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Isolation and Characterization of Endophytic Actinobacteria from Drought-Tolerant Rice Genotypes with Plant Growth-Promoting Potential

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Abstract

Endophytic actinobacteria are recognized as an important group of beneficial microorganisms that colonize internal plant tissues and contribute to plant growth promotion, nutrient mobilization, and stress tolerance. The present study aimed to isolate, characterize, and identify endophytic actinobacteria associated with the drought-tolerant rice variety Nagina 22 and rice landrace 'Thoka Odlu'. A total of thirty actinobacterial isolates were obtained from surface-sterilized root and stem tissues using ISP2 medium. The isolates exhibited characteristic actinobacterial morphology, including filamentous mycelial growth, dry powdery colonies, and diverse pigmentation patterns. Functional screening of the isolates revealed multiple plant growth-promoting (PGP) traits, including phosphorus, potassium, and zinc solubilization, siderophore production, and indole-3-acetic acid (IAA) production. Among the isolates, eight promising strains (ACB-2, ACB-5, ACB-9, ACB-11, ACB-15, ACB-24, ACB-27, and ACB-28) exhibited all evaluated PGP traits, indicating their multifunctional potential in plant growth promotion. Molecular identification based on 16S rRNA gene amplification and Sanger sequencing demonstrated that seven isolates belonged to the genus *Streptomyces*, while one isolate was identified as *Nocardia* sp., with sequence similarities ranging from 99-100%. The predominance of *Streptomyces* sp. highlights their ecological adaptability and beneficial association with rice tissues. The findings suggest that these endophytic actinobacteria possess significant potential for application as bioinoculants in sustainable rice cultivation through enhancement of nutrient availability, phytohormone production, and stress mitigation which helps to the development of eco-friendly microbial formulations for climate-resilient agriculture.

Keywords: Endophytic actinobacteria; *Streptomyces*; Rice endophytes; Plant growth promotion; 16S rRNA sequencing

Introduction

Rice (*Oryza sativa* L.) is one of the most important staple food crops worldwide and serves as the primary source of nutrition for more than half of the global population. However, rice productivity is severely affected by several abiotic stresses such as salinity, drought, nutrient deficiency, and temperature fluctuations, which limit crop growth and yield under changing climatic conditions. Excessive dependence on chemical fertilizers and pesticides to overcome these constraints has resulted in soil degradation, environmental pollution, and loss of soil microbial diversity. Consequently, there is growing interest in the exploration of beneficial plant-associated microorganisms as sustainable alternatives for improving crop productivity and stress resilience. Endophytic microorganisms inhabit internal plant tissues without causing disease symptoms and establish mutually beneficial associations with their host plants. Among them, endophytic actinobacteria have attracted considerable attention due to their remarkable metabolic diversity and ability to synthesize a wide range of bioactive compounds (Qin *et al.*, 2011) [19]. Members of the genus *Streptomyces* are the most dominant and extensively studied endophytic actinobacteria because of their capacity to produce antibiotics, extracellular enzymes, siderophores, phytohormones, and other secondary metabolites that contribute to plant growth promotion and disease suppression (Barka *et al.*, 2016) [3]. These microorganisms improve plant growth directly through nutrient solubilization and phytohormone production, and indirectly by suppressing

phytopathogens and inducing systemic resistance in plants (Viaene *et al.*, 2016) ^[25].

Plant growth-promoting (PGP) traits such as phosphorus solubilization, potassium mobilization, zinc solubilization, siderophore production, and indole-3-acetic acid (IAA) synthesis play crucial roles in enhancing nutrient availability and plant development. Phosphorus and potassium are essential macronutrients required for energy transfer, root development, and metabolic regulation, but their availability is often limited in soils due to insoluble forms. Endophytic actinobacteria capable of solubilizing these nutrients can significantly improve nutrient uptake and plant productivity (Jog *et al.*, 2014) ^[14]. Similarly, zinc-solubilizing microorganisms contribute to improved micronutrient availability, which is essential for enzyme activation and plant metabolism. Siderophore-producing endophytes enhance iron acquisition under iron-limited conditions while simultaneously restricting pathogen growth through iron competition (Wang *et al.*, 2014) ^[26]. In addition, IAA-producing actinobacteria stimulate root elongation, root branching, and overall plant vigor, thereby enhancing water and nutrient absorption under stress conditions.

