

The Gracilariaceae Germplasm Bank of the University of São Paulo, Brazil—a DNA barcoding approach

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Abstract The University of São Paulo Gracilariaceae Germplasm Bank has 50 strains collected mostly in Brazil, but also elsewhere in the world. This bank has been used as a source of material for research developed locally and abroad. With over 200 species, some of which have high economic value, the family Gracilariaceae has been extensively studied. Nonetheless, taxonomic problems still persist by the existence of cryptic species, phenotypic plasticity, and broad geographic distribution. In the case of algae kept in culture for long periods of time, the identification is even more problematic as a consequence of considerable morphological modification. Thus, the use of molecular markers has been shown to be an efficient tool to elucidate taxonomic issues in the group. In this work, we sequenced the 5'-end of the *cox1* gene for 41 strains and the universal plastid amplicon (UPA) plastid region for 45 strains, covering all 50 strains in the bank. In addition, the *rbcL* for representatives of the *cox1*/UPA clusters was sequenced for 14 strains. The original species identification based on morphology was compared with the molecular data obtained in this work, resulting in the identification of 13 different species. Our analyses indicate that *cox1* and UPA are suitable markers for the delineation of species of Gracilariales in the germplasm bank. The addition of DNA barcode tags to the samples in the Gracilariaceae germplasm bank and

the molecular identification of the species will make this bank even more useful for future research as the species can be easily traced and confirmed.

Keywords *cox1* · DNA barcoding · Germplasm bank · Gracilariales · *rbcL* · UPA

Introduction

The family Gracilariaceae is widely distributed on tropical and temperate marine coasts of the world. The main genera in the family are *Gracilaria* Greville with around 167 species and *Gracilariopsis* E.Y. Dawson with 20 species (Algaebase, Guiry and Guiry 2010). These seaweeds have considerable economic importance as the main global source of agar (Oliveira et al. 2000), which is largely used by the pharmaceutical and food industries (Oliveira and Plastino 1994). The quantity and quality of agar vary among species of Gracilariales; therefore, a precise identification may be very important (Macchiavello et al. 1999; Skriptsova and Nabivailo 2009).

In spite of the great effort applied to understand the biology of the group, precise taxonomic identification is limited by phenotypic plasticity, the occurrence of cryptic species, and the absence of male and cystocarpic reproductive structures (e.g., Fredericq and Hommersand 1989; Gurgel et al. 2003, 2004; Oliveira 1984). Many alternative approaches to conventional morphological analysis have been attempted (cf. Oliveira and Plastino 1994; Plastino and Oliveira 1996), including, for example, hybridization (Plastino and Oliveira 1988, 1990). To accomplish that, E.C. Oliveira and E.M. Plastino established the Germplasm Bank of the Laboratory of Marine Algae of the University of São Paulo (LAM-USP) for crossing experiments (Plastino et al. 1995; Plastino and Oliveira 1988, 1990, 1996, 1997, 2000). The germplasm bank currently has

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50 strains of Gracilariaceae in culture, some of which have been kept in vitro for more than 30 years. These strains were mostly collected in Brazil, but also elsewhere in the world (Lourenço and Vieira 2004).

This bank has been used as a source of material for several investigations, contributing to the knowledge of different aspects of this economically important group of algae. The life history of some species has been completed in vitro: *Gracilaria birdiae* (Costa and Plastino 2001); *Gracilaria caudata* and *Gracilaria cornea* (Oliveira and Plastino 1984); *Gracilaria chilensis* (Plastino and Oliveira 1984); *Gracilaria domingensis* (Guimarães et al. 1999); and *Gracilaria tenuis-tipitata* (Barufi et al. 2010). Physiological aspects related to growth rates (Ferreira et al. 2006; Plastino et al. 1998, 2004; Ursi et al. 2008; Ursi and Plastino 2001; Yokoya and Oliveira 1992a, b, 1993), pigment characterization (Barufi et al. 2010; Costa and Plastino 2011; Guimarães et al. 2003; Plastino et al. 2004), photosynthetic and respiratory characterization (Ursi et al. 2003), enzymatic activity (Chow et al. 2004, 2007; Chow and Oliveira 2008; Collén et al. 2003; Lopes et al. 1997, 2002; Rossa et al. 2002), and polysaccharide content (Guimarães et al. 2007) have been studied using strains from the germplasm bank. Furthermore, some strains have been used in color inheritance studies (Costa and Plastino 2001, 2011; Guimarães et al. 2003; Plastino et al. 1999, 2004), ultrastructure characterization (Bouzon et al. 2000, 2011; Guimarães and Plastino 1999; Plastino and Costa 1999, 2001), axenic tissue cultures (Ramlov et al. 2009; Yokoya 2000), phylogeny and systematic studies (Bellorin et al. 2002; Bird and Oliveira 1986), and gene sequencing and expression studies (Falcão et al. 2008, 2010; Hagopian et al. 2002, 2004; Nyvall et al. 2011).

However, once in culture, strains of *Gracilaria* and *Gracilariaopsis* may change their morphology, usually remaining infertile, thus making species identification very difficult, if not impossible. Therefore, it is necessary to implement a more direct approach, based on the use of molecular markers, for the identification and tracking of species in the bank.

