

1 This is an Accepted Manuscript of an article published by Elsevier in *Molecular*
2 *Phylogenetics and Evolution* on 21st June 2020, available at:
3 <https://doi.org/10.1016/j.ympev.2020.106909>

4 Extensive cryptic diversity in the widely distributed *Polysiphonia scopulorum*
5 (Rhodomelaceae, Rhodophyta): molecular species delimitation and morphometric analyses

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20

21 ABSTRACT

22 Our knowledge of seaweed diversity and biogeography still largely relies on information
23 derived from morphological identifications, but the use of molecular tools is revealing that
24 cryptic diversity is common among algae. *Polysiphonia scopulorum* is a turf-forming red alga
25 widely reported in tropical and temperate coasts worldwide. The only study based on material
26 collected from its Australian type locality and the Iberian Peninsula indicates that it is a
27 species complex, but the extent of cryptic diversity across its geographical range is not
28 known. To investigate the species diversity in *P. scopulorum*, the geographical distribution of
29 species-level lineages and their morphological characterization, we collected 135 specimens
30 from Australia, South Africa and southern Europe. Two gene datasets (*cox1* and *rbcL*) were
31 used to delimit species using three methods (GMYC, PTP, ABGD), leading to a consensus
32 result that our collections of the *P. scopulorum* complex comprise 12 species. Five of these
33 species were resolved in a highly supported clade, while the other seven species were related
34 to other taxonomically accepted species or in unresolved parts of the tree. Morphometric and
35 statistical analysis of a set of ten quantitative characters showed that there are no clear
36 morphological correlates of species boundaries, demonstrating true cryptic diversity in the *P.*
37 *scopulorum* complex. Distribution patterns of the 12 species were variable, ranging from
38 species only known from a single site to species with a wide distribution spanning three
39 continents. Our study indicates that a significant level of undiscovered cryptic diversity is
40 likely to be found in algal turfs, a type of seaweed community formed by small entangled
41 species.

42

43 *Keywords:* Algal turfs; Biogeography; *cox1*; Morphology; *Polysiphonia caespitosa*; *rbcL*

44 **1. Introduction**

45 Marine macroalgae show a wide morphological diversity ranging from tiny filamentous to
46 highly complex morphologies (Coomans and Hommersand, 1990). Morphological species
47 delineation in algae is often problematic due to a lack of useful characters and phenotypic
48 plasticity, and this problem is more severe for algae with simple morphologies (Verbruggen,
49 2014). For this reason, it has become common practice to use molecular tools to delimit
50 species in algae, leading to the discovery of substantial cryptic diversity (e.g. Guillemin et al.,
51 2016; Leliaert et al., 2014, 2018; Yang et al., 2018; Pezolesi et al., 2019; Camacho et al.,
52 2019; Kang et al., 2019).

53 Algal turf is an assemblage that consists of densely entangled small macroalgae
54 (Connell et al., 2014). It comprises of many species of red, brown and green algae, many of
55 which evolved a similar body plan consisting of prostrate axes attached to the substratum by
56 rhizoids and erect axes where the reproductive structures develop (Price and Scott, 1992;
57 Díaz-Tapia and Bárbara, 2013, 2014). The small size, similar overall morphology and
58 densely entangled nature of turf algae makes biodiversity surveys and taxonomic work
59 particularly challenging and labour-intensive. Because of their structural simplicity and
60 similar body plan, it seems likely that cryptic diversity will be prevalent among turf algae
61 (e.g. Verbruggen et al., 2009; Díaz-Tapia and Bárbara, 2013; Díaz-Tapia et al., 2018b, 2020).

62 While the use of molecular data is well established as a primary source of information
63 for algal species delineation, it remains important to characterise morphological traits of the
64 discovered species. This information allows an understanding of whether and how
65 morphological data can be used as a proxy trait to recognise species defined through DNA
66 data, and to arrive at satisfactory nomenclatural decisions that reconcile the newly proposed
67 taxonomies with previously described species names. Most taxonomists prefer to work with

68 discrete morphological traits, but those are not always available, particularly in structurally
69 simple taxa. In such situations like that, morphometric analyses focusing on measurable traits
70 can be used, and there are several examples of their application in algal taxonomy
71 (Verbruggen et al., 2005a,b, 2017; Meynard et al., 2019).