Drought-tolerant rice genotypes serve as important reservoirs of stress-adaptive traits and diverse endophytic microbial communities. Nagina 22, a well-known drought- and heat-tolerant rice variety, has been extensively utilized in rice breeding programmes because of its ability to perform under adverse environmental conditions and is regarded as a promising source of stress-associated beneficial microorganisms. Similarly, the traditional rice landrace *Thoka Odlu*, adapted to water-limited ecosystems, is likely to harbour stress-resilient endophytic microbiota. Investigating the endophytic actinobacterial populations associated with these stress-adapted rice genotypes may facilitate the identification of novel microbial resources possessing enhanced plant growth-promoting potential and stress-alleviating capabilities.

Previous studies have reported the beneficial role of endophytic actinobacteria in improving plant growth, nutrient mobilization, and tolerance to abiotic stresses in several crop plants including rice, wheat, and maize (Palaniyandi *et al.*, 2013) ^[17]. Furthermore, *Streptomyces* species isolated from plant tissues have demonstrated strong antagonistic activity against phytopathogens and the ability to improve plant performance under adverse environmental conditions (El-Tarabily and Sivasithamparan, 2006) ^[8]. Despite increasing reports on rhizospheric microorganisms, information regarding endophytic actinobacteria associated with stress-tolerant rice genotypes remains limited.

Therefore, the present investigation was undertaken to isolate and characterize endophytic actinobacteria from Nagina 22 and the rice landrace 'Thoka Odlu', evaluate their plant growth-promoting traits, and identify promising isolates through 16S rRNA gene sequencing. The study aims to identify multifunctional endophytic actinobacteria with potential application as biofertilizers and microbial inoculants for sustainable rice cultivation under stress-prone environments.

Materials and Methods

Sample Collection

The rice variety Nagina 22, a drought-tolerant genotype, was collected from ICAR- Indian Institute of Rice Research (ICAR-IIRR) fields, Hyderabad, India. The rice landrace 'Thoka Odlu' was collected from Raichur, Karnataka, India. Root and stem tissues from both rice genotypes were used for the isolation of endophytic actinobacterial cultures.

Isolation of Endophytic Actinobacterial Cultures from Rice Samples

Root and stem tissues of Nagina 22, and 'Thoka Odlu' were collected for the isolation of endophytic actinobacteria. The plant samples were surface-sterilized using 1% sodium hypochlorite solution, followed by rinsing with sterile distilled water to remove residual sterilizing agents. The surface-sterilized tissues were aseptically macerated separately using a sterile mortar and pestle. The resulting homogenates were serially diluted and spread-plated onto Yeast Malt Agar (ISP2) medium containing 4 g yeast extract, 10 g malt extract, 4 g dextrose, and 20 g agar per liter of distilled water. The inoculated plates were incubated under appropriate conditions until the appearance of distinct colonies. Filamentous colonies exhibiting typical actinobacterial morphology were selected and purified through repeated streaking on fresh ISP2 medium. The purified isolate was subsequently used for morphological, biochemical, and molecular characterization.

Screening of Endophytic actinobacterial isolates for Plant Growth Promoting Traits

These purified isolates were functionally screened for plant growth promotion traits viz., phosphorus solubilization, potassium solubilization, zinc solubilization, production of siderophore, and Indole acetic acid (IAA).

Phosphorous solubilizing ability

The phosphorous solubilizing ability of the isolates was assessed by inoculating them on Pikovskaya's medium and incubated for 48 h. Following incubation, the plates were examined for the presence of clear halo zones surrounding actinobacterial colonies, which indicates positive P solubilizing activity.

