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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

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Cover: Digital illustration of *Impatiens chamchumroonii* in Krita by Dupati Poojitha.

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COMMUNICATION

Analysis revealed minuscule DNA sequence data availability for Indian marine macroalgal diversity

Digvijay Singh Yadav [1], Aswin Alichen [2] & Vaibhav A. Mantri [3]

[1,2,3] Applied Phycology and Biotechnology Division, CSIR- Central Salt and Marine Chemicals Research Institute, Gijubhai Badheka Marg, Bhavnagar, Gujarat 364002, India.
[3] Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh 201002, India.
[1] digvijaysingh.yadav@gmail.com, [2] aswinalichan12@gmail.com, [3] vaibhav.csmcri@csir.res.in (corresponding author)

Abstract: Seaweeds hold immense economic potential due to multifarious applications in pharmaceuticals and everyday products. India's 11,099 km coastline harbours a rich diversity of seaweeds in the Indian Ocean. Identifying seaweeds based on morphology is challenging due to high phenotypic and reproductive plasticity, so DNA barcoding is often used. This initiative marks the first national effort to compile relevant scientific information on DNA barcoding of Indian marine macroalgae, the current-status of knowledge and the scope for study. Despite decades of molecular research on Indian macroalgae, the resulting sequence data remain scattered across online repositories without systematic integration or quality assessment. The study is a comprehensive analysis of current barcode coverage of Indian seaweeds available on GenBank. With 207 unique sequences, only 11% of total Indian macroalgal diversity has been studied yet. The priority gaps that demonstrate direct benefits such as accurate taxonomic identification, cultivation strain authentication, and assessment of invasive species and surveillance of algal blooms, and indirect benefits like policy support, conservation planning, reference libraries for eDNA, training, and capacity building were identified. We consider that DNA barcoding at the national level would not only help in the sustainable commercial utilisation of economically important species but also in the conservation of endemic taxa. This is identified as a major research gap. It needs to be addressed through concentrated efforts by national research organisations and universities, ascertaining the availability of adequate infrastructure, and focused efforts on capacity building. A comprehensive and collaborative research program is urgently needed at the Pan-India level.

Keywords: AlgaeBase, aquaculture, bioprospecting, conservation, DNA barcoding, GenBank, genetic resources, molecular systematics, species identification, taxonomy.

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Author details: Digvijay Singh Yadav has PhD in Biosciences with expertise in molecular taxonomy and pharmaceutical application of seaweeds. Currently working as a postdoctoral researcher at the CSIR-Central Salt and Marine Chemicals Research Institute (CSMCRI) in India, his work focuses on seaweed-propagule transport, biostimulant application, and large-scale seaweed cultivation along the Indian coast. Aswin Alichen has completed his post graduation and is a young and motivated researcher with strong interest in seaweed biology and seaweed-based climate changes studies. The research work in the current publication was carried out during his dissertation work at CSMCRI, India. Vaibhav A. Mantri is the chief principal scientist at CSMCRI, Dr. Mantri advances year-round Indian seaweed farming through improved cultivation techniques. His research focuses on strain enhancement, artificial seedling protocols to minimize epiphytic infestation, and developing viable farming methods by analyzing environmental determinants.

Author contributions: DSY—investigation, formal analysis, methodology, validation, visualization, data curation, manuscript preparation. AA—investigation, formal analysis, methodology, validation, visualization, data curation. VAM—conceptualization, methodology, project administration, supervision, writing – review & editing, funding acquisition. All authors provided critical feedback and helped shape the research analysis and manuscript.

