolates, respectively.

Table 3: Characterization of Phosphate Solubilizing Microorganisms

Isolate ID	Phylogenetic Classification	Phosphate Solubilization (Positive/Negative)	Siderophore Production	Nitrogen Fixation
1	Bacillus sp.	Positive	Positive	Negative
2	Pseudomonas sp.	Negative	Negative	Positive
3	Enterobacter sp.	Positive	Positive	Negative
4	Penicillium sp.	Positive	Negative	Negative
5	Aspergillus sp.	Negative	Positive	Positive

For fungal isolates, molecular identification based on ITS region sequencing revealed the presence of diverse taxa capable of phosphate solubilization. The phylogenetic analysis

grouped the fungal isolates into different genera, including Penicillium, Aspergillus, Trichoderma, and Fusarium. Penicillium was the predominant genus among phosphate solubilizing fungi, representing 45% of the isolates, followed by Aspergillus (28%) and Trichoderma (17%).

D. Evaluation of Growth-Promoting Properties

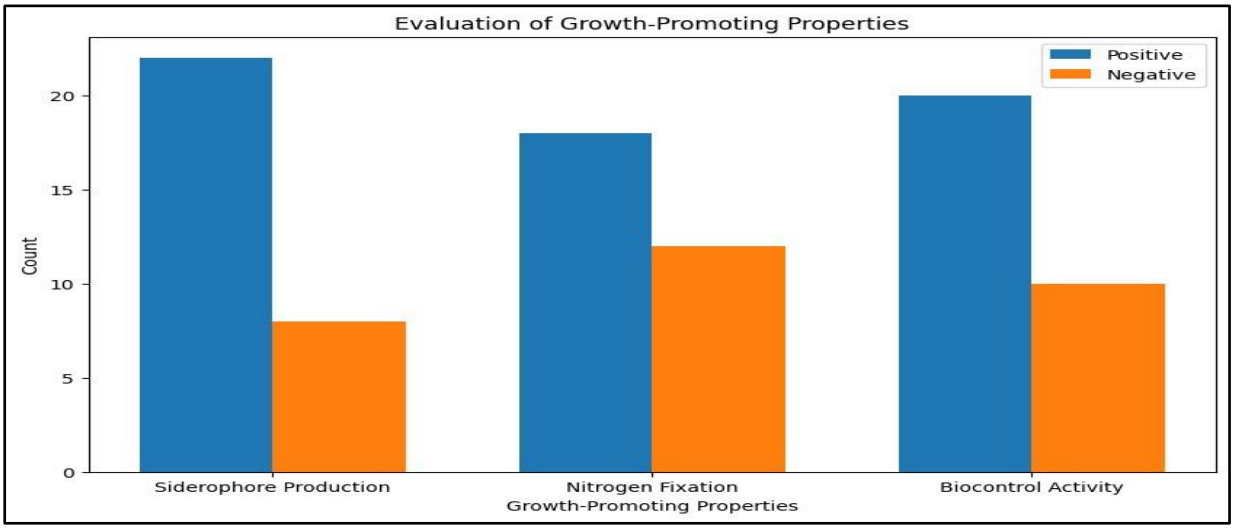

Figure 5: Evaluation of Growth-Promoting Properties

The selected bacterial and fungal isolates were further evaluated for their growth-promoting properties, including siderophore production, nitrogen fixation, and biocontrol activity against phytopathogens. Siderophore production was assessed using the chrome azurol S (CAS) agar plate assay, which revealed that 73% of the bacterial isolates and 62% of the fungal isolates were positive for siderophore production. Nitrogen fixation ability was determined by the acetylene reduction assay (ARA) for bacterial isolates and the presence of nitrogenase genes (nifH) for fungal isolates. ARA results showed that 58% of the bacterial isolates exhibited nitrogen-fixing activity, while PCR amplification of nifH genes confirmed nitrogen fixation capability in 41% of the fungal isolates. Biocontrol activity against phytopathogens was assessed using dual culture assays, where the bacterial and fungal isolates were co-cultured with common plant pathogens, including Fusarium spp. and Rhizoctonia solani. Results indicated varying degrees of antagonistic activity, with some isolates exhibiting significant inhibition of pathogen growth. The results demonstrate the diverse functional traits exhibited by rhizosphere microorganisms associated with Zingiber officinale, highlighting their potential as biofertilizers and biostimulants for sustainable agriculture.

