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Gracilaria viridis sp. nov. (Gracilariales, Rhodophyta): a new red algal species from the Mediterranean Sea

Adriano Sfriso[1]§*, Marion Adelheid Wolf[2]§, Katia Sciuto[2], Marina Morabito[3], Carlo Andreoli[2] and Isabella Moro[2]

[1]*Department of Environmental Sciences, Informatics & Statistics, University of Venice, Calle Larga 2137, 30123 Venice, Italy*
[2]*Department of Biology, University of Padova, Via U. Bassi, 58/B 35131 Padova, Italy*
[3]*Department of Life Sciences "Marcello Malpighi", University of Messina, V. Ferdinando Stagno d'Alcontres, 31 98166 Messina, Italy*

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We characterized a new *Gracilaria* species from the Venice Lagoon, Italy, using molecular analyses based on the plastid large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase gene (*rbc*L) and the intergenic RuBisCO spacer (*rbc*L-*rbc*S), combined with morphology data. This new entity was recorded on the artificial substrata of the Venice Gulf from March to July, adding to 12 *Gracilaria* taxa already recorded in the Mediterranean and Adriatic seas. Thalli exhibited a green-yellowish pigmentation with pink shades, and there was dense branching in the distal portions. Tetrasporangia were scattered on thallus cortex and distributed mostly on short, stipitate branchlets. The inner pericarp was connected to the gonimoblast by tubular nutritive cells. The male gametophytic plants formed round-elliptical spermatangial *verrucosa*-type conceptacles. This species grew attached on artificial rocky substrata of the low midlittoral and upper sublittoral zone in spring and early summer. Molecular analyses based on the plastid-encoded *rbc*L gene showed a 99.66% nucleotide identity with another *Gracilaria* sp. from southern Sicily. We compared our *rbc*L-*rbc*S spacer sequences with those of two cryptic species, and the phylogenetic analyses confirmed that the Venice populations were a new species. We suggested that the discovery of this new species was not due to an extra-Mediterranean introduction but the consequence of its misidentification as *Gracilaria gracilis*, which has a similar gross morphology.

Key Words: *Gracilaria viridis* sp. nov., Gracilariaceae, Mediterranean Sea, New species, *rbc*L, *rbc*L-*rbc*S spacer

INTRODUCTION

Gracilaria Greville is an important economic red algal genus because it is the major agarophyte resource in the world (Troell *et al*. 2003). It is characterized by a wide phenotypic variability and great species diversity. Thalli of this genus range from erect to prostrate and from terete to broadly flattened, with species forming branched fronds composed of cylindrical or irregularly shaped units (Guiry & Guiry 2011).

Gross morphological characters of the vegetative and reproductive structures have distinguished many genera and for years have provided the basis of Mediterranean seaweeds identification (Gargiulo *et al*. 1987, 1992; Fredericq & Hommersand 1989a, b, 1990). Unfortunately, morphological features are often limited and ambiguous, leading to misidentifications caused by convergent evolution or morphological plasticity caused by environmental influences. This makes the systematics of this group very problematic (Bird 1995).

Progress in molecular techniques solved problems in species identification and led systematic revisions for many algal groups including *Gracilaria* (Bellorin *et al*. 2002; Gurgel & Fredericq 2004). Several molecular markers have been used: the plastid-encoded large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase gene (*rbc*L) (Freshwater *et al*. 1994; Fredericq *et al*. 1996; Hommersand *et al*. 1999; Gurgel & Fredericq 2004) and the *rbc*L-*rbc*S intergenic spacer region (Cho *et al*. 2003; Skage *et al*. 2005; Wolf *et al*. 2011), the mitochondrial-encoded *cox*1 gene (Saunders 2005), and the nuclear-encoded rRNA internal transcribed spacer (Hayden & Waaland 2004).

At present Guiry & Guiry (2011) report 170 specific and intraspecific accepted taxa for *Gracilaria* and 12 species (Table 1) are present in the Mediterranean Sea (Gargiulo *et al*. 1992; Furnari *et al*. 1999, 2003; Sfriso & Curiel 2007; Cecere & Petrocelli 2009; Sfriso *et al*. 2009). However, the development of taxonomy, especially on molecular systematics, and the occurrence of introduced taxa (Sfriso *et al*. 2010) are increasing this number.

Here we report the characterization of specimens collected in the Venice Lagoon (Italy); specimens are identified using morphological features and molecular analyses of the *rbc*L gene and the more variable intergenic *rbc*L-*rbc*S spacer; the spacer is useful for distinguishing between cryptic species (strictly correlated species) (Maggs *et al*. 2002). The *rbc*L results show that the Venice specimens are conspecific with another *Gracilaria* species (named *Gracilaria*-LI02) from southern Sicily, Italy (Gargiulo *et al*. 2006). On the basis of our results, we propose the name *Gracilaria viridis* sp. nov.

* Corresponding authors (adriano.sfriso@unive.it, isabella.moro@unipd.it).
§ These authors contributed equally to this work.

Table 1. Morphology of the vegetative and reproductive features for the Mediterranean *Gracilaria* species.