Potassium solubilization

The potassium solubilization ability of the isolates was assessed by inoculating them on Aleksandrov's media containing insoluble potassium aluminum silicate and incubating for 48 h as described by Sugumaran and Janarthanam (2007). Following incubation, the plates were examined for the presence of clear halo zones surrounding actinobacterial colonies, which indicates positive potassium solubilization activity.

Zinc solubilization

The zinc solubilization ability of the isolates will be screened by inoculating them on Tris minimal media containing 0.1% zinc oxide as a source of zinc according to Fasim *et al.* 2002 ^[9], and after incubation for 48 h, the plates will be examined for the presence of halo zones surrounding the colonies, which indicates positive zinc solubilization as the microorganisms solubilize the insoluble zinc compound.

Siderophore production

Siderophore production will be estimated using Chrome Azurol S (CAS) agar medium according to Schwayn and Neiland (1987), where the isolates will be inoculated and incubated for 48 h at 28 °C, and the appearance of an orange-colored zone around the colony will be considered positive for siderophore production as it indicates the chelation of iron from the blue CAS-iron complex.

Indole Acetic Acid production

Indole Acetic Acid (IAA) production was estimated quantitatively according to Gordon and Weber (1951) ^[11] by inoculating the isolates in Tryptic soy broth containing 0.1% L-

Tryptophan and without L-Tryptophan, followed by incubation for 7 days at 30 °C, after which 2ml of culture broth was centrifuged at 10,000 rpm for 10 minutes and the supernatant tested for IAA production by adding 2ml of Salkowski reagent and 2 drops of orthophosphoric acid. The development of pink color after 30 minutes of incubation indicates IAA production.

Genomic DNA Isolation and Quantification

A single filamentous actinobacterial colony was isolated, purified and used for molecular identification. Genomic DNA was extracted from the purified culture using the Gsure Bacterial DNA Isolation Kit (Cat. No. G46211) according to the manufacturer's protocol. The quantification of the extracted DNA was determined by using a NanoDrop Lite Plus spectrophotometer (Thermo Fisher Scientific Inc., USA). Quantification of DNA was further evaluated by electrophoresis on 0.8% (w/v) agarose gel.

PCR Amplification and Molecular Identification of Actinobacterial Isolate

Molecular identification of the actinobacterial isolate was carried out through amplification of the 16S rRNA gene using universal bacterial primers targeting the V3–V4 hypervariable region. The primer sequences used were V3F (5'–CCTACGGGNGGCWGCAG–3') and V4R (5'–GACTACHVGGGTATCTAATCC–3'). PCR amplification was performed in a total reaction volume of 10 µL containing 1 µL genomic DNA template (50 ng), 1 µL of 10× Taq buffer, 0.8 µL dNTP mixture (0.2 mM), 0.5 µL (10 pM) each of forward and reverse primers, 0.1 µL Taq DNA polymerase (1.25 U), and nuclease-free water to make up the final volume. Amplification was carried out in a T100 Thermal Cycler (Bio-Rad, USA) with the following cycling conditions: initial denaturation at 95 °C for 5 min; followed by 30 cycles of denaturation at 95 °C for 30 s, annealing at 60 °C for 30 s, and extension at 72 °C for 1 min; with a final extension at 72 °C for 7 min. The amplified PCR product (428 bp) was resolved on 2% (w/v) agarose gel.

The amplified PCR product was purified using the FavorPrep PCR Clean-Up Mini Kit (Genaxy, Cat No- FAGCK001) following the manufacturer's instructions and quantified using a NanoDrop Lite Plus spectrophotometer (Thermo Fisher Scientific Inc., USA). The purified PCR amplicon product was subjected to Sanger sequencing. The obtained nucleotide sequence was analyzed using the BLASTn program available at the National Center for Biotechnology Information (NCBI) GenBank database for sequence similarity analysis and taxonomic identification.

