Building evidence for conservation globally

Journal of Threatened Taxa

Open Access

10.11609/jott.2025.17.6.27035-27170
www.threatenedtaxa.org

26 June 2025 (Online & Print)
17(6): 27035-27170
ISSN 0974-7907 (Online)
ISSN 0974-7893 (Print)

40 Years zoo reach Zoo Outreach Organisation

ISSN 0974-7907 (Online); ISSN 0974-7893 (Print)

Publisher
Wildlife Information Liaison Development Society
www.wild.zooreach.org

Host
Zoo Outreach Organization
www.zooreach.org

Srivari Illam, No. 61, Karthik Nagar, 10th Street, Saravanampatti, Coimbatore, Tamil Nadu 641035, India
Registered Office: 3A2 Varadarajulu Nagar, FCI Road, Ganapathy, Coimbatore, Tamil Nadu 641006, India
Ph: +91 9385339863 | www.threatenedtaxa.org
Email: sanjay@threatenedtaxa.org

For Focus, Scope, Aims, and Policies, visit https://threatenedtaxa.org/index.php/JoTT/aims_scope
For Article Submission Guidelines, visit https://threatenedtaxa.org/index.php/JoTT/about/submissions
For Policies against Scientific Misconduct, visit https://threatenedtaxa.org/index.php/JoTT/policies_various

continued on the back inside cover

Cover: A mesmerising Indian Luna moth *Actias selene* is dancing through the starry night (by Vincent van Gogh) moonlit sky, displaying its ballistic display of feather tail. Digital artwork by Vyshnavee Sneha Jaijar.

Journal of Threatened Taxa | www.threatenedtaxa.org | 26 June 2025 | 17(6): 27087–27097

ISSN 0974-7907 (Online) | ISSN 0974-7893 (Print)

https://doi.org/10.11609/jott.9565.17.6.27087-27097

#9565 | Received 18 December 2024 | Final received 27 February 2025 | Finally accepted 19 June 2025

OPEN ACCESS

ARTICLE

Collection and lipid analysis of marine unialgal cyanobacteria: a case study from the southeastern coast of India

Selvam Selvapriya [1] & **Sundaram Rajakumar** [2]

[1,2] Department of Marine Biotechnology, Bharathidasan University, Tiruchirappalli, Tamil Nadu 620024, India.
[1] priyaselvam1919@gmail.com, [2] srajakumar@bdu.ac.in (corresponding author)

Abstract: Cyanobacteria are capable of surviving in extreme environments such as rocky shorelines, drought, desiccation, osmotic stress, salinity stress, UV radiation, and nitrogen starvation. The study collects and analyse cyanobacterial samples from ponds, seashores, and salt pans along the southeastern coastline of Tamil Nadu—specifically from Mimisal, Thondi, Tuticorin, and Tiruchendur. The study involved the isolation and purification of samples using various techniques, including plating, cell disruption, and mechanical separation methods. Cultures were incubated at optimal temperature, photoperiod, and light intensity using artificial sea nutrient and blue-green (BG11) media. Samples were subjected to phototactic movement on 0.4% soft agar plates under both field and laboratory conditions for rapid isolation. Once visible filaments or single colonies were observed, unialgal cells were isolated using a micromanipulator, resulting in the collection of 17 cyanobacterial and three green algal strains. Identification was carried out to the genus level unless distinct species-level characteristics were evident, based on the morphological criteria described for Cyanophyta. Among the 20 strains screened, four marine microalgae exhibited lipid contents of 15% or higher and were classified as high lipid-yielding strains. These selected strains were further evaluated for functional group composition using Fourier Transform Infrared spectroscopy.

Keywords: 16S rRNA, BDUM19, BLAST, diversity, isolation, Lipid and FTIR, marine cyanobacteria, microalgae, physio-chemical, survey, *Synechococcus* sp.

Editor: R. Ravinesh, University of Kerala, Thiruvananthapuram, India.

Date of publication: 26 June 2025 (online & print)

Citation: Selvapriya, S. & S. Rajakumar (2025). Collection and lipid analysis of marine unialgal cyanobacteria: a case study from the southeastern coast of India. *Journal of Threatened Taxa* 17(6): 27087–27097. https://doi.org/10.11609/jott.9565.17.6.27087-27097

Funding: The authors would like to thank the funding resource from RUSA 2.0 the Ministry of Education (MoE) and the Government of Tamil Nadu and University Research Fellow (URF) – awarded university research fellowship for pursuance of Ph.D., in the Department of Marine Biotechnology, Bharathidasan University.

Competing interests: The authors declare no competing interests.

Author details: Selvam Selvapriya, research scholar, Department of Marine Biotechnology, Bharathidasan University, Tiruchirappalli, Tamil Nadu 620024, India. Dr. S. Rajakumar, Associate professor and dead, Department of Marine Biotechnology, Bharathidasan University, Tiruchirappalli, Tamil Nadu 620024, India.

Author contributions: SS—conceptualization, methodology, writing - original draft. SR—supervision, investigation, validation, writing – review, editing, visualization.

Acknowledgements: The authors acknowledge RUSA 2.0 the Ministry of Education (MoE) and the Government of Tamil Nadu and National Facility for Marine Cyanobacteria (NFMC) Govt.of India, for providing necessary laboratory facilities.

INTRODUCTION

Cyanobacteria are a diverse group of prokaryotes containing chlorophyll a and capable of performing oxygenic photosynthesis. They contribute substantially to global biological nitrogen fixation (Haselkor & Buikema 1992). Traditionally, cyanobacterial identification has relied on morphological characteristics, including the shape and size of trichomes, cell types, the size, and position of heterocysts & akinetes, and the planes of cell division (Rippka et al. 1979). Within the nostocalean genera, species differentiation is primarily based on the morphology of trichomes, heterocytes, and akinetes (Hindák 2000).

According to Garrity & Stanley (2001), cyanobacteria are classified into five taxonomic groups or subsections. The dichotomous key used for this classification is based on morphological criteria, including whether the organism is unicellular or quasi-multicellular (trichomatous), the mode of cell division (binary or multiple), and the presence or absence of baeocyte formation. Baeocytes are single-celled reproductive units formed through multiple fission. The baeocyte finally develops into a vegetative cell. Additionally, determine whether specialised cells such as akinetes and heterocysts are present or absent, whether there are any branches in the trichome and whether they are real or not (Chaurasia 2015). The modern taxonomic system of cyanobacteria involves morphological, physiological, biochemical, and genetic characterisations based on axenic strains (Stanier et al. 1971; Waterbury 2006).

Cyanobacteria can survive in extreme environments like rocky coasts, hot springs, dryness, dehydration stress, osmotic stress, salinity stress, UV stress, oxidative stress, heat & cold shock, anaerobiosis, and nitrogen deficiency (Sinha & Hader 1996). A vital component of the global nutrient cycle is cyanobacteria. By supplying other living things with carbon and nitrogen, their capacity to fix atmospheric CO_2 through photosynthesis, and N_2 through nitrogen fixation, sustains life on Earth. This highlights the essential function that cyanobacteria play in maintaining life on Earth by being essential to the marine food chain as well as the control of climate and nutrient levels (Sinha et al. 1995). Some cyanobacteria form heterocysts and can fix atmospheric nitrogen (Bonnet et al. 2010).