Different molecular markers have been used for Gracilariaceae, such as the nuclear gene coding for the small subunit of ribosomal RNA, the internal transcribed spacers of ribosomal genes, and the *rbcL* gene coding for RUBISCO large subunit (Bellorin et al. 2002, 2008; Bhattacharya et al. 1990; Goff et al. 1994; Gurgel et al. 1999). These markers proved to be suitable for species identification and phylogenetic analysis within the group, but they are of relatively large size, requiring some effort for amplification and sequencing with the need for several internal primers, which results in additional cost in both time and resources.

On the other hand, the technique of DNA barcoding is a fast, practical, and uniform system based on polymerase chain reaction (PCR) amplification of relatively short (~400–700 bp) DNA fragments that can be fully sequenced

with the same two primers used in PCR (Savolainen et al. 2005). Hebert et al. (2003) proposed the use of the 5'-end of the mitochondrial gene *cox1* coding for cytochrome oxidase 1 to facilitate the rapid identification of specimens and as a powerful ally in understanding biodiversity. Given the difficulties that exist in species identification in several red algae, Saunders (2005) proposed and developed primers for the use of *cox1* for DNA barcoding in this group of organisms. Another region that has been proposed by Sherwood and Presting (2007) as a DNA barcode for photosynthetic organisms is the universal plastid amplicon (UPA), which is part of the chloroplast gene coding for the large ribosomal RNA (23SRNAr).

In this work, we first sequenced the 5'-end of *cox1* and the UPA region of Gracilariaceae kept in culture in the LAM-USP Germplasm Bank. These sequences were compared and grouped. Moreover, chloroplast DNA sequences for *rbcL* were obtained for each of the different groups. In this way, the original species identification based on morphology was compared with the molecular data obtained in this work, leading to the identification of 13 different species in the bank.

Materials and methods

Samples were collected from several locations (Table 1) and transported to the laboratory. The unialgal cultures were established from apical segments or spores. As soon as the algae were brought to the lab, a careful process for the removal of contaminants using brushes under stereoscopic microscope was performed. Successive cleanups were performed at 2–4 days, with the algae kept in sterile seawater without nutrients (Plastino and Oliveira 1990). Once isolated, cultures were maintained in modified von Stosch (Ursi and Plastino 2001) enriched seawater, diluted to 50 % with sterile seawater (32 psu). The cultures were kept at $25 \pm 1^\circ\text{C}$ under $30 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ photosynthetically active radiation (PAR) provided by 40-W daylight fluorescent tubes on a 14-h light/10-h dark cycle. The medium was renewed monthly.

Before DNA extraction, the apical fragments of each sample were transferred to Erlenmeyer flasks with 50 mL of enriched seawater for 2 weeks. Cultures were maintained under $150 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ PAR and aerated for 30 min h^{-1} . The medium was renewed weekly. After this period, the algae were rapidly rinsed in fresh water, blotted dry, frozen in liquid nitrogen, and stored at -70°C .

DNA extraction, PCR amplification, and sequencing

DNA was extracted from approximately 30 mg of frozen samples by grinding in liquid nitrogen and using the method

described by Bellorin et al. (2002). The mitochondrial *cox1* was amplified and sequenced using the synthetic primers GazF1 and GazR1 described by Saunders (2005). The plastidial UPA was amplified and sequenced using the primers p23Sv_f1 and p23Sv_r1 described by Sherwood and Presting (2007). The plastidial *rbcL* was amplified with the primers FrbcL and RbcS and sequenced with the addition of internal primers described by Freshwater et al. (1994). PCR amplification, purification, and sequencing are described in Milstein et al. (2011).

Molecular analyses

The consensus *Gracilaria* and *Gracilariopsis cox1*, UPA, and *rbcL* sequences were each aligned using ClustalW within BioEdit (Hall 1999) together with sequences of the same markers available from the GenBank. For *rbcL*, the sequences of *Curdiea racovitzia* Hariot and *Melanthalia abscissa* (Turner) J.D. Hooker and Harvey were used as outgroups. The following matrices were assembled: 57 sequences (41 sequences generated in this work and 16 obtained from databanks) and 664 positions for *cox1*; 56 sequences (45 sequences generated in this work and 11 obtained from databanks) and 370 positions for UPA; and 78 sequences (14 sequences generated in this work and 64 obtained from databanks) and 1,393 positions for *rbcL*. For all three markers, positions corresponding to amplification primers were excluded.

For *cox1* and UPA only, a neighbor-joining (NJ) analysis using PAUP* 4.0b10 (Swofford 2002) with 2,000 replicates of bootstrap was performed to visualize the species groups. For *rbcL*, an evolution model was selected using MrModeltest 2.2 (Posada and Crandall 1998), and phylogenetic analyses were inferred by: (1) NJ with 2,000 replicates of bootstrap; (2) maximum parsimony heuristic search, using starting trees obtained by stepwise addition, with random sequence addition (ten replicates) using tree bisection–reconnection branch-swapping algorithm and with 2,000 replicates of bootstrap, using the PAUP* 4.0b10 (Swofford 2002); and (3) Bayesian analysis with two runs of four chains and with 4,000,000 generations sampled every 100 (initial 100,000 generations were discarded as burn in) using MrBayes (v3.1.2) (Huelsenbeck and Ronquist 2001).

Results

The germplasm bank has a total of 50 samples of Gracilariaceae; out of which 33 originated from Brazil and 17 from abroad (Table 1). Sequences for the 5'-end of *cox1* were obtained for 41 samples and presented 16 unique sequences that grouped into nine clusters representing different species (Fig. 1). Sequences for the UPA plastid region were obtained

for 45 samples and presented 13 unique sequences that grouped into clusters representing different species (Fig. 2).