	Maximum axis				Cystocarp	
Taxa	Length (cm)	Diameter (mm)	Shape	Medullary cells	Position	Size (μm)
G. armata (C. Agardh) Greville	15–25	2–4	terete	50–250	distal branches	520–700 × 700–800
G. bursa-pastoris (Gmelin) Silva	25–35	1–2(−3)	partially flattened	250–500	entire thallus	500–800 × 700–900
G. conferta (Schousboe *ex* Montagne) Montagne	6–8	0.15	terete	180–200	distal branches	700–800 × 800–950
G. corallicola Zanardini	5–10	3–7(−15)	flattened	100–180(−300)	distal branches	700–800 × 800–900
G. dendroides Gargiulo *et al.*	25–30	0.2	terete with lanceolate branchets	150–200	lanceolate branches	600–700 × 800–900
G. dura (Agardh) Agardh	20–25	1–1.8	terete	75–100(−180)	entire thallus	700–800 × 800–900
G. gracilis (Stackhouse) Steentoft *et al.*	15–35	0.8–1.2	terete	100–150(−200)	entire thallus	500–700
G. heteroclada Zhang & Xia	25–35	3–5(−8)	flattened with spatulated apices	80–120	on club-shaped branches	300–350 × 350–400
G. longa Gargiulo *et al.*	100–200	1.5–3(−4)	terete	150–300(−500)	entire branches	750–850(−1200)
G. multipartita (Clemente) Harvey	20–60[1]	6–10	flattened	60 × 65–132 × 180[1]	entire thallus	—
G. vermiculophylla (Ohmi) Papenfuss	50-100-200	1.5–3(−4)	terete	200–250(−300)	entire thallus	700–900 × 800-1300
G. verrucosa (Hudson) Papenfuss	15	1	terete	100–200	entire thallus	600–700 × 700–750
G. viridis sp. nov	5–35	0.5–1.3	terete	(100–)150–200	entire thallus	800-1050

[1] Neto *et al.* (2002).
[2] Gurgel & Fredericq (2004).
[3] Smith (1954).
[4] Bellorin *et al.* (2004).

MATERIAL AND METHODS

Samples of *Gracilaria viridis* sp. nov. were collected on the artificial stone breakwaters perpendicular to the shore coastline of the Lido and Pellestrina islands, along the Venice sea coastline and in the jetty 'dikes' formed by limestone blocks placed between the sea and the Venice Lagoon (Italy) to protect the wide sea inlets of Lido, Malamocco and Chioggia (Lido: 45°23′N, 12°21′E; Malamocco: 45°20′N, 12°19′E; Pellestrina: 45°17′N, 12°18′E). Moreover, thalli of *G. viridis* were sampled in Licata (Agrigento, Sicily, Italy) (37°05′N, 13°55′E), at Marianello beach, west of the fishing harbour. Thalli were deposited in the herbarium, University of Messina (MS).

Gross morphological observations were carried out on fresh samples or on specimens fixed in 4% buffered formaldehyde–seawater solution; a stereo zoom microscope E-1654ZT45 (Euromex microscopes, Holland) and a compound light microscope-353Ph (Optika microscopes, Italy) were employed. Spermatangial conceptacles were observed on semithin sections. Parts of thalli were fixed overnight in 6% glutaraldehyde in 0.1 M cacodylate buffer (pH 6.9), and postfixed overnight in 1% OsO_4 in the same buffer. The postfixed samples were dehydrated in a graded ethanol series followed by propylene oxide, and then they were embedded in araldite resin. Semithin sections were cut with an ultramicrotome (Reichert Ultracut S), stained with 1% toluidine blue and examined with a DMR Leica microscope (Wetzlar, Germany) equipped with a digital image acquisition system.

Genomic DNA was extracted from dried samples using the Genomic DNA purification kit (Fermentas International Inc., Burlington, Ontario, Canada) following the manufacturer's instructions. For amplification and sequencing reactions of the plastid *rbc*L gene, two primer pairs (F7-R753, F577-R1381) were used (see Freshwater & Rueness 1994). For the *rbc*L-*rbc*S spacer amplification and sequencing, the forward primer F1320 (Freshwater *et al.* 2006) was used in combination with the reverse primer RrbcSstart (Freshwater & Rueness 1994). PCR amplifications were performed as follows: an initial denaturation step of 2 min at 94°C; 30 cycles at 94°C for 40 s, at 50°C for 40 s, and at 72°C for 50 s; and a final extension step at 72°C for 5 min. The amplification products were cleaned with ExoSAP-ITTM kit (GE Healthcare, Uppsala, Sweden, Europe) following the manufacturer's protocol. DNA sequencing was performed at the BMR Genomics Sequencing Service (Padova University, Italy) on automated ABI DNA sequencers (Applied Biosystem, Foster City, CA, USA). Final consensus sequences were assembled using the SeqMan II program from the Lasergene software package (DNAStar©, Madison, WI, USA). Identity of new sequences was checked with the BLAST program (Altschul *et al.* 1990) available at the USA National Center for Biotechnology Information (NCBI) web server (http://www.ncbi.nlm.nih.gov), and the sequence alignments were obtained by the ClustalW computer program (Thompson *et al.* 1994).

For phylogenetic analyses of the *rbc*L gene, a dataset of 73 sequences was constructed using our new sequences plus sequences obtained from DDBJ/GenBank/EBI Data Bank.