The distribution of cyanobacteria in the water is influenced by a number of factors, including competition, light, temperature, nutrients, symbiotic relationships, and predation. Understanding the interactions between these components will help us better understand how cyanobacteria impact marine ecosystems, including nitrogen cycle, primary production, and harmful algal blooms. Basic knowledge of ecological factors is important for understanding the ecology and biodiversity of cyanobacteria (Silambarasan et al. 2012). With this in mind, marine cyanobacteria were studied on seashore, and salt pan samples from the southeastern coast of Tamil Nadu, India. In the present study, cyanobacteria strains were collected from the Thondi, Mimisal, Tiruchendur, and Tuticorin regions. The isolated strains were purified, identified, cultured in the laboratory, and pure strains were deposited in the National Repository for Microalgae and Cyanobacteria - Marine (NRMC-M), Bharathidasan University

MATERIALS AND METHODS

Examination and sample collection of Marine Cyanobacteria

Samples of cyanobacteria were collected from ponds, shorelines, and salt pans along the southeastern coast of Tamil Nadu, including Thondi, Mimisal, Tiruchendur, and Tuticorin. The geographical coordinates of each sampling site were recorded. Specimens were collected using sterile forceps and stored in polyethene bags, and vials, following the method described by Thajuddin & Subramanian (2005).

Isolation, Purification and Maintenance of Marine Cyanobacteria

Unialgal cyanobacterial isolates were obtained using a combination of isolation techniques developed during this study. All samples were serially diluted, vortexed, and plated onto soft agar (0.8% concentration) using a sterile micropipette. The plates were then incubated under continuous illumination to promote the clear spread of unialgal cyanobacterial filaments. Individual filaments were carefully isolated using sterile needles with the aid of a microscope-assisted micromanipulator. The resulting unialgal strains were preserved in both liquid and solid agar media at the NRMC(M) using ASN III growth medium, maintained at a pH of 7.5 ± 0.2. Liquid cultures (100 ml volume) were maintained in triplicate and subcultured every 15 days. Strain purity was assessed every 45 days. Culture flasks were manually agitated every 24 hours and inspected for any physical contamination. For long-term preservation, ASN III agar medium was dispensed into rubber-sealed glass bottles. All culture flasks and agar bottles were stored in a culture room maintained at 25 ± 2°C, under white fluorescent light at an intensity of 20 µmol photonsm $^{-2}$ s $^{-2}$.

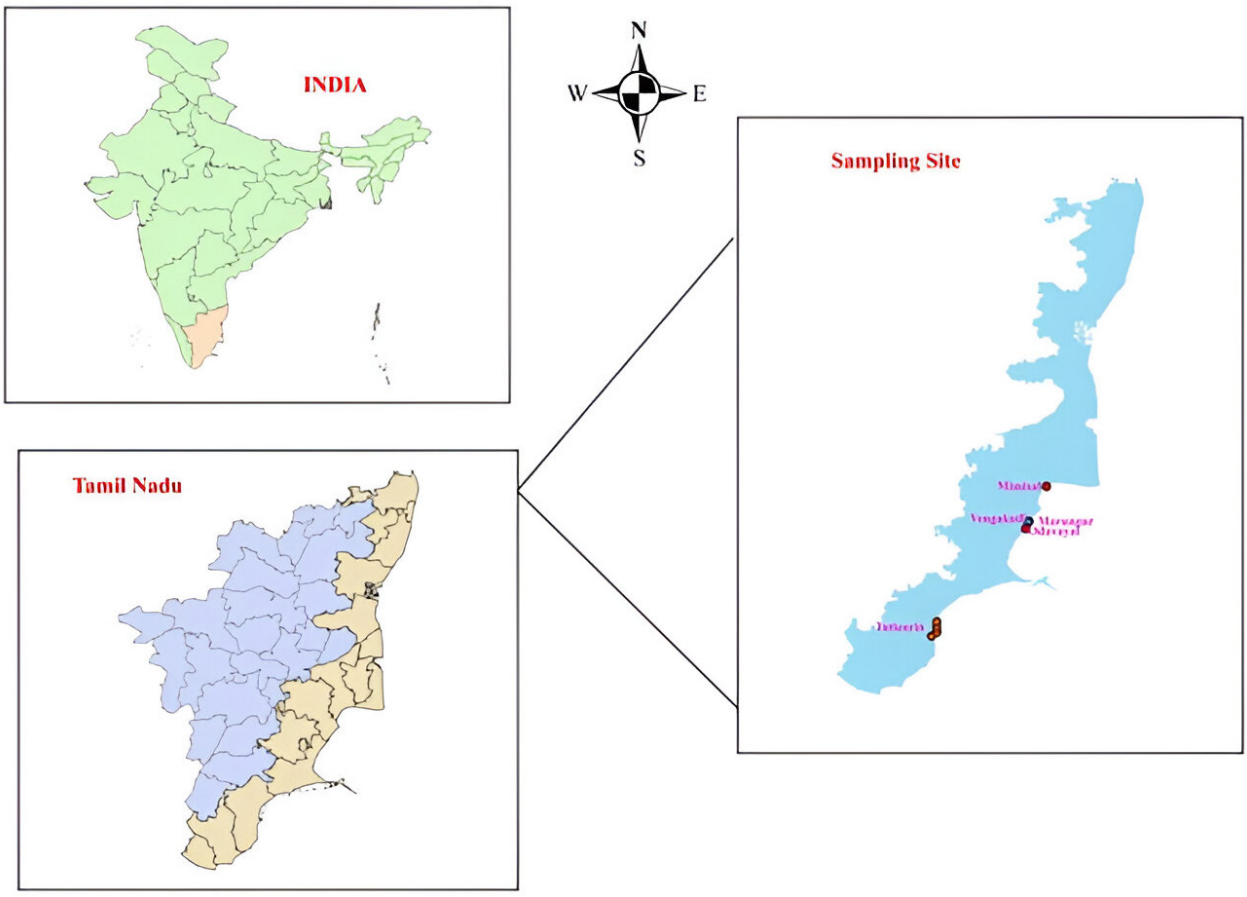

Figure 1. Sampling location of marine cyanobacteria from southeastern coast of Tamil Nadu, India.

Morphological Observation and Identification Marine Cyanobacteria

Morphological documentation of an unialgal axenic cyanobacterial isolates was carried out using an inverted light microscope (Leica DMI 3000B). Identification was performed up to the genus level, unless distinct species-level characteristics were evident. Taxonomic identification was based on morphological features following the classification system of Cyanophyta (Desikachary 1959).