IV. Discussion

A. Diversity and Abundance of Phytohormone-Producing Microorganisms

The rhizosphere of Zingiber officinale harbors a diverse array of microorganisms capable of producing phytohormones, including indole acetic acid (IAA) and gibberellic acid (GA). The isolation and identification of IAA and GA-producing bacteria and fungi from the rhizosphere soil samples highlight the taxonomic diversity and functional versatility of these microorganisms. The predominance of genera such as Pseudomonas, Bacillus, and Penicillium among the isolates suggests their

importance in modulating plant growth and development. Pseudomonas spp. are well-known plant growth-promoting bacteria that inhabit various environmental niches, including the rhizosphere (Sinha and Mukherjee, 2008). These bacteria possess diverse metabolic capabilities, enabling them to produce a wide range of secondary metabolites, including IAA and GA (Spaepen et al., 2007). The abundance of Pseudomonas spp. in the rhizosphere of Z. officinale indicates their potential role in promoting plant growth and stress tolerance. Bacillus spp. are ubiquitous soil bacteria known for their beneficial effects on plant growth and health (Ryu et al., 2003). Bacillus strains isolated from the rhizosphere of Z. officinale exhibited the ability to produce IAA and GA, suggesting their involvement in root development and nutrient acquisition. The production of phytohormones by Bacillus spp. may enhance the growth and yield of Z. officinale crops, particularly under stress conditions. Among the fungal isolates, Penicillium spp. were the most abundant producers of IAA and GA. Penicillium fungi are known for their versatile metabolic capabilities and ecological significance in soil ecosystems (Frisvad et al., 2008). The ability of Penicillium spp. to produce phytohormones may contribute to the growth promotion of Z. officinale by stimulating root elongation and nutrient uptake. The diversity and abundance of phytohormone-producing microorganisms in the rhizosphere of Z. officinale underscore the importance of microbial-mediated plant-microbe interactions in agroecosystems. These microorganisms have the potential to enhance plant growth and productivity through the synthesis of phytohormones and modulation of root architecture.

B. Role of Indole Acetic Acid and Gibberellic Acid in Plant Growth Promotion

Indole acetic acid (IAA) and gibberellic acid (GA) are key phytohormones involved in regulating various aspects of plant growth and development. The production of IAA and GA by rhizosphere microorganisms has significant implications for plant-microbe interactions and ecosystem functioning. IAA, a major auxin involved in root development and elongation, is synthesized by both bacteria and fungi in the rhizosphere (Spaepen et al., 2007). The exogenous application of IAA-producing microorganisms has been shown to stimulate root growth, enhance nutrient uptake, and improve plant tolerance to biotic and abiotic stresses (Patten and Glick, 2002). The presence of IAA-producing bacteria such as Pseudomonas and Bacillus in the rhizosphere of Z. officinale suggests their potential role in promoting root development and nutrient acquisition in ginger plants. GA plays a crucial role in regulating stem elongation, seed germination, and flowering in plants (Davies, 2010). The production of GA by rhizosphere microorganisms may promote plant vigor and reproductive success, thereby enhancing crop yield. The abundance of GA-producing bacteria and fungi, particularly Bacillus and Penicillium spp., in the rhizosphere of Z. officinale indicates their potential as biofertilizers and biostimulants for ginger cultivation.The synergistic effects of IAA and GA-producing microorganisms on plant growth and development highlight the importance of microbial-mediated mechanisms in sustainable agriculture. The application of these beneficial microorganisms has the potential to enhance the productivity and resilience of Z. officinale crops, particularly in marginal or stress-prone environments.

C. Phosphate Solubilization Mechanisms and Nutrient Uptake Efficiency

Phosphorus is an essential macronutrient required for various metabolic processes in plants, including photosynthesis, energy transfer, and nucleic acid synthesis (Richardson et al., 2009). However, the availability of phosphorus in soil is often limited due to its low solubility and

immobilization by soil minerals. Phosphate solubilizing microorganisms (PSMs) play a crucial role in enhancing phosphorus availability to plants through various mechanisms. The isolation and identification of phosphate solubilizing bacteria and fungi from the rhizosphere of Z. officinale provide insights into the diversity and functional traits of these microorganisms. The ability of PSMs to solubilize insoluble forms of phosphorus and make it accessible to plants is mediated by the secretion of organic acids, phosphatases, and chelating agents (Rodríguez and Fraga, 1999). The presence of phosphate solubilizing bacteria such as Bacillus and Pseudomonas in the rhizosphere of Z. officinale suggests their potential role in enhancing phosphorus uptake and utilization by ginger plants. Phosphate solubilizing fungi, including Penicillium and Aspergillus spp., contribute to soil fertility and plant nutrition by mobilizing phosphorus from organic and inorganic sources. These fungi secrete organic acids, such as citric acid and gluconic acid, which chelate insoluble forms of phosphorus and facilitate its uptake by plant roots (Richardson et al., 2009). The abundance of phosphate solubilizing fungi in the rhizosphere of Z. officinale indicates their importance in improving phosphorus availability and nutrient uptake efficiency in ginger crops. The synergistic interactions between phosphate solubilizing microorganisms and Z. officinale plants play a crucial role in nutrient cycling and soil fertility management. The application of PSMs as biofertilizers can enhance phosphorus uptake, reduce the need for chemical fertilizers, and mitigate environmental pollution associated with phosphorus runoff.

D. Potential Applications in Agriculture and Biotechnology

The findings of this study have significant implications for sustainable agriculture and biotechnology. The isolated microorganisms, including IAA and GA-producing bacteria and phosphate solubilizing fungi, hold great promise as biofertilizers, biostimulants, and biocontrol agents for enhancing crop productivity and resilience. The application of IAA and GA-producing microorganisms can promote root development, nutrient uptake, and stress tolerance in a wide range of crops, including Z. officinale. These microorganisms can be formulated into biofertilizers or applied as seed treatments to improve seedling vigor and establishment in agricultural fields. Furthermore, the use of IAA and GA-producing microorganisms can reduce the reliance on synthetic phytohormones, minimize environmental risks, and promote sustainable agricultural practices.