Table 1. Extended

Tubular nutritive cells to			Male conceptacles		Tetrasporangia	
Inner pericarp	Outer pericarp	Fusion cell type	Type	Size (μm)	Position	Size (μm)
+	+	restricted	*textorii*	25–38 × 25–38	distal branches	15–20 × 25–30
+	+	expanded	*textorii*	20–25 × 20–25(−38)	entire thallus	15–25 × 20–35
+	+	restricted	*verrucosa*	15–20 × 20–25	distal branches	18–20 × 25–35
+	+	restricted	*chorda*	8–10 × 15–20	entire thallus	18–20 × 22–26
+	+	expanded	*verrucosa*	30–50 × 65–75	lanceolate branches	35–40 × 50–60
−	+	expanded	*verrucosa*	25–30 × 40–50	distal region	25–30 × 35–40
−	+	expanded	*verrucosa*	25–30 × 30–40	entire thallus	25–30 × 30–40
+	+	restricted	*chorda*	30–40 × 40–50	spatulated branches	18–20 × 30–40
−	+	expanded	*verrucosa*	30–45 × 50–70	entire thallus	15–20 × 18–40(−50)
+[2]	+[2]	expanded[3]	*textorii*[2]	—	scattered, younger parts of the blade[1]	23–29 × 34–60[1]
−[4]	+ (rare)	restricted[4]	*verrucosa*	25–40(−50) × 40–100(−125)	entire thallus	20–30 × 20–40(−50)
−	+	expanded	*verrucosa*	20–25 × 30–40	entire thallus	25–30 × 30–40
+	+	restricted	*verrucosa*	15–35(−50) × 50–100(−125)	entire thallus	12–15 × 20–35

Analyses were performed according to maximum likelihood (ML) method with the PHYML 2.4.4 program (Guindon & Gascuel 2003) applying the GTR+I+Γ evolutionary model (Lanave *et al*. 1984). Nonparametric bootstrap resampling (Felsenstein 1985) was performed to test the robustness of the tree topology (1000 replicates). The models that best fitted our data were found using the program jMODELTEST under the Akaike Information Criterion (Posada & Crandall 1998; Posada & Buckley 2004). Bayesian Inference analyses were carried out using MrBayes version 3.1 (Ronquist & Huelsenbeck 2003). The substitution model was the GTR+I+Γ and the Bayesian analyses were performed with four search chains for 3,000,000 generations, sampling trees every 100 generations. The first 7500 trees were discarded as burn-in. Parameter stability was estimated by plotting log-likelihood values against generation time, and a consensus tree with posterior probabilities was then produced. The nexus files for the Bayesian analyses were generated with the Mesquite 2.71 software package (Maddison & Maddison 2009).

The *rbc*L gene and the *rbc*L-*rbc*S spacer sequences of the Venice isolate were deposited in DDBJ/GenBankTM/EBI Data Bank with the accession numbers HE614144 and HE614145, respectively, while the *rbc*L sequence of *Gracilaria conferta* Montagne from Morocco was assigned the accession number HE964956.

RESULTS

Gracilaria viridis Sfriso, Wolf, Sciuto, Morabito, Andreoli & Moro sp. nov.

Figs 1–11

DIAGNOSIS: *Thalli tereti 0.5–1.3 mm diametro, 5–35 cm alti, saxicolae, irregularis, fere horizontaliter effusi, haptero parvo discoideo affixi. Color viridis-flavidus, aliquando purpureus. Rami alterni, dense fructicosis, ad apices angustati et saepe incurvati. In transversa sectio frondes multistrato constitutas: ab exterior parte cellulae corticalis per 1–2 stratos; mediae cellulae medullariae subcorticalesque, 10–20 μm diametro, per 2–3 stratos; interioris cellulae medullariae magnae, 100–200 μm diametro, parietibus tenuibus. Cystocarpia matura ellipsoidea, ∼ 900 μm diametro, basi constricta, per totem fronda sparsa. Gonimoblasti per cellulas nutrices tubulares ad cellulas basales pericarpii affixi. Tetrasporangia, ∼ 30 μm longa ∼ 13 μm lata, filamentis corticalibus circumcinctis, in brevis ramulis, per totam frondem sparsa. Spermatangia in concectaculis, ∼ 35 μm diametro ∼ 75 μm altis, in cellula corticalis et subcorticalibus mersi.*

HOLOTYPE DESIGNATED HERE: A000008, a voucher specimen deposited at the Herbarium Patavinum (PAD); a tetrasporophytic plant with short stipitate unibranched to tribranched branchlets (see Fig. 1).