Growth and Maintenance of Marine Cyanobacteria

Isolated marine cyanobacterial cultures were grown in ASN III medium (Rippka et al. 1979) in Erlenmeyer flasks, under continuous illumination using white fluorescent light at an intensity of 1500 lux. Cultures were maintained at 25 ± 2°C in a controlled culture facility and preserved at the NRMC (M).

Analysis of physicochemical parameters

The physico-chemical parameters like temperature, pH & salinity, Calcium, Magnesium, and Ammonia were estimated by the standard method- APHA 1998 (Rice et al. 2012). Temperature was measured with a mercury thermometer with an accuracy of 0.5°C. The pH was measured using a calibrated pH pen with an accuracy of 0.1. Salinity was measured with a hand-held refractometer (Strickland & Parsons 1972). The pH was measured by using a calibrated pH pen (pHep, Hanna Instruments, Mauritius Ltd., Portugal) with an accuracy of ± 0.1.

Molecular characterisation of cyanobacteria

Molecular characterisation of the selected strains was carried out using the partial gene sequence of 16S rRNA.

Extraction of DNA and 16S rRNA gene amplification by PCR of Marine Cyanobacteria

Total genomic DNA was extracted from selected strains using the xanthogenate nucleic acid isolation method described by Tillett & Neilan (2000). To obtain the complete sequence of the 16S rRNA gene, PCR amplification was performed in three regions using

different primer sets. One such amplified region utilised the forward primer 16S A2F (AGAGTTTGATCCTGGCTCAG) and the reverse primer S17R (GGCTACCTTGTTACGAC) as described by Seo & Yokota (2003), specifically for marine cyanobacterial isolates. Primers were synthesised by Eurofins Genomics India Pvt. Ltd. (Bangalore). PCR reactions were carried out in a final volume of 50 µl containing 1 µl (10 pmol) of each primer, 1 µl of 1.25 mM dNTPs, 1 µl (50 ng) of cyanobacterial DNA, and 1 unit of DreamTaq DNA polymerase (Thermo Scientific, USA), using the buffer provided by the manufacturer. Amplification was performed in a DNA thermal cycler (Applied Biosystems, CA, USA). The thermal cycling conditions for 16S rRNA gene amplification were as follows: an initial denaturation at 95°C for seven minutes; followed by 30 cycles of denaturation at 95°C for one minute, annealing at 58°C for one minute, and extension at 72°C for one minute; with a final extension step at 72°C for 10 minutes. Following PCR, 10 µl of the amplified product was resolved on a 1.2% low-melting-point agarose gel (Sigma, USA), stained with ethidium bromide, and visualised under UV transillumination using a Bio-Rad documentation system.

Sequencing of 16S rRNA gene

The nucleotide sequences of the PCR amplicons were determined using a Mastercycler® pro S (Eppendorf) and an ABI 3130 genetic analyser (Applied Biosystems) available at Genurem Bioscience LLP, Bangalore. Sequence identity was established by comparing the obtained sequences with reference sequences available in public databases using the BLAST algorithm (Altschul et al. 1997).

Bioprospecting of marine cyanobacteria for lipid production

A total of 20 marine cyanobacteria, new isolates obtained through this study, were screened for bioprospecting of lipids. The strains represented unicellular and filamentous forms. The selected strains were grown in Erlenmeyer flasks with continuous illumination using white fluorescent light at an intensity of 1,500 lux at 25 ± 2 °C in a controlled culture room and lipid content was estimated gravimetrically at the end of the tenth day. All the extractions were carried out in triplicates.

Extraction of total lipids from Marine Cyanobacteria

A known mass of the cyanobacterial sample was obtained by centrifugation at 5,000 × g for 10 minutes. The resulting pellet was rinsed twice with distilled water and dried in a hot air oven at 50°C. A known weight of the dried biomass was then pulverised using a mortar and pestle for the extraction of total lipids, employing a binary solvent mixture of chloroform and methanol in a 2:1 ratio. Lipid extraction from the pellet was carried out repeatedly until complete extraction was achieved. The pooled extract was centrifuged at 5,000 × g for 10 minutes, and the supernatant was transferred to a fresh tube. To remove water-soluble impurities, one-third volume of 1% NaCl solution was added to the supernatant, and vortexed thoroughly. To eliminate residual moisture, the extract was passed through a column packed with sodium sulphate crystals. The resultant filtrate was dried using a rotary evaporator (EVATORII), and the total lipid yield was calculated gravimetrically following the method of Bligh & Dyer (1959).

FTIR analysis of lipids from marine cyanobacteria

Crude total lipid isolated from the chosen strain was homogenized using a mortar and pestle to conform to the lipid functionality. 150 mg of the mixture was analysedusing a Spectrum 8900 IR spectrometer (Shimadzu, Japan). The following were the scanning settings: spectral range of 4000–400 cm^{-1}, resolution of 32 scans cm^{-1}.

RESULTS AND DISCUSSION

Identification and Isolation of Cyanobacteria from Marine Environments

Floating and substrate-attached cyanobacteria were carefully located and isolated using sterile forceps, following the method of Nikam et al. (2010). A total of 50 samples were collected during the survey from the coastal regions of Mimisal, Thondi, Tiruchendur, and Tuticorin (Figure 1). Microalgae belonging to seven different families, Chlorellaceae, Dunaliellaceae, Merismopediaceae, Synechococcaceae, Pseudanabaenaceae, Spirulinaceae, and Oscillatoriaceae have been found in the seawater ecosystems of Rameswaram, and Tuticorin Districts. Each species has its unique size and shape, which allows it to be placed in different families. Each species has its importance in the ecosystem in which it lives. Standardised taxonomic keys were used to identify the transformed unialgal marine cyanobacteria species based on their morphological characteristics (Desikachary 1959). All the strains deposited in the repository have been updated in the germplasm database (www.nfmc.bdu.ac.in), given unique identification

numbers, and geographically tagged (Table 1).

Identification of Cyanobacteria

The identified unialgal species of cyanobacteria belong to seven genera (Table 1). These marine cyanobacteria families all contribute to primary production, nitrogen fixation, and nutrient cycling, all of which are essential to their respective habitats. Comprehending these families facilitates the recognition of their ecological importance, possible economic worth (e.g., *Spirulina*), and contributions to global biological processes. The majority of the species have been found in the families Chlorellaceae and Dunaliellaceae. These families include microalgae species such as *Dunaliella* sp. BDUC001, *Dunaliella* sp. BDUT10, and *Chlorella* sp. BDUC003. The cyanobacteria species were classified as *Aphanocapsa* sp. BDUM42 belongs to the family Merismopediaceae, *Synechococcus* sp. BDUM19 belongs to Synechococcaceae, *Pseudanabaena* sp. BDUM034 belongs to Pseudanabaenaceae, *Spirulina* sp. BDUT005 classified under the family Spirulinaceae. Also, the family Oscillatoriaceae, including species such as *Osicillatoria* sp. BDUM4, *Phormidium* sp BDUD059, *Phormidium* sp. BDUD072, *Phormidium* sp. BDUT80, *Phomidium* sp. BDUC002, *Phormidium* sp. BDUD008, *Phormidium* sp. BDUD058, *Phormidium* sp. BDUM116, *Phormidium* sp. BDUT003, *Phormidium* sp. BDUT02, *Phormidium* sp. BDUT1, *Phormidium* sp. BDUC002, *Phormidium* sp. BDUC003, *Phormidium* sp. BDUC80 were shown in Image 1.