72 The red algal genus *Polysiphonia* is a very commonly encountered member of algal
73 turfs. It is the largest genus in the red algal family Rhodomelaceae, with 191 currently
74 accepted species (Guiry and Guiry, 2020). The morphological complexity of *Polysiphonia* is
75 relatively high, with many macroscopic and microscopic qualitative diagnostic characters for
76 species delineation (Stuercke and Freshwater, 2008). However, the high diversity of species
77 within this genus still makes many species share an identical set of qualitative characters,
78 imposing limits to basing taxonomy on morphology (Díaz-Tapia et al., 2017a). *Polysiphonia*
79 *scopulorum* Harvey is a turf-forming species originally described from Rottnest Island
80 (Western Australia) that has since been reported in tropical and temperate regions of the
81 Indian, Pacific and Atlantic oceans based on morphological identifications (Harvey, 1855;
82 Guiry and Guiry, 2020). Specimens from South Africa were described as a separate species,
83 *P. caespitosa* (Pocock) Hollenberg, that was later synonymised with *P. scopulorum* based on
84 morphological studies (Stegenga et al., 1997; Rull Lluçh, 2002). The taxonomy of these two
85 names was never studied using molecular information and is still unclear. The *rbcL*
86 sequences of *P. scopulorum* presently available on GenBank from Spain and Western
87 Australia suggest that *P. scopulorum* might be a species complex with separate species in
88 these two regions (Huisman et al., 2017).

89 Our goal in this study is to investigate species boundaries in the *Polysiphonia*
90 *scopulorum* complex using a large collection of samples from the Indian, Pacific and Atlantic
91 oceans. We aim to determine the number of species present in the *P. scopulorum* complex,
92 their geographical distributions, and whether morphological information can be used to

93 differentiate among them. Our approach consists of analyses of *rbcL* and *cox1* alignments
94 using a range of species delimitation algorithms. Quantitative morphometric analyses are
95 used to identify the morphological correlates of species boundaries.

96

97 **2. Material and methods**

98 *2.1 Field collections and morphological identification*

99 Samples of *Polysiphonia* were collected from Europe (Atlantic Iberian Peninsula, Azores,
100 Canary Islands, Mediterranean), Australia (Western Australia, South Australia, Victoria,
101 Tasmania) and South Africa (Table S1 in Supplementary Material). Samples were collected
102 using a knife for scraping the algal turfs in the intertidal during low tide, or in the upper
103 subtidal by snorkelling. Samples were placed in plastic bags and transported to the laboratory
104 where they were carefully cleaned and isolated using a stereomicroscope. Materials for DNA
105 extraction were dried in silica gel desiccant. Plants for morphological examination were
106 preserved in 4% formalin seawater at 4°C and stored in the dark.

107 Specimens of *Polysiphonia scopulorum* were morphologically identified using the
108 available references for each sampled region (Rojas-González, 1997; Stegenga et al., 1997;
109 Womersley, 1979, 2003; Díaz-Tapia and Bárbara, 2013). Specimens morphologically
110 identified in this study as *P. scopulorum* presented the following key characters that are in
111 agreement with previous descriptions of the species and differ from other recorded species in
112 the respective regions: dorsiventral habit with extensive prostrate axes that lack trichoblasts
113 in their apical cells and that bear short erect axes (up to 2 cm in length), thallus brownish-red
114 to black in colour with a fairly rigid texture, rhizoids unicellular in open connection with the
115 pericentral cells, axes with four pericentral cells and (35-) 50-100 (-110) µm in diameter,
116 erect axes unbranched or bearing irregularly arranged branches that are often adventitious,

117 branches independent of trichoblasts, apical cells dome-shaped and trichoblasts from absent
118 to well developed spirally arranged on every segment. According to this definition, we
119 excluded from our analysis specimens referred to *P. villum* J.Agardh or *P. scopulorum* var.
120 *villum* (J.Agardh) Hollenberg, that are red in colour and flaccid in texture (PD pers. obs. on
121 our own collections and images available at <http://www.boldsystems.org/>), making them easily
122 distinguishable from specimens here assigned to the *P. scopulorum* complex.