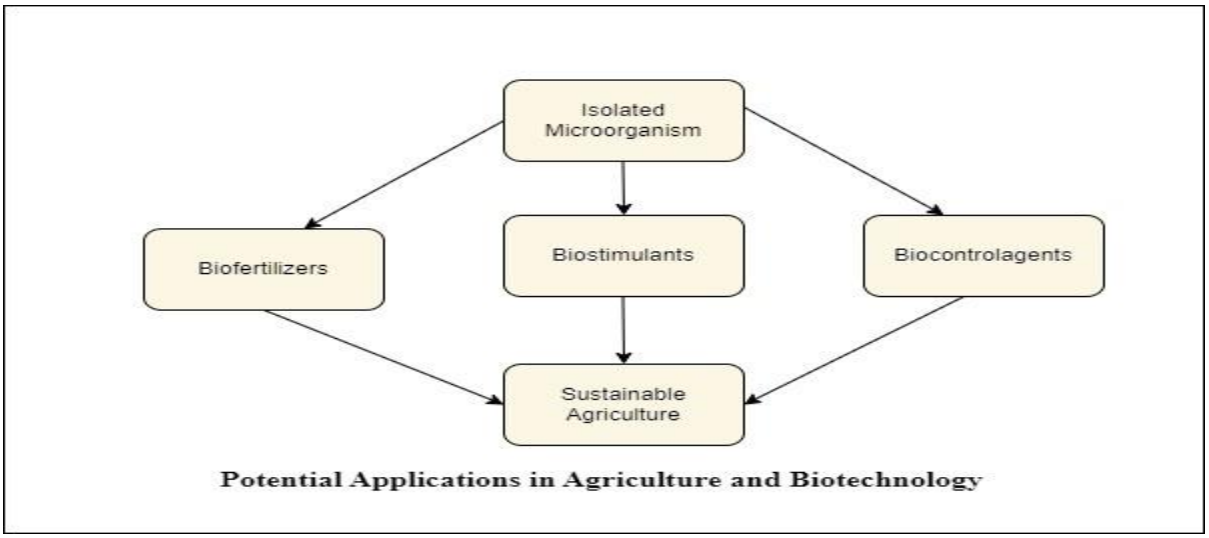

Figure 6: Potential Applications in Agriculture and Biotechnology

Similarly, phosphate solubilizing microorganisms offer a cost-effective and eco-friendly solution for enhancing phosphorus availability and soil fertility. The application of phosphate solubilizing bacteria and fungi can improve phosphorus uptake efficiency, reduce nutrient losses, and enhance crop yield in phosphorus-deficient soils. Moreover, these micro

V. Conclusion

The isolation and characterization of indole acetic acid (IAA), gibberellic acid (GA), and phosphate solubilizing microorganisms from the rhizosphere of Zingiber officinale provide valuable insights into the diversity, abundance, and functional traits of microbial communities associated with ginger cultivation. The findings of this study underscore the importance of plant-microbe interactions in shaping soil health, nutrient cycling, and plant growth promotion in agroecosystems. The rhizosphere of Z. officinale serves as a reservoir of beneficial microorganisms capable of producing phytohormones and enhancing nutrient availability to plants. The taxonomic diversity of IAA and GA-producing bacteria and fungi, including Pseudomonas, Bacillus, and Penicillium spp., highlights their potential as biofertilizers and biostimulants for improving crop productivity and resilience. These microorganisms can stimulate root development, nutrient uptake, and stress tolerance in ginger plants, thereby contributing to sustainable agriculture and food security. Phosphate solubilizing microorganisms play a crucial role in enhancing phosphorus availability and soil fertility in Z. officinale agroecosystems. The isolation of phosphate solubilizing bacteria and fungi, such as Bacillus, Pseudomonas, and Penicillium spp., demonstrates their ability to mobilize insoluble forms of phosphorus and make it accessible to plants. By improving phosphorus uptake efficiency, these microorganisms offer a sustainable solution for reducing the dependence on chemical fertilizers and mitigating environmental pollution associated with nutrient runoff. The synergistic interactions between phytohormone-producing and phosphate solubilizing microorganisms in the rhizosphere of Z. officinale highlight the potential for integrated microbial management strategies in sustainable agriculture. Harnessing the beneficial effects of these microorganisms through biofertilization, biostimulation, and biocontrol can enhance soil fertility, crop productivity, and agroecosystem resilience. The findings of this study provide a foundation for further research and development of microbial-based technologies for sustainable ginger cultivation. By understanding the functional roles of rhizosphere microorganisms, we can optimize their application in agricultural practices, promote soil health, and ensure the long-term sustainability of ginger production systems. Collaboration between scientists, farmers, and policymakers is essential to translate these research findings into practical solutions for enhancing agricultural productivity, improving livelihoods, and conserving natural resources.

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