Analysis of physico-chemical variables

The details of the environmental parameters prevailing in the seashore and saltpan areas of Mimisal,

Table 1. Habitat and geographical origin of marine cyanobacteria and microalgae from southeastern coast of Tamil Nadu, India.

	Place of collection	Habitat	GPS	Organisms
1	Mimisal	A dense collection of marine algae from the ocean is known as the dark green floating mat	9.909° N 79.144° E	*Pseudanabaena* sp. BDUM03
2	Odavayal	Stagnant sea water	9.909° N 79.144° E	*Aphanocapsa* sp. BDUM42
3	Mimisal	Marine cyanobacteria generate a dark green floating mat.	10.278° N 79.319° E	*Synechococcus* sp. BDUM19
4	Marungur (Thondi)	Salt evaporation pond	9.909° N 79.135° E	*Osicillatoria* sp. BDUM4
5	Odavayal (Thondi)	Salt evaporation pond	9.832° N 79.089° E	*Phormidium* sp. BDUM7
6	Mimisal	Sea shore	9.909° N 79.144° E	*Phormidium* sp. BDUD059
7	Marungur (Thondi)	Salt evaporation pond	9.909° N 79.135° E	*Phormidium* sp. BDUD072
8	Vengakudi (Mimisal)	Salt evaporation pond	9.903° N 79.129° E	*Phormidium* sp. BDUD008
9	Marungur (Thondi)	Formation of mats in the backwater sea	9.832° N 79.089° E	*Phormidium* sp. BDUD058
10	Mimisal	Sea shore	9.909° N 79.144° E	*Phormidium* sp. BDUM11669
11	Tuticorin	The saltpan's dark green floating mat	8.843° N 79.160° E	*Phormidium* sp. BDUT003
12	Tuticorin	A jelly formation in saltpan's corner	8.843° N 79.160° E	*Spirulina* sp. BDUT005
13	Tuticorin	Inside the PVC pipe-salt pan, greenish	8.787° N 78.159° E	*Dunaliella* sp. BDUT10
14	Tuticorin	Saltpan	8.843° N 79.160° E	*Phormidium* sp. BDUT02
15	Tuticorin	Stagnant water-saltpan	8.843° N 79.160° E	*Phormidium* sp. BDUT1
16	Tiruchendur	Mud that is dark green in the saltpan	8.693° N 79.104° E	*Chlorella* sp. BDUC003
17	Tiruchendur	Floating on the surface of the rock like green	8.693° N 79.104° E	*Phormidium* sp. BDUC003
18	Tiruchendur	Mud that is blue-green in the saltpan region	8.734° N 78.159° E	*Dunaliella* sp. BDUC001
19	Tiruchendur	Yellowish-green foam that floats in the form of cyanobacteria	8.693° N 79.104° E	*Phormidium* sp. BDUC002
20	Tiruchendur	Saltpan foam with dark green mud	8.734° N 78.159° E	*Phormidium* sp. BDUC80

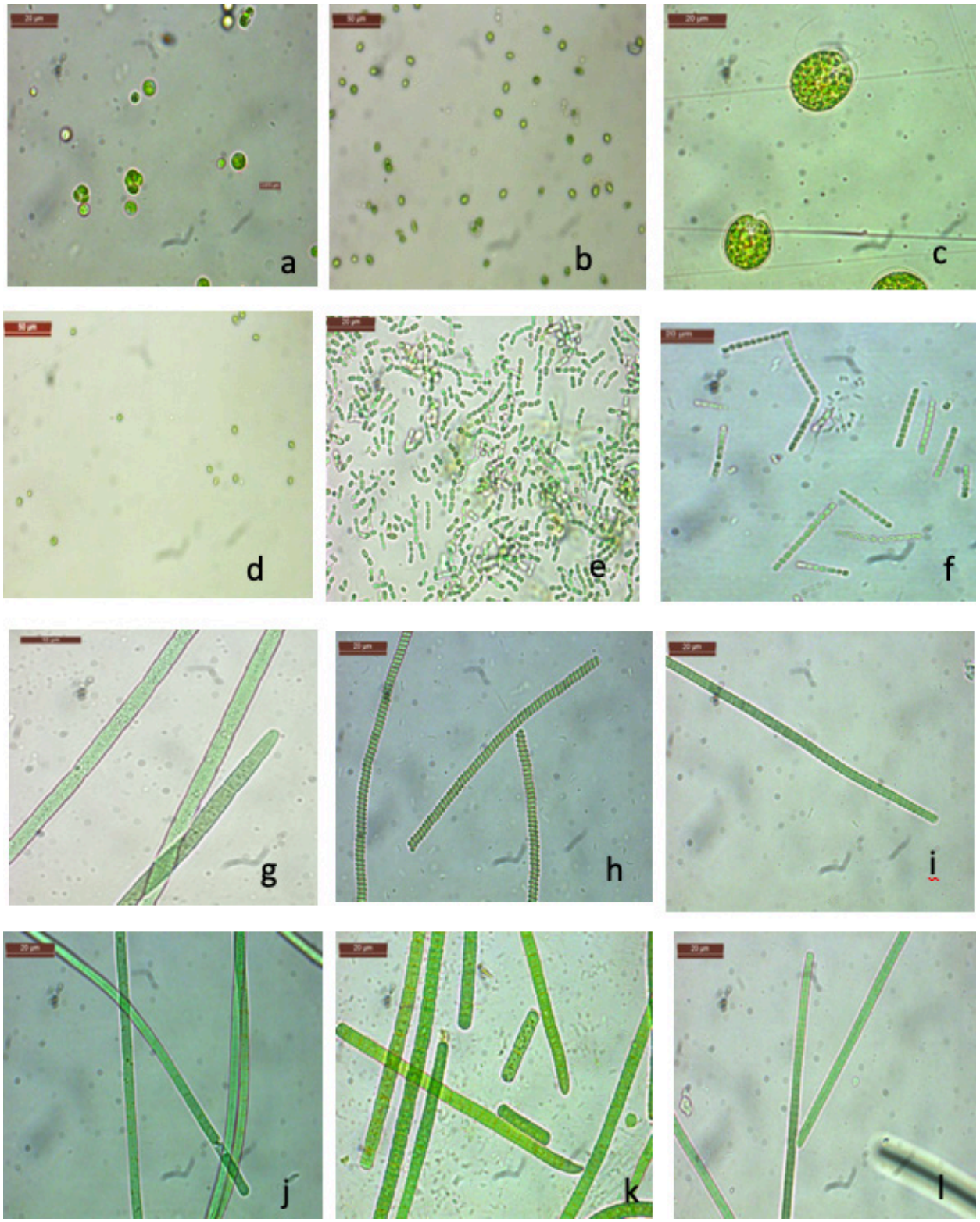

Image 1. Microphotographs of Marine unialgal cyanobacteria from different marine regimes of Rameshwaram and Tuticorin Districts. a—*Aphanocapsa* sp. BDUM42 | b—*Dunaliella* sp. BDUC001 | c—*Dunaliella* sp. BDUT10 | d—*Chlorella* sp. BDUC003 | e—*Synechococcus* sp. BDUM19 | f—*Pseudanabaena* sp. BDUM034 | g—*Osicillatoria* sp. BDUM4 | h—*Spirulina* sp. BDUT005 | i—*Phormidium* sp. BDUD059 | j—*Phormidium* sp. BDUD072 | k—*Phormidium* sp. BDUT80 | l—*Phomidium* sp. BDUC002. © Selvam Selvapriya.

