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Molecular data demonstrate the occurrence of *Compsopogon caeruleus* (Compsopogonophyceae, Rhodophyta) in Bahia state, Brazil

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Key words:
- Brazilian northeast
- COI-5P
- Compsopogononales
- *rbc*L
- red algae

Abstract
The freshwater red macroalga C*ompsopogon caeruleus* is ubiquitously distributed in tropical and subtropical regions and has been reported in many Brazilian states. Here, we report the first record of this species in the state of Bahia, constituting the third record of this species in the northeast region. This population was found on an oyster farm in the Graciosa Quilombola Fishing Community, Taperoá, Bahia, Brazil. We conducted a detailed morphological assessment and analyzed of the sequences of the molecular markers COI-5P and *rbc*L.

Palavras-chave:
- nordeste brasileiro
- COI-5P
- Compsopogononales
- *rbc*L
- algas vermelhas

Resumo
Embora seja ubiquamente distribuída em regiões tropicais e subtropicais, e seja relatada para muitos estados brasileiros, a macroalga vermelha de água doce C*ompsopogon caeruleus* é relatada pela primeira vez para o estado da Bahia, constituindo a terceira citação para a região Nordeste. A população foi encontrada em uma fazenda de ostras na Comunidade de Pesca Quilombola Graciosa, Taperoá, Bahia, Brasil. Neste estudo, descrevemos sua morfologia em detalhes, corroborando com análises das sequências dos marcadores moleculares COI-5P e *rbc*L.

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Introduction

The freshwater macroalgae *Compsopogon caeruleus* (Balbis *ex* C.Agardh) Montagne (1846:154) (Compsopogonophyceae, Rhodophyta) is widely distributed in tropical and subtropical regions (Oliveira Filho & Pereira 1973; South & Skelton 2002; Liu & Wang 2004; Ratha *et al*. 2007; Sherwood *et al*. 2010; Kitayana 2011; Bautista & Necchi Junior 2014; Vis & Necchi Junior 2021). The species has even been reported in temperate regions (Nichols 1964; Chapman & Cameron 1967; Žáková *et al*. 2013; Zaburlín *et al*. 2019; Vis & Necchi Junior 2021), where it is often considered an invasive species (Žáková *et al*. 2013; Zaburlín *et al*. 2019).

Compsopogon caeruleus is well adapted to adverse environmental conditions, including aquariums and artificial lakes, natural water bodies affected by the discharge of industrial effluents (Szymanska & Krupinska 1983; Scott *et al*. 1988; Scott & Broadwater 1989; Stoyneva *et al*. 2006; Žáková *et al*. 2013; Bautista & Necchi Junior 2014),

and water discharge regions that are used to cool power plants (Chapman & Cameron 1967).

Advancements in morphological taxonomic studies and, subsequently, the emergence of molecular taxonomy have resulted in the consolidation of most *Compsopogon* taxa, with 19 heterotypic synonyms now included in *C. caeruleus* (Guiry 2022). This has expanded its global distribution, demonstrating its remarkable phenotypic plasticity and adaptability. Molecular studies have revealed that although *C. caeruleus* populations are geographically isolated, they exhibit low genetic diversity (Necchi Junior *et al.* 2013; Nan *et al.* 2016; Zaburlín *et al.* 2019).

According to Flora e Funga do Brasil 2025 (continuously updated), *C. caeruleus* is documented from the north to the south of Brazil, in the states of Amazonas, Pará, Maranhão, Espírito Santo, Rio de Janeiro, São Paulo, Paraná, and Rio Grande do Sul; Necchi Junior *et al.* (2013) also mentioned its presence in the state of Sergipe. However, the species has not been confirmed in the state of Bahia. Here, we report the first documented occurrence of *C. caeruleus* in Bahia and provide morphological and molecular analyses.

Materials and Methods

Sample collection

A population of *Compsopogon caeruleus* was discovered growing in great abundance on an estuarine oyster farm in Graciosa, a community of quilombola fishermen (descendants of enslaved people), in the municipality of Taperoá, Bahia, Brazil (13°28′46.26″S, 39°05′34.50″W). The estuary is surrounded by mangroves, and the land is occupied by extensive palm oil plantations.

The highest occurrence of algae occurred in autumn 2022, the region's rainiest period, when local oyster farmers recorded salinities ranging from approximately 8 at low tide to 24 at high tide. The algae were growing in the oyster farming lanterns in dense populations, harming cultivation because of the weight of the floating structures.

Sampling was conducted in July 2022, and the collected material was preserved in 70% alcohol. The material was subsequently used for morphological and molecular analyses. A voucher specimen was deposited in the Herbarium Alexandre Leal Costa (ALCB) at the Federal University of Bahia, Brazil (Tab. 1).