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INTRODUCTION

Marine macroalgae are gaining importance globally due to their multifarious applications in commodity products being used in day-to-day life. They are the only source of polysaccharides such as, ulvan, agar, alginates, mannitol, and carrageen having niche applications in biomedical, and pharmaceutical domains (Pereira & Cotas 2024). Studying the marine macro-algal biodiversity is pivotal for understanding the health of marine ecosystems, searching for potent bioactive compounds, and finding latent alternatives for food, feed, and fuels (Rajauria et al. 2015). Conventional morphology-based identification often yields inaccuracies due to phenotypic plasticity coupled with lack of specialized taxonomic expertise. Therefore, DNA barcoding offers a universal and standardized approach including for seaweeds (Hebert et al. 2003; Kowalska et al. 2019). This technique is less susceptible to errors caused by phenotypic variation, life stage, reproductive age, and does not require specialized traditional taxonomy knowledge. Further, it is also important to learn evolutionary lineages, discover novel species, and identify commercially valuable species (Saunders 2005; Chac & Thinh 2023). DNA barcoding provides legally defensible scientific evidence-based lab-to-market species identification, ensuring traceability and linking product authenticity to performance outcomes. For example, use of DNA barcoding for identifying novel seaweed species (Lagourgue et al. 2022), uncover genetic groups and morphospecies of *Saccharina* sp. (Saunders and McDevit 2014), or correctly identify *Bulung sangu* (*Gracilaria* sp.) to decide specific and correct cultivation methods to meet falling supply to high demands (Wirawan et al. 2021). For seaweeds such as *Gracilaria dura* known for high gel strength (> 1,900 g cm^{-2} at 1%) if misidentified with other *Gracilaria* spp. may lead to performance failure and economic loss (Mantri et al. 2022a). Further DNA barcode information may be used to track and stop illegal trade of endangered species (Mishra et al. 2017).

India is globally recognized as a megadiverse country, with 7–8% of the world's recognized flora and fauna and ranks fourth among the 34 biodiversity hotspots across the 17 megadiverse countries of the world (Mantri et al. 2020). Indian coastline stretches over 11,099 km and the highest number of marine macro-algal taxa have been reported from India compared to countries neighbouring the Indian Ocean (Sahoo 2001). Despite decades of research involving molecular identification of species, the online sequence data for Indian seaweeds is scarce, for example DBIndalgae, first centralized database effort in India to systematically compile information on native marine algae (Bhushan et al. 2016). However, repositories like DIDI (Diatoms image database of India), and Algal Database exist to address the challenges and discrepancies in identifying diatoms and freshwater microalgae respectively (Sharma et al. 2013; Pandey et al. 2016). The studies encompassing systematic integration or quality assessment are highly desired to ensure accuracy and reliability. To our knowledge, this is the first attempt to comprehensively analyse the online available sequence data for Indian seaweeds based on the sequences available in GenBank. The current study aims to provide a comprehensive, scientific inventory of publicly available DNA sequence database of Indian seaweeds. Such analyses would establish an integrated, quality-assured national baseline by consolidating decades of fragmented DNA sequence records. Standardized markers and metadata would enhance comparability across national laboratories, strengthening research and policy synthesis practices. Molecular identification would enhance value-chain growth and product traceability, along with accurate detection of potential invasive, harmful bloom-forming taxa thereby reinforcing biosecurity. Further this effort would be also crucial in identification of rare and threatened taxa, those need immediate conservation attention. Thus, we emphasize the urgent need for continued research, including marker-based sequencing efforts and standardized methodologies to enhance our knowledge base and unlock the full potential of Indian macroalgal biodiversity.

METHODS

DNA-barcode sequences for Indian macroalgal species reported in the checklist of Indian marine algae by Rao & Gupta (2015) were obtained from the GenBank database (GenBank 2025). The search terms used were: "India" + "Chlorophyta", "India" + "Rhodophyta", "India" + "Phaeophyta", and "India" + "Ochrophyta" for all the data available throughout the database, irrespective of submission date range. All records for Phaeophyta were combinedly presented under Ochrophyta throughout the manuscript. For each record, accession, organism name, marker/gene, publication, and collection location were extracted. The results were then verified against Web of Science, Scopus, and PubMed databases to confirm species name, marker usage, and sampling locations. Entries without peer-reviewed published record, geographical locations, and the duplicate entries were removed and not considered for the analysis. The accepted taxonomic nomenclature was confirmed from AlgaeBase (Guiry & Guiry 2024). The cleaned data of collected sequences were then categorized based on phylum, class, and primer used to generate the DNA barcodes. The dataset thus obtained was used for the analysis against the latest checklist by Rao & Gupta (2015). The checklist represents 865 macro-algal species from India, including 212 green algae from 46 genera, 211 brown algae from 50 genera, and 442 red algae in 138 genera.