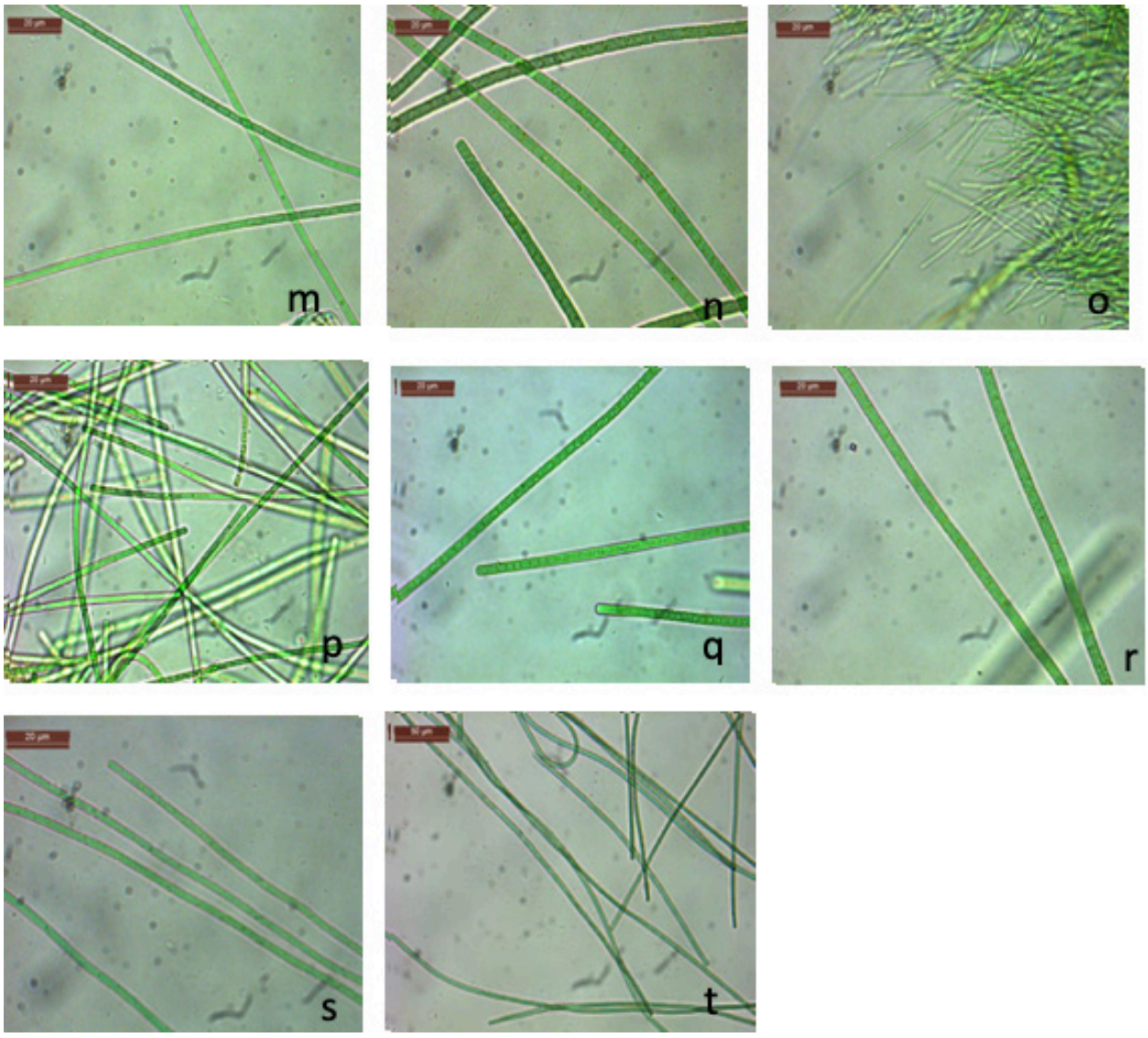

Image 1. cont. Microphotographs of Marine unialgal cyanobacteria from different marine regimes of Rameshwaram and Tuticorin Districts. m—*Phormidium* sp. BDUD008 | n—*Phormidium* sp. BDUD058 | o—*Phormidium* sp. BDUM116 | p—*Phormidium* sp. BDUC003 | q—*Phormidium* sp. BDUC003 | r—*Phormidium* sp. BDUT1 | s—*Phormidium* sp. BDUT02 | t—*Phormidium* sp. BDUM7. © Selvam Selvapriya.

Thondi, Tuticorin, and Tiruchendur are presented in Table 2. The physico-chemical characteristics of these sites revealed significant spatial variation, reflecting the ecological diversity of these coastal regimes. Temperature ranged from a minimum of 29 ± 2°C in Tuticorin to a maximum of 36 ± 2°C in Tiruchendur. Such thermal variation plays a key role in regulating cyanobacterial metabolism, enzymatic activity, and growth dynamics. Salinity also exhibited substantial variation, with the highest range recorded in Mimisal (40–47 PPT), followed by Thondi (25–50 PPT), while Tuticorin showed a more stable, and lower value (30 PPT). Salinity influences osmotic regulation and species distribution, especially in hypersaline habitats where only well-adapted cyanobacteria can thrive.