Morphological analysis

Aspects of external and internal morphology were analyzed using a stereomicroscope MoticTM-SMZ-168 Series (Hong Kong, China), and further microscopic analyses were conducted under an optical microscope (Olympus-CX 31, São Paulo, SP, Brazil), coupled to a digital camera (Motic-Motican 3.0 MP). The images were analyzed using Motic software (Images Plus 2.0 ML). The analyses were conducted based on the observation of the filaments and cuts made with the aid of steel blades. Minimum and maximum measurements were taken for morphometric characteristics from a set of 10 measurements for each analyzed structure.

Molecular analysis

Total DNA was extracted after grinding in liquid nitrogen using the NucleoSpin© Plant II-Macherey-Nagel kit (Bethlehem, PA, USA), following the manufacturer's instructions. For polymerase chain reaction (PCR), the *rbc*L marker was amplified using three overlapping pairs of primers: F*rbc*LS-R492a, F492a-R1150a, and F993-R*rbc*S (Freshwater & Rueness 1994; Cassano 2009). The COI-5P marker was amplified using the primer pair GAZF1-GAZR1 (Saunders 2005). For PCR amplification, two GoTaq kits were used following the manufacturer's instructions: Flexi DNA Polymerase Kit (Promega, Madison, WI, USA) and G2 Hot Start Polymerase Kit (Promega); the final volume of the reaction was 25 μL. As a way of solving problems in the amplification, bovine serum albumin (0.5 μL) or magnesium chloride (1.5 μL at 25 mM) were added to the PCR solution, always maintaining the final volume at 25 μL. For *rbc*L, the amplification cycle involved an initial denaturation step at 94 °C for 4 min, followed by 35 cycles of 1 min at 94 °C, 1 min at 45 °C, and 1 min 30 s at 72 °C with a final 10 min extension cycle at 72 °C. For COI-5P, the amplification involved an initial denaturation step at 94 °C for 5 min, followed by 34 cycles of 30 s at 94 °C, 1 min at 45 °C, and 2 min at 72 °C with a final 7 min extension cycle at 72 °C. The reactions were performed using a Techne TC-330 thermocycler (Ramsey, MN, USA). All PCR products were analyzed via electrophoresis on 0.7% agarose gel and stained with Gel Loading Buffer GelRed™ (Biotium) to check product size. PCR products were purified using the PureLinkTM PCR Purification Kit (Invitrogen, Carlsbad, CA, USA) following the manufacturer's instructions.

Purified amplicons for both markers were sequenced in both directions using the same PCR primers mentioned above, and the BigDye Terminator Cycle Sequencing Ready Reaction kit (Applied Biosystems, Foster City, CA, USA) on an ABI PRISM 3130DNA Genetic Analyzer (Applied Biosystems) using 40 cycles of 10 s at 96 °C, 20 s at 54 °C and 4 min at 60 °C.

The sequences obtained in the forward and reverse directions for each marker were compared using the BlastN algorithm of GenBank (<http://www.ncbi.nlm.nih.gov>), and alignment was performed using BioEdit 7.0.4.1 (Hall 1999). Ambiguous nucleotides were checked in the original electropherograms. For each marker, an alignment

Table 1 – Species, collection information, and voucher and accession numbers of COI-5P and *rbc*L sequences.