123

124 2.2 DNA extraction and sequencing

125 DNA was extracted from silica gel-dried material following Saunders and McDevit
126 (2012) or an adapted cetyltrimethylammonium bromide (CTAB) protocol (Doyle and Doyle,
127 1987). PCR amplification of *rbcL* was carried out using primers F57/*rbcL*revNEW, F2/
128 R1008, F2/R1464 or F2/R1452 (Saunders and Moore, 2013; Díaz-Tapia et al., 2018b). PCR
129 amplification of *cox1* was carried out using the newly designed forward primer 97F (5'
130 GCTTTTGCWGGWRTTTTAGGAGG 3'), and reverse primer 1023R (5'
131 CCTTCCTCACATWGTWGCAATTCA 3'). Reactions were performed in a total volume of
132 25 µl, consisting of 5 µl 5× MyTaq™ reaction buffer, 0.7 µl 10 µM of forward and reverse
133 primers, 0.125 µl 1U µl⁻¹ My Taq™ DNA Polymerase (Bioline, London, UK), 17.475 µl
134 MilliQ® water and 1 µl template DNA. The PCR profile consisted of initial denaturation
135 (93°C for 3 min), 35 cycles of denaturation (94°C for 30 s), primer annealing (45°C for 30 s),
136 and extension (74°C for 90 s) and final extension (74°C for 5 min). The PCR products were
137 purified and sequenced by Macrogen (Korea) or the sequencing service of the University of
138 A Coruña.

139

140 2.3 Molecular species delimitation

141 Sequences of the *rbcL* and *cox1* genes of samples morphologically identified as *Polysiphonia*
142 *scopulorum* collected from Australia, South Africa and Europe were used for the molecular
143 analysis. We also included in our analyses sequences from 11 other species that were
144 resolved in the same major clade in previous studies, as well as four species placed in a sister
145 clade that were used as the outgroup (Díaz-Tapia et al., 2017b). GenBank accession numbers
146 of the used sequences are provided in Table S1 (in Supplementary Material). The sequences
147 were checked for quality, corrected and aligned in Geneious Prime using MUSCLE (Kearse
148 et al., 2012). Two alignments were produced with 214 *rbcL* sequences (135 of *P. scopulorum*
149 and 79 sequences of other species) and 158 *cox1* sequences (128 of *P. scopulorum* and 30
150 sequences of other species). Identical sequences were removed from both alignments with the
151 longest sequences retained, leaving 55 *rbcL* sequences (25 of *P. scopulorum* and 30
152 sequences of other species) and 42 *cox1* sequences (33 of *P. scopulorum* and 9 sequences of
153 other species). Ultrametric trees were built with the unique alignments in BEAST v1.8.4
154 (Suchard et al., 2018) using GTR and Gamma + Invariant Sites models, uncorrelated relaxed
155 clock and Coalescent: Constant Size tree prior, run for the default number of states.
156 Maximum Likelihood (ML) trees were also built for both unique alignments using RAxML
157 8.1 (Stamatakis, 2014). GTR-Gamma was used as the nucleotide substitution model and
158 branch support was estimated with 1000 bootstrap replicates.

159 Three species delimitation algorithms were applied to both the *rbcL* and *cox1*
160 alignments; Automatic Barcode Gap Discovery (ABGD; Puillandre et al., 2012a),
161 Generalized Mixed Yule Coalescent (GYMC; Fujisawa and Barraclough, 2013), and Poisson
162 tree processes (PTP; Zhang et al., 2013). ABGD was run on the full alignments using default
163 settings from an online server (<http://wwwabi.snv.jussieu.fr/public/abgd/abgdweb.html>),
164 GMYC was run on the BEAST trees in R v3.5.2 and PTP on the RAxML trees in Python.

165 The results of each of the analyses were then compared and used to inform the samples used
166 for the morphometric analysis.

167 In order to visualise haplotype variability in the *cox1* gene and the geographical
168 distribution of haplotypes for the resolved clade that included the largest number of samples,
169 we clustered them using the TCS method (Clement et al., 2000) in POPART (Leigh and
170 Bryant, 2015).