In our experience, the UPA region was easier to amplify and sequence compared to *cox1* based on the number of PCR and sequencing reactions needed to obtain each consensus sequence. For 45 UPA sequences, 47 PCR and 106 sequencing reactions were performed, whereas to obtain 41 *cox1* sequences, 76 PCR and 284 sequencing reactions were performed. As a consequence, around 2.5-fold more reagents were needed to obtain *cox1* sequences than to obtain a similar number of UPA sequences.

The *cox1* and UPA sequences obtained for the germplasm bank samples, plus the few available sequences in the GenBank, were clustered using NJ (Figs. 1 and 2). In both analyses, the genera *Gracilaria* and *Gracilariopsis* were segregated. For the *cox1* analysis, four groups were formed for *Gracilariopsis*: one containing all the *Gp. tenuifrons* from several locations of Brazil and Venezuela with an intraspecific variation of 0–0.3 %; one for *Gp. longissima* from the eastern North Atlantic; one for *Gp. lemaneiformis* from Ecuador; and one for *Gp. andersonii* from Canada (Fig. 1). For the UPA, the same clusters were formed, with the exception of *Gp. andersonii*, which was not included in the analyses by the lack of UPA sequences, and with the addition of the only UPA sequence of *Gp. mclachlanii* (Fig. 2).

Analyses of *cox1* and UPA sequences of *Gracilaria* sequences from the germplasm bank grouped in clusters or isolated branches represent six and nine lineages, respectively (Figs. 1 and 2). *G. caudata* samples from northeastern Brazil (CE/BR) formed a sister cluster to a sample from southeastern Brazil (SP/BR), albeit at a distance of some 3,000 km from each other, with a *cox1* intraspecific divergence of 6 bp (0.8 %) between them (Fig. 1). For UPA, a *G. caudata* cluster was also formed, but without intraspecific variation (Fig. 2). Samples of *Gracilaria cornea* cultivated in Israel (originally collected in the Caribbean), Brazil, and Mexico formed a cluster in both the *cox1* and UPA analyses with a *cox1* intraspecific variation of 0–5 bp (0–0.8 %). For *G. birdiae*, only a UPA sequence was obtained, showing the close relationship of this species to *G. cornea* (only 0.3 % divergence). Samples of *Gracilaria gracilis* from Argentina, Portugal, Namibia, Brazil, and Norway grouped in both the *cox1* analysis, with an intraspecific variation of 0–2 bp (0–0.5 %), and the UPA analysis without intraspecific variation. Samples of *G. isabellana* from Brazil grouped both in the *cox1* and UPA analyses without intraspecific variation. The other samples, *G. domingensis*, *G. tenuistipitata*, *G. sp.* BG0057, and *G. rangiferina*, did not group with significant support to other species in either the *cox1* or UPA analyses.

The *rbcL* was sequenced for 14 samples selected from one or more representatives of each of the *cox1* and/or UPA clusters (Table 1): *G. caudata*, *G. cornea*, *G. domingensis*, *G. gracilis*,

Table 1 Strains maintained in culture in the Gracilariaceae Germplasm Bank at the University of São Paulo