Sample	Collection data	Voucher	GenBank acc. no.	
			COI-5P	*rbc*L
Erythrotrichia carnea (Dillwyn) J.Agardh	USA, California, Pebble Beach, May 1965, J. Ramus	UTEX1690	-	AF087118
E. carnea	Australia, Tasmania, Tinderbox	JAW4398.1	-	EF660274
Sahlingia subintegra (Rosenvinge) Kornmann	India, Pondicherry, July 20, 2012, F. Bast	POD-49	MH107767	-
S. subintegra	India, Elathur, May 25, 2012, F. Bast	ELA-11	MH107768	-
Boldia erythrosiphon Herndon	USA, Tennessee, Hiawassee River, June 22, 1993, R. Holton		-	AF087122
B. erythrosiphon	-	UTEX LB2858	-	KY709208
Boldia sp.	Canada, K.M. Muller	CRON	HQ699256	-
Compsopogon caeruleus	Vanuatu, Efate Island, June 16, 2005	JAW4530	JX028181	JF292657
C. caeruleus	Vanuatu, Cressionnieres Cascades, 2 km North of Eton Beach waterfall, June 16, 2005, J. West	BHO VU-4531	JX028193	-
C. caeruleus	Argentina, Misiones, Candelaria, High Parana River, 2016, N. Pividori, D. Aichino	-	MH638995	-
	Argentina, Misiones, Yabebiry, High Parana River, 2017, N. Pividori, D. Aichino	-	MH638996	-
C. caeruleus	Australia, Victoria, Hopkins River mouth, March 1995, J. West	BHO A-0893	JX028190	JX028170
C. caeruleus	Austria, Pernhofen, Pulkava River, October 19, 2010, Z. Žáková	BIOTES Lab, AT	JX028189	JX028148
C. caeruleus	Brazil, São Paulo, Conchas, Muquém River, June 13, 2008, O. Necchi Jr.	SJRP BR-CO	-	JX028149
C. caeruleus	Brazil, Espírito Santo, Domingos Martins, Rodovia ES 164, July 18, 2006, O. Necchi Jr.	SJRP BR-ES3	JX028172	JX028150
C. caeruleus	Brazil, Espírito Santo, Cachoeira, Guandú River. July 19, 2006, O. Necchi Jr.	SJRP BR-ES06	JX028173	JX028151
C. caeruleus	Brazil, Espírito Santo, Afonso Cláudio, Route ES-165, waterfall beside the road, July 19, 2006, O. Necchi Jr.	SJRP BR-ES7	JX028174	JX028152
C. caeruleus	Brazil, Espírito Santo, Santa Teresa, Country Club Waterfall. July 21, 2006, O. Necchi Jr.	SJRP BR-ES10	JX028175	JX028153
C. caeruleus	Brazil, São Paulo, Pereiras, near the railroad station, June 13, 2008, O. Necchi Jr.	SJRP BR-PE	JX028176	JX028154
C. caeruleus	Brazil, São Paulo, Pontes Gestal, Rio Preto, Cachoeira de São Roberto, June 1, 2009, O. Necchi Jr.	SJRP BR-PG2	JX028177	JX028155
C. caeruleus	Brazil, Sergipe, Lagarto, Route SE-110, 3,5 km from Campo de Brito, Rio das Traíras, June 8, 2006, O. Necchi Jr.	SJRP BR-SE4	JX028178	JX028156
C. caeruleus	Brazil, São Paulo, Ubatuba, Itamambuca Beach, Itamambuca River, 200 m from the sea, January 17, 2011, O. Necchi Jr.	SJRP BR-Cl	JX028184	JX028165
C. caeruleus	Brazil, São Paulo, Guaraqueçaba, Sebuí Ecological Reserve, mouth of Sebuí River, September 21, 2008, O. Necchi Jr.	SJRP BR-CL	JX028185	JX028166
C. caeruleus	Brazil, Bahia, Taperoá, Graciosa Quilombola Fishing Community, oyster farm, 22 July 2022	ALCB 145987	PP445213	OR820778

Sample	Collection data	Voucher	GenBank acc. no.	
			COI-5P	*rbc*L
C. caeruleus	China, Shanxi province, Niangziguan	MM1	KR706536	KR706528
C. caeruleus	China, Shanxi province, Niangziguan	MM2	KR706537	KR706529
C. caeruleus	China, April 18, 2019, K. Fang	SXU-YN19045	MT649410	MT653121
C. caeruleus	China, December 2020, K. Fang	SXU-GD20005	-	OM171262
C. caeruleus	Indonesia, Central Java, downstream from hot spring near Tegal, August 19, 2011, E. Johnston, N. Buhari, F. Saint Amour	IR-34	-	KF557555
C. caeruleus	Guam, Mahlack River, Talofofo branch, December 1, 2007, M.L. Vis, D.L. House, C. Lobban	BHO:A-0223	JX028182	JX028160
C. caeruleus	Malaysia, Johor, Sungai Mupur off the highway between Kota Tinngi and Mersing, September 3, 2011, E. Johnston, F. Saint Amour	MR-16	-	KF557565
C. caeruleus	Federated States of Micronesia, Wachen Falls. December 3, 2007, M. Vis, D. House	BHO A-1515	JX028186	JX028167
C. caeruleus	Spain, Lleida, Segre River, September 13, 2010, P. Tomás	MUB ES-209	JX028191	JX028157
C. caeruleus	Spain, Zaragoza, Ebro River, September 8, 2010, P. Tomás	MUB ES-210	-	JX028158
C. caeruleus	Spain, Zaragoza, Ebro River, September 8, 2010, P. Tomás	MUB ES-211	-	JX028159
C. caeruleus	USA, Florida	US-FLa	-	AF087114
C. caeruleus	USA, Louisiana, Whiskey Chitto	US-LAa	-	AF087116
C. caeruleus	USA, Florida, Marion County, Juniper Springs, March 23, 2011, M.L. Vis, W.B. Chiasson, K.W. Chiasson.	BHO A-0415	JX028179	JX028161
C. caeruleus	USA, Hawaii, O'ahu, Kahana stream, Kahana State Park, Ko'olau Poko district, August 7, 2001, M.L. Vis, A.R. Sherwood	BHO A-1518	-	JX028162
C. caeruleus	USA, Covington, Virginia, Jackson River, November 2006, J. Zalack	BHO A-1445	JX028180	JX028163
C. caeruleus	USA, Hawaii, Kaua'i, north fork of Wailua stream, Kawaihua district, August 11, 2001, M.L. Vis, A.R. Sherwood	BHO US-HI11	JX028187	JX028168
C. caeruleus	USA, Louisiana, Spring Creek, Athus-Melder Rd, July 26, 2008, M.L. Vis, W.B. Chiasson	BHO A-1517	JX028188	JX028169
C. caeruleus	USA, Hawaii, Oahu	00216-00001	-	KC596170
C. caeruleus	USA, Hawaii	01159-00001	-	KC596173
C. caeruleus	USA, Hawaii, Maui	04155-00005	KC596325	-
C. caeruleus	USA, Hawaii, Maui	ARS 02676	HQ423112	-
C. caeruleus	Venezuela, Edo Sucre, Rio Guaire, April 10, 1991, J. West	BHO A-0894	JX028192	JX028171
C. caeruleus	From an aquarium, November 1, 2007, J. Bonham	BHO:A-0938	JX028183	JX028164
C. caeruleus	Germany, River Erft	FD Ott O646	-	DQ308425
C. caeruleus	Japan	FD Ott O1123	-	DQ308426