171

172 *2.4 Morphometric analysis and morphological observations*

173 For morphometric data collection, wet preserved samples were mounted in 20% Karo®
174 Syrup solution (ACH Foods, Memphis, Tennessee, USA) and photographs of all parts of the
175 samples were taken under a light microscope. Measurements of characters for each sample
176 were then made digitally using the photographs in ImageJ (Schneider et al., 2012).

177 Quantitative data was collected for 10 characters (Fig. 1), taken from non-branching areas of
178 mature, non-damaged tissue, with five replicates of each measurement per sample. Data was
179 collected from 28 samples in total, including representatives of each of the species inferred
180 by the molecular data analysis. The number of samples available for each inferred species
181 was unequal, ranging from 1 to 43 (Table S1 in Supplementary Material), and at least two
182 samples were selected when possible.

183 The morphometric data were analysed with multivariate statistics in R v3.5.2. The
184 measurements were averaged across replicates within a sample to produce a dataset with one
185 entry per sample. In order to visualise the overall morphospace of *P. scopulorum*, a principal
186 components analysis was carried out with the FactoMineR package (Lê et al. 2008).

187 Discriminant analysis was carried out to identify the morphological differences between the *a*
188 *priori* groups (i.e., the candidate species based on molecular data) using the candisc package.

189 A second DA was performed on samples from a subset of candidate species to further
190 distinguish between them.

191

192 **3. Results**

193 *3.1 Phylogeny and molecular species delimitation*

194 The summary of the results for the GMYC, PTP and ABGD analyses for the *rbcL* and *cox1*
195 datasets were mapped onto a RAxML tree constructed using the *rbcL* dataset (Fig. 2).

196 For the *rbcL* sequence data, the delimitation analyses were completely congruent and
197 suggest there are 12 separate molecular candidate species within the *Polysiphonia*
198 *scopulorum* complex, which are numbered 1-12 in the figure (Fig. 2). The relationships
199 among candidate species were resolved in some cases but not in others, and it is clear from
200 the RAxML phylogeny that the *P. scopulorum* complex is not monophyletic, with other
201 named species present in the lineage (Fig. 2). *Polysiphonia scopulorum* 2-6 were resolved in
202 a highly supported clade and *P. scopulorum* 10 and 11 were placed as sister taxa but this
203 relationship was unsupported. These two independent clades were placed as sister to clades
204 including other currently recognized species. *Polysiphonia scopulorum* 7 was placed with
205 high support as sister to *P. adamsiae* Womersley. *Polysiphonia scopulorum* 1, 7, 8, 9 and 12
206 were placed in the phylogeny among other currently recognized species and their
207 phylogenetic relationships were unresolved.

208 The delimitation analyses of the *cox1* sequence data were fairly congruent, but they
209 differed slightly in the number of delimited molecular species hypothesis (11, 10 and 9 in
210 GMYC, PTP and ABGD, respectively) and the clades resolved as separate species (Fig. 2).
211 *Polysiphonia scopulorum* 7 was separated as two hypothetical species in GMYC and *P.*
212 *scopulorum* 11 was divided into two hypothetical species in GMYC and PTP. *Polysiphonia*

213 *scopulorum* 2, 10 and 12 were not represented in *cox1* dataset due to PCR amplification
214 failure.

215 Divergences between the candidate species were higher than intraspecific divergences
216 for both *rbcL* and *cox1* in the analysed dataset. Interspecific divergences ranged from 0.9% to
217 8.7% while intraspecific variability was $\leq 0.5\%$ for the *rbcL* gene (Table S2 in Supplementary
218 Material). Interspecific divergences were higher in *cox1*, ranging from 3.1% to 11.7%, while
219 intraspecific divergence $\leq 2.6\%$ (Table S3 in Supplementary Material).