RESULTS AND DISCUSSION

A total of 207 unique sequences were obtained for Indian macro-algal species (Table 1) across chloroplast (*rbc*L, *tuf*A, UPA, *atp*B, *psb*A), mitochondria (COI-5P, cox), nucleus (ITS), and ribosome (LSU rDNA, 23S rRNA,18S rRNA) (Figure 1) loci from GenBank establishing a unified baseline for national-scale assessment and reuse. The study found that only 11% of the India marine macro algae were documented from India. The data revealed that in Chlorophyta, only nine genera containing 33 species from six unique orders have been amplified based on chloroplast (39), mitochondrial (5), nuclear (22), and ribosomal (16) gene markers. *Ulva sapora* and *U. paschima* are now recognized as synonyms of *Ulva tepida* and *Caulerpa peltata* is synonymised with *Caulerpa chemnitzia* (Guiry & Guiry 2024). For Ochrophyta, 13 species of six genera were identified from three unique orders, with 55% of the generated sequences from chloroplast, 25% from mitochondria, and 10% each from nuclear and ribosomal genes. Moreover, 49 species of 22 genera from 10 unique orders and four varieties have been studied for Rhodophyta. *Gracilaria verrucosa* has now been renamed *Gracilariopsis longissima* (Guiry & Guiry 2024). Results revealed an uneven focus on molecular studies, with only 19% of green, 12% of brown, and 16% of red algae species globally. This depends largely on availability and due to more focused attention towards economically important seaweeds that are given priority. The observed seaweeds species of genus *Kappaphycus*, *Gracilaria*, *Porphyra*, *Sargassum*, *Turbinaria, Padina* are cultivated at scale for high value compound extraction (carrageenan, agar, alginates, pigments) and to be used as food (*Ulva and Caulerpa* species). Further, *Laurencia*, *Acanthophora*, *Caulerpa*, *Bryopsis* were studied for their bioactive properties due to presence of halogenated and terpenoid metabolites. At the genus level, it is only nine of the 46 reported green algal genera (20%), six out of 50 brown algal genera (12%), and 22 of the 138 reported red algal genera (16%) were reported from India. Further, among the 11 molecular markers that were investigated *rbc*L is the most studied marker (81 sequences), while *atp*B is the least (only one sequence) investigated marker for Indian marine macro algae (Figure 1). An effective DNA barcode couples sufficient interspecific sequence variation and ease of amplification across diverse taxa

