

Isolation and screening of halotolerant endophytic bacteria with plant growth-promoting properties from *Avicennia alba* Blume

J. Lavanya*¹, D. Sandhya Deepika², M. Sri Devi³ & M. Ramesh Chowdary⁴

Department of Botany, Andhra University, Visakhapatnam (Andhra Pradesh), 530003 India.

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Abstract

This current research explores the bacterial endophytes and their attributes from *Avicennia alba*, a mangrove plant growing in the region of Coringa Wildlife Reserve, Andhra Pradesh, India. The objective of this study is to identify salt-tolerant endophytes from *Avicennia alba*, revealing the phosphate solubilizing ability, and to explore the IAA producing capacity of endophytes promoting plant growth. Leaves and roots were collected from the *Avicennia alba* to isolate endophytes. The leaves and pneumatophores yielded sixteen endophytic isolates. To evaluate their ability to resist salt, all endophytic isolates were cultivated in nutrient agar containing 0 to 12% NaCl. AAP5 (*Avicennia-A alba-A* Pneumatophore-P Isolate 5) isolate (7.1 ppm) had the highest phosphate solubilizing ability, followed by AAP9 (5.3 ppm) and AAP3 (4.0 ppm) isolates. The endophytic organisms' capacity to produce Indole-3-acetic acid (IAA) ranged from 18 µg/ml (AAL2 isolate) (*Avicennia-A alba-A* Leaf-L Isolate 2) to 57.0 µg/ml (AAP9 isolate). Based on preliminary identification, strain AAL2 isolated from *Avicennia alba*, identified as *Exiguobacterium mexicanum* and AAP3, AAP5 and AAP9 isolates obtained from *Avicennia alba* belongs to Gram-positive non-spore forming bacilli, vibrio sp. and *Chryseomicrobium amylolyticum*, respectively. Endophytic bacterial strains AAP10 (Gram-positive bacteria), AAP9 (*Chryseomicrobium amylolyticum*), and AAP4 (*Bacillus* sp.) were recorded as suitable inoculants for producing plant growth-promoting hormones and phosphate solubilization. Various sets of bioenzymes and *Chryseomicrobium amylolyticum* were reported for the first time in *Avicennia alba* with potential application from an unexplored resource at the Coringa mangrove ecosystem.

Keywords: *Avicennia alba*, *Chryseomicrobium amylolyticum*, Endophytes, Phosphate solubilisation, Plant growth promoting hormones

Introduction:

Mangrove ecosystem are the most salt tolerant plants known and play a key ecological part for the preservation and productivity of tropical coastal ecosystems (Donato et al., 2011; Ezcurra et al., 2016; Sutton-Grier et al., 2015). Unlike other plant species growing in naturally saline conditions, mangroves host halo-tolerant and halophilic bacteria (Castro et al., 2014) and were anticipated as a valuable source of plant growth promoting bacteria (PGPB) (Bashan & Holguin, 2002). Extreme deforestation and mass exploitation of important mangrove plants cause too many of this mangrove plants becoming endangered. Apart from being an eco-hazard, extracting biological active substance from plants is also very costly, time consuming and laborious. For this reason, searching mangrove endophytic bacteria which are eco-friendly sources of valuable

phytochemicals is extremely desirable (Jamwal & Gandhi, 2019). Endophytic bacterial isolates has been employed as a resource for the production of biological active compounds. However, reports on the mangrove as the source of endophytic bacteria are still limited (C. Jose & Christy, 2013). Endophytes are the microorganisms found within the plant tissue for at least, a part of the cycle of the plant life. Such microorganisms do not cause any damage or disease to the host plant and generally offer many benefits favouring production of biologically active compounds, production of plant growth promoting phytohormones, fixes nitrogen, phosphates solubilization and antimicrobial activity (Le Cocq et al., 2017; Ludwig Muller et al., 2015). In the study conducted by Deivanai et al., (2014) isolated endophytic bacteria namely *Bacillus amyloliquefaciens* (3MPE1) and *Pantoea ananatis* (1MSE1) isolated from mangrove plant *Rhizophora apiculata* Blume. Inoculation of these endophytic bacterial isolates (EBI) with rice seeds resulted in increased root and shoot growth with significant increase in the chlorophyll content.

Avicennia alba Blume. belongs to the family Acanthaceae is an evergreen shrub or small tree widely found in tropical and subtropical regions of the world, grows in tidal forests near river mouths. It predominantly grows in humid tropical ecosystems. The geographical range of this species is from Tropical Asia to the North western Pacific. Scabies, rheumatism, paralysis, asthma, snake bites, skin diseases, and ulcers are among the problems that it is used to cure in the Indian medical system (The Wealth of India; Colin Field, 1995). According to Bandaranayake (1995), the plant is a rich source of alkaloids, triterpenes, steroids, saponins, flavonoids, and tannins.