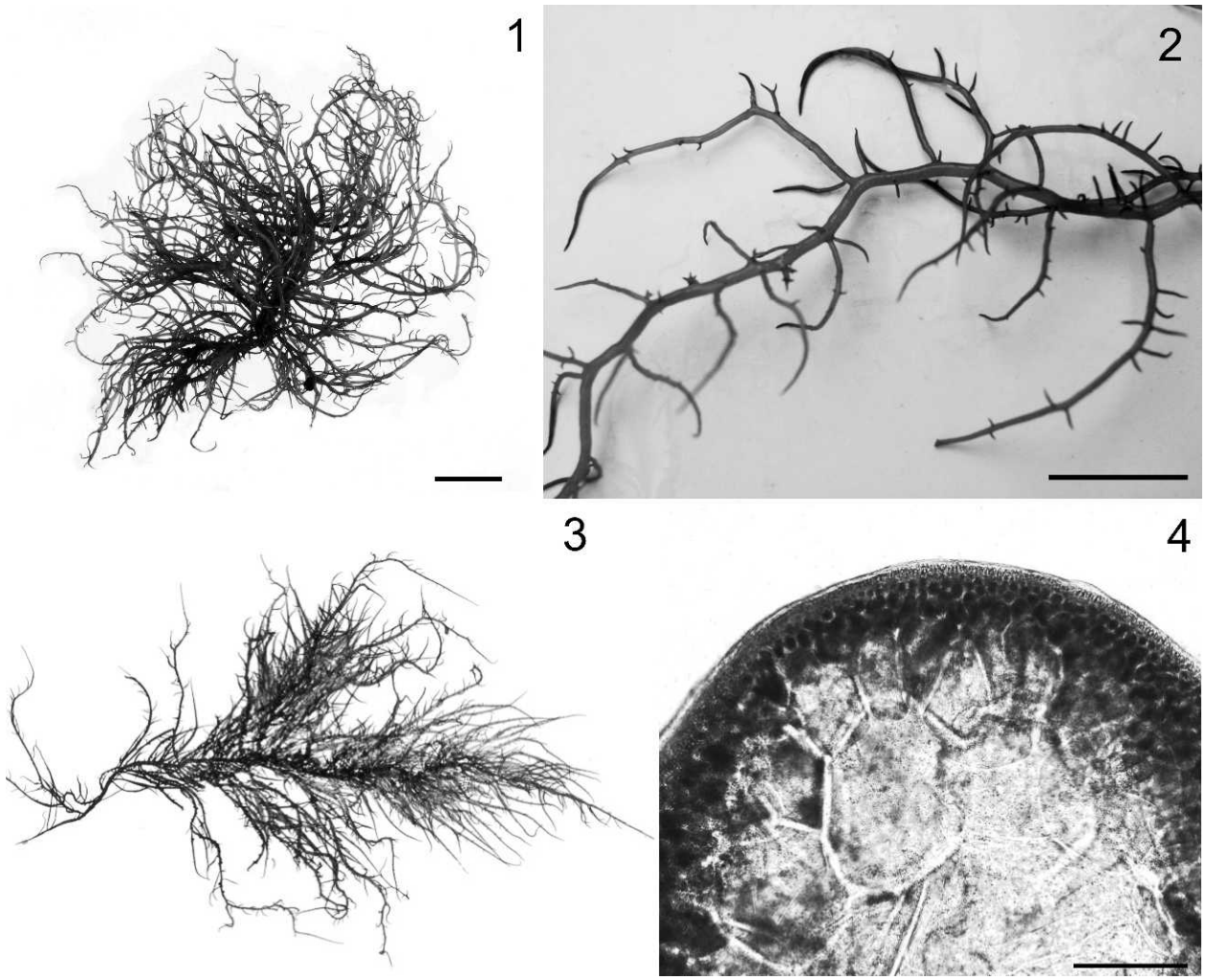
TYPE LOCALITY: Jetty, marine coast, Lido, Venice, Italy (45°22′140″N, 12°20′362″E).

ETYMOLOGY: *viridis* (Latin) = green, and refers to the green-yellowish thallus colour.

HABITAT: Artificial rocky substrata of the low midlittoral and upper sublittoral zones.

DISTRIBUTION: Gulf of Venice, Adriatic Sea; Licata, Agrigento, southern Sicily.

The thallus was green-yellowish in colour but sometimes it was a partially reddish colour (Figs 1,2). Thalli were



Figs 1–4. *Gracilaria viridis*.
Fig. 1. Habit of the thallus collected in the Venice Lagoon, Italy (image of the holotype, A000008). Scale bar = 2 cm.
Fig. 2. Branches and branchlets of thallus (A000008). Scale bar = 0.5 cm.
Fig. 3. Habit of the thallus collected in Sicily, Italy (*Gracilaria*-LI02). Scale bar = 2 cm.
Fig. 4. Cross-section of an axis showing cortical, sub-cortical and medullar cells (A000008). Scale bar = 200 μm.

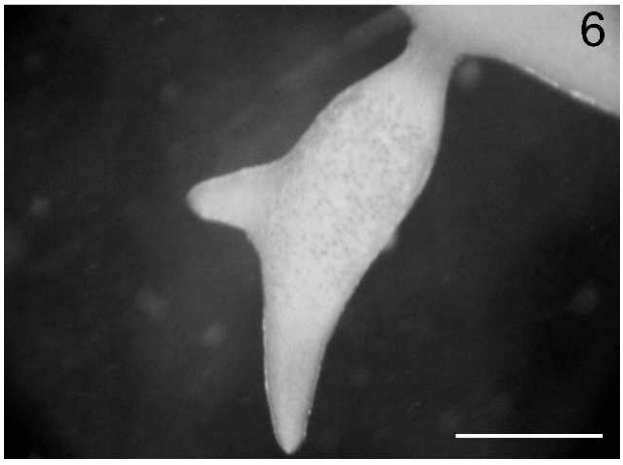
attached by a small discoid holdfast bearing erect fronds; thalli were 5–35 cm high and 0.5–1.3 mm thick, they were smooth throughout, and they were irregularly branched at the basal and median regions, with dense entangled branching in the apical parts, especially on the oldest specimens. Branches and branchlets formed without order, but they were mostly perpendicular and frequently sigmoid or recurvate (Fig. 3). Branching insertions were feebly restricted at the base.