was constructed using the sequences generated in the present study and those available in GenBank (Tab. 1).

The most appropriate models of sequence evolution for maximum likelihood (ML) and Bayesian inference (BI), GTR+F+I+G4 for *rbc*L and HKY+I for COI-5P, were selected based on the Akaike Information Criterion, as implemented on the IQ-Tree webserver (Trifinopoulos *et al*. 2016). ML analysis was performed using 2,000 bootstrap replicates on the IQ-Tree web server. BI analysis was performed using MrBayes v3.2.2 (Ronquist *et al*. 2012), with the following parameters: four chains of the Markov chain Monte Carlo (one hot and three cold) for two independent runs, sampling one tree every 1,000 generations for 5,000,000 generations, starting with a random tree. We discarded the first 20,000 generations in both runs as burn-in to build a consensus tree and compute the posterior probabilities. The best tree was visualized using FigTree v1.4.4 (Rambaut 2018). *Boldia*, *Erythrotrichia,* and *Sahlingia* were used as outgroups. For *rbc*L and COI-5P matrices, genetic distances were calculated using uncorrected '*p*' distances in PAUP v4.0 beta10 (Swofford 2002).

Results and Discussion

For *rbc*L, 44 sequences were used in an alignment of 1117 bp, including one new accession obtained in the present study (Tab. 1). The *rbc*L consensus tree (Fig. 1) containing all global populations of *Compsopogon caeruleus* sequenced thus far recovered the species as monophyletic with full support. The same was observed for COI-5P, for which 33 sequences (one new accession) were used in an alignment of 664 bp (Fig. 2). The divergence values between our sequences and those from GenBank were 0.13%–1.2% for *rbc*L and 1.15%–1.48% for COI-5P. Other studies reported similar results, demonstrating low genetic diversity in *C. caeruleus* samples from around the world (Necchi Junior *et al*. 2013; Nan *et al*. 2016).