Species	Original identification	Bank #	Collection site	Collector	Date	SPF	Life cycle phase	cox1 (664 bp)	rbcL (1,393 bp)	UPA (370 bp)
<i>Gracilaria caudata</i> J. Agardh	<i>Gracilaria caudata</i>	BG00028	Ubatuba, SP, Brazil	E. Plastino	25 April 1985	–	Female gametophyte	JQ843317 ⁿ		JQ952643
		BG00058	Guajiru, Trairi, CE, Brazil	E. Oliveira	16 September 1989	55510	Male gametophyte	JQ935789	JQ843355	JQ952644
		BG00059	Guajiru, Trairi, CE, Brazil	E. Oliveira	16 September 1989	55511	Female gametophyte	JQ843318		JQ952645
		BG00060	Guajiru, Trairi, CE, Brazil	E. Oliveira	16 September 1989	55512	Tetrasporophyte	JQ843319	JQ843356	JQ952646
		BG00081	Ubatuba, SP, Brazil		July 1993	52029	Female gametophyte			JQ907427
		BG00087	Praia do Meireles, Fortaleza, CE, Brazil	E. Plastino	28 February 1992	55807	Tetrasporophyte			JQ952642
		BG00088	Praia do Meireles, Fortaleza, CE, Brazil	E. Plastino	28 February 1992	55807	Male gametophyte	JQ843320		JQ952647
		BG00091	Praia do Pacheco, Fortaleza, CE, Brazil	E. Plastino	26 February 1992	55813	Tetrasporophyte	JQ935790		JQ952648
		BG00055	Guajiru, Trairi, CE, Brazil	E. Oliveira	16 September 1989	54946	Tetrasporophyte	JQ843324		JQ907432
		BG00067	Israel	A. Critchley	September 1992	–	Infertile plant	JQ843322		JQ907429
<i>Gracilaria cornea</i> J. Agardh	<i>Gracilaria cornea</i>	BG01112	Guajiru, Trairi, CE, Brazil	E. Plastino	February 1992	55662	Tetrasporophyte	JQ843321		JQ907428
		BG01113	Guajiru, Trairi, CE, Brazil	E. Plastino	February 1992	55662	Tetrasporophyte	JQ935791		JQ952650
		BG01115	Guajiru, Trairi, CE, Brazil	E. Plastino	February 1992	55662	Tetrasporophyte	JQ843323	JQ843357	JQ952649
		BG01040	Rio do Fogo, RN, Brazil	M. Amaral		–	Tetrasporophyte			JQ907430
		BG00005	Ubatuba, SP, Brazil	E. Oliveira	28 October 1981	26055	Male gametophyte		JQ843358	
		BG00007	São Sebastião, SP, Brazil	E. Plastino	11 December 1982	26774	Male gametophyte	JQ843329	JQ843359	JQ907438
		BG00033	Puerto Madryn, Argentina	E. Oliveira	29 March 1986	27985	Tetrasporophyte	JQ935792		JQ952651
		BG00045	Puerto Madryn, Argentina	E. Oliveira	24 March 1986	27985	Tetrasporophyte	JQ935793		JQ952652
		BG00061	Luderitz, Namibia	A. Critchley	December 19 1989	–	Infertile plant	JQ843331		JQ907440
		BG00084	Pajuçara, AL, Brazil	E. Plastino	03 March 1994	55734	Tetrasporophyte	JQ843332	JQ843360	JQ907442
<i>Gracilaria gracilis</i> (Stackhouse) M. Steentoft, L.M. Irvine & W.F. Farnham	<i>Gracilaria gracilis</i> <i>Gracilaria tenuifrons</i> <i>Gracilaria verrucosa</i>	BG00094	Norway	E. Oliveira	1982	–	Male gametophyte			JQ907441
		BG00095	Norway	E. Oliveira	1982	–	Tetrasporophyte	JQ843333		
		BG00036	Cabo Frio, RJ, Brazil	E. Plastino	06 November 1987	52189	Tetrasporophyte	JQ843335		JQ907448
		BG00037	Cabo Frio, RJ, Brazil	E. Plastino	06 November 1987	52190	Male gametophyte	JQ843338	JQ843361	JQ907454
		BG00038	Cabo Frio, RJ, Brazil	E. Plastino	06 November 1987	52191	Female gametophyte	JQ843337		JQ907453
		BG00048	Cabo Frio, RJ, Brazil	E. Plastino	06 November 1987	52191	Tetrasporophyte	JQ935794		JQ952653
		BG00092	Guajiru, Trairi, CE, Brazil	E. Plastino	08 April 1993	56055	Tetrasporophyte		JQ843362	JQ907456
		BG00062	Haikou, Hainan Island, China	E. Oliveira		–	Gametophyte		AY 673996	AY 673996
		BG00057	Guajiru, Trairi, CE, Brazil	E. Oliveira	16 September 1989	54948	Tetrasporophyte			JQ907443
		BG00078	Ecuador	E. Oliveira		–		JQ843342		JQ907465
<i>Gracilaria rangiferina</i> (Kütz.) Piccone	<i>Gracilaria rangiferina</i> <i>Gracilaria tenuisipitata</i> C.F. Chang & B.M. Xia <i>Gracilaria</i> sp. <i>Gracilaria lemaneiformis</i> (Bory de Saint-Vicent) E.Y. Dawson, Acleto & Foldvik <i>Gracilaria mclachlanii</i> Buryo, Bellorin & M.C. Oliveira <i>Gracilaria longissima</i> (S.G. Gmelin) M. Steentoft, L.M. Irvine & W.F. Farnham	BG00079	Ecuador (tank)	E. Oliveira		–		JQ843343	JQ843363	JQ907466
		BG00072	Zanzibar, Tanzania	E. Oliveira	June 1992	–	Infertile plant		JQ843365	JQ907469
		BG00051	England			–	Male gametophyte	JQ843345		JQ907468
		BG00052	England			–	Female gametophyte	JQ843344	JQ843364	JQ907467

Table 1 (continued)

Species	Original identification	Bank #	Collection site	Collector	Date	SPF	Life cycle phase	cox1 (664 bp)	rbcL (1,393 bp)	UPA (370 bp)
<i>Gracilariopsis tenuifrons</i> (C.J. Bird & E.C. Oliveira) Fredericq & Hommersand	<i>Gracilariopsis tenuifrons</i>	BG0039	Cabo Frio, RJ, Brazil	E. Plastino	06 November 1987	52192	Female gametophyte	JQ935796		JQ952655
		BG0040	Cabo Frio, RJ, Brazil	E. Plastino	06 November 1987	52192	Male gametophyte	JQ843354		JQ952663
		BG0042	Arraya, La Peña, Venezuela	M. Aponle	30 March 1989	52027	Tetrasporophyte	JQ843353		JQ952662
		BG0043	Arraya, La Peña, Venezuela	M. Aponle	30 March 1989	52027	Tetrasporophyte	JQ935800	JQ843368	JQ952661
		BG0044	Arraya, La Peña, Venezuela	M. Aponle	30 March 1989	–	Tetrasporophyte	JQ843351		JQ907472
<i>Gracilaria</i> sp.	<i>Gracilaria caudata</i>	BG0047	Valença, BA, Brazil	E. Oliveira	16 December 1987	27958	Tetrasporophyte	JQ935795		JQ952654
		BG0050	Punta Banda, Baja California, México	E. Oliveira	07 June 1989	54484	Male gametophyte	JQ935798	JQ843366	JQ952659
<i>Gracilariopsis tenuifrons</i>	<i>Gracilariopsis tenuifrons</i>	BG0054	Arraya, La Peña, Venezuela	M. Aponle	30 March 1989	–	Male gametophyte	JQ843346		JQ907470
		BG0064	Itanhaém, SP, Brazil		11 May 1990	55323	Tetrasporophyte	JQ843349		JQ952657
		BG0073	Lagoa de Mundau, AL, Brazil	E. Plastino	21 January 1993	55700	Infertile plant	JQ935799	JQ843367	JQ952660
		BG0073a	Lagoa de Mundau, AL, Brazil	E. Plastino	21 January 1993	55700	Infertile plant	JQ843347		JQ952656
		BG0073b	Lagoa de Mundau, AL, Brazil	E. Plastino	21 January 1993	55700	Infertile plant	JQ843348		
		BG0082	Ubatuba, SP, Brazil	E. Plastino	July 1993	56086	Male gametophyte	JQ935801		
		BG0083	Ubatuba, SP, Brazil	E. Plastino	July 1993	56087	Female gametophyte	JQ843350		
		BG0085	Pajuçara, AI, Brazil	E. Plastino	03 March 1994	55734	Female gametophyte	JQ935797		JQ952658
BG0086	Mundau, AL, Brazil	E. Plastino	03 March 1994	55734	Female gametophyte			JQ907471		