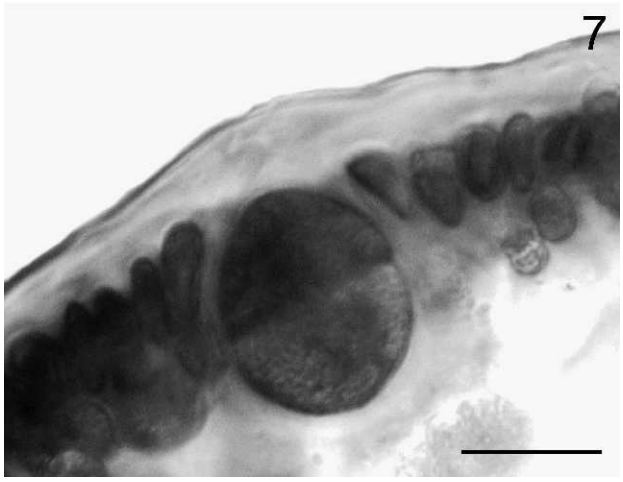
The same thallus morphology was observed for the Sicily strain, which was collected in 2002 (Fig. 3).

Cortical cells had a rounded-polyhedric shape, *c*. 7–10 μm in surface view. In cross-section, they were 3–6 μm in width and 7–10 μm long. There were one or two layers of subcortical cells, 10–20 μm in diameter, and these were surrounded by the larger colourless thin-walled medullary cells (*c*. 150–200 to 300 μm in diameter; Fig. 4). Subspherical tetrasporangia, *c*. 12–15 × 20–35 μm, were produced throughout the main branches (Fig. 5) and on short stipitate unibranched to tribranched branchlets that were frequently enlarged in the median region (branches 0.3–0.45 μm diameter 1–2(–3) mm in length) (Fig. 6). Tetrasporangia were ∼ 30 μm long and 13 μm broad, and they were immersed in the cortex (Fig. 7).

Dark red mature ostiolate cystocarps, *c*. 800-1050 μm in diameter but constricted at the base, were borne throughout the main axis and branches (Figs 8,9). Their dark-red pigmentation stands out on the green-yellowish plants. The inner pericarp was connected to the gonimoblast by tubular nutritive cells (Fig. 10). The gonimoblast tissue consisted of cellular rows producing ovoid carposporangia of 15–18 × 20–30 μm.

The male gametophytic plants formed round to elliptical spermatangial *Gracilaria verrucosa*–type conceptacles that were scattered on the cortical layer (Fig. 11). Sometimes they were confluent, showing a cristated shape in surface view. Conceptacle cavities were ∼ 20–30 μm diameter and 25–35 μm deep.





Figs 5–7. *Gracilaria viridis*.
Fig. 5. Tetrasporophytic branches with short stipitate unitribranched branchlets (A000008). Scale bar =1 mm.
Fig. 6. Tetrasporophytic branches with short stipitate bibranched branchlets (A000008). Scale bar = 0.5 mm.
Fig. 7. Tetrasporangium immersed in the cortex (A000008). Scale bar = 20 μm.

Thalli were common from March to July in the artificial stone breakwaters along the Lido and Pellestrina islands; the alga also occurred on the first part of the limestone block jetties (dikes) that were placed between the seaside and the lagoon side for protection of the wide lagoon inlets of Lido, Malamocco and Chioggia. They colonized the lower intertidal and the upper sublittoral zones where they formed a fringe of isolated thalli that were strongly entangled with many epiphytic taxa, especially *Ceramium*, *Polysiphonia* and *Centroceras*. Thalli were always haptophytic and were not able to grow in a free-floating form.