MATERIAL AND METHODS

The current investigation was carried out at the Botany Department of Andhra University, Visakhapatnam, Andhra Pradesh. Plant tissue samples of *Avicennia alba* were collected from the mangrove forests zone of Coringa Wildlife Sanctuary, East Godavari district, of Andhra Pradesh. All the plant samples were collected in sterile bags and transported immediately to the laboratory for isolation of bacterial endophytes.

Gram staining reaction

The Gram staining was carryout as per modified Gram's staining protocols (2005). Gram staining was carried out to know the morphology i.e. cocci, rods, cocco-bacilli, and spiral shape and their reaction to gram staining as Gram's Positive and Gram's Negative. Heat fixed 24 hours bacterial smear was taken in the clean glass slide and first stained with crystal violet solution for one minute and washed with running tap water and then the slide was given Gram's Iodine solution for one minute followed by washing in running tap water. 90% ethanol was used for 10 seconds to decolorize the surface, and then tap water was used once again. Lastly, the slide was counterstained with Safranin solution, washed with water and dried with blotting paper. Then the slide was examined under microscope using oil immersion objective lens (100 X). The Gram-Negative bacteria appeared as pink colour while the Gram-positive bacteria appeared as purple colour.

Effect of salt concentration on growth

All isolated cultures were grown on nutrient agar using varied salt concentrations i.e. 0% (no salt), 3%, 6%, 8%, 10% and 12% Sodium chloride incubated at 32°C for 24 to 48 hours in thermostat incubator. Observations on growth were recorded for every 24 and 48 hours of incubation.

Production of plant growth promoting characters

IAA production ability:

Indole-3-acetic acid (IAA) is the most prevalent phytohormone produced by endophytic bacteria isolated from mangrove plant sp. and other secondary metabolites. IAA production was assessed for Indole compounds using a colorimetric assay with Salkowski reagent. A loop full of cultures were inoculated in 1ml of 3% NaCl Nutrient broth in Eppendorf tubes and kept for rotation in a rotary mixer for 4hrs for activation of bacteria. The 4hrs activated cultures were inoculated (50µl) into 4ml of 3% Nutrient broth containing 0.2% (v/v) of L-Tryptophan in ria vials. The vials are vortexed and kept for rotation in a rotary mixer for 48hrs at 32°C. After 48hrs, the cultures from the ria vials are subjected to centrifugation at 2000rpm for 20mins. Uninoculated Control was maintained for comparison. After centrifugation, the supernatant is used for analysis. 1.5ml of the supernatant mixed with 1.5ml of Salkowski's reagent and incubated for about 20mins. Cultures positive for IAA production, show different range of colours from orange to dark purple. Using a UV Spectrophotometer, the colours in the combination were measured spectrophotometrically at 536 nm. The readings are compared with the standard graph of IAA and estimated the approximate quantity. The standard graph was prepared with standards of 10µg/ml to 60µg/ml with Indole 3-Acetic Acid.

Phosphate solubilizing ability:

Loop full of culture were inoculated in 1ml of 3% NaCl Nutrient broth in Eppendorf tubes and kept for rotation in a rotary mixer for 4hrs for activation of the isolates. The activated cultures were inoculated (50µl) into 4ml of Pikovskaya's broth enriched with 3% NaCl in ria vials. The vials are vortexed and kept for rotation in a rotary mixer for 48hrs. Uninoculated control was maintained for comparison. After 48hrs, the cultures from the ria vials are subjected to centrifugation at 2000rpm for 20mins. After centrifugation, the supernatant is used for analysis. 50µl of the supernatant is mixed with 3.95ml of distilled water to make 4ml of sample. To the 4ml of the sample, 750µl of phosphate reagent was added and waited for 5mins and observations for development of blue colour of different intensities were recorded by measuring the different colour intensities, spectrophotometrically at 680nm and compared with phosphate standard graph.

Molecular Identification using 16S ribosomal RNA gene method

According to Dighe et al., (2004) and Green wood et al., (2012) if the similarity of 16S rRNA coding genes base sequence more than 97% couple considered the same species. Sequence data of 16S rRNA gene could describe the degree of similarity between two taxa. Hence, it could be used to construct phylogenetic trees that present the relationship among ancestors and association of organisms (Godini and Fallahi, 2019). 16S rRNA gene is used widely for constructing phylogenetic trees, in addition to this they also found in all

prokaryotes. This 16S rRNA had variable and conserve areas that reflects the phylogenetic relationship among species (Van de Peer, 2009; Mitreva, 2017).

Extraction of 16S ribosomal RNA bacteria gene

Individually 1.5 ml of bacterial culture grown in nutrient broth for 24 hours was placed in a 2 ml eppendorf tube. The tubes then centrifuged at 10,000 rpm for 10 minutes. The supernatant was removed and another 1.5 ml of bacterial isolates was further added into the tube. The tubes were again centrifuged at 10,000 rpm for 10 minutes. 200 µl of lysis buffer was added to the eppendorf tube and mixed well. The mixture then kept in minibath for 10 minutes at 100°C. These tubes were again centrifuged for 10 minutes at 10,000 rpm. After centrifugation 100µl of sample was taken in 0.5 ml of eppendorf tubes and stored at -20°C and directly used for amplification.

Amplification of 16s rRNA through Polymerase Chain Reaction and BLAST analysis.

Nucleic acid was extracted from a bacterial sample, and its purity was assessed through the application of 1.0% agarose gel electrophoresis. The amplification of 16S ribosomal RNA gene fragments was conducted utilizing 16SrRNA-Forward and 16SrRNA-Reverse primers. The purification of the 1500 bp PCR template was successfully completed. A consensus genome sequence of the 16S ribosomal RNA gene was generated from both forward and reverse data sequences utilizing the Aligner Software tool. The sequencing of 16S rRNA was conducted utilizing BLAST with the 'nr' database given by the National Center for Biotechnology Information (NCBI), especially GenBank. Utilizing the highest identity scores, ten gene sequences were selected and aligned using the Multiple Alignment software tool Clustal W. Using MEGA10, a distance matrix and phylogenetic tree were created.

Results and Discussion:

Sixteen endophytic bacterial isolates were obtained from different parts (leaves, roots, and pneumatophores) of *Avicennia alba* and coded based on host, plant part, and isolate number (e.g., AAL1). Among these, 11 isolates were Gram-positive and 5 were Gram-negative. Most isolates tolerated salinity up to 10% NaCl, while a few (AAL1, AAP2, and AAP6) showed tolerance up to 12%. All isolates exhibited optimal growth between 3–8% NaCl, confirming their halophytic nature, with some also capable of growth in the absence of NaCl.

Biochemical characterization revealed that all isolates were catalase-positive. Significant protease activity (3.0 cm zone) was observed in isolates AAP2, AAP6, and AAP13. A majority of isolates produced indole-3-acetic acid (IAA), with AAP10 showing the highest production (59 µg/ml), followed by AAP9, AAP8, and AAP11. Preliminary identification indicated that AAP10, AAP8, and AAP11 are Gram-negative bacilli, while AAP9 was identified as *Chryseomicrobium amylolyticum* through 16S rRNA analysis. Phosphate solubilization was highest in isolate AAP5 (7.1 ppm).

Table-1: Biochemical properties of endophytic bacterial isolates

Mangrove plant sp.	Bacterial isolates	String test	Catalase	Oxidase	Indole	Methyl Red	VogesProskauer	Citrate
<i>Avicennia alba</i>	AAL1	+	+	+	+	+	-	+
	AAL2	-	+	-	-	-	-	-
	AAL3	-	+	-	-	-	-	-
	AAP1	-	+	-	-	+	-	-
	AAP2	-	+	-	-	-	-	-
	AAP3	-	+++	-	-	+	-	-
	AAP4	-	+	-	-	+	-	-
	AAP5	+	+	+	-	-	-	-
	AAP6	-	+	-	-	+	-	-
	AAP7	-	+	-	-	-	-	-
	AAP8	+	++	-	-	-	-	-
	AAP9	-	+++	-	-	+	-	-
	AAP10	+	++	-	-	-	-	-
	AAP11	+	++	-	-	+	-	-
	AAP12	-	+	-	-	-	-	-
	AAP13	-	+	+	-	+	-	-

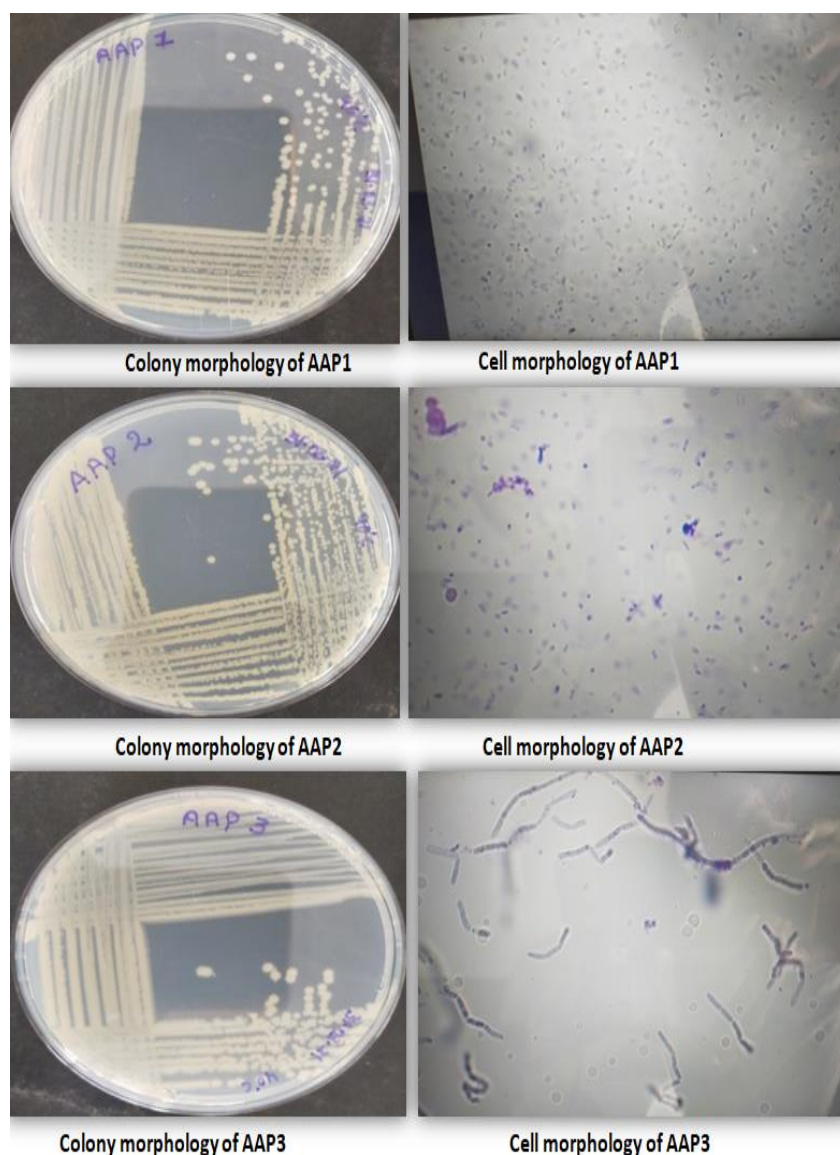


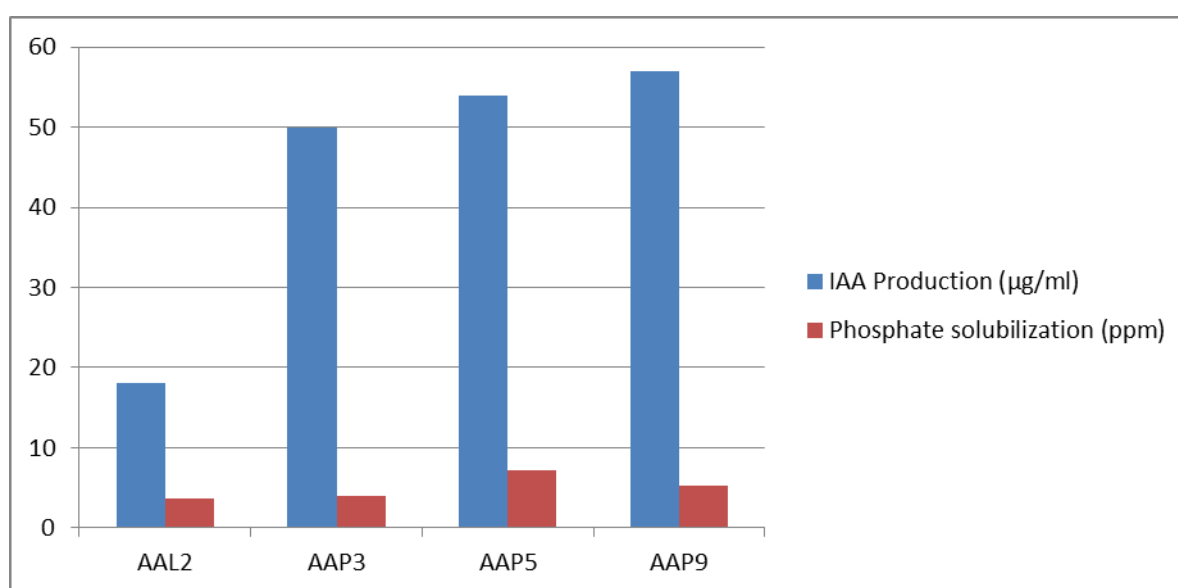
Fig:1 Colonies of samples from *Avicennia alba* pneumatophore

Endophytic bacterial isolates showing both IAA production and Phosphate solubilization.

The endophytic bacterial strains were screened for their ability to produce both IAA and solubilize Phosphate. Strain AAL2 isolated from *Avicennia alba* was recorded with 18 $\mu\text{g/ml}$ and 3.7 ppm for IAA production and Phosphate solubilization characters, respectively whereas strains AAP3, AAP5, and AAP9 isolated from *Avicennia alba* were recorded with 50 $\mu\text{g/ml}$ & 4.0 ppm, 54 $\mu\text{g/ml}$ and 7.1 ppm, 57 $\mu\text{g/ml}$, and 5.3 ppm for IAA production and phosphate solubilization ability respectively. Based on preliminary identification, strain AAL2 isolated from *Avicennia alba* identified as *Exiguobacterium mexicanum*, and AAP3, AAP5, and AAP9 obtained from *Avicennia alba* belongs to Gram-positive non-spore-forming bacilli, vibrio sp, and *Chryseomicrobium amylolyticum* respectively. The results are placed in the table 2.

Table-2: Endophytic bacterial isolates showing both IAA production and Phosphate solubilization.

Mangrove plant sp.	Endophytic bacterial isolates	IAA Production ($\mu\text{g/ml}$)	Phosphate solubilization (ppm)	Preliminary identification
<i>Avicennia alba</i>	AAL2	18	3.7	<i>Exiguobacterium mexicanum</i>
	AAP3	50	4.0	Bacilli sp. Gram positive non-spore forming
	AAP5	54	7.1	Vibrio sp.
	AAP9	57	5.3	<i>Chryseomicrobium amylolyticum</i>

**Fig 2. Endophytic isolates recorded both IAA production and Phosphate solubilization characters.**

Molecular Identification using 16S ribosomal RNA gene method

Individual strains with distinct characters and properties were selected and subject to 16S rRNA sequencing as described in the material and methods. The sequences received were analyzed, and the phylogenetic tree was used to evaluate the relationship between the isolated endophytic bacteria and other species of bacteria. Based on 16S rRNA molecular methods, the following endophytic strains were identified and presented in Table 3.

Based on preliminary phenotypic and biochemical characteristics, Plant growth-promoting ability, and phosphate solubilization ability, three isolates were randomly selected for identification by the 16S rRNA molecular method. Based on the results obtained, nucleotide sequencing of the nearly full length of the 16S rRNA gene from all isolates was 99-100% similar to the species already recorded in the GenBank database.

Table-3: Molecular identification of isolated endophytic strains

Endophytic Strain	Source of the endophytes	Identify as	Nearest Accession No.
AAL2	<i>Avicennia alba</i>	<i>Exiguobacterium mexicanum</i>	MK920159.1
AAP9	<i>Avicennia alba</i>	<i>Chryseomicrobium amylolyticum</i>	MZ680359.1
AAP10	<i>Avicennia alba</i>	<i>Vibrio alginolyticus</i>	NR_122059.1

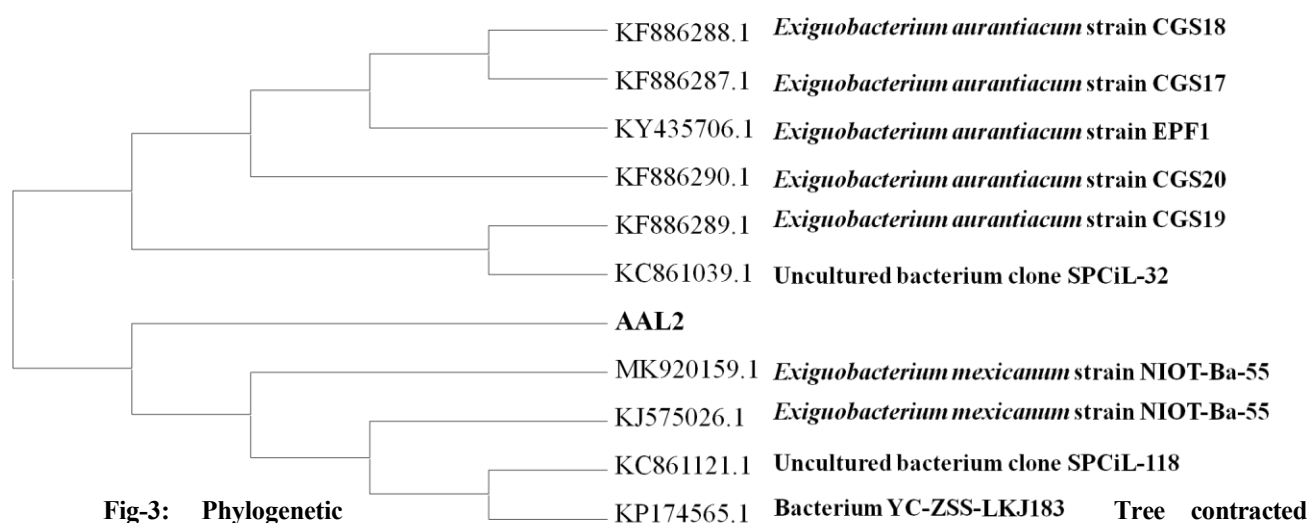
Evolutionary analysis by Maximum Likelihood method

The evolutionary history was drawn by using the Maximum Composite Likelihood method and the Tamura Nei model (Kimura, 1980). The highest log-likelihood (-3537.00) tree was obtained. The initial tree was constructed by applying Neighbour-Join and Bio NJ algorithms. The analysis involved 11 nucleotide sequences and codon positions, including 1st + 2nd + 3rd + Noncoding. The final data set contains 1481 positions. Using MEGA X, an evolutionary analysis was carried out ((Kumar et al., 2018).

Sequence analysis revealed that the endophytic bacterial isolate AAL2 isolated from *Avicennia alba* showed 99% 16S rRNA gene sequence similarity to *Exiguobacterium mexicanum* strain NIOT-Ba-55 (Nearest Accession No. MK920159.1) (Table-4). A phylogenetic tree was constructed using partial 16S rRNA sequences of isolated endophytic bacteria and representative bacterial type strains of related taxa generated by the neighbor-joining method and presented in Fig-3.

Table-4: Sequence producing significant alignment

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Nearest Accession
<i>Exiguobacterium mexicanum</i> strain NIOT-Ba-55	2760	2760	0.99	0	0.9993	MK920159.1
Uncultured bacterium clone SPCiL-118	2760	2760	0.99	0	0.9993	KC861121.1
<i>Exiguobacterium aurantiacum</i> strain CGS20	2758	2758	0.99	0	1	KF886290.1
<i>Exiguobacterium aurantiacum</i> strain CGS18	2752	2752	0.99	0	0.9993	KF886288.1
<i>Exiguobacterium aurantiacum</i> strain CGS17	2752	2752	0.99	0	0.9993	KF886287.1
<i>Exiguobacterium mexicanum</i> strain NIOT-Ba-55	2750	2750	0.99	0	0.9993	KJ575026.1
<i>Exiguobacterium aurantiacum</i> strain CGS19	2750	2750	0.99	0	0.9993	KF886289.1
<i>Exiguobacterium aurantiacum</i> strain EPF1	2748	2748	1	0	0.998	KY435706.1
Bacterium YC-ZSS-LKJ183	2748	2748	0.99	0	0.998	KP174565.1
Uncultured bacterium clone SPCiL-32	2748	2748	0.99	0	0.998	KC861039.1



Sequence analysis revealed that endophytic bacterial isolate AAP9 isolated from *Avicennia alba* showed 98% 16S rRNA gene sequence similarity to *Chryseomicrobium amylolyticum* strain SICr03 (Nearest Accession No. MZ680359.1) (Table-5). A phylogenetic tree was constructed using partial 16S rRNA sequences of isolated endophytic bacteria and representative bacterial type strains of related taxa generated by the neighbor-joining method and presented in Fig-4.

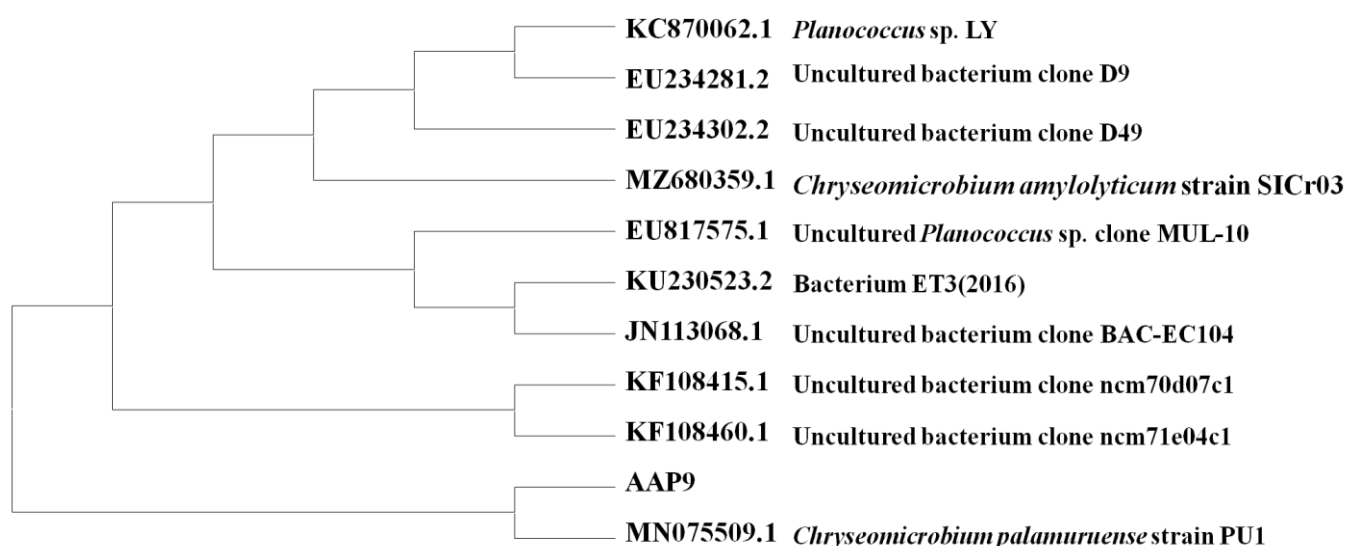


Table-5: Sequence producing significant alignment

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Nearest Accession
<i>Chryseomicrobium amylolyticum</i> strain SICr03	2261	2261	1	0	0.9852	MZ680359.1
Uncultured bacterium clone ncm70d07c1	2255	2255	1	0	0.9844	KF108415.1
<i>Chryseomicrobium palamuruense</i> strain PU1	2252	2252	1	0	0.9836	MN075509.1
Uncultured bacterium clone D49	2250	2250	1	0	0.9836	EU234302.2
Uncultured bacterium clonncm71e04c1	2244	2244	1	0	0.9828	KF108460.1
<i>Planococcus</i> sp. LY	2244	2244	1	0	0.9828	KC870062.1
Bacterium ET3(2016)	2239	2239	1	0	0.982	KU230523.2
Uncultured bacterium clone D9	2233	2233	1	0	0.9813	EU234281.2
Uncultured bacterium clone BAC-EC104	2233	2233	1	0	0.9813	JN113068.1
Uncultured <i>Planococcus</i> sp. clone MUL-10	2233	2233	1	0	0.9813	EU817575.1

Sequence analysis revealed that endophytic bacterial isolate AAP10 isolated from *Avicennia alba* showed 99% 16S rRNA gene sequence similarity to *Vibrio alginolyticus* strain NBRC 15630 (Nearest Accession No. NR_122059.1). A phylogenetic tree was constructed using partial 16S rRNA sequences of isolated endophytic bacteria and representative bacterial type strains of related taxa generated by the neighbor-joining method and presented in Fig-5.

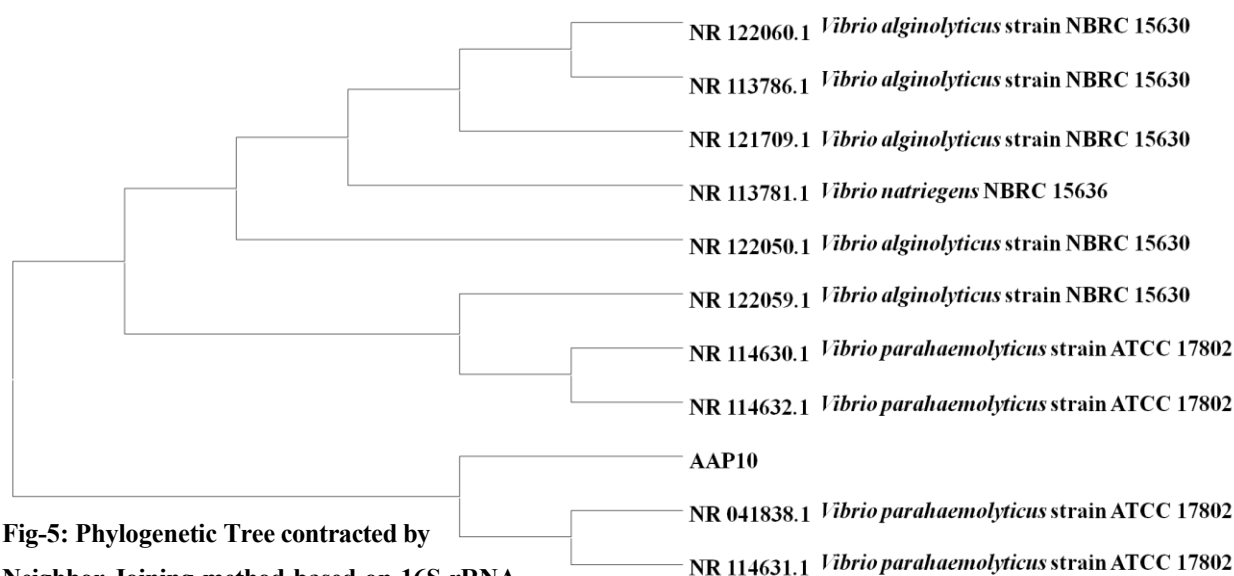


Fig-5: Phylogenetic Tree contracted by Neighbor-Joining method based on 16S rRNA

gene sequencing showing the phylogenetic position of the type strain of *Vibrio alginolyticus* strain NBRC 15630

Conclusion:

Endophytes have several potential applications in various fields of agriculture, medicine, and biotechnological sectors. Exploration of bacterial endophytes from unexplored resources is crucial to find their possible applications. In this present study, attempts were made to isolate, identify, and screen the mangrove endophytic bacteria for their halotolerant, plant growth-promoting ability, and phosphate solubilization characteristics from the unexplored source of coring wildlife sanctuary, a mangrove ecosystem located in Andhra Pradesh.

Strains AAP10 (Gram-positive bacteria), AAP9 (*Chryseomicrobium amylolyticum*), and AAP4 (*Bacillus* sp.) were recorded as suitable inoculants for producing plant growth-promoting hormones, phosphate solubilization, producing various sets of bioenzyme. They were the first to report endophytic bacteria with potential application from the Coringa wildlife mangrove ecosystem. The results revealed that using these endophytic isolates as inoculants to grow plants in sustainable agricultural and allied sectors was also used for further research studies.

References:

1. Bandaranayake WM. Survey of mangrove plants from Northern Australia for phytochemical constituents and UV absorbing compounds. *Current Topical Phytochemistry*, 1995; 14: 69-78.
2. Bashan, Y., & Holguin, G. (2002). Plant growth-promoting bacteria: a potential tool for arid mangrove reforestation. *Trees*, 16(2-3), 159-166.
3. C. Jose, A., & Christy, P. H. (2013). Assessment of antimicrobial potential of endophytic bacteria isolated from *Rhizophora mucronata*. *International Journal of Current Microbiology and Applied Sciences*, 2(10), 188–194.
4. Castro, R. A., Quecine, M. C., Lacava, P. T., Batista, B. D., Luvizotto, D. M., Marcon, J., ...&Azevedo, J. L. (2014). Isolation and enzyme bioprospection of endophytic bacteria associated with plants of Brazilian mangrove ecosystem. *Sprjinger Plus*, 3(1), 1-9.
5. Coico R. (2005). Gram staining. *Current protocols in microbiology*, Appendix 3, .<https://doi.org/10.1002/9780471729259.mca03cs00>
6. Colin Field, (1995). Impact of expected climate change on mangroves. *Hydrobiologia* 295, 75–81 <https://doi.org/10.1007/BF00029113> .
7. Deivanai, S., Bindusara, A. S., Prabhakaran, G., & Bhore, S. J. (2014). Culturable bacterial endophytes isolated from Mangrove tree (*Rhizophora apiculata* Blume) enhance seedling growth in Rice. *Journal of natural science, biology, and medicine*, 5(2), 437.
8. Dighe AS, Jangid K, Gonzalez JM, Pidiyar VJ, Patole MS, Ranade DR, Shouche YS. (2004). Comparison of 16S rRNA Gene Sequences of Genus *Methanobrevibacter*. *BMC Microbiol* 4: 20. DOI: :10.1186/1471-2180-4-20.
9. Donato, D. C., Kauffman, J. B., Murdiyarso, D., Kurnianto, S., Stidham, M, etal. , Mangroves among the most carbon-rich forests in the tropics, *Nat Geosci*, 4(5) (2011), 293-297.
10. Ezcurra, P., Ezcurra, E., Garcillán, P. P., Costa, M. T., &Aburto-Oropeza, O. Coastal landforms and accumulation of mangrove peat increase carbon sequestration and storage, *Proc Nat Acad Sci*, 113(16), (2016) 4404-4409.

11. Godini R, Fallahi H. (2019). A brief overview of the concepts, methods and computational tools used in phylogenetic tree construction and gene prediction. *Meta Gene* 21: 100586.
12. Greenwood D, Barer M, Slack R, Irving W. (2012). *Medical Microbiology A Guide to Microbial Infections: Pathogenesis, Immunity, Laboratory Investigation and Control*, 18th ed. Elsevier Ltd., New York
13. Jamwal, V. L., & Gandhi, S. G. (2019). Endophytes as a source of High-value phytochemicals: Present scenario and future outlook. *Endophytes Second. Metabolites Reference Ser. Phytochemistry*, 571-590.
14. Kimura, M. 1980. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *J. Mol. Evol.*16:111-120.
15. Kumar S et al, MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. *Mol Biol Evol.* 2018 Jun 1;35(6): 1547-1549.
16. Le Cocq, K., Gurr, S. J., Hirsch, P. R., &Mauchline, T. H. (2017). Exploitation of endophytes for sustainable agricultural intensification. *Molecular Plant Pathology*, 18(3), 469-473.
17. Ludwig-Müller, J. (2015). Plants and endophytes: equal partners in secondary metabolite production. *Biotechnology letters*, 37, 1325-1334.
18. Mitreva M. 2017. The Microbiome in infectious diseases. In: *Infection Diseases*, Vol. 1, 4th ed. Elsevier, Dordrecht
19. Sutton-Grier, A. E., Wowk, K., &Bamford, H. Future of our coasts: The potential for natural and hybrid infrastructure to enhance the resilience of our coastal communities, economies and ecosystems., *Environ Sci Policy*, 51, (2015) 137-148.
20. Van de Peer Y, Lemey P, Salemi M, Vandamme AM. (2009). *The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing*. Cambridge University Press, London