^a GenBank accession numbers

Gp. isabellana, *G. rangiferina*, *Gp. tenuifrons*, *Gp. lemaneiformis*, *Gp. longissima*, and *Gp. mclachlanii*. The *rbcL* for *G. tenuistipitata* was previously sequenced for the same strain used in this work and was available from GenBank. The phylogenetic analyses for these *rbcL* sequences with others from the Genbank are shown in Fig. 3. By using two other Gracilariaceae genera, *Curdiea* and *Melanthalia*, as outgroups, the species of the genus *Gracilariopsis* formed a monophyletic assemblage highly supported in all analyses, but *Gracilaria* was monophyletic only in the Bayesian analysis (0.89 a posteriori probability). The sequences obtained from the samples in the germplasm bank clustered with other available sequences from the same species obtained in the GenBank. The germplasm bank strains of *Gp. tenuifrons* from Brazil, Mexico, and Venezuela grouped with a *Gp. tenuifrons* from Guadalupe in the Caribbean. The sample of *Gp. longissima* from England grouped with another sample from the same species from Italy. The sample of *Gp. lemaneiformis* from Ecuador grouped with another one from Peru. The sample of *Gp. mclachlanii* grouped with a previously sequenced sample from Tanzania.

The *Gracilaria* species formed different clades with varying support. A basal clade was formed only in the Bayesian analyses joining *G. vermiculophylla*, *G. chilensis*, and *G. tenuistipitata*. The following groupings were observed: (1) Strains of *G. caudata* from Brazil grouped with *G. caudata* from FL, USA; (2) *G. cornea* from Brazil grouped with one strain from Venezuela; (3) *G. domingensis* from Brazil formed a clade; (4) *G. isabellana* from Brazil grouped with a sample from Venezuela (as *G. lacinulata* in GenBank); and (5) *G. tenuistipitata* from China grouped with a sample attributed to the same species from India.

Discussion

The LAM-USP Germplasm Bank has been a very useful resource for several studies on Gracilariales. Successful unialgal isolation is a key step in setting up cultures. Once isolated, samples of *Gracilaria* and *Gracilariopsis* can be maintained in vitro for a long time at relatively low cost and with little labor, as the medium only needs to be replaced once a month by the requirement of low irradiance. For experimental purposes, apices are progressively cultivated in higher irradiance and nutrients. Depending on the treatment, the species can be successfully propagated in 1 month.

Only rarely is it possible to identify *Gracilaria* species without the presence of cystocarps and male reproductive structures. Identification based on gross morphology and vegetative anatomy is generally subjective and cumbersome because of high morphological plasticity, which explains the frequent misidentifications and extensive synonymy in this

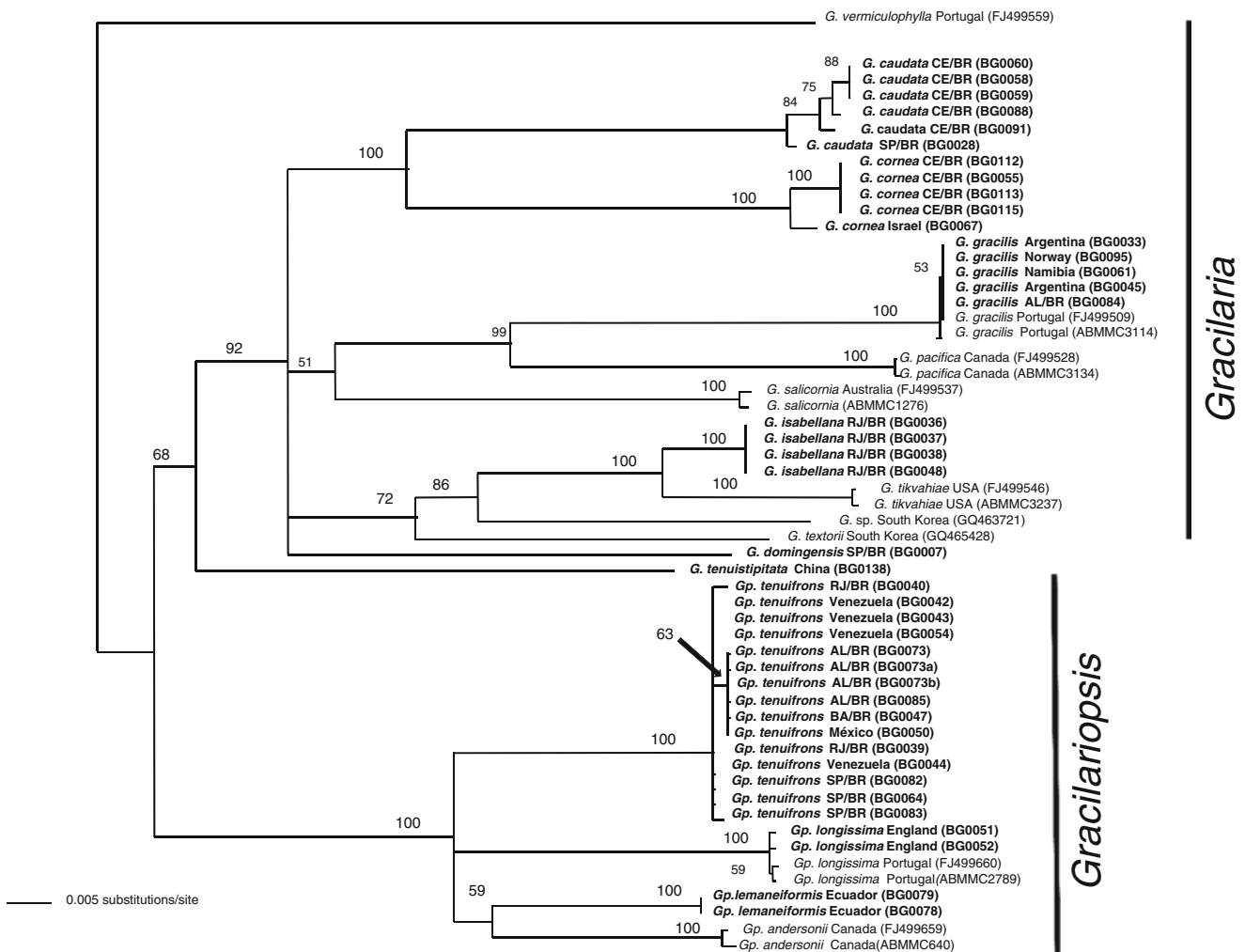


Fig. 1 Neighbor-joining phylogram for the *cox1* region showing the grouping of the Gracilariaceae sequenced in this study (*in bold*) and available from databanks (GenBank and BOLD). Strain numbers are *in*

brackets (see Table 1 for information on each strain). Bootstrap support values for 2,000 replicates are indicated on branches

group. Most species have no economic value, but for the few that do, this confusion in nomenclature has practical consequences (Bellorin et al. 2002, 2004; Saunders 2009).

Although *Gracilariopsis* has a much smaller biodiversity, species identification is even more difficult in the genus. With the sole exception of *Gracilariopsis silvana* Gurgel, which is flattened, all *Gracilariopsis* taxa are terete and stringy, looking very much alike. Therefore, in this genus, species are separated mostly based on geographical distribution, rather than on morphology and anatomy. This seemed adequate until some papers showed that some species of Gracilariales have a broad distribution and may be invasive (Bellorin et al. 2004; Saunders 2009).

Consequently, in addition to its inherent academic value, the use of short molecular tags for species identification is also demanded by industry, as a matter of economic exigency. Furthermore, molecular tags can be quite useful for field studies and to pinpoint the occurrence of invasive species.

For instance, Saunders (2009) identified the invasive species *G. vermiculophylla* in Canadian waters using the 5' region of *cox1* in routine DNA barcoding of Gracilariales.

Based on the work of several investigators, the data obtained so far indicate that a significant amount of intraspecific variation (~1 %) for *cox1* may occur in some in *Gracilaria* species. For example, intraspecific variation for *cox1* found for the *Gracilaria* and *Gracilariopsis* species in this work was, in some cases, higher (up to 0.8 %) than that found by Saunders (2005) (1 or 2 bp ~0.2 %) for several genera of Rhodophyta. Yang et al. (2007) used *cox1* (1,245 bp) to evaluate intraspecific variation in *G. vermiculophylla* from Asia and found a pairwise divergence up to 11 bp (0.9 %). Similar to the results of Yang et al. (2007), *G. caudata* from the southeast coast diverged by 0.8 % from strains of the same species from the northeastern coast of Brazil, and *G. cornea* cultivated in Israel (but originally collected in the Caribbean region, Alvaro Israel personal com.) diverged by 0.8 % from strains of the same species from Brazil.

