



RESEARCH ARTICLE

ISOLATION, IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF ACTINOMYCETE STRAIN FROM THE LATERITE SOIL OF KANDUKURU

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ABSTRACT

The laterite soil was collected from the Kandukuru of Prakasahm District and analyzed for its physico-chemical properties and pretreated and used for isolation of actinomycetes. The isolated strain was designated as CN-4. The morphological charecterisation carried with genomic (16 rDNA gene sequencing) analysis. The amplified and sequenced 16S rDNA was compared with the sequences in GenBank using BLAST and aligned with the sequences retrieved from NCBI GenBank database using the Clustal W method. The phylogenetic tree was constructed based on Maximum Likelihood method using bootstrap analysis and micro morphology of the strain through Scanning Electron Microscopy (SEM) was also carried out. Based on the scanning electron microscopic observation and phylogenetic tree construction the isolated strain from the laterite soil of Kandukuru was identified as *Streptomyces albus* CN-4.

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INTRODUCTION

Microorganisms from environments have gained considerable attention in recent years. This is mainly due to the fact that they hold about the molecular evolution of life. Natural products are the leading sources of novel biomolecules that have been used in the pharmaceutical industries since their inception. The majority of the natural products currently used in the market as therapeutic agents or as health supplements are derived from the terrestrial organisms including plants, animals and microorganisms. Microbial secondary metabolites are the important sources of natural compounds with potential bioactivities. In general, natural products including the microbial metabolites may be practically utilized in different ways including in the fields of medicine and agriculture industries, material for subsequent chemical or microbiological modification (derivatization), lead compounds in the synthesis of new analogs or as templates in Rational Drug Design studies. Soil is the perfect laboratory for the creation of natural medicines. It holds a wide array of tiny microhabitats that creates a vast variation in the appearance and survival strategies of soil microbes. The actinomycetes which represent a transitional form between the bacteria and fungi compose a large proportion of the soil flora. They are Gram positive bacteria, filamentous and sporulating with DNA rich in G+C ranging from 55-75% (Ho *et al.*, 2002). they are generally considered as terrigenous bacteria due to their wide distribution and abundance in soil. The name actinomycetes derived from Greek aktis (a ray) and mykes (fungus) was given to these organisms from initial observation of their morphology. These

members are grouped into the class Actinobacteria belonging to the division of Firmicutes of the domain Bacteria. The class Actinobacteria is categorized into five subclasses namely Actinobacteridae, Acidimicrobidae, Coriobacteridae, Sphaerobacteridae and Rubrobacteridae. Except Actinobacteridae, the other four subclasses contain only one order subsequently delineated into one family each. On the other hand, subclass Actinobacteridae consists of two orders, the Actinomycetales and Bifidobacteriales. The order Actinomycetales has ten suborders, each sub order again categorized into a total of about 38 families. The order Bifidobacteriales constitute only one family namely Bifidobacteriaceae. Classification of actinomycetes proposed by Stackebrandt *et al.* (1997). In this context, a study was conducted on the isolation of actinomycetes from the laterite soil of Kandukuru, Prekasam (Dist), A.P., micro morphology of the strain through Scanning Electron Microscopy (SEM) as per the procedure described by the Yassin *et al.* (1997). morphological characteristics of the strain with those reported in Bergey's Manual.

The search for the pharmacological targets as well as the synthesis of modified natural compounds will keep on moving Microbiologists, Biotechnologists and Chemists in the process of new drugs discovery. In connection with the excellent track record of actinomycetes with antimicrobial activity, an attempt was made to exploit the laterite soil for the isolation of actinomycetes

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MATERIALS AND METHODS

Isolation and screening of actinomycete strains from laterite Soil sample

Laterite soil sample collected for the isolation of potent actinomycete strains was initially analysed for physico-chemical properties such as moisture content (%), pH, organic carbon (%) and total nitrogen content (%).

Soil Characteristics

Moisture content

To determine the moisture content, 10 g of soil sample was dried in a hot air oven at 105°C until a constant weight is obtained. The difference between the weights of pre-drying and post-drying was taken as the moisture content of the initial soil sample.

Soil pH

To identifying the pH of the collected soil sample was determined with the help of digital pH meter of model Di-707 (Jackson, 1973). 20 g of soil sample was taken in a 100 ml beaker and 40 ml of distilled water was added. The suspension was mixed thoroughly and allowed to settle the suspended clay particles from the suspension for about 1h before recording the pH.

Organic carbon

Organic carbon content of the soil sample was estimated by following Walkey and Black method (1934). 10 g of soil sample was taken into 500 ml Erlenmeyer flask. To this 10 ml of 1N K₂Cr₂O₇ was added and shaken gently to disperse the soil into the solution. 20 ml of Conc. H₂SO₄ was added followed by vigorous agitation for 1min. 200 ml of distilled water was added and filtered. Few drops of *O* - phenanthroline indicator was added to the filtered solution and titrated against 0.5N FeSO₄. 7H₂O. Sample without soil served as blank. The amount of organic carbon in the soil sample was calculated by using the following formula.

(milliequivalents of K₂Cr₂O₇ – milliequivalents of FeSO₄. 7H₂O) x 0.003 x 100

Organic carbon (%) = -----

----x f Soil weight (g)

f = correlation factor = 1.24

Total nitrogen

Total nitrogen in the soil sample was determined by Micro - Kjeldahl method.

Reagents

Conc. H₂SO₄, mercuric oxide, K₂SO₄, sodium hydroxide – sodium thiosulphate solution (60% NaOH and 5% Na₂SO₃. 5H₂O in distilled water), 0.02N standard HCl, 4% boric acid solution, mixed indicator solution (10ml of 0.2% methyl red in ethanol mixed with 50ml of 0.2% bromocresol green in ethanol)

Procedure

To the finely sieved soil sample (100 g) taken into a digestion flask, 2 g of K₂SO₄, 90 mg of mercuric oxide and 2 ml of

Conc. H₂SO₄ were added, mixed thoroughly and kept for digestion on heater. Before carrying out of distillation process, limited addition of distilled water (5 ml) to the flask was followed by the addition of Sodium hydroxide – sodium thiosulphate solution was added. Ammonia was collected in boric

acid. The distillate (20ml) collected was titrated against 0.02N HCl. Appearance of violet colour is the end point. Blank was maintained using equal volume of distilled water instead of distillate. Total nitrogen present in the soil sample was calculated by using the formula

[{HCl (ml) in sample – HCl (ml) in blank x normality of acid x 14.01 x 100}]

Total nitrogen = -----

Soil weight (mg)

Isolation of actinomycete strains

Laterite soil sample collected from Kandukuru, Prakasam (Dist) a depth of 5 – 8 cm was pretreated with calcium carbonate (1:1 w/w) and dried at 45°C for 1 h in order to reduce the abundance of bacteria and fungi (El-Nakeeb and Lechhevalier, 1963). Yeast extract malt extract dextrose agar (YMD) and starch casein salts agar media were prepared, sterilized at 15 lbs pressure (120°C) for 15 min and poured into Petri plates under aseptic conditions. Both streptomycin (50 µg/ml) and nystatin (50 µg/ml) were added to the media just before pouring into Petri plate. Soil dilution plate technique was employed for isolation of actinomycetes strains (Williams and Cross, 1971). The pretreated soil (1 g) sample was suspended in 100 ml of sterile distilled water. Serial dilutions were prepared and 0.1ml of 10⁻³ and 10⁻⁴ dilutions were placed on media with the help of a spreader. The inoculated plates were incubated at 30°C for 7-14 days. After incubation, actinomycete colonies were isolated from soil. Streak plate method was used to purify the cultures of actinomycete strains. The colonies were picked with the loop according to the condition. The picked up specks of the colonies were streaked over YMD agar medium followed by incubation at 30°C for 7 days. Further, pure cultures were maintained on YMD agar slants and stored at 4°C for further study (Williams and Cross, 1971).

Taxonomic studies of the actinomycete strain

Cultural, morphological, biochemical and physiological characteristics together with genomic (16s rDNA gene sequencing) analysis of the strain CN-4 were studied.

Morphological studies

ISP-2 grown culture was used to observe the detailed micro morphology of the strain through Scanning Electron Microscopy (SEM) as per the procedure described by the Yassin *et al.* (1997). The culture was fixed in 2.5% glutaraldehyde prepared in 0.1 M phosphate buffer (pH 7.2) for 24 h at 4°C followed by the post fixation step in 2% aqueous osmium tetroxide for 4 h in the same buffer. The sample was then dehydrated in ethanol and then dried up to critical with the help of Electron Microscopy science CPD unit (Ruska Labs, Acharya NG Ranga University, Hyderabad, India). The dried sample was mounted on aluminum stubs covered with double-sided carbon tape. A thin layer of gold coating was applied over the sample by

using automated sputter coater for 3 min (JEOL JFC -1600, Japan). Finally, the samples were examined under SEM at various magnifications (Model: JOEL-JSM 5600, Japan).

Molecular identification of the strain based on 16s rDNA sequence analysis

The strain was grown in YMD broth for 3 days and was centrifuged at 10,000 rpm for 20 min and the pellet was used for the extraction of DNA (Mehling *et al.*, 1995). PCR mixture consisted of 2.5 µl of 10× buffer, 3.5 µl of MgCl₂ (25 mM), 2 µl of dNTP (0.4 mM), 1 µl of 16S rDNA actino specific primer – forward (10 pmol/µl), 1 µl of 16S rDNA actino specific primer- reverse (10 pmol/µl), Taq polymerase (2 U/µl) and 2 µl template DNA. PCR amplification was carried out as follows: Initial denaturation step at 94 °C for 3 min followed by 30 cycles of denaturation at 94°C for 1 min, annealing at 65°C for 1min and extension at 72°C for 1 min, with a further 5 min extension at 72°C. The PCR product was purified with Agarose Gel DNA Purification Kit SoluteReady® Genomic DNA purification kit, PCR Master Mix, Agarose gel electrophoresis consumables and Primers from HELINI Biomolecules, Chennai, India). The 750 bp 16S rDNA sequence was determined with 16S rDNA actino specific forward and reverse primers. The 16S rRNA gene fragment was amplified using Universal Primers. (Actino specific forward Primer -5'-GCCTAACACATGCAAGTCGA-3' and Actino Specific Reverse primer - 5'-CGTATTACCGCGGCTGCTGG-5') (Nilsson and Strom,2002). The deduced 16s rDNA sequence was compared with the sequences in GenBank (<http://www.ncbi.nlm.nih.gov/>) using the Basic Local Alignment Search Tool (BLAST) then aligned with the related reference sequences retrieved from NCBI GenBank databases using the Clustal W method. Phylogenetic and molecular evolutionary analyses were conducted using Molecular Evolutionary Genetic analysis (MEGA) version 5.0 (Tamura *et al.* 2007).

RESULTS AND DISCUSSION

Isolation of actinomycete strains from laterite soil **Soil characters**

Isolation of actinomycetes from the laterite soil, the soil sample collected from kandhukuru was tested for soil characters such as moisture content, soil pH, organic matter and soil nitrogen content following standard protocols and the results were recorded as moisture content - 10%, pH - 7.2, organic matter - 1.0% and total nitrogen - 0.12%.

Isolation of actinomycete strains

For the isolation of actinomycete strains, the soil sample amended with calcium carbonate was air - dried at 45°C for 1 h. Serial dilution plate technique was employed for the isolation of actinomycetes. Serially diluted soil sample (0.1 ml) was plated on YMD agar (ISP-2) and starch casein agar media amended with streptomycin (50 µg/ml) and nystatin (50 µg/ml) and the Petri dishes were incubated at 28±2°C for 7-14 days. After incubation, the plates were observed for the growth of tough, leathery actinomycete colonies. Treatment of soil samples with calcium carbonate was reported to be the most efficient technique for the preferential isolation of actinomycetes (Alferova *et al.*, 1989). A total of ten actinomycete strains were isolated from laterite soil (figure 2).

One of the strains designated as CN-4 was found to be more active when compared to the other isolates; hence the strain was maintained as pure culture on yeast extract, malt extract, dextrose (YMD) agar slants and preserved at 4°C.

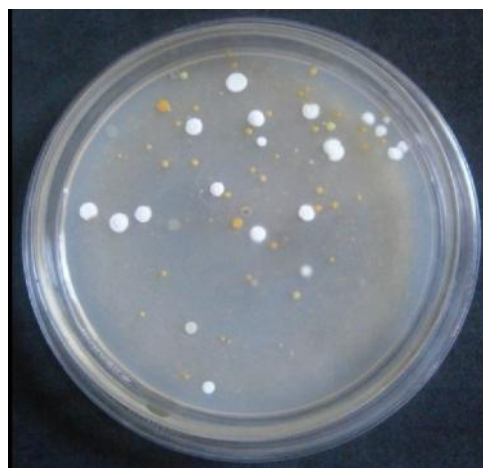


Fig 1 Isolation of actinomycetes on Starch- casein agar medium

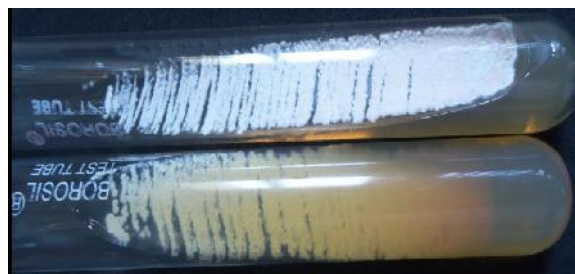


Fig 2 Growth of *Streptomyces albus* CN-4 on Yeast extracts malt extract- dextrose agar medium substrate and aerial mycelium.

Morphological characteristics

Slide culture technique was employed to observe the micromorphology of the strain grown on ISP - 2 medium through light microscopy and the detailed morphology of the strain was examined through Scanning Electron Microscopy (SEM). The colour of the aerial mycelium was creamy white with pale yellow substrate mycelium when grown on ISP - 2 medium. The sporophore morphology of the strain was observed as spiral with rough surface and hence placed under the spira group of the family Streptomycetaceae (Pridham *et al.*, 1958; Williams *et al.*, 1972). SEM images of the strain CN-4 are presented in figure 4.

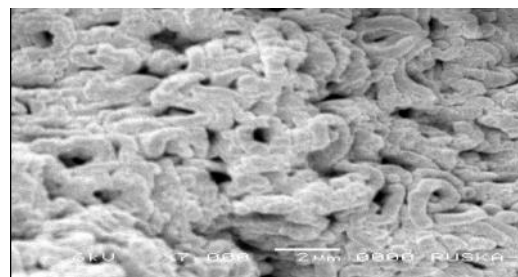


Fig 3 Scanning Electron microscopic photograph of *Streptomyces albus* CN4(x7000).

Phylogenetic study of the strain CN-4

The taxonomic position of the strain CN-4 was established based on 16s rDNA analysis. The 16s rDNA sequence of the strain was compared with the sequences in GenBank using BLAST and aligned with the sequences retrieved from NCBI GenBank database using the Clustal W method. The

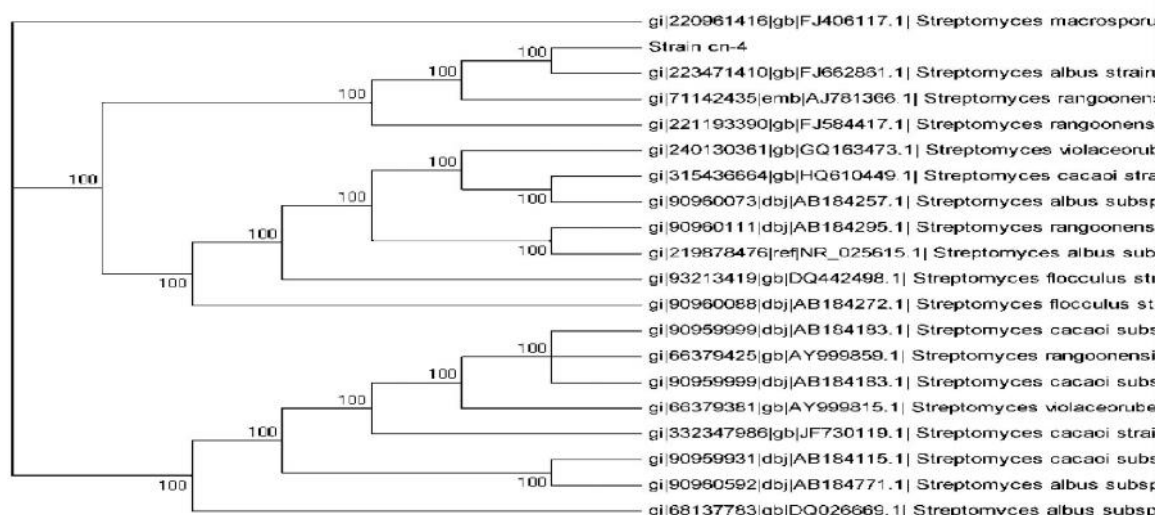


Fig 4 Phylogenetic tree derived from partial 16S rRNA gene sequence showing relationship between strain CN-4 and related members of the genus streptomyces spp, was constructed by using Maximum Likelihood method. Bootstrap values are expressed as percentages of 1000 replications.

phylogenetic tree was constructed based on Maximum likelihood method using bootstrap analysis (Fig. 6). The strain was close to *Streptomyces albus* with a bootstrap value of 100. Based on the cultural, morphological, physiological and molecular analysis, the strain CN-4 was identified as *Streptomyces albus* CN-4.

CONCLUSION

The sporophore morphology of the strain was observed as spiral with rough surface and hence placed under the spira group of the family Streptomycetaceae. The phylogenetic tree was constructed based on Maximum likelihood method using bootstrap analysis. The strain was close to *Streptomyces albus* with a bootstrap value of 100. Based on the morphological, and molecular analysis, the strain CN-4 was identified as *Streptomyces albus* CN-4.

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