The pH levels ranged from slightly neutral in Tuticorin (7.0) to highly alkaline in Mimisal (up to 11.0), indicating strong buffering capacities, and intense biological activity in some areas. Alkaline environments are particularly conducive to the growth of specific cyanobacterial taxa such as *Spirulina* and *Oscillatoria*. Calcium concentrations varied between 298 and 454 mg L^{-1}, with the highest level recorded in Tuticorin. Similarly, magnesium levels ranged from 267 mg L^{-1} in Mimisal to 362 mg L^{-1} in Tuticorin. Both values are within acceptable environmental limits. Magnesium, often paired with calcium in natural waters, is a critical component for chlorophyll synthesis and serves as a

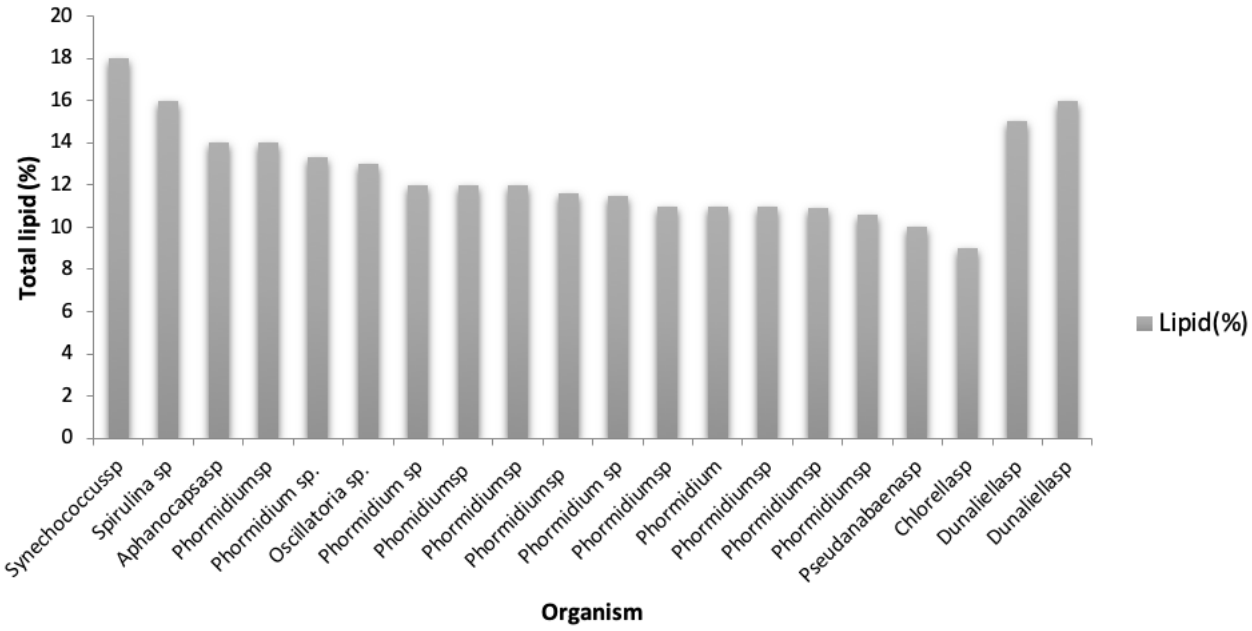

Figure 2. Lipid production of marine unicellular cyanobacteria.

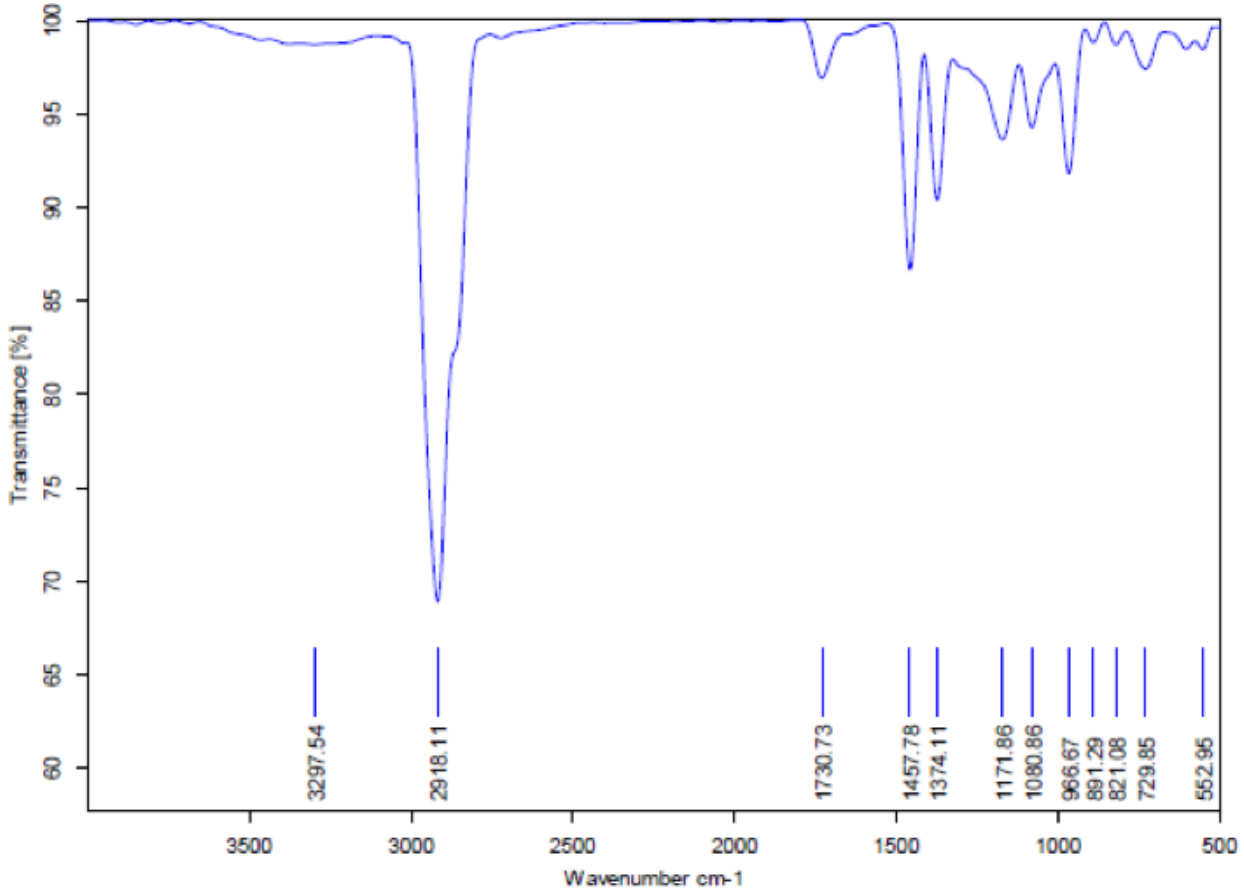

Figure 3. FTIR analysis of cyanobacterial strains for lipid production.

Table 2. Physico-chemical parameters of seashore and saltpan areas—Mimisal, Thondi, Tuticorinand, and Tirchendur.

Parameters	Mimisal	Thondi	Tuticorin	Tirchendur
Temperature	31±2 ^{0}C	35±2 ^{0}C	29±2 ^{0}C	36±2 ^{0}C
Salinity (PPT)	40–47	25–50	30	28–33
pH	7.3–11	7.3–10	7–8	8–9
Calcium (mg L^{-1})	343	423	454	298
Magnesium (mg L^{-1})	267	351	362	287
Chloride (g L^{-1})	23	27	19	17
Ammonia (mg L^{-1})	0.05	0.03	0.02	0.01

limiting factor for the growth of marine microalgae and cyanobacteria.