220 Only four of the candidate species identified in this study matched with sequences
221 deposited in GenBank, while molecular data was not previously published for the other eight
222 candidate species. Four *rbcL* sequences of *Polysiphonia scopulorum* newly determined in this
223 study were identical to three available sequences in GenBank (MF139308-10, Huisman et al.,
224 2017). An *rbcL* sequence of *P. scopulorum* from GenBank (JX828149, Bárbara et al., 2013)
225 was identical to several of our sequences of *P. scopulorum* 4. An *rbcL* sequence extracted
226 from the complete plastid genome of a specimen identified as *P. scopulorum* (MF093999,
227 Díaz-Tapia et al., 2017b) was identical to several of the newly determined sequences
228 assigned to *P. scopulorum* 6. Finally, an *rbcL* sequence assigned in GenBank to *Polysiphonia*
229 sp. (MH101826, Díaz-Tapia et al., 2018a) matched *P. scopulorum* 7.

230

231 3.2 Species distributions

232 Four of the candidate species were abundant in the sampling sites and were collected in at
233 least four different localities (Fig. 3). *Polysiphonia scopulorum* 7 was abundantly collected in
234 South Australia, Victoria and Tasmania. Other three of the abundant candidate species (3, 4
235 and 6) were resolved in the same clade with high support (Fig. 2). *Polysiphonia scopulorum* 4
236 had the widest distribution, as it was found in several localities from South Africa, southern

237 Europe, the Azores, as well as a single site in South Australia. The haplotype network of *cox1*
238 sequences from three regions shows six haplotypes that differ among regions, one found in
239 Azores, one in South Australia and four in South Africa (Fig. 4). The closely related *P.*
240 *scopulorum* 3 was only found in the Canary Islands where it was common and a single *cox1*
241 haplotype was detected (Figs 3 and 4). *Polysiphonia scopulorum* 6 was abundantly collected
242 in the Australian states Victoria and Tasmania, as well as a single site in South Australia (Fig.
243 3). Six *cox1* haplotypes were identified, two found in both Tasmania and eastern Victoria,
244 one exclusive to Tasmania, two only found in western Victoria and one in South Australia
245 (Fig. 4). In the same clade were also resolved *P. scopulorum* 5, a rare species collected only
246 in two sites from Western Australia, and *P. scopulorum* 2 that was found in a single site of
247 the French Riviera (Fig. 3).

248 Eight of the candidate species were rare, collected from one or two localities only
249 (Fig. 3). Among them, only *Polysiphonia scopulorum* 9 had a wide distribution in Australia
250 that included Western Australia and Queensland. However, the sample from Queensland was
251 collected on a pontoon in a marina, suggesting that this could be an introduced species in this
252 region. Most of the rare candidate species were found in Australia, except *P. scopulorum* 2
253 from the French Riviera.

254 In most sampling sites, only one candidate species was found, but some of the
255 Australian localities yielded up to three candidate species. On Rottnest Island, the type
256 locality of *Polysiphonia scopulorum*, we identified three different candidate species (Fig. 3).

257

258 *3.3 Morphometric analysis*

259 The principal components analysis of the morphometric data reveals the overall structure of
260 the morphospace of *Polysiphonia scopulorum* (Fig. 5). The variable structure (grey dotted

261 vectors) indicates that there are three major groups of correlated variables, the first composed
262 of axes and rhizoid diameters (4th quadrant: PAXsegdia, EAXsegdia, RHdia), the second
263 related to cell lengths of the erect axes (1st quadrant: EAXcytlen, EAXseglen), and the third
264 related to overall cell size of prostrate axes (along x-axis: PAXcytlen, PAXcytdia,
265 PAXseglen). Samples are spread continuously across the first two axes, indicating that no
266 groupings clearly stand out and that there is morphological continuity across the various
267 candidate species. Samples belonging to the same candidate species tend to cluster near one
268 another on the biplot, but there is substantial overlap between the candidate species.
269 Generally speaking, no clear separation of any candidate species is apparent on the biplot,
270 except perhaps for some candidate species found on the extremity of the morphospace (e.g.
271 *P. scopulorum* 10 and 11 on the left on the biplot), but only a single sample of each of these
272 candidate species was available to us and the full range of morphological variability of these
273 species is likely to be larger.

274 A discriminant analysis was carried out aiming to find those dimensions in the
275 morphometric data with which the species are best separated. The biplot of this analysis (Fig.
276 6) shows wider separation of some candidate species, especially along the x-axis, but many
277 species remain very close to one another and the polygons for the best represented candidate
278 species (*Polysiphonia scopulorum* 4, