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Exploring the Multifaceted Applications of *Streptosporangium terrae*: From Antibacterial Activity to Microbial Fuel Cells

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Abstract

The present study explored the dual potential of *Streptosporangium terrae*, isolated from the Western Ghats of Tamil Nadu, India, for antibiotic production and bioelectricity generation using microbial fuel cells (MFCs). The optimization of growth conditions, including pH, temperature, incubation time, and nutrient sources, was conducted to enhance the production of bioactive metabolites and electricity. Antibiotic sensitivity was tested against vancomycin, tetracycline, amikacin, and amoxicillin, revealing resistance to tetracycline and sensitivity to the other antibiotics tested. The antibacterial activity was evaluated against pathogenic strains such as *Escherichia coli*, *Staphylococcus pyogenes*, *Pseudomonas aeruginosa*, *Klebsiella oxytoca*, and *Proteus mirabilis*. The secondary metabolites were characterized using FT-IR spectroscopy, which identified functional groups such as amines, alkenes, and carboxyl groups. The MFCs utilizing *S. terrae* demonstrated the conversion of chemical energy into electrical energy, with a peak voltage of 1.204 mV observed on the 5th day. This study highlights the potential of *S. terrae* in sustainable energy production and antimicrobial applications, contributing to environmental sustainability.

Keywords: *Streptosporangium terrae*, Microbial Fuel Cells, Bioelectricity, Antibacterial activity, FT-IR.

Introduction

The increasing global demand for sustainable energy sources and the urgent need to combat antibiotic resistance have driven researchers to explore innovative solutions to address environmental and biomedical challenges in recent years. Microbial fuel cells (MFCs) have emerged as a promising technology for sustainable energy production, utilizing microorganisms to convert organic matter into electricity. MFCs are bioelectrochemical

systems that harness the metabolic activity of microorganisms to generate electricity from organic substrates. Bioelectrochemical systems are innovative bioengineering technologies that combine microorganisms or enzymes with electrochemical methods for in-situ energy harvesting and resource recovery in wastewater treatment. Bioelectrochemical systems include Microbial Fuel Cells (MFCs) and Microbial Solar Cells (MSCs) (1). However, the use of actinomycetes in MFCs has not been extensively explored, despite their metabolic versatility and ability to produce redox-active compounds. This represents a significant research gap, as actinomycetes can potentially enhance MFC efficiency while simultaneously producing valuable secondary metabolites. Simultaneously, gram-positive actinomycetes, particularly *Streptomyces* species, have long been recognized for their ability to produce bioactive secondary metabolites, including antibiotics, which are crucial in the fight against multidrug resistance (MDR). Synthetic antibiotics and antimicrobial medicines threaten human health and cause antibiotic resistance (2). Integrating fields such as bioelectricity generation and antibiotic production offers a unique opportunity to develop sustainable technologies that address energy needs while contributing to public health concerns. Pharmacognosy has provided various natural compounds, including antibacterial and antifungal agents, as potential drug candidates (3).

Actinomycetes are gram-positive bacteria that thrive in soil, particularly in alkaline and nutrient-rich soils. They are known for their ability to produce a wide range of secondary metabolites, including antibiotics and anticancer agents (4). Among actinomycetes, *Streptomyces* species are the most studied, accounting for nearly half of all known bioactive compounds. Actinomycetes inhabit terrestrial and marine ecosystems and are highly proficient in producing a wide range of natural products with diverse biological functions, including antitumor, immunosuppressive, antimicrobial, and antiviral activities. However, the potential of lesser-known genera, such as *Streptosporangium*, remains unexplored. *Streptosporangium terrae*, a soil-dwelling actinomycete, has shown promise in producing bioactive metabolites with antibacterial, antifungal, and anticancer properties, offering promise for novel drug discovery (5).

Its enzymatic capabilities, including cellulase and protease production, have industrial applications in the biofuel and waste management sectors. Additionally, *S. terrae* has the potential to generate bioelectricity through MFCs by converting organic substrates into sustainable energy. Its ability to degrade environmental pollutants further highlights its role in this process. However, its potential for bioelectricity generation has not been thoroughly investigated yet. With its diverse metabolic activities, *S. terrae* is a valuable resource for addressing global challenges in healthcare, energy, and environmental sustainability and warrants further exploration.

This study aimed to bridge this gap by investigating the dual potential of *Streptosporangium terrae* for antibiotic production and bioelectricity generation. By optimizing the growth conditions and evaluating its performance in MFCs, this study aimed to demonstrate the feasibility of using *S. terrae* as a sustainable biocatalyst for electricity generation in MFCs. These findings could pave the way for the development of integrated systems that simultaneously address energy needs and antibiotic resistance, thereby contributing to environmental sustainability and public health.

Materials and Methods

Isolation and identification of S. terrae

Soil samples were collected from the Western Ghats, Shenpagathoppu, Tamil Nadu, India. The samples were transported to the laboratory in sterile containers and stored at

room temperature for 48 h prior to analysis. Actinomycetes were isolated using starch casein nitrate agar (SCNA) through serial dilution and spread-plating techniques. Cycloheximide (50 µg/mL) and nalidixic acid (25 µg/mL) were added to the medium to inhibit fungal and bacterial growth, respectively. The plates were incubated at 27°C for 7-10 days. Colonies exhibiting typical actinomycete morphology, including dry, earthy, and pigmented colonies, were selected for further identification using morphological and molecular characterization (6).

Genomic DNA extraction

The isolated bacterial strain was grown in 2 mL Zobell marine broth overnight at 35 °C. The culture was spun at 7000 rpm for 3 min to remove the supernatant. The pellet was resuspended in 400 µL sucrose TE (Tris-EDTA). Lysozyme was added to a final concentration of 8 mg/ml and incubated for 1h at 35°C. To this tube, 100 µL of 0.5 M ethylene diamine tetraacetic acid (EDTA) (pH 8.0), 60 µL of 10% sodium dodecyl sulfate (SDS), and 3 µL of proteinase K from 20 mg/mL were added and incubated overnight at 55°C. The supernatant was extracted twice with phenol: chloroform (1:1) and once with chloroform: isoamyl alcohol (24:1) and precipitated with ethanol. Finally, the DNA pellet was resuspended in sterile buffer and quantified using a microplate reader (Synergy H1, BioTek, USA).

PCR protocol

In this study, polymerase Chain Reaction (PCR) was used to amplify the 16S rRNA gene to identify and classify the bacteria. The M2F primer used to amplify the 16S rRNA was as follows: 5P-SAGAAGAAGCGCCGGCC-3P (7). Polymerase chain reaction (PCR) reaction mixture included 1X Taq buffer, 100 µM dNTPs, 1.5 mM $MgCl_2$, 5 pmol forward and reverse primers, 10-50 ng DNA template, and 1 U Taq DNA polymerase. The PCR amplification process involved initial denaturation at 94 °C for 4 min, followed by 30 cycles of denaturation, annealing, extension, and final extension at 72 °C for 8 min (8). Upon successful amplification, the PCR product was purified using Roche Life Science's High Pure PCR product purification kit and sequenced at Eurofins Genomics India Pvt. Ltd. (Bengaluru, India). The molecular identification of The strain was identified through BLAST analysis (9).

Optimization of cultural conditions for S. terrae growth

The growth conditions for *S. terrae* were optimized to maximize biomass and secondary metabolite production. Parameters such as pH (3–9), temperature (20–50°C), incubation time (1–7 days), carbon sources (glucose, starch, galactose), nitrogen sources (tryptone, ammonium chloride, yeast extract), and metal ions ($FeCl_3$, $MgSO_4$, $ZnSO_4$, and $CuSO_4$) were evaluated. The optimal conditions were determined by measuring the optical density (OD) at 600 nm and the secondary metabolite yield (10).

Antibiotic sensitivity test

The antibiotic sensitivity of *S. terrae* was assessed using the disc diffusion method. Antibiotic discs (vancomycin, tetracycline, amikacin, and amoxicillin) were placed on Mueller-Hinton agar plates inoculated with *S. terrae*. The plates were incubated at 28°C for 5 days, and the inhibition zones were measured to determine sensitivity (11).

Antibacterial activity

The antibacterial activity of *S. terrae* was determined against five clinical bacterial pathogens (*Escherichia coli, Staphylococcus pyogenes, Pseudomonas aeruginosa, Klebsiella oxytoca,* and *Proteus mirabilis*) using the well-diffusion method. The 24-hour-old cultures were swabbed on Muller Hinton agar (microbiological grade) plates using a sterile cotton swab, and 20 µl of the sample was placed into the wells aseptically. The plates were incubated at 35°C for 24 h. The results were obtained by measuring the diameter of the inhibition zone for each well and expressed in millimeters (12,13).

FT-IR analysis

Secondary metabolites were extracted using ethyl acetate and analyzed using Fourier-transform infrared (FT-IR) spectroscopy. The functional groups were identified based on the absorption spectra in the range of 400–4000 cm^{-1} (14).

Microbial fuel cells (MFC) setup and operation

Oxidative fermentation test

The oxidative fermentation capability of *S. terrae* was evaluated using the Oxidative Fermentation Test. The basal medium was prepared in test tubes, and the *S. terrae* culture was inoculated by stabbing into the medium. To create anaerobic conditions, the tubes were sealed with paraffin wax and incubated at 28°C for 3–7 days. The presence of facultative anaerobes was confirmed by a color change in the medium from green to yellow, indicating oxidative metabolic activity.

Double-chamber MFC design

A double-chamber MFC was constructed to evaluate the bioelectricity generation potential of *S. terrae*. The MFC consisted of two sterile plastic containers serving as anode and cathode chambers, each with a working volume of 1000 mL. The chambers were connected by a 50 mL salt bridge to facilitate the proton transfer. To prevent leakage, the joints were sealed using M-seal. Cylindrical copper (anode) and zinc (cathode) electrodes were placed in the respective chambers, each measuring 6.5 cm long. The electrodes were connected via copper wires to an external digital multimeter for voltage and current measurements. The cathode chamber contained 100 mM potassium ferricyanide in phosphate-buffered saline as the electron acceptor, whereas the anode chamber was inoculated with 10 g of *S. terrae* biomass suspended in rice wastewater. The MFC was operated in batch mode, and measurements were recorded daily (15).

MFC reactor measurement and analysis

The MFC electrical output was monitored using a digital multimeter. Voltage (V) and current (i) were measured, and the power (P) was calculated using the following formula:

$$P=iV$$

where P is the power in watts (W), i is the current in amperes (A), and V is the voltage in volts (V). Closed-circuit voltage measurements were conducted using an ammeter, voltmeter, breadboard, and resistors (1 kΩ and 100 kΩ). The anode of the MFC was connected to the positive terminal of the ammeter, and the cathode was connected to the negative terminal of the ammeter. The circuit was completed by linking the ammeter to the voltmeter and resistors to ensure accurate measurement of the constant current. This experimental setup was designed to assess the bioelectrochemical performance of *S. terrae* in MFCs, providing insights into its potential for sustainable energy generation and environmental applications.

Statistical analysis

All experiments were conducted in triplicate, and the data were analyzed using one-way ANOVA to determine the significant differences ($p < 0.05$). The results are expressed as mean ± standard deviation.

Results and Discussion

Isolation and identification of S. terrae

Isolation and Identification of *S. terrae* were confirmed through morphological and molecular characterization, aligning with previously reported traits of *Streptosporangium* species. In this study, the selective medium supplemented with cycloheximide and nalidixic acid effectively inhibited fungal and bacterial contaminants, ensuring the purity of *S. terrae* cultures. The colonies exhibited typical actinomycete morphology, characterized by a dry, earthy appearance and pigmented growth on starch casein nitrate (SCN) agar (Fig. 1) (16). Thus,

S. terrae was successfully isolated from soil samples collected from the Western Ghats in Tamil Nadu using starch casein nitrate (SCN) agar. The identification of bacteria was further confirmed by molecular characterization.

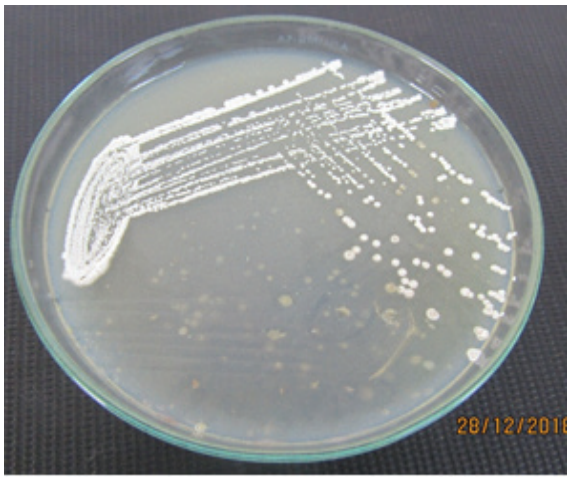

Fig. 1 Isolation of *S. terrae* on starch casein nitrate (SCN) agar plate

Phylogenetic analysis

The sequence of *Streptosporangium terrae* was submitted to GenBank under the accession number OQ118100. A phylogenetic tree was constructed (Fig. 2).

Streptosporangium terrae strain SMG01 16S ribosomal RNA gene, partial sequence

GenBank: OQ118100.1 in the FASTA format.

OQ118100.1 *Streptosporangium terrae* strain SMG01 16S ribosomal RNA gene, partial sequencese

GAACGCTGGCGGCGTGCTTAACACATG-
CAAGTCGAGCGGAAAGGCCCTTCGGG-
GTACTCGAGCGGCGAACGGTGAGTAA-
CACGTGAGCAACCTGCCCCTGACTCTGG-
GATAAGCCCGGGAAACTGGGTCTAATAC-
CGGATACGACCGCTTCCCGCATGGGATGG-
CGGTGGAAAGTTTTTTCGGTTGGGGATG-
GGCTCGCGGCCTATCAGTTGTTGGTGG-
GGTAGTGGCCTACCAAGGCGACGACGG-
GTAGCCGGCCTGAGAGGGCGACCGGC-
CACACTGGGACTGAGACACGGCCCA-
GACTCCTACGGGAGGCAGCAGTGGG-
GAATATTGCGCAATGGGCGAAAGCCTG-
CAGCGACGCCGCGTGGGGGATGACG-
GTCGGGTTGTAAACCTCTTTCAGCAGG-
GACGAAGTTGACGTGTACCTGCAGAA-
GAAGCGCCGGCTAACTACGTGCCAGCAGC-
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GTGGCTT.

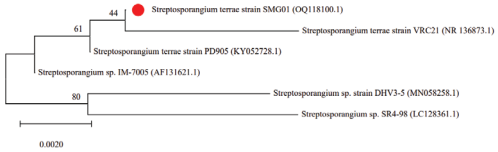

Fig. 2. Phylogenetic tree of Streptosporangium terrae

Previous studies have reported that Streptosporangium was observed in relation to the rhizosphere of buckwheat without waste rock, which can colonize not only rhizosphere soil but also plant tissues and play a significant role in promoting plant growth through nitrogen-fixing processes and inducing plant resistance (17,18).

Optimization of S. terrae

Effect of pH

The pH of the growth medium significantly influenced the growth and metabolic activity of S. terrae. Cultures were incubated at varying pH levels (3–9) and 35°C. The maximum biomass production, measured as optical density (OD) at 600 nm, was observed at pH 7 (OD 1.08 ± 0.03), indicating that neutral pH is optimal for S. terrae growth. Acidic conditions (pH 3) resulted in minimal growth (OD 0.17 ± 0.02), whereas alkaline conditions (pH 9) also showed reduced growth (OD 0.75 ± 0.04). These findings are consistent with previous studies on actinomycetes, which typically thrive in neutral-to-slightly alkaline environments. The pH-dependent growth pattern suggests that S. terrae require a stable pH for optimal enzymatic

activity and metabolism (Fig. 3a). Similarly, the optimum pH was 7-7.5. Streptomyces sp secondary metabolite production was highest at pH 7.5, with a minor decrease in antibiotic synthesis at pH 8.5 (19).

Effect of temperature

Temperature is a critical factor influencing microbial growth and secondary metabolite production. S. terrae cultures were incubated at temperatures ranging from 20°C to 50°C. Maximum biomass production was observed at 35°C (OD 1.51 ± 0.05), whereas growth was significantly reduced at lower (20°C, OD 0.29 ± 0.01) and higher (50 °C, OD 0.45 ± 0.03) temperatures. The optimal temperature range for S. terrae aligns with the mesophilic nature of most actinomycetes, which typically grow best between 25°C and 35°C. The decline in growth at extreme temperatures may be attributed to enzyme denaturation and disruption of cellular processes (Fig. 3b). In support of our study, the optimum growth of the bacterium Calidithermus terrae was observed at 30-50°C (20).

Effect of incubation time

The effect of incubation time on S. terrae growth was evaluated over 7 days. Maximum biomass production (OD 1.74 ± 0.02) occurred on the 5th day, corresponding to the exponential growth phase of the culture. Growth was minimal on the 1st day (OD 0.09 ± 0.01) and declined after the 5th day, reaching an OD of 1.32 ± 0.02 by the 7th day, indicating the onset of the stationary growth phase. The optimal incubation time of 5 days aligned with the peak secondary metabolite production. These findings highlight the importance of timing in maximizing biomass and metabolite yields, providing a basis for the efficient industrial-scale cultivation of S. terrae (Fig. 3c). The incubation and inoculation times were at 9-day intervals. Actinomycete cultures inoculated with inoculum broth secreted more bioactive compounds than those inoculated with a spore suspension. In both situations, extending the incubation time to 12 days increased the bioactive metabolite content (21).

Effect of carbon source

Carbon sources are vital for microbial growth and metabolite production. The effects of different carbon sources (glucose, starch, and galactose) on S. terrae growth were evaluated. Glucose was the most effective carbon source, supporting maximum biomass production (OD 1.43 ± 0.04), followed by galactose (OD 1.12 ± 0.03) and starch (OD 0.51 ± 0.02). The preference for glucose is consistent with its role as a readily metabolizable sugar that provides energy and carbon skeletons for biosynthesis. The lower growth observed with starch may be due to its complex structure, which requires additional enzymatic activity for its degradation (Fig. 3d). Glucose, galactose, and arabinose produced applicable values of bioactive metabolites (55–83 percent of that recorded by starch), despite some researchers claiming that monosugars, particularly glucose, are a good source of growth but inhibit the production of bioactive metabolites (21).

Effect of nitrogen source

Nitrogen is essential for protein synthesis and secondary metabolite production. The influence of various nitrogen sources (tryptone, ammonium chloride, and yeast extract) on S. terrae growth was investigated. Tryptone emerged as the most effective nitrogen source, supporting the highest biomass production (OD 1.01 ± 0.06), followed by yeast extract (OD 0.85 ± 0.04) and ammonium chloride (OD 0.33 ± 0.02) in that order. The superior performance of tryptone may be attributed to its high amino acid content, which supports robust microbial growth. Inorganic nitrogen sources, such as ammonium chloride, were less effective, likely due to their limited ability to provide essential nutrients for secondary metabolite synthesis (Fig. 3e). Evaluating different culture media is crucial because the production of specialized metabolites, including pigments, is influenced by changes in the primary carbon and nitrogen

sources of the medium. These changes can either increase the supply or limit access to key precursors, triggering the activation of biosynthetic enzymes or simultaneously affecting both processes. Similarly, nitrogen source preference (nitrogen repression) affects the expression of primary nitrogen metabolism and subsequently the biosynthesis of specialized metabolites, which require nitrogen compound precursors (22).

Effect of metal ions

Metal ions are crucial cofactors for enzymatic activity and cellular metabolism. The impact of various metal ions ($FeCl_3$, $MgSO_4 \cdot 6H_2O$, $ZnSO_4 \cdot 7H_2O$, $CuSO_4 \cdot 5H_2O$, $AgNO_3$, and $BaCl_2 \cdot 2H_2O$) on S. terrae growth was evaluated. $CuSO_4 \cdot 5H_2O$ supported the highest biomass production ($OD\ 0.77 \pm 0.03$), followed by $ZnSO_4 \cdot 7H_2O$ ($OD\ 0.65 \pm 0.02$) and $MgSO_4 \cdot 6H_2O$ ($OD\ 0.58 \pm 0.03$). In contrast, FeCl3 had the least effect (OD 0.26 ± 0.02). The positive influence of copper and zinc ions may be due to their role as cofactors for key enzymes involved in secondary metabolite biosynthesis. The low growth observed with $FeCl_3$ could be attributed to its potential toxicity at higher concentrations (Fig. 3f). Metal ions Mn2+, Cu2+, and NH4+were present in Streptomyces sp. B-PNG23 synthesis (23).

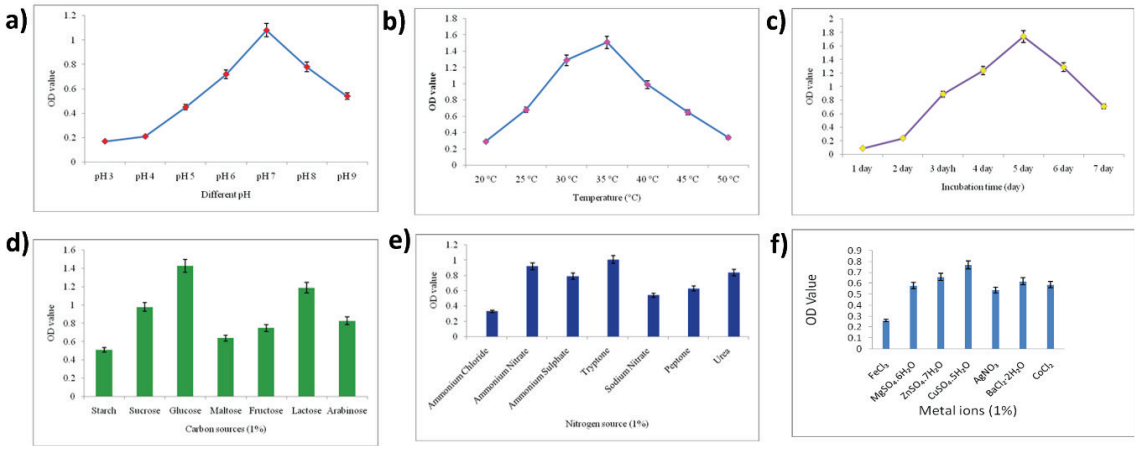

Figure 3: Effect of (a) pH, (b) temperature, (c) incubation time, (d) carbon source, (e) nitrogen source, and (f) metal ions on the growth of isolated S. terrae.

Antibiotic sensitivity test

S. terrae was sensitive to vancomycin, amikacin, and amoxicillin, with inhibition zones of 15.24 ± 0.31 mm, 18.42 ± 0.36 mm, and 14.18 ± 0.12 mm, respectively. However, it showed resistance to tetracycline, with a minimal inhibition zone of 3.15 ± 0.22 mm (Table 1). Sensitivity to vancomycin and amikacin suggests that S. terrae lacks resistance mechanisms against these antibiotics, making them effective for controlling its growth in laboratory settings. Resistance to tetracycline may be attributed to the presence of efflux pumps or enzymatic degradation mechanisms, which are common in Actinobacteria. These findings are consistent with those of previous studies showing that actinomycetes often exhibit multiple antibiotic resistances owing to their complex genetic makeup and exposure to diverse environmental conditions. The antibiotic sensitivity profile of S. terrae highlights its potential as a model organism for studying antibiotic resistance mechanisms in actinomycetes. Additionally, the sensitivity to vancomycin and amikacin suggests that these antibiotics can be used to selectively isolate S. terrae from mixed microbial communities. Antibiotic sensitivity against

ampicillin, penicillin, gentamycin, ciprofloxacin, and tetracycline in Staphylococcus aureus (24). In support of our study, Kotrbová et al. reported resistance to ampicillin, erythromycin, tetracycline, gentamycin, amoxicillin, and penicillin in Streptomyces spp. (25).

Table 1: Antibiotic sensitivity of S. terrae

S. No.	Antibiotic disc	Zone of inhibition (mm)
1	Vancomycin	15.24 ± 0.31
2	Tetracycline	3.15 ± 0.22
3	Amikasin	18.42 ± 0.36
4	Amoxicillin	14.18 ± 0.12

Antibacterial activity

The antibacterial activity of S. terrae against all tested pathogens demonstrated significant inhibition against Klebsiella oxytoca (9.16 ± 0.27 mm) and the lowest against Staphylococcus pyogenes (2.36 ± 0.11 mm). The inhibitory zones for Escherichia coli, Pseudomonas aeruginosa, and Proteus mirabilis were 5.24 ± 0.19 mm, 5.24 ± 0.19 mm, and 7.42 ± 0.34 mm, respectively (Table 2). The variation in the size of the inhibitory zones may be attributed to differences in the cell wall structure and resistance mechanisms of the pathogens. Gram-negative bacteria, such as Klebsiella oxytoca and Pseudomonas aeruginosa, were more susceptible to S. terrae metabolites, possibly because of the presence of bioactive compounds that disrupt their outer membrane. The antibacterial activity of S. terrae is likely due to the production of secondary metabolites, such as alkaloids, polyketides, and peptides, which interfere with bacterial cell wall synthesis, protein synthesis, and other essential cellular processes. These findings align with previous studies on actinomycetes, known for their ability to produce a wide range of bioactive compounds with antimicrobial properties. Bioactive compounds from Streptomonospora arabica VSM-25 have demonstrated antibacterial and antifungal activities (26). The concentration of the extract plays an important role in its antimicrobial activity. The higher the concentration of the extract, the higher the antimicrobial activity (27). In support of our study, Nofiani et al. reported Streptosporangium sp. antibacterial activity against bacteria such as S. mutant, E. coli, and P. aeruginosa (28).