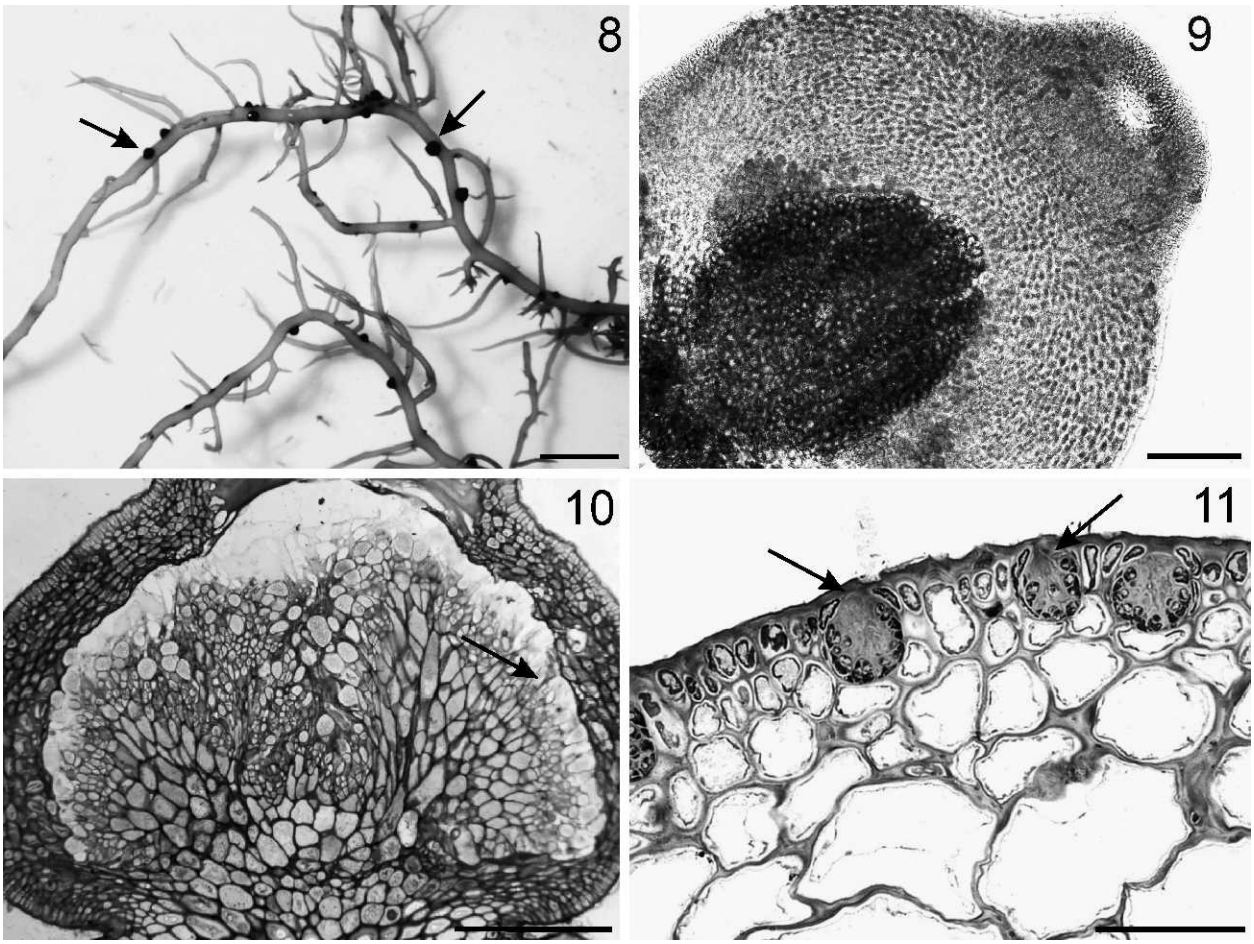
The *rbc*L and *rbc*L-*rbc*S spacer sequences from the five isolates were all identical. The partial *rbc*L sequence showed 99.66% identity with *Gracilaria* sp. (GenBank AY651040). The *rbc*L-*rbc*S spacer was most similar to *Gracilaria conferta* (Schousboe *ex* Montagne) Montagne and *Gracilaria gracilis* (Stackhouse) Steentoft, Irvine & Farnham. The *rbc*L-*rbc*S spacer region sequences were 220 bp long; they consisted of the *rbc*L-*rbc*S spacer (116 bp), a fragment of the *rbc*L gene (85 bp) and a fragment of the *rbc*S gene (19 bp). The spacer region showed a nucleotide divergence of 2.27% with *G. conferta* and of 5.45 % with *G. gracilis*.

The *rbc*L dataset (1191 bp) included one sequence from a Venice specimen, a *G. conferta* sequence, obtained from an herbarium specimen kindly provided by Prof. C. Destombe (Morocco), 70 *Gracilaria* sequences from public databases and the outgroup sequence of *Hypnea spinella* (C. Agardh) Kützing (AF385635). The tree showed the Venice specimen in a well-supported clade with *Gracilaria* sp. from Sicily (100% of bootstrap support, 100 BT, and 1.00 of posterior probability, 1.00PP) (Fig. 12). *Gracilaria conferta* from Morocco was placed as sister taxon (100BT/1.00PP), while *G. pacifica* from Indian Island (USA) and two specimens of *G. gracilis* from France (AY049399) and Italy (EF434946) occupied a basal position.

DISCUSSION

The molecular and morphological features strongly suggest that our strain represents a new species, which we named *Gracilaria viridis* sp. nov. The *rbc*L phylogenetic analyses (Fig. 12) show that our strain is not conspecific with the cryptic species *G. gracilis* or with another Mediterranean terete species, *G. conferta*. *Gracilaria viridis* forms a separate clade with *Gracilaria* sp. LI02 from Sicily, and the clade is supported by 100BT/1.00PP values. Moreover, the small nucleotide divergence between the Sicilian and the Venetian specimens (0.34%) strongly suggests that they could be considered the same species.

The comparison of *rbc*L-*rbc*S spacer sequences shows that the closest species, *G. gracilis* and *G. conferta*, are distinctly different (divergence = 5.45% and 2.27%, respectively). That is, although the divergences are small, they fall with interspecific range reported for this genus (1.05–17.07%) and these differences are comparable with other *Gracilaria* species [1.94% for *G. gracilis* and *G. dura* (C. Agardh) J. Agardh; 2.72% for *G. conferta* and *G. dura* and 3.92% for *G. conferta* and *G. gracilis*] (Iyer *et al.* 2005). Moreover our results agree with those of other authors, i.e. no sequence variation was found between individuals assigned to the same morphospecies (Guillemin *et al.* 2008; Hommersand & Freshwater 2009).



Figs 8–11. *Gracilaria viridis*.
Fig. 8. Dark red ostiolate cystocarps (arrows) on green-yellowish thalli (*Gracilaria* VE01). Scale bar = 2 mm.
Fig. 9. Longitudinal section of cystocarp (*Gracilaria* VE01). Scale bar = 200 μm.
Fig. 10. Longitudinal section of cystocarp with tubular nutritive cells (arrow) (*Gracilaria* LI02). Scale bar = 250 μm.
Fig. 11. Cross-section of a male gametophytic plant showing round-elliptical spermatangial *verrucosa*-type conceptacles (arrow) scattered on the cortical layer (*Gracilaria* VE02). Scale bar = 50 μm.

Thalli of *Gracilaria viridis* are distinguishable from other Mediterranean terete species of *Gracilaria* (Table 1). For example, *G. longa* Gargiulo, De Masi & Tripodi and *G. vermiculophylla* (Ohmi) Papenfuss differ for the much bigger size of the thallus and *G. armata* (C. Agardh) Greville for thicker axes. The phylogenetically related species *G. conferta* presents both cystocarps and tetrasporangia only on distal branches and not on the entire thallus as occurs on *G. gracilis* and *G. viridis*. Therefore when only vegetative thalli are examined, *G. viridis* could be misidentified as *G. conferta* or *G. gracilis* (e.g. Sfriso & Curiel 2007; Sfriso *et al*. 2009). Superficially, *G. gracilis* thalli resemble those of our new species except for the dark red to purple colour of *G. gracilis*. However, with careful examination, *G. gracilis* has bigger cortical cells (10-μm width, 14 μm long), subcortical cells (40–80 in diameter) and tetrasporangia (30 × 40 μm) (Iyer *et al*. 2004); furthermore, *G. gracilis* has smaller cystocarps (500–700 μm) and less deep male conceptacles (30–40 μm).

In 1992 Gargiulo and collaborators identified an exsiccata from Chioggia (Levi, no date, MS-33076-04) as *G. conferta*; the thalli were characterized by some morphological features similar to those of *G. viridis*, e.g. terete filaments with a main axis diameter < 1.5 μm and dense bushy or spiny branching in the distal portions. However, our new species is larger, reaching an height of 30–35 cm, instead of the 8 cm reported by Gargiulo *et al*. (1992). Also, our species never has a wine-red colour – it is always green-yellowish, with at most a few

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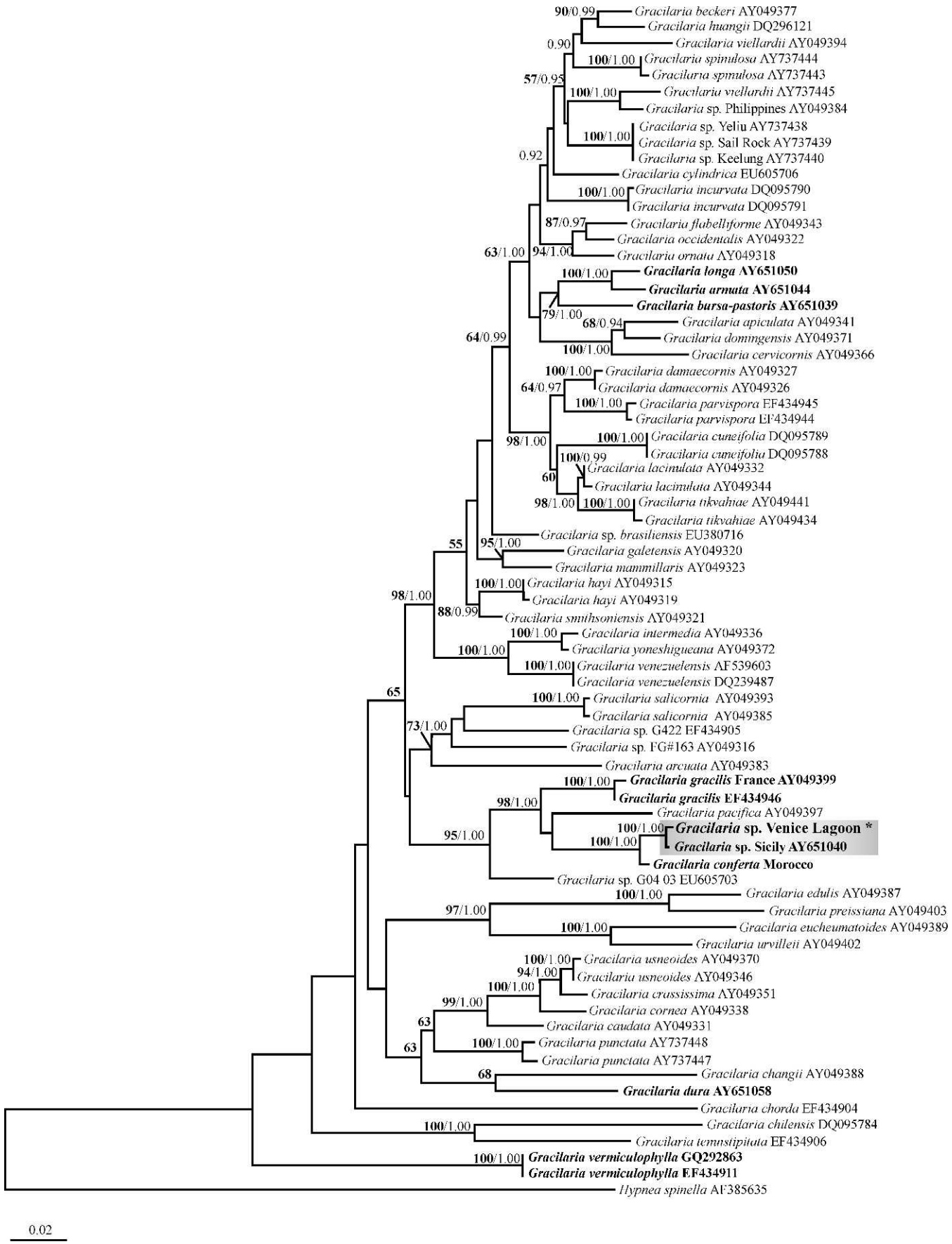
Fig. 12. ML tree inferred from *rbc*L gene sequences, calculated using the GTR+I+Γ model of evolution. Numbers near nodes indicate bootstrap values (>50%) for ML analysis (in bold black font), and posterior probabilities (in normal font). The new species sequence determined in this work is evidenced in bold, in higher size and marked with an asterisk. The Mediterranean species sequences are indicated in bold. Scale bar = 0.02 nucleotide substitutions per site.