Results and Discussion

Isolation and Biochemical Characterization of Endophytic Actinobacteria

Thirty actinobacterial cultures were isolated from surface-sterilized root and shoot tissues of rice plants, Nagina 22 and Thoka odlu. Isolation of these isolates from interior tissues

confirmed their endophytic nature (Table-1). The isolates had actinobacteria-like morphology, including dry and powdery colonies, filamentous mycelial growth, and varied pigmentation on the isolation medium (ISP2). These morphological characteristics are typical of members of the *Streptomyces* genus, which is widely known as the dominant endophytic actinobacteria found on crop plants.

Table1: Isolation details of endophytic actinobacterial cultures obtained from root and stem tissues of Nagina 22 and 'Thoka Odlu'

S.No	Culture ID	Variety	Isolated from	Location
1	ACB-1	Nagina 22	Stem	ICAR- IIRR, Hyderabad
2	ACB-2	Nagina 22	Stem	ICAR- IIRR, Hyderabad
3	ACB-3	Nagina 22	Stem	ICAR- IIRR, Hyderabad
4	ACB-4	Nagina 22	Stem	ICAR- IIRR, Hyderabad
5	ACB-5	Nagina 22	Root	ICAR- IIRR, Hyderabad
6	ACB-6	Nagina 22	Root	ICAR- IIRR, Hyderabad
7	ACB-7	Nagina 22	Root	ICAR- IIRR, Hyderabad
8	ACB-8	Nagina 22	Root	ICAR- IIRR, Hyderabad
9	ACB-9	Nagina 22	Root	ICAR- IIRR, Hyderabad
10	ACB-10	Nagina 22	Root	ICAR- IIRR, Hyderabad
11	ACB-11	Nagina 22	Root	ICAR- IIRR, Hyderabad
12	ACB-12	Nagina 22	Root	ICAR- IIRR, Hyderabad
13	ACB-13	Nagina 22	Root	ICAR- IIRR, Hyderabad
14	ACB-14	Nagina 22	Root	ICAR- IIRR, Hyderabad
15	ACB-15	Nagina 22	Root	ICAR- IIRR, Hyderabad
16	ACB-16	Thoka Odlu	Stem	Raichur, Karnataka
17	ACB-17	Thoka Odlu	Stem	Raichur, Karnataka
18	ACB-18	Thoka Odlu	Stem	Raichur, Karnataka
19	ACB-19	Thoka Odlu	Stem	Raichur, Karnataka
20	ACB-20	Thoka Odlu	Stem	Raichur, Karnataka
21	ACB-21	Thoka Odlu	Root	Raichur, Karnataka
22	ACB-22	Thoka Odlu	Root	Raichur, Karnataka
23	ACB-23	Thoka Odlu	Root	Raichur, Karnataka
24	ACB-24	Thoka Odlu	Root	Raichur, Karnataka
25	ACB-25	Thoka Odlu	Root	Raichur, Karnataka
26	ACB-26	Thoka Odlu	Root	Raichur, Karnataka
27	ACB-27	Thoka Odlu	Root	Raichur, Karnataka
28	ACB-28	Thoka Odlu	Root	Raichur, Karnataka
29	ACB-29	Thoka Odlu	Root	Raichur, Karnataka
30	ACB-30	Thoka Odlu	Root	Raichur, Karnataka

Among the 30 actinobacterial isolates tested for plant growth promoting (PGP) properties, zinc solubilization was the most common trait in the 26 isolates. 16 of the isolates exhibited phosphorus solubilization activity and 12 of the isolates showed potassium solubilization activity. A total of 17 isolates were found to produce siderophores and 13 isolates had exhibited IAA production ability. Several isolates were shown to be capable of stimulating plant growth by the production of phytohormones, namely indole-3-acetic acid (IAA) (13 isolates). ACB-2, ACB-5, ACB-9, ACB-11, ACB-15, ACB-24, ACB-27 and ACB-28 were all the isolates found to have all the evaluated PGP traits, showing their multifunctional plant growth promoting potential (Fig-1).

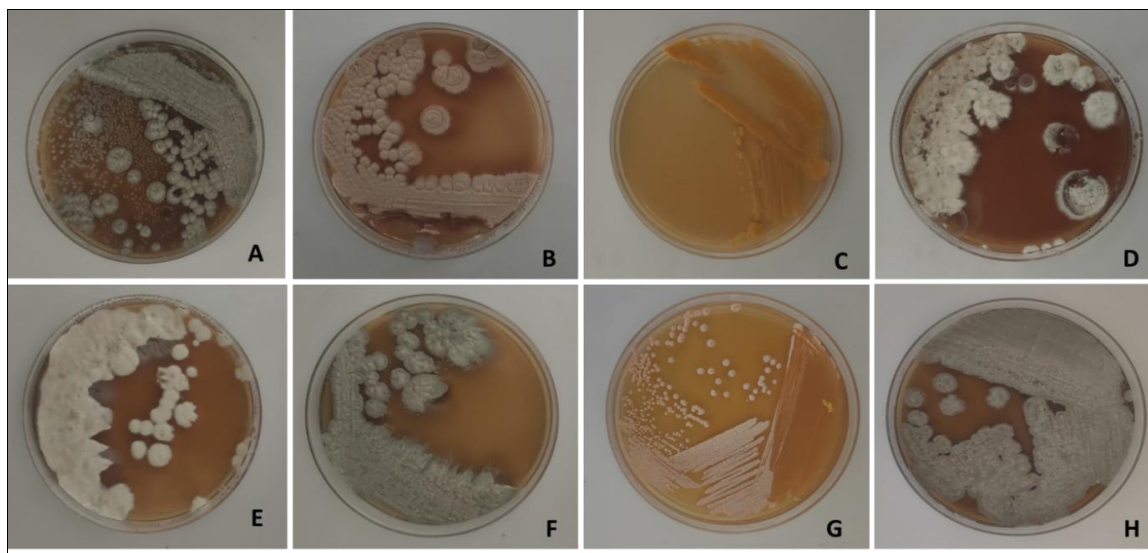


Fig 1: Colony morphology of endophytic actinobacterial isolates obtained from stress-tolerant rice genotypes. A-ACB-2, B- ACB-5, C- ACB-9, D- ACB-11, E- ACB-15, F- ACB-24, G- ACB-27, H- ACB-28

The successful isolation of endophytic actinobacteria from rice tissues suggests that rice plants contain a variety of microbial communities that can form close relationships within plant tissues without causing symptoms of disease. It is known that endophytic actinobacteria colonize vascular tissues and intercellular spaces, where they aid in the generation of phytohormones, the mobilization of nutrients, and defense against phytopathogens (Qin *et al.*, 2011, Mengistu 2020) [19, 15]. According to similar research, *Streptomyces* species are prevalent endophytes in cereal crops as rice, wheat, and maize (Palaniyandi *et al.*, 2013) [17].

The present study showed that a significant percentage of the isolates produced mineral solubilization and growth promoting activities which showed endophytic actinobacteria plays a functional role in the plant-microbe interactions. One of these properties most commonly found among the isolates was the ability to solubilize zinc. The zinc-solubilizing capacity of actinobacteria endophytes indicates the potential of these microorganisms to increase the plant micronutrient availability and uptake within the plant system (Suriyachadkun *et al.*, 2022) [22]. Similarly, solubilization of phosphorus and potassium for several isolates was observed, which suggests their ability to release insoluble nutrient fractions into the plant available form (Boubekri *et al.*, 2021) [6]. The siderophore production by many of these isolates further confirms the plant protection and plant acquisition role of endophytic actinobacteria. Under iron limited conditions, the uptake of iron is mediated by low molecular weight compounds called siderophores. Besides enhancing Fe availability, siderophore-producing microorganisms also inhibit the growth of phytopathogens by reducing the availability of Fe for other pathogens (Wang *et al.*, 2014) [26].