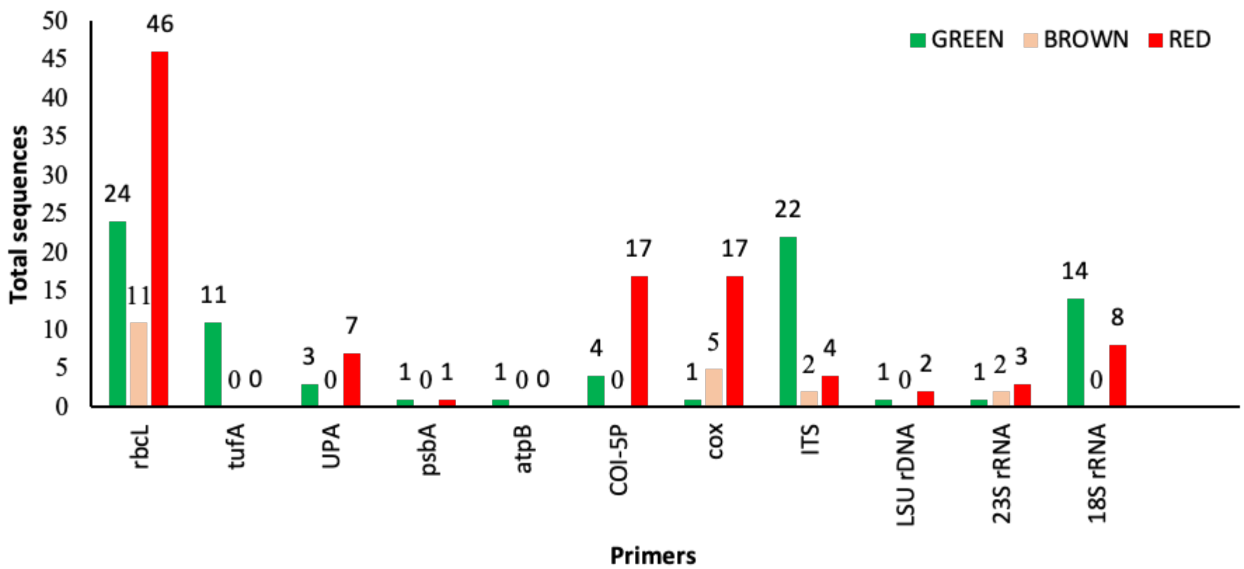

Figure 1. Marker-wise distribution of publicly available DNA barcode sequences for Indian marine macroalgae, showing counts per locus for Green (Chlorophyta), Brown (Ochrophyta), and Red (Rhodophyta) seaweeds.

Table 1. Marker-wise distribution of publicly available DNA barcode sequences from GenBank for Indian marine macroalgae by phylum, class, order and taxonomically accepted scientific names of seaweeds from India.

Phylum	Class	Order	Scientific Name	Primers
Chlorophyta	Ulvophyceae	Bryopsidales	*Bryopsis* sp.	*rbc*L
			Caulerpa racemosa var. *lamourouxii*	ITS
			Caulerpa agardhii	*rbc*L, 18S rRNA
			Caulerpa fergusonii	ITS
			Caulerpa mexicana var. *pluriseriata*	*tuf*A
			Caulerpa mexicana.	*rbc*L, 18S rRNA, *tuf*A, ITS
			Caulerpa microphysa	*rbc*L, 18S rRNA, *tuf*A, ITS
			Caulerpa peltata (*C. chemnitzia*)	*rbc*L, 18S rRNA, *tuf*A, ITS
			Caulerpa racemosa	*rbc*L, 18S rRNA, *tuf*A, ITS
			Caulerpa scalpelliformis	*rbc*L, 18S rRNA, *tuf*A, ITS
			Caulerpa serrulata	*rbc*L, 18S rRNA, *tuf*A, ITS
			Caulerpa sertularioides	*rbc*L, 18S rRNA, *tuf*A, ITS
			Caulerpa taxifolia	*rbc*L, 18S rRNA, *tuf*A, ITS
			Caulerpa veravalensis	*rbc*L, 18S rRNA, *tuf*A, LSU rDNA
			Caulerpa verticillata	*rbc*L, 18S rRNA, *tuf*A, ITS
		Cladophorales	*Chaetomorpha antennina*	*rbc*L
			Cladophora goaensis	ITS
		Dasycladales	*Acetabularia jalakanyakae*	18S rRNA
		Ulvales	*Ulva chaugulei*	*rbc*L, ITS
			Ulva compressa	*rbc*L, COI-5P, UPA
			Caulerpa chemnitzia	*rbc*L
			Ulva flexuosa	*rbc*L, COI-5P, UPA
			Ulva intestinalis	*rbc*L, ITS, cox
			Ulva lactuca	*rbc*L, 18S rRNA, ITS
			Ulva ohnoi	*rbc*L, ITS
			Ulva paschima (*U. tepida*)	*rbc*L, COI-5P, UPA
			Ulva reticulata	*rbc*L, ITS
			Ulva sapora (*U. tepida*)	ITS, *atp*B, 23S rRNA
			Ulva uniseriata	ITS
			Ulvella leptochaete	*rbc*L, ITS, COI-5P
			Ulvella sp.	*rbc*L, ITS
	Ulvophyceae	Ulotrichales	*Gayralia brasiliensis*	ITS
	Chlorodendrophyceae	Chlorodendrales	*Tetraselmis indica*	18S rRNA
Ochrophyta	Phaeophyceae	Ectocarpales	*Chnoospora implexa*	*rbc*L, cox
			Chnoospora sp.	*rbc*L, cox
		Dictyotales	*Dictyota bartayresiana*	*rbc*L
			Dictyota dichotoma	*rbc*L
			Padina tetrastromatica	*rbc*L
		Fucales	*Sargassum aquifolium*	23S rRNA
			Sargassum linearifolium	*rbc*L
			Sargassum plagiophyllum	23S rRNA
			Sargassum polycystum	*rbc*L
			Sargassum swartzii	*rbc*L
			Sargassum tenerrimum	*rbc*L
			Sargassum zhangii	ITS, cox
			Turbinaria ornata	ITS, cox
			Anthophycus longifolius	*rbc*L
			Anthophycus sp.	*rbc*L, cox

Phylum	Class	Order	Scientific Name	Primers
Rhodophyta	Bangiophyceae	Bangiales	*Phycocalidia acanthophora* var. *robusta*	*rbc*L, COI-5P
			Phycocalidia sukshma	*rbc*L, COI-5P
			Phycocalidia vietnamensis	*rbc*L, COI-5P
			Porphyra kanyakumariensis	*rbc*L, COI-5P
			Porphyra tenera	*rbc*L
			Porphyra yamadae	*rbc*L, cox
			Porphyra yezoensis	*rbc*L
			Pyropia acanthophora var. *robusta*	*rbc*L, cox
			Pyropia vietnamensis	cox
	Florideophyceae	Batrachospermales	*Lemanea manipurensis*	*rbc*L
			Sirodotia assamica	*rbc*L, COI-5P
			Sheathia assamica	*rbc*L
		Ceramiales	*Caloglossa fluviatilis*	*rbc*L
			Palisada perforata	*rbc*L
			Caloglossa beccarii	*rbc*L, LSU rDNA
			Acanthophora spicifera	*rbc*L
			Laurencia thyrsifera	*rbc*L, ITS, COI-5P
Rhodophyta	Florideophyceae	Ceramiales	*Herposiphonia akidoglossa*	*rbc*L, COI-5P, *psb*A
			Spyridia hypnoides	*rbc*L, UPA, cox, LSU rDNA
		Corallinales	*Jania rubens*	*rbc*L
		Gelidiales	*Gelidiella acerosa*	*rbc*L, COI-5P
			Gelidiella indica	*rbc*L, COI-5P, cox
		Gigartinales	*Hypnea bullata*	*rbc*L, COI-5P, UPA
			Hypnea indica	*rbc*L, COI-5P, UPA
			Hypnea musciformis	*rbc*L
			Hypnea nidifica	*rbc*L, COI-5P, UPA, cox
			Hypnea nigrescens	*rbc*L, COI-5P, UPA
			Hypnea spinella	*rbc*L, COI-5P, UPA
			Hypnea valentiae	*rbc*L, ITS
			Kappaphycus alvarezii	*rbc*L, ITS, COI-5P, UPA, cox
			Sarconema filiforme	*rbc*L, COI-5P, cox
		Gracilariales	*Gracilaria corticata*	*rbc*L, ITS, COI-5P, cox
			Gracilaria corticata var. *corticata*	*rbcL,*18s RNA, cox
			Gracilaria dura	*rbc*L, 18s RNA, cox
			Gracilaria corticata var. *cylindrica*	*rbc*L, 18s RNA, cox
			Gracilaria debilis	*rbc*L, 18s RNA, cox
			Gracilaria edulis	23S rRNA
			Gracilaria fergusonii	23S rRNA
			Gracilaria foliifera	*rbc*L, 18s RNA, cox
			Gracilaria gracilis	*rbc*L, 18s RNA, cox
			Gracilaria salicornia	*rbc*L
			Gracilaria textorii	*rbc*L, 18s RNA, cox
			Gracilaria verrucosa (*Gracilariopsis longissima*)	*rbc*L, 23S rRNA
			Gracilariopsis lemaneiformis	*rbc*L, 18s RNA, cox
			Hydropuntia edulis	*rbc*L
		Halymeniales	*Grateloupia catenata*	*rbc*L
			Grateloupia orientalis	*rbc*L
			Grateloupia sp.	*rbc*L
		Nemaliales	*Liagora albicans*	*rbc*L

(Hollingsworth et al. 2009). Based on assessments of recoverability, sequence quality, and levels of species discrimination, a 2-loci combination of *rbc*L+matK as the plant barcode is recommended to provide a universal framework for the routine use of DNA sequence data to identify specimens and contribute toward the discovery of overlooked species of land plants (Leliaert et al. 2012). Because land plants evolved from green algal ancestors, the use of *rbc*L succeeded for seaweed DNA barcoding, as its conserved priming sites and informative variation support dependable amplification and species discrimination. The species delineation in marine macro-algal taxa poses a considerable challenge due to high morphological, anatomical, and reproductive plasticity. Nevertheless, taxonomic concepts in this group are fast evolving globally with the advent of DNA barcoding techniques. This is the first national effort to compile relevant scientific information on DNA barcoding pertaining to Indian marine macro-algae, which was scattered and difficult to access. The analysis revealed minuscule DNA sequence data availability.

Seaweeds offer socio-economic benefits to coastal communities through aquaculture and represent a valuable, yet underexplored resource (Mantri et al. 2020). The seaweed aquaculture industry is valued at USD 14 billion globally, producing 34.7 million tonnes of wet weight annually (FAO 2022) encompassing 51.3% of the global aquaculture industry with 6.2% annual growth (Duarte et al. 2022), but India contributes only 0.01% of the cultivated seaweeds, indicating a colossal gap (Mantri et al. 2022b). The lack of DNA sequence data significantly hinders our ability to understand the full spectrum of seaweed biodiversity range (endemic, exotic, and migratory species), abundance (dominant, rare, vulnerable, and endangered species), ecological roles, and correct taxonomic placement of Indian macro-algal species. We consider, DNA barcoding data at the national level would not only help us in the sustainable commercial utilisation of economically important species (Rao & Mantri 2006) but also in the conservation of endemic taxa (Rathod et al. 2023). This is identified as a major research gap. It needs to be addressed through concentrated efforts by national research organizations and universities, ascertaining the availability of adequate infrastructure, and focused efforts on capacity building (Mantri et al. 2020). However, the reliance on public-domain with heterogenous quality, incomplete metadata, and marker bias may limit resolution for certain clades and addressing these gaps would require coordinated national sampling, sequencing efforts, and capacity building.

The results provide first national current coverage of barcodes for Indian seaweed species, marker bias, and the availability of miniscule molecular data compared to the huge biodiversity. This calls for a comprehensive and collaborative research program urgently needed at the Pan-India level. India is investing large amounts of money in seaweed farming and value-chain development, and dependable species authentication underpins quality, traceability of high value products (Mantri et al. 2022a). Early detection of invasive species, surveillance of harmful algae, and identifying species at risk would aid in strengthening coastal biosecurity, select germplasm banking, risk management, and conservation and policy formation (Armstrong & Ball 2005; Hofmann et al. 2025). Multi-gene and method-integrated barcoding frameworks further improve resolution for difficult groups, enhancing surveillance sensitivity and reliability. This efficiency compounds benefits across ecology, systematics, and bioprospecting, where barcoding underpins access to novel bioactives and authentic species-level insights.

Data availability

The datasets generated during and/or analysed during the current study are available from the corresponding author upon reasonable request.

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