90/0.99 Gracilaria beckeri AY049377
Gracilaria huangii DQ296121
0.90 Gracilaria viellardii AY049394
100/1.00 Gracilaria spinulosa AY737444
Gracilaria spinulosa AY737443
57/0.95
100/1.00 Gracilaria viellardii AY737445
Gracilaria sp. Philippines AY049384
Gracilaria sp. Yeliu AY737438
100/1.00 Gracilaria sp. Sail Rock AY737439
Gracilaria sp. Keelung AY737440
0.92 Gracilaria cylindrica EU605706
100/1.00 Gracilaria incurvata DQ095790
Gracilaria incurvata DQ095791
87/0.97 Gracilaria flabelliforme AY049343
Gracilaria occidentalis AY049322
63/1.00 94/1.00 Gracilaria ornata AY049318
100/1.00 Gracilaria longa AY651050
Gracilaria armata AY651044
Gracilaria bursa-pastoris AY651039
79/1.00
68/0.94 Gracilaria apiculata AY049341
64/0.99 Gracilaria domingensis AY049371
100/1.00 Gracilaria cervicornis AY049366
100/1.00 Gracilaria damaecornis AY049327
64/0.97 Gracilaria damaecornis AY049326
100/1.00 Gracilaria parvispora EF434945
Gracilaria parvispora EF434944
98/1.00 100/1.00 Gracilaria cuneifolia DQ095789
Gracilaria cuneifolia DQ095788
100/0.99 Gracilaria lacinulata AY049332
60 Gracilaria lacinulata AY049344
98/1.00 100/1.00 Gracilaria tikvahiae AY049441
Gracilaria tikvahiae AY049434
Gracilaria sp. brasiliensis EU380716
55 95/1.00 Gracilaria galetensis AY049320
Gracilaria mammillaris AY049323
100/1.00 Gracilaria hayi AY049315
98/1.00 Gracilaria hayi AY049319
88/0.99 Gracilaria smithsoniensis AY049321
100/1.00 Gracilaria intermedia AY049336
100/1.00 Gracilaria yoneshigueana AY049372
100/1.00 Gracilaria venezuelensis AF539603
Gracilaria venezuelensis DQ239487
65 100/1.00 Gracilaria salicornia AY049393
Gracilaria salicornia AY049385
73/1.00 Gracilaria sp. G422 EF434905
Gracilaria sp. FG#163 AY049316
Gracilaria arcuata AY049383
100/1.00 Gracilaria gracilis France AY049399
Gracilaria gracilis EF434946
98/1.00 Gracilaria pacifica AY049397
100/1.00 Gracilaria sp. Venice Lagoon *
95/1.00 100/1.00 Gracilaria sp. Sicily AY651040
Gracilaria conferta Morocco
Gracilaria sp. G04 03 EU605703
100/1.00 Gracilaria edulis AY049387
97/1.00 Gracilaria preissiana AY049403
100/1.00 Gracilaria eucheumatoides AY049389
Gracilaria urvillei AY049402
100/1.00 Gracilaria usneoides AY049370
94/1.00 Gracilaria usneoides AY049346
100/1.00 Gracilaria crassissima AY049351
99/1.00 Gracilaria cornea AY049338
63 Gracilaria caudata AY049331
100/1.00 Gracilaria punctata AY737448
63 Gracilaria punctata AY737447
68 Gracilaria changii AY049388
Gracilaria dura AY651058
Gracilaria chorda EF434904
100/1.00 Gracilaria chilensis DQ095784
Gracilaria temnstipitata EF434906
100/1.00 Gracilaria vermiculophylla GQ292863
Gracilaria vermiculophylla EF434911
Hypnea spinella AF385635
0.02

reddish parts. Unfortunately, there is only a morphological description for the exsiccata, and no molecular data are available for a comparison.

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