The endophytes that produce IAA are known to increase plant growth, root elongation, branching of roots and uptake of nutrients and water. The presence of several PGP traits in the same isolates confirms the multifunctional nature of these endophytic actinobacteria, and the possibility of synergistic activity in the plant growth promotion process (Aguennouz *et al.*, 2025) [1]. The findings of the present study are consistent with previous studies, which also showed that endophytic actinobacteria contribute significantly to nutrient mobilization, plant growth promotion, and biocontrol properties through the synthesis of different kinds of beneficial metabolites and enzymes (Mingma *et al.*, 2018, Borah *et al.*, 2021, Hazarika *et*

al., 2022) [22, 5, 12]. The results obtained in the present study are in agreement with earlier reports indicating that endophytic actinobacteria play an important role in nutrient mobilization, plant growth promotion, and biocontrol activity through the production of various beneficial metabolites and enzymes (Mingma *et al.*, 2018, Borah *et al.*, 2021; Hazarika *et al.*, 2022) [16, 5, 12].

Among the thirty isolates, eight promising actinobacterial isolates, ACB-2, ACB-5, ACB-9, ACB-11, ACB-15, ACB-24, ACB-27, and ACB-28, were selected based on the PGPR traits and *in vitro* plant growth promotion on the agar medium (Prasad Babu KV *et al.*, 2026) [24] (Table-2) were further carried out for the molecular identification.

Table 2: Screening of Endophytic actinobacterial isolates for Plant Growth Promoting Traits

S.No	Culture ID	zinc	Phosphorus	Potassium	Siderophore	IAA
1	ACB-1	+	+	-	-	-
2	ACB-2	+	+	+	+	+
3	ACB-3	+	-	+	+	+
4	ACB-4	+	-	-	+	-
5	ACB-5	+	+	+	+	+
6	ACB-6	+	-	-	-	-
7	ACB-7	-	+	-	+	+
8	ACB-8	+	-	-	-	-
9	ACB-9	+	+	+	+	+
10	ACB-10	+	-	-	+	-
11	ACB-11	+	+	+	+	+
12	ACB-12	-	+	-	-	-
13	ACB-13	+	+	-	-	-
14	ACB-14	+	+	-	+	-
15	ACB-15	+	+	+	+	+
16	ACB-16	+	-	-	+	-
17	ACB-17	+	+	+	-	-
18	ACB-18	+	-	+	+	+
19	ACB-19	+	+	-	-	-
20	ACB-20	+	-	-	-	-
21	ACB-21	-	-	-	+	-
22	ACB-22	+	+	+	-	+
23	ACB-23	+	-	-	-	-
24	ACB-24	+	+	+	+	+
25	ACB-25	+	-	-	+	+
26	ACB-26	+	-	-	-	-
27	ACB-27	+	+	+	+	+
28	ACB-28	+	-	+	+	+
29	ACB-29	+	-	-	+	-
30	ACB-30	-	+	-	-	-

Genomic DNA Extraction and PCR Amplification of 16S rRNA Gene

Genomic DNA was extracted from all eight promising bacterial isolates using a bacterial genomic DNA extraction kit. The quantified and qualified DNA was used for molecular analysis. PCR amplification of the 16S rRNA gene (V3- V4) produced clear and distinct amplicons corresponding to the expected fragment size (428bp) in all isolates (Fig. 2), indicating

successful amplification of bacterial genomic DNA.

The 16S rRNA gene is considered a highly conserved molecular marker widely used for bacterial identification and phylogenetic analysis because of its conserved and hypervariable regions that enable discrimination among bacterial taxa (Janda and Abbott, 2007) [13]. Amplification of the 16S rRNA gene confirmed the bacterial identity of the isolates and facilitated accurate molecular characterization through sequencing analysis.

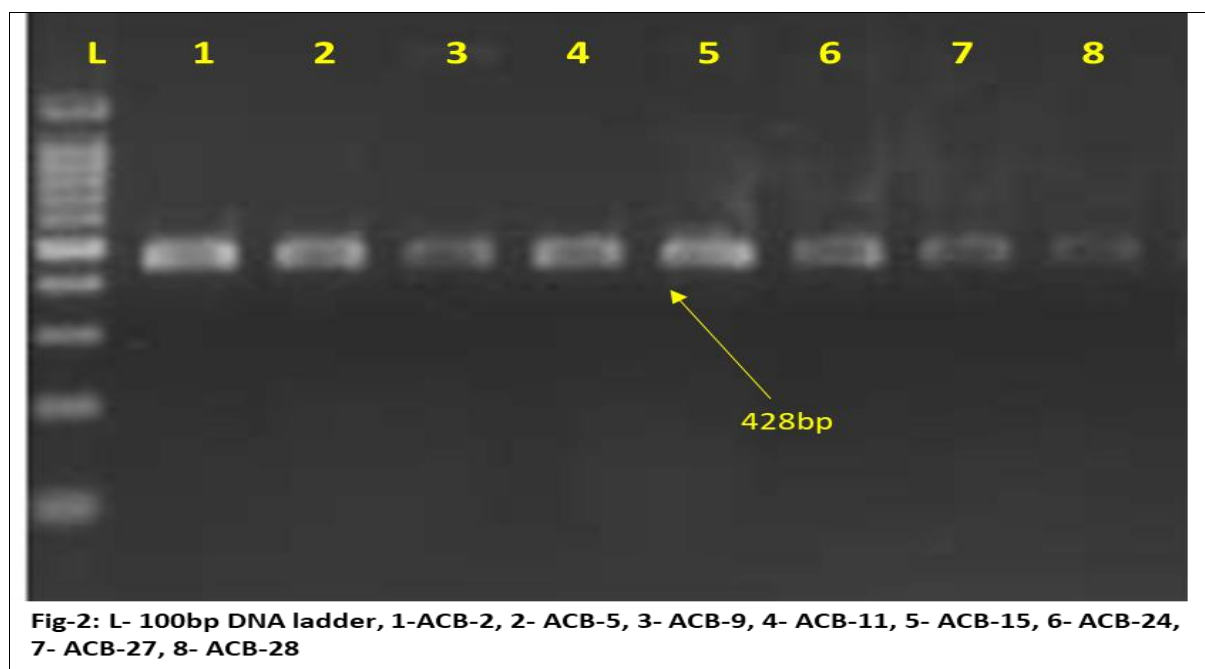


Fig 2: PCR amplification of V3-V4 gene from the genomic DNA of the bacterial isolates

Molecular Identification of Actinobacterial Isolates through Sanger Sequencing

The amplified PCR products were subjected to Sanger sequencing, and sequence analysis was performed using the NCBI BLAST database. The sequencing results revealed that seven isolates belonged predominantly to the genus *Streptomyces*, whereas one isolate (ACB-24) showed close similarity with *Nocardia* sp. The percentage similarity ranged from 99-100%, confirming the taxonomic identity of the isolates with high confidence (Table 3).

Table 3: Molecular identification of promising endophytic actinobacterial isolates based on 16S rRNA gene sequencing

S.NO	Sample ID	Identified organism	Percentage of Similarity
1	ACB-2	<i>Streptomyces aureovorticillatus</i> strain CNS244	99.6
2	ACB-5	<i>Streptomyces</i> sp. R107-2	100
3	ACB-9	<i>Streptomyces</i> sp. strain CXM4-1	100
4	ACB-11	<i>Streptomyces galbus</i> strain MP15-5	100
5	ACB15	<i>Streptomyces</i> sp. D828	99
6	ACB24	<i>Nocardia</i> sp. S20-46	99
7	ACB27	<i>Streptomyces</i> sp. D828	99
8	ACB-28	<i>Streptomyces</i> sp.	100

The predominance of *Streptomyces* species among the isolates indicates their ecological adaptability and successful colonization within rice tissues. Members of the genus *Streptomyces* are well known for producing a broad spectrum of secondary metabolites including antibiotics, siderophores, extracellular enzymes, and phytohormones that contribute to plant growth promotion and disease suppression (Barka *et al.*,

2016) [3]. The high sequence similarity observed among the isolates suggests that these strains are closely related to previously reported beneficial actinobacteria.

Endophytic Association and Functional Significance of the Isolates

The successful isolation and molecular identification of endophytic *Streptomyces* spp. from rice tissues highlight their potential ecological role in plant- microbe interactions. Endophytic actinobacteria establish symbiotic associations with host plants and often enhance plant growth through multiple direct and indirect mechanisms such as phosphate solubilization, production of indole-3-acetic acid (IAA), siderophore production, and induction of systemic resistance (Viaene *et al.*, 2016) [25]. Previous studies have demonstrated that endophytic *Streptomyces* species improve root architecture, nutrient uptake, and stress tolerance in plants under adverse environmental conditions. In rice, these microorganisms have been associated with enhanced seedling vigor, improved chlorophyll content, and increased tolerance to drought and salinity stress (Jog *et al.*, 2014) [14]. The presence of these endophytic actinobacteria within internal tissues may therefore contribute significantly to plant fitness and productivity.

The identification of *Streptomyces galbus* among the isolates is particularly important because this species has been reported to possess strong antagonistic activity against fungal pathogens and the ability to produce plant growth-promoting metabolites (El-Tarabily and Sivasithamparam, 2006) [8]. Similarly, *Streptomyces aureovorticillatus* and related species are known producers of bioactive compounds with antimicrobial and stress-mitigating properties. These findings suggest that the isolated

strains may serve as potential candidates for development of microbial bioinoculants for sustainable rice cultivation. The detection of *Nocardia* sp. among the isolates also demonstrates the diversity of endophytic actinobacteria colonizing rice tissues. Although *Nocardia* species are less commonly reported as plant-associated endophytes, they have been shown to produce bioactive metabolites and participate in organic matter degradation and nutrient cycling (Goodfellow and Williams, 1983) [10]. Their coexistence with *Streptomyces* sp. may contribute synergistically to the microbial ecology of rice plants.

Conclusion:

The present investigation revealed the presence of diverse endophytic actinobacteria associated with the root and stem tissues of the drought-tolerant rice variety *Nagina 22* and the drought-tolerant rice landrace 'Thoka Odlu'. A total of thirty actinobacterial isolates were successfully recovered and screened for important plant growth-promoting traits. Several isolates exhibited the ability to solubilize phosphorus, potassium, and zinc along with siderophore and indole-3-acetic acid production, indicating their multifunctional role in improving nutrient availability and plant growth. Among them, eight isolates showed superior plant growth-promoting potential and were selected for molecular characterization.

Molecular identification based on 16S rRNA gene sequencing demonstrated that the majority of the promising isolates belonged to the genus *Streptomyces*, while one isolate showed close similarity to *Nocardia* sp. The predominance of *Streptomyces* among the isolates suggests their successful adaptation as endophytes within rice tissues and highlights their ecological significance in plant-microbe interactions. The identified isolates possess characteristics that may contribute to enhanced plant growth, nutrient acquisition, and tolerance to environmental stress conditions. The findings of the present study indicate that stress-adapted rice genotypes harbor beneficial endophytic actinobacteria with considerable agricultural importance. These isolates may serve as potential candidates for the development of microbial bioinoculants aimed at reducing dependence on chemical fertilizers and promoting sustainable rice cultivation and crop improvement programs.

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