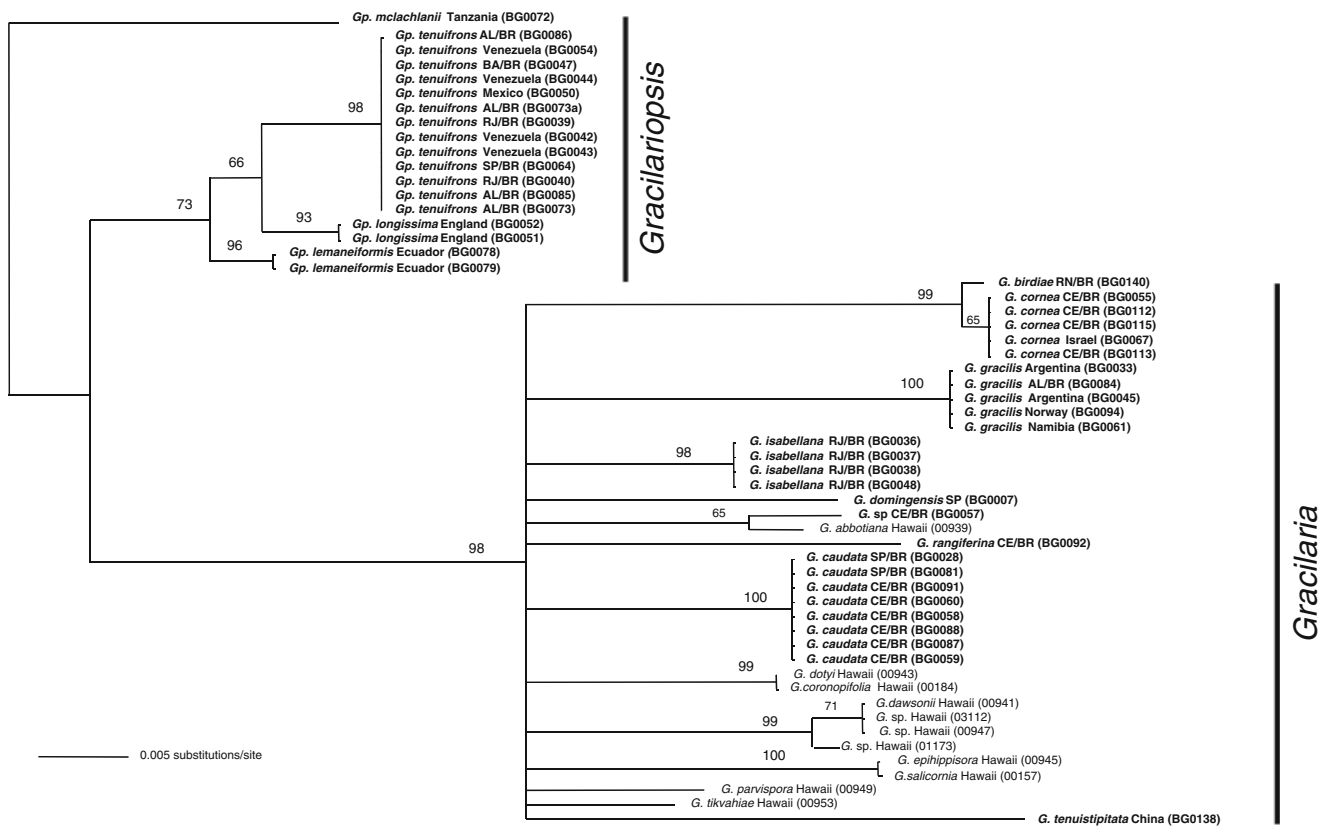


Fig. 2 Neighbor-joining phylogram for the UPA region showing the grouping of the Gracilariaceae sequenced in this study (*in bold*) and available from the Hawaiian Algal Database. Strain numbers are *in*

brackets (see Table 1 for information on each strain). Bootstrap support values for 2,000 replicates are indicated on branches

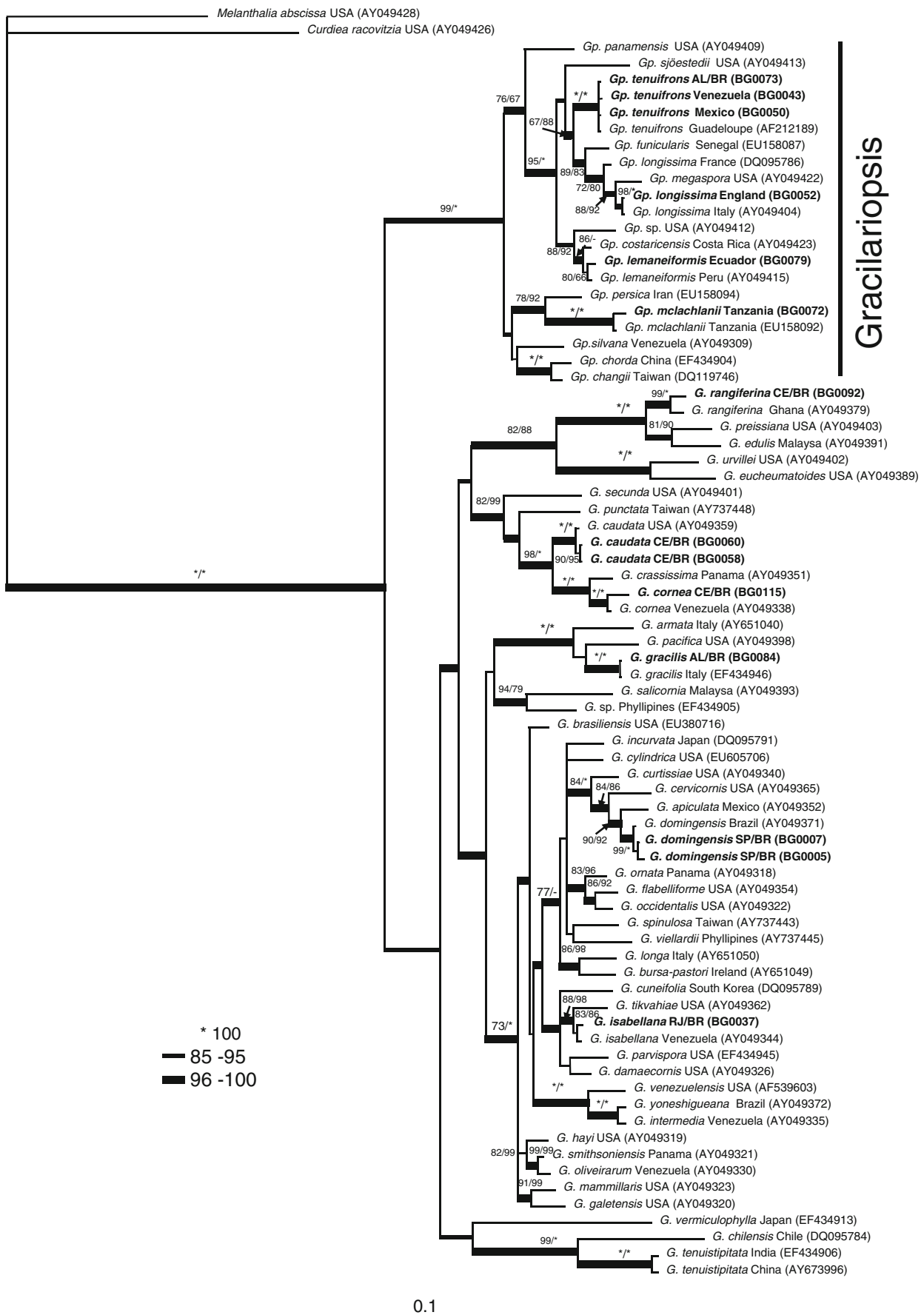
The interspecific variation for *cox1* found for *Gracilariopsis* (5.8–6.5 %; 38–43 bp) was similar to the one found by Saunders (2005), but for *Gracilaria* (9.1–13.7 %; 60–91 bp), the values were higher. For this region, Saunders (2005) found that interspecific variation in several genera of Rhodophyta was around 30–40 bp, with some exceptions. For *cox1*, Yang et al. (2007) found that the interspecific nucleotide difference was also high among different species of Gracilariales (>41 bp, 3.2–16.1 % of 1,245 bp). Thus, the use of *cox1* seems to be adequate for DNA barcoding of species in the Gracilariales, as previously demonstrated in various red algae (Robba et al. 2006; Saunders 2005, 2009).

As expected, the UPA sequences were more conserved and showed less interspecific and no intraspecific variation, and as in *cox1* (Sherwood et al. 2010), interspecific variation for UPA was relatively higher for *Gracilaria* species (2.2–5.2 %; 8–19 bp) than that observed for *Gracilariopsis* (0.8–3.7 %; 3–14 bp). Nonetheless, the interspecific variation found for UPA was enough to separate the species in the germplasm bank. Considering that UPA is easier to amplify and sequence than *cox1*, UPA is a reliable molecular marker that can be used as a routine tag for the addition and tracking of strains in culture collections.

Relatively few sequences of *cox1* and UPA for Gracilariales species are to be found in the databanks. Therefore, to help in species identification, *rbcL* was sequenced for one or more representatives of each of the *cox1* and/or UPA clusters, as there are *rbcL* sequences for several species of Gracilariales available in the GenBank. The use of *rbcL* confirmed the previous identification of most samples or helped in the identification of those that were not given a species name when first included in the germplasm bank (Table 1).

In a few cases, the molecular marker results did not corroborate the original morphological identification. For example, based on the molecular markers, BG0007, originally identified as *G. cervicornis*, and BG0005, originally identified as *G. mammillaris*, both correspond to *G. domingensis*, while BG0050, originally identified as *G. caudata* (collected in Mexico), was identified as *Gp. tenuifrons* based on molecular markers. These discrepancies indicate a possible mislabeling during the manipulation of the isolates along the 20 years of

Fig. 3 Consensus tree derived from Bayesian analyses of *rbcL* sequences obtained in this study (*in bold*) and available from Genbank (accession numbers *in brackets*). Thickness of the branches indicates Bayesian a posteriori probabilities. Bootstrap supports (2,000) replicates which are shown on the branches as follows: maximum parsimony/neighbor-joining



media and vial changes. This is further supported by the fact that *G. domingensis* is not found on the coast of São Paulo State (both BG0007 and BG0005 were originally collected from the São Paulo coast). *Gp. tenuifrons* has not been cited to Mexico, thus reinforcing the idea that some mistake was made with the labeling of specimens in the laboratory. Besides, the original algae have a *verrucosa*-type spermatangia distribution, which is different from *Gp. tenuifrons* that presents a *chorda*-type. These results highlight the importance of routinely using molecular markers to identify species kept in the germplasm bank.

Conclusions

Implementing the use of molecular markers for strains contained in the germplasm bank allowed us to define the existence of 13 different species in the bank. Unpublished sequences for *cox1* and UPA were generated for 7 and 12 species of Gracilariales, respectively. Both *cox1* and UPA were suitable DNA barcode markers to help track species of Gracilariaceae kept in culture in the germplasm bank, although UPA demanded considerably less effort and material for amplification. On the other hand, *cox1* presents, in some cases, a low level of intraspecific variation and could be used to track individual strains of different populations of the same species, which can be also useful for the purpose of germplasm bank management. The addition of the DNA barcode tag to the samples in the Gracilariaceae germplasm bank and the molecular identification of the species will make this bank even more useful for future research as the species can be easily traced and confirmed.

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