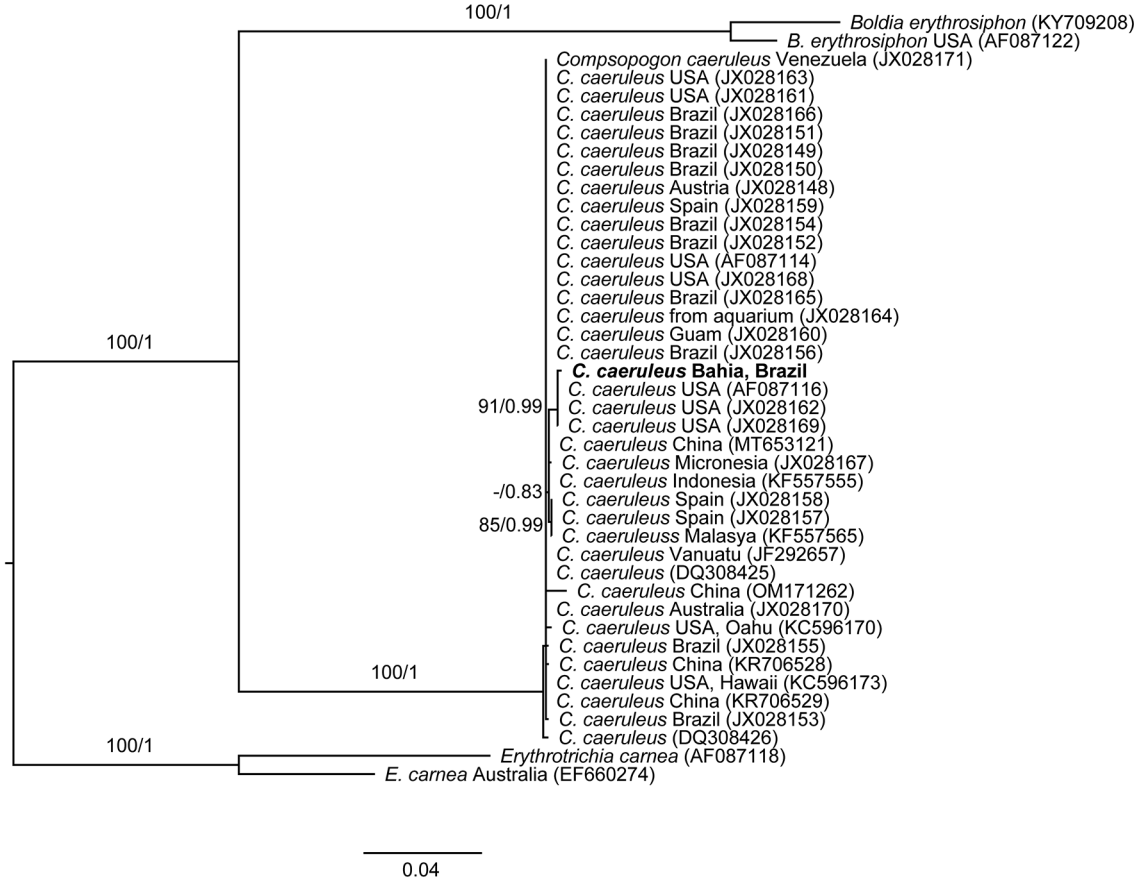

Figure 1 – Consensus tree derived from maximum likelihood (ML) analysis of *rbc*L sequences. Bootstrap values (BP) and posterior probabilities (PP) are shown at the nodes ML/PP. The sample generated in this study is in bold; '-' indicates lack of bootstrap support or values < 70.

Compsopogon caeruleus (Fig. 3a-i) has a densely branched filamentous thallus, with alternate to irregular branching, green to gray in color, and up to 30 cm. Thalli, which is heterotrichous, is composed of pluriseriate main axes and uniseriate lateral branches, corticated in older portions. The pluriseriate portion contains numerous spine-like branchlets. Uniseriate branches are 12–50 μm in diameter. Pluriseriate branches have 1–2 layers of cells, 87–300 μm thick; axial cell is 40–200 μm in diameter. In surface view, cortical cells of the outermost layer are polygonal to irregular, and of the second layer, when it occurs, are globose; cortical cells measure 12.5–50 μm in diameter and 10–50 μm length. Monosporangia present in corticated filaments, spherical to polygonal, and 9–16 μm in diameter.

Compared with other studies (for example: Thaxter 1900; Oliveira Filho & Pereira 1973; Necchi Junior *et al*. 1999, 2013; Bautista & Necchi Junior 2014), few morphological differences exist; however, some studies have highlighted the absence of spine-like branchlets (South & Skelton 2002) and the presence of more layers of cortical cells (Liu & Wang 2004; Ratha *et al.* 2007; Vis & Necchi Junior 2021). A summary of the comparison of *C. caeruleus* characteristics from the present study with those from other regions of the world is presented in Table 2.

The hydrology of the Graciosa region, characterized by the influence of rivers, such as the Rio Graciosa and major tributaries entering the Canal de Taperoá (*e.g.*, Rio do Engenho, Rio das Almas, and Rio Una), generates a highly dynamic estuarine environment (Araujo *et al.* 2013, Ferraz & Accioly 2015). This pronounced salinity range and the transitional nature of the Graciosa/Taperoá estuarine system provide an ecological context that is consistent with the observed distribution of *C. caeruleus*. Although primarily considered a freshwater taxon, *C. caeruleus* has been recorded in estuarine and brackish lagoon environments worldwide. Early studies attested to this brackish water tolerance, reporting the species as "frequent" in tidal creeks within estuarine regions of the United States (Thaxter 1900; Taylor 1960). In India, this species has been collected directly from an estuarine channel and the brackish Chilika Lagoon (Ratha *et al*. 2007). Kitayana (2011) reported the presence of *C. caeruleus* along the Pacific coast of Japan, indicating a distribution pattern associated with coastal and estuarine habitats.