Chloride concentrations were found to be 23, 27, 19, and 17 g L^{-1} in Mimisal, Thondi, Tuticorin, and Tiruchendur respectively, aligning with standard marine values. Chloride ions are ecologically significant in maintaining the ionic balance and regulating salinity in marine ecosystems. Ammonia levels across all sites were within prescribed environmental limits, ranging from 0.01 mg L^{-1} in Tiruchendur to 0.05 mg L^{-1} in Mimisal. Although present in low concentrations, ammonia provides an important nitrogen source for cyanobacteria, especially under nutrient-depleted conditions.

Molecular identification of Marine Cyanobacteria

An organism's genetic makeup defines a species' characteristics. Therefore, the smaller ribosomal subunit, 16S rRNA, is well known for conserved regions, and the genomic DNA extraction process was performed for marine cyanobacteria in which a prospective strain demonstrated strong band formation following agarose gel electrophoresis, suggesting the high genomic DNA content. Thus, it is thought that one of the helpful tools for molecularly characterising the specified isolates is the amplification of such a segment of genomic DNA. The current results were in line with operational taxonomic groups based on 16S rRNA genes that are part of the Synechococcaceae family (Taton et al. 2006). Moreover, strains in the genus *Synechococcus* exhibit significant divergence and are dispersed widely over the cyanobacteria evolutionary tree (Turner et al. 1999). 16S rRNA gene sequences from a potential strain were annotated, trimmed for high-quality sequences, and subjected to a BLAST search analysis (http://www.ncbi.nlm.nih.gov/BLAST). Individual accession numbers have been allocated to the sequences, which were submitted to the NCBI with Accession Number OP237032

Identification of Lipid-Producing Marine Cyanobacterial Isolates

Twenty marine cyanobacteria were screened for lipid accumulation as part of a bioprospecting initiative aimed at discovering new bio-based resources. (Figure 2). Four marine cyanobacteria possessed a maximum lipid of 15 % and above, and were designated as high lipid yielders. *Synechococcus* sp. BDUM19, a unicellular marine cyanobacterium that does not experience stress, produced 18% of the high lipid output species.

The lipid content analysis of cyanobacterial and microalgal isolates revealed considerable interspecific variation, with total lipid percentages ranging from approximately 10% to 18% of dry biomass (Figure 2). *Synechococcus* sp. exhibited the highest lipid content (~18%), followed closely by *Dunaliella* sp. and *Spirulina* sp., which recorded lipid levels around 16% and 15%, respectively. These results highlight the potential of these taxa as promising candidates for lipid-based biotechnological applications, particularly in biofuel production. *Aphanocapsa* sp. also showed substantial lipid accumulation (~14%), reinforcing its utility as a bioresource. In contrast, *Chlorella* sp. demonstrated the lowest lipid yield (~10%), suggesting limited application in high-lipid-demand processes unless optimised. Among the multiple isolates of *Phormidium* sp., lipid levels remained relatively consistent, ranging between 11% and 14%, indicating a stable but moderate lipid-producing capacity within the genus. Notably, *Pseudanabaena* sp. and *Oscillatoria* sp. also recorded moderate lipid levels. The presence of high lipid-yielding strains across diverse genera underscores the significance of strain-specific screening in selecting suitable candidates for bioenergy and value-added product development.

Lipid Profiling of Marine Cyanobacteria using FTIR Spectroscopy

The strains were assessed for the functional group analysis using FTIR spectroscopy. The Lipid of the tested strain pertained to major functional groups namely carboxyl, hydroxyl, and amine groups. Spectroscopy of the lipid for *Synechococcus* sp BDUM19 showed a peak at 2918 - Stretching of > CH 2 (asymmetric) and COO- which indicates the functional group of lipid (Figure 3).

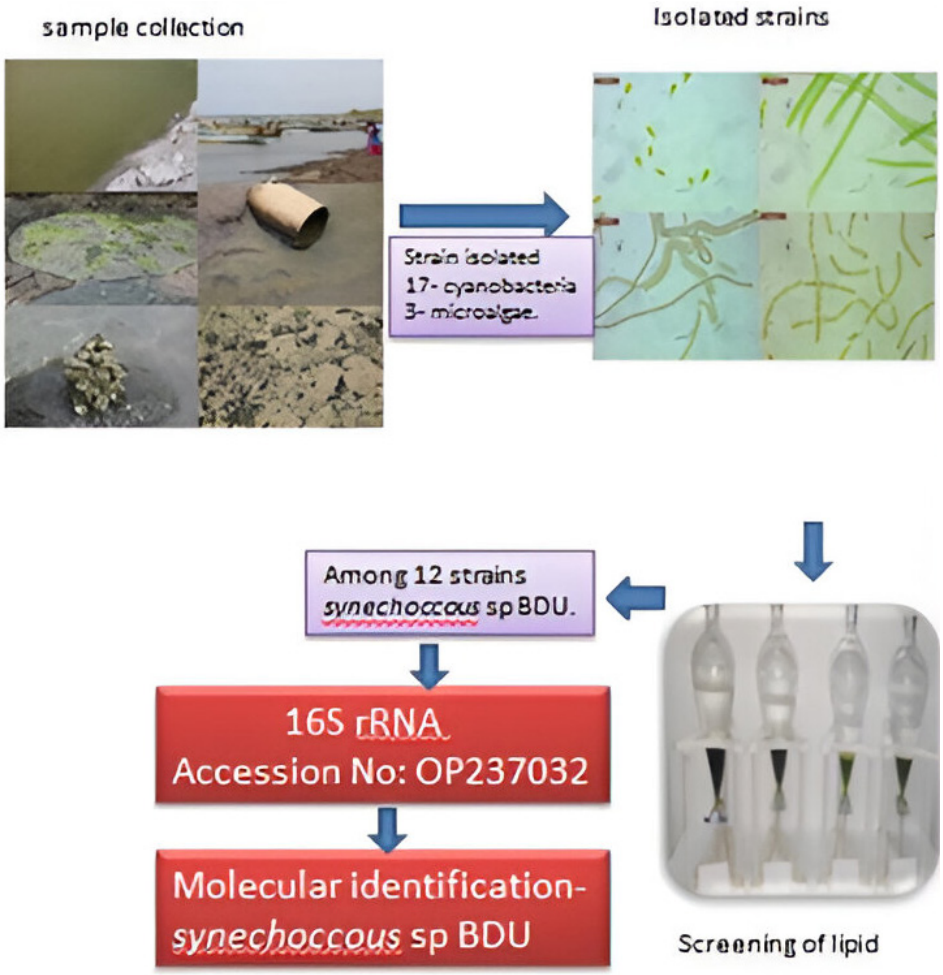

Image 2. Marine cyanobacteria collection and lipid analysis (southeastern coast of India).

CONCLUSION

In the present study, it was observed that the diverse ecosystems of coastal and estuarine regions support varying levels of cyanobacterial diversity. These environments, characterised by dynamic physicochemical conditions, offer distinct ecological niches that influence species composition and abundance. Optimal levels of sunlight, temperature, salinity, humidity, and nutrient availability, particularly nitrogen & phosphorus, create favourable conditions for the proliferation of cyanobacteria. The interplay of these environmental factors contributes significantly to the spatial and temporal variability in cyanobacterial distribution across the studied sites. In each sample (Image 2), over 20 cyanobacteria species and isolates with various morphologies were identified. Morphological identification of cyanobacteria showed that both filamentous and unicellular growth were observed. The sequences were submitted to NCBI, and individual accession numbers were assigned with accession number OP237032. The selected strain is assessed for the functional group analysis using FTIR spectroscopy pertaining to major functional groups, namely carboxyl, hydroxyl, and amine groups. These groups are essential for cyanobacterial activity and lipid synthesis. The amine group is necessary for the metabolism of proteins and nitrogen, the carboxyl group aids in the formation of fatty acids, and the hydroxyl group maintains the stability of compounds. It is noteworthy that the most productive lipid producers are unicellular types.

REFERENCES

Altschul, S.F., T.L. Madden, A.A. Schäffer, J. Zhang, Z. Zhang, W. Miller & D.J. Lipman (1997). Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25(17): 3389–3402.

Bligh, E.G. & W.J. Dyer (1959). A rapid method of total lipid extraction and purification. *Canadian Journal of Biochemistry and Physiology* 37(8): 911–917.

Bonnet, S., E.A. Webb, C. Panzeca, D.M. Karl, D.G. Capone & S.A.S. Wilhelmy (2010). Vitamin B12 excretion by cultures of the marine cyanobacteria Crocosphaera and Synechococcus. *Limnology and Oceanography* 55(5): 1959–1964.

Chaurasia, A. (2015). Cyanobacterial biodiversity and associated ecosystem services: introduction to the special issue. *Biodiversity and Conservation* 24(4): 707–710. https://doi.org/10.1007/s10531-015-0908-6

Desikachary, T.V. (1959). *Cyanophyta*. Indian Council of Agricultural Research. New Delhi, 686 pp.

Garrity, G.M. & J.T. Stanley (2001). *Bergey's Manual® of Systematic Bacteriology: Volume 1 - The Archaea and the Deeply Branching and Phototrophic Bacteria*. Springer, New York, 931 pp.

Haselkorn, R. & W.J. Buikema (1992). Nitrogen fixation in cyanobacteria. Biological Nitrogen Fixation, 166–190 pp.

Hindák, F. (2000). Morphological variation of four planktic nostocalean cyanophytes–members of the genus *Aphanizomenon* or *Anabaena*? *Hydrobiologia* 438: 107–116.

Nikam, T.D., J.N. Nehul, Y.R. Gahile, B.K. Auti, M.L. Ahire, K.M. Nitnaware, B. Joshi & N. Jawali (2010). Cyanobacterial diversity in Western Ghats region of Maharashtra, India. *Bioremediation, Biodiversity and Bioavailability* 7(1): 70–80.

Rice, E.W., L. Bridgewater & A.P.H. Association (2012). *Standard Methods for the Examination of Water and Wastewater, Vol. 10*. American Public Health Association, Washington, DC.

Seo, P.S. & A. Yokota (2003). The phylogenetic relationships of cyanobacteria inferred from 16S rRNA, gyrB, rpoC1 and rpoD1 gene sequences. *The Journal of General and Applied Microbiology* 49(3): 191–203.

Silambarasan, G., T. Ramanathan & K. Kathiresan (2012). Diversity of marine cyanobacteria from three mangrove environment in Tamil Nadu Coast, south east coast of India. *Current Research Journal of Biological Sciences* 4(3): 235–238.

Sinha, R.P. & D.P. Hader (1996). Invited Review Photobiology and Ecophysiology of Rice Field Cyanobacteria. *Photochemistry and Photobiology* 64(6): 887–896.

Sinha, R.P., H.D. Kumar, A. Kumar & D.P. Häder (1995). Effects of UV-B irradiation on growth, survival, pigmentation and nitrogen metabolism enzymes in cyanobacteria. *Acta Protozoologica* 34: 187.

Stanier, R.Y., R. Kunisawa, M. Mandel & G. Cohen-Bazire (1971). Purification and properties of unicellular blue-green algae (order Chroococcales). *Bacteriological Reviews* 35(2): 171–205.

Strickland, J.D.H. & T.R. Parsons (1972). *A Practical Handbook of Seawater Analysis*. Fisheries Research Board of Canada, 310 pp.

Taton, A., S. Grubisic, D. Ertz, D.A. Hodgson, R. Piccardi, N. Biondi, M.R. Tredici, M. Mainini, D. Losi & F. Marinelli (2006). Polyphasic study of Antarctic cyanobacterial strains 1. *Journal of Phycology* 42(6): 1257–1270.

Thajuddin, N. & G. Subramanian (2005). Cyanobacterial biodiversity and potential applications in biotechnology. *Current Science* 89(1): 47–57.

Tillett, D. & B.A. Neilan (2000). Xanthogenate nucleic acid isolation from cultured and environmental cyanobacteria. *Journal of Phycology* 36(1): 251–258.

Turner, S., K.M. Pryer, V.P.W. Miao & J.D. Palmer (1999). Investigating deep phylogenetic relationships among cyanobacteria and plastids by small subunit rRNA sequence analysis 1. *Journal of Eukaryotic Microbiology* 46(4): 327–338.

Wang, W., Y. Liu, D. Li, C. Hu & B. Rao (2009). Feasibility of cyanobacterial inoculation for biological soil crusts formation in desert area. *Soil Biology and Biochemistry* 41(5): 926–929.

Waterbury, J.B. (2006). The cyanobacteria—isolation, purification and identification. *The Prokaryotes* 4: 1053–1073.

Journal of Threatened Taxa is indexed/abstracted in Bibliography of Systematic Mycology, Biological Abstracts, BIOSIS Previews, CAB Abstracts, EBSCO, Google Scholar, Index Copernicus, Index Fungorum, JournalSeek, National Academy of Agricultural Sciences, NewJour, OCLC WorldCat, SCOPUS, Stanford University Libraries, Virtual Library of Biology, Zoological Records.

NAAS rating (India) 5.64

Print copies of the Journal are available at cost. Write to:
The Managing Editor, JoTT,
c/o Wildlife Information Liaison Development Society,
3A2 Varadarajulu Nagar, FCI Road, Ganapathy, Coimbatore,
Tamil Nadu 641006, India
ravi@threatenedtaxa.org & ravi@zooreach.org

www.threatenedtaxa.org

ISSN 0974-7907 (Online) | ISSN 0974-7893 (Print)

June 2025 | Vol. 17 | No. 6 | Pages: 27035–27170
Date of Publication: 26 June 2025 (Online & Print)
DOI: 10.11609/jott.2025.17.6.27035-27170

Articles

Communications

Review

Short Communications

Publisher & Host

Threatened Taxa