Table 2: Antibacterial activity of S. terrae against pathogens

S. No.	Test organisms	Inhibition zone (mm)
1	Escherichia coli	5.24 ± 0.19
2	Staphylococcus pyogenes	2.36 ± 0.11
3	Pseudomonas aeruginosa	5.24 ± 0.19
4	Klebsiella oxytoca	9.16 ± 0.27
5	Proteus mirabilis	7.42 ± 0.34

Microbial fuel cells of oxidative fermentation test and measurement of the MFC reactor

The bioelectricity generation potential of S. terrae was evaluated using a double-chamber MFC with Cu and Zn electrodes. The MFC was inoculated with S. terrae biomass, and the voltage and current were monitored daily for seven days. A peak voltage of 1.204 mV was observed on the 5th day, indicating optimal metabolic activity and electron transfer efficiency of the MFC. The power output, calculated using the formula P=iV, reached its maximum during this period, demonstrating the ability of S. terrae to convert chemical energy from organic substrates into electrical energy. The voltage declined after the 5th day, likely due to substrate depletion or reduction in metabolic activity. The MFC performance highlights the potential of S. terrae as a biocatalyst for sustainable energy production, with applications in wastewater treatment and renewable energy generation. These findings align with those of previous studies on MFCs, emphasizing the importance of optimizing the operational parameters to enhance the bioelectricity output. Further research should focus on improving electrode materials, substrate utilization, and MFC design to maximize the energy efficiency of S. terrae-based systems, as the current declined from the seventh day (Fig.

4). Microbial fuel cells (MFC) are promising, eco-friendly, and emerging techniques. In this technique, microorganisms play an important role in the bioremediation of water pollutants while simultaneously generating electric current (29). MFCs are preferable to conventional wastewater treatment methods because they use microbial metabolic activities for energy generation during wastewater treatment instead of consuming energy (30). MFC designs to reduce the system's internal resistance, cost-effective electrode materials with high surface area, cheaper cation exchange membranes, modifications of the electrode material with nanomaterials (e.g., gold nanoparticles, nickel nanoparticles), and other physical (e.g., heat treatment of stainless-steel electrode) or chemical (nitric acid) modifications are among the amendments in MFCs.

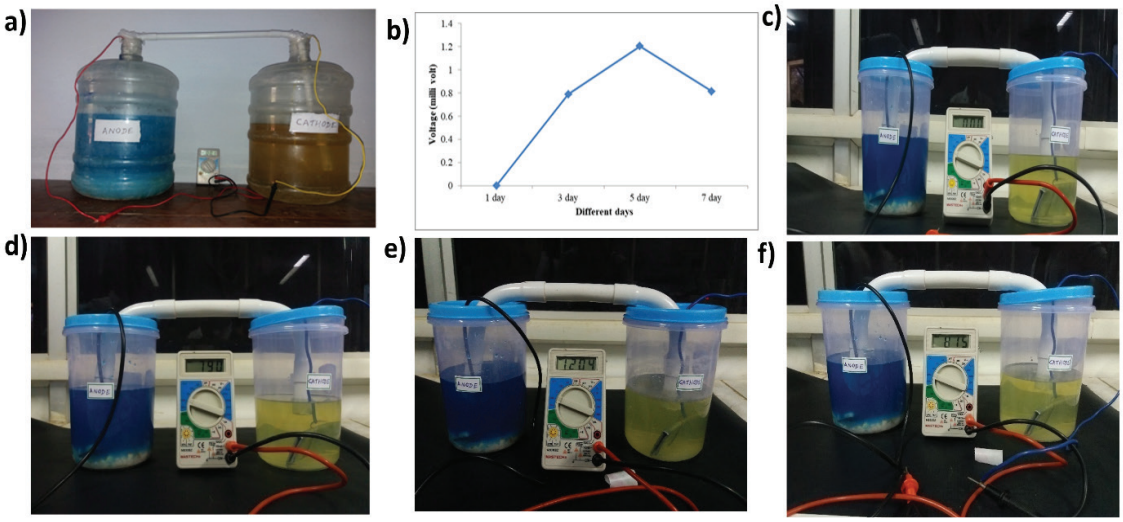

Figure 4: (a) Microbial fuel cell (MFC) setup for current generation. (b) Voltage vs. number of days produced by MFC. Open-circuit voltage of the cell at (c) Control (0 day), (d) 3rd day, (e) 5th day, and (f) 7th day.

FT-IR analysis

FT-IR spectroscopy was used to characterize the functional groups present in the secondary metabolites produced by S. terrae. The FT-IR spectra revealed distinct absorption peaks corresponding to various functional groups, including amines, alkenes, carboxyl groups, and aromatic compounds. A strong peak at 3062.75 cm^{-1} indicated C-H stretching vibrations, while peaks at 1664.45 cm^{-1} and 1540.05 cm^{-1} were attributed to C=C stretching (alkenes) and N-O asymmetric stretching (nitro compounds), respectively. The presence of hydroxyl groups was confirmed by a broad peak at 3444.63 cm^{-1}, and a medium peak at 1047.27 cm^{-1} suggested C-N stretching in aliphatic amines. Additionally, peaks at 1176.50 cm^{-1} (C-O stretching) and 1361.65 cm^{-1} (C-H rocking) indicate the presence of alcohols, carboxylic acids, and alkanes (Fig. 5). These findings align with previous studies on actinomycete metabolites, confirming the diverse bioactive potential of S. terrae. The FT-IR spectrum of the ethyl acetate extracts of G614 C1 revealed absorption at 3411 cm-1, indicating hydroxyl groups, absorption at 2856 and 2915 cm-1, indicating hydrocarbon chassis, and absorption at 1649 cm-1, indicating a double bond of a polygenic compound (31,32). The identification of these functional groups provides valuable insights into the chemical composition of secondary metabolites, highlighting their

potential for antimicrobial, anticancer, and other pharmacological applications.

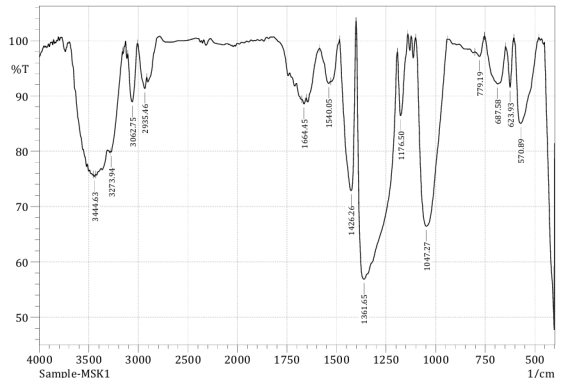

Fig. 5. FT-IR spectrum for isolated S. terrae

Conclusion

This study demonstrates the multifaceted potential of S. terrae as a valuable resource for both antibiotic production and sustainable bioelectricity generation. The optimization of growth conditions revealed that S. terrae thrives at neutral pH 7, moderate temperature (35°C), and glucose and tryptone as optimal carbon and nitrogen sources, respectively. The antibiotic sensitivity profile highlighted its resistance to tetracycline and sensitivity to vancomycin, amikacin, and amoxicillin. Its broad-spectrum antibacterial activity against pathogenic bacteria underscores its potential for combating antibiotic-resistant infections. Furthermore, the successful integration of S. terrae into the MFC demonstrated its ability to generate bioelectricity, with a peak voltage of 1.204 mV observed on the 5th day. These findings collectively emphasize the dual potential of S. terrae in addressing global challenges in healthcare and energy sustainability. By leveraging its bioactive metabolite production and bioelectrochemical capabilities, S. terrae offers a promising avenue for the development of novel antibiotics and renewable energy technologies. Future research should focus on scaling up production, optimizing MFC configurations, and exploring the full spectrum of bioactive compounds to unlock the untapped potential of this versatile Actinomycete species.

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Conflicts of Interest

The authors declare no conflicts of interest.

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