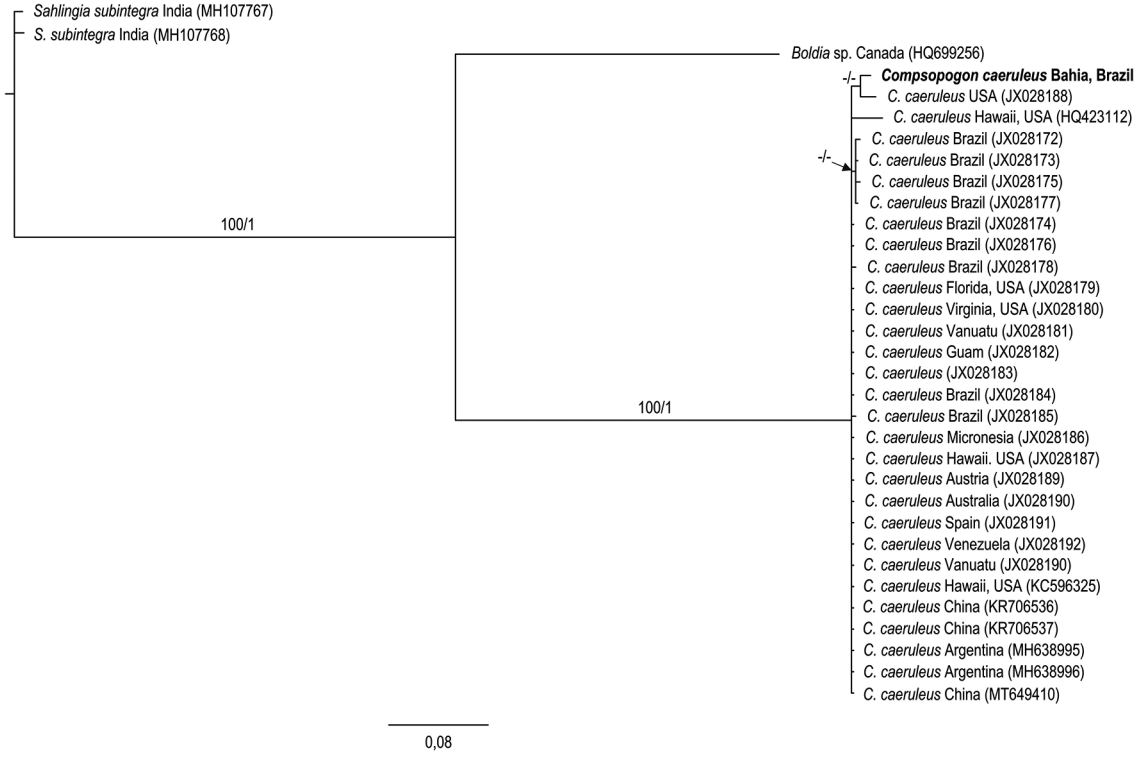

Figure 2 – Consensus tree derived from maximum likelihood (ML) analysis of COI-5P sequences. Bootstrap values and Bayesian posterior probabilities (BP/PP) are shown at the nodes. The sample generated in this study is in bold; '-' indicates lack of bootstrap support or values under 70.

Figure 3 – a-i. Morphological characters of *Compsopogon caeruleus* from Taperoá, Bahia, Brazil – a. aspect of corticated and uniseriate filaments (scale bar = 200 μm); b. details of uniseriate branches (scale bar = 100 μm); c. aspect of spine-like branchlets (scale bar = 200 μm); d. details of spine-like branchlets (scale bar = 200 μm); e. cross section of an apical corticate filament, showing one layer of cortical cells (scale bar = 50 μm); f. cross section of a corticated filament of the median portion, showing one layer of cortical cells; arrow indicates a monosporagia (scale bar = 20 μm); g. cross section of a corticated filament of the basal portion, showing two layers of cortical cells (scale bar = 50 μm); h. details of a corticated branch of the median portion; arrows indicate monosporangia (scale bar = 100 μm); i. details of a corticated branch of the basal portion; arrows indicate monosporangia (scale bar = 100 μm).

Table 2 – Comparison of morphological characters of *Compsopogon caeruleus* from the present and other studies.

Characteristics	Present study	Champman and Cameron (1967)	as *C. aeruginosus* and *C. chalybeus* (Oliveira Filho and Pereira, 1973)	South and Skelton (2002)	as *C. chalybeus* and *C. tenellus* (Liu and Wang, 2004)	Stoyneva *et al.* (2006)	Ratha *et al.* (2007)	Kitayana (2011)	Zaburlín *et al.* (2019)	Vis and Necchi Junior (2021)
Country	Brazil	New Zealand	Brazil	Fiji	Taiwan	Belgium	India	Japan	Argentina-Paraguay	Puerto Rico
Thallus color	Green to gray	Green, blue, gray, purplish, or variations	Greenish blue, yellowish green	Bluish green	Green	-	Bluish green, greenish grey	Bluish green or reddish brown	Violet, dark red, olive green, to bluish	-
Thallus length (cm)	Up to 30	20–60	6–20	Up to 20	Up to 15	-	Up to 35	Up to 40	Up to 18	-
Branch angle	Acute	Over 45°	-	45°	-	-	Acute	Acute	Acute	Acute
Spine-like branchlets	Present	-	Present	Absent	Absent	Absent	Absent	Absent	Present	Present
Uniseriate branches (μm, diam.)	12–50	Up to 20	17–43	Up to 35	-	7.1–21.4	5–24.5	-	20–66	10–55
Corticated branches										
Corticated branches (diam.)	87–300 μm	Up to 1.5 mm	Up to 360 μm	1–2 mm	50–320 μm	210–220 μm	Up to 2.8 mm	Up to 360 μm	Up to 250 μm	Up to 2 mm
Cortical layers	1–2	One to several	1–2	1–2	1–3	1	2–3	1–3	1	1–4
Cortical cells shape	Polygonal to irregular	Polygonal	Polygonal	Rounded to angular	Polygonal to ovoid	-	Polygonal	Spherical / Cuboidal	Polygonal to irregular	Polygonal
Cortical cells (μm, diam.)	12.5–50	20–40	10–15	Up to 20	17–30	23–38	10–33	12–32	14–22	15–30
Cortical cells (μm, length)	10–50	-	12–20	Up to 20	22–40	23–38	14–43	15–48	16–32	15–55
Axial cells (μm, diam.)	40–200	Up to 200	-	-	-	-	-	-	-	45–450
Monosporangia (μm, diam.)	9–16	10–15	12–17	Absent	12–22	13–16	8.6–22.3	12–16	12–20	10–20

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Data availability statement

In accordance with Open Science communication practices, the authors inform that all data supporting the findings of this study are included in the article.

References

Araujo QR, Krause LRO, Santana SO, Araujo TG, Mendonça JR, Trindade AV & Epps KY (2013) Characterization of a mangrove soil in the Graciosa River estuary, in Bahia, Brazil: highlighting heavy metals and microbial populations. Agrotrópica 25: 149-162.

Bautista AIN & Necchi Júnior O (2014) Physiological performances of two populations of *Compsopogon caeruleus* (Rhodophyta) to inorganic nitrogen and phosphorus impoverishment. Revista Brasileira de Botânica 37: 391-398.

Cassano V (2009) Taxonomia e filogenia do Complexo *Laurencia* (Ceramiales, Rhodophyta), com ênfase no estado do Rio de Janeiro, Brasil. Tese de Doutorado. Instituto de Botânica da Secretaria de Estado do Meio Ambiente, São Paulo. 328p.

Chapman VJ & Cameron H (1967) *Compsopogon* in New Zealand. New Zealand Journal of Botany 5: 548-552.

Ferraz CVH & Accioly MC (2015) Experiência de extensão em comunidades tradicionais pesqueiras para regularização de produção aquícola - estudo de caso: Comunidade da Graciosa, Taperoá - BA. Revista Extendere 3: 37-51.

Flora e Funga do Brasil 2025 (continuously updated) Compsopogonophyceae in Flora e Funga do Brasil. Jardim Botânico do Rio de Janeiro. Available at <https://floradobrasil.jbrj.gov.br/FB125661>. Access on 2 April 2025.

Freshwater DW & Rueness J (1994) Phylogenetic relationships of some European *Gelidium* (Gelidiales, Rhodophyta) species, based on *rbc*L nucleotide sequence analysis. Phycologia 33: 187-194. DOI: 10.2216/i0031-8884-33-3-187.1

Guiry MD (2022) *Compsopogon caeruleus* (Balbis *ex* C.Agardh) Montagne 1846. *In*: Guiry MD & Guiry GM (eds.) AlgaeBase. National University of Ireland, Galway. Available at <https://www.algaebase.org/search/species/detail/?species_id=583>. Access on 2 April 2025.

Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium 41: 95-98.

Kitayana T (2011) First record of *Compsopogon caeruleus* (Balbis *ex* C.Agardh) Montagne (Compsopogonophyceae, Rhodophyta) from Ogasawara Islands, Japan. Bulletin of the National Museum of Nature and Science, Series B (Botany) 37: 169-174.

Liu S-L & Wang W-L (2004) Two new members of freshwater red algae in Taiwan: *Compsopogon tenellus* Ling et Xie and *C. chalybeus* Kützing (Compsopogonaceae, Rhodophyta). Taiwania 49: 32-38. DOI: 10.6165/tai.2004.49(1).32

Montagne [JF]C (1846) Flore d'Algérie. Ordo I. Phyceae Fries. *In*: Durieu De Maisonneuve MC (ed.) Exploration scientifique de l'Algérie pendant les années 1840, 1841, 1842. Sciences physiques. Botanique. Cryptogamie. Vol. 1. Imprimerie Royale, publiée par ordre du Gouvernement et avec le concours d'une Commission Académique, Paris. Pp. 1-197.

Nan F, Feng J, Lv J, Liu Q & Xie S (2016) Evolutionary history of the monospecific *Compsopogon* genus (Compsopogonales, Rhodophyta). Algae 31: 303-315. DOI: 10.4490/algae.2016.31.10.22

Necchi Junior O, Branco CCZ & Gomes RRV (1999) Microhabitat and plant structure of *Compsopogon coeruleus* (Compsopogonaceae, Rhodophyta) populations in streams from São Paulo state, southeastern Brazil. Cryptogamie Algologie 20: 75-87. DOI: 10.1016/S0181-1568(99)80008-7

Necchi Junior O, Garcia Fo AS, Salomaki ED, West JA, Aboal M & Vis ML (2013) Global sampling reveals low genetic diversity within *Compsopogon* (Compsopogonales, Rhodophyta). European Journal of Phycology 48: 152-162. DOI: 10.1080/09670262.2013.783626

Nichols HW (1964) Culture and developmental morphology of *Compsopogon coeruleus*. American Journal of Botany 51: 180-188. DOI: 10.1002/j.1537-2197.1964.tb06618.x

Oliveira Filho EC & Pereira SMB (1973) Notas sobre o gênero *Compsopogon* Montagne (Rhodophyta - Compsopogonales) no Brasil. Boletim de Botânica 1: 85-94.

Rambaut A (2018) FigTree v.1.4.4. Available at <http://tree.bio.ed.ac.uk/software/figtree/>. Access on 30 September 2023.

Ratha SK, Jena M, Rath J & Adhikary SP (2007) Three ecotypes of *Compsopogon coeruleus* (Rhodophyta) from Orissa state, East Coast of India. Algae 22: 87-93. DOI: 10.4490/algae.2007.22.2.087

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA & Huelsenbeck JP (2012) MRBAYES 3.2: efficient Bayesian phylogenetic inference and model selection across a large model space. Systematic Biology 61: 539-542. DOI: 10.1093/sysbio/sys029

Saunders GW (2005) Applying DNA barcoding to red macroalgae: a preliminary appraisal holds promise for future. Philosophical Transactions of the Royal Society B: Biological Sciences 360: 1879-1888. DOI: 10.1098/rstb.2005.1719

Scott J, Thomas J & Saunders B (1988) Primary pit connections in *Compsopogon coeruleus* (Balbis) Montagne (Compsopogonales, Rhodophyta). Phycologia 27: 327-333. DOI: 10.2216/i0031-8884-27-3-327.1

Scott J & Broadwater S (1989) Ultrastructure of vegetative organization and cell division in the freshwater red alga *Compsopogon*. Protoplasma 152: 112-122. DOI: 10.1007/BF01323070

Sherwood AR, Kurihara A, Conklin KY, Sauvage T & Presting GG (2010) The Hawaiian Rhodophyta Biodiversity Survey (2006-2010): a summary of principal findings. BMC Plant Biology 10: 258. DOI: 10.1186/1471-2229-10-258

South GR & Skelton PA (2002) Occurrence and use of *Compsopogon coeruleus* (Rhodophyta: Compsopogonaceae) in Fiji, South Pacific. New Zealand Journal of Marine and Freshwater Research 36: 879-882. DOI: 10.1080/00288330.2002.9517139

Stoyneva MP, Vanhoutte K & Vyverman W (2006) First record of the tropical invasive alga *Compsopogon coeruleus* (Balbis) Montagne (Rhodophyta) in Flanders (Belgium). *In*: Ognajanova-Rumenova N & Monoyloy K (eds.) Advances in phycological studies. Pensoft Publishers and University Publishing House, Sofía (Moscow). Pp. 203-212.

Swofford D (2002) PAUP 4.0 b10: Phylogenetic Analysis Using Parsimony (and other methods). Sinauer Associates, Sunderland. DOI: 10.1111/j.0014-3820.2002.tb00191.x

Szymanska H & Krupinska I (1983) The finding of *Compsopogon coeruleus* (Balbis) Montagne in Poland. Acta Societatis Botanicorum Poloniae 52: 101-103. DOI: 10.5586/asbp.1983.011

Taylor WR (1960) Marine algae of the Eastern Tropical and Subtropical coasts of the Americas. The University of Michigan Press, Ann Arbor. PP. xi-870, 14 figs, 80 pls.

Thaxter R (1900) Note on the structure and reproduction of *Compsopogon*. Botanical Gazete 29: 259-267. DOI: 10.1086/327978

Trifinopoulos J, Nguyen LT, von Haeseler A & Minh BQ (2016) W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Research 44: W232-W235. DOI: 10.1093/nar/gkw256

Vis ML & Necchi Junior O (2021) Freshwater red algae: phylogeny, taxonomy and biogeography. Springer Nature Switzerland AG, Cham. 338p.

Žáková Z, Pum M, Sedláček P, Mlejnková H & Hindák F (2013) New records of *Compsopogon aeruginosus* (Rhodophyta) in rivers of central Europe. Oceanological and Hydrobiological Studies 42: 412-419. DOI: 10.2478/s13545-013-0097-4

Zaburlín NRM, Guzmán LB, Escalada MC, Llano VM & Vogler RE (2019) First record of the red alga *Compsopogon caeruleus* (Balbis *ex* C. Agardh) Montagne 1846 in the High Paraná River, Argentina-Paraguay. BioInvasions Records 8: 753–763. DOI: 10.3391/bir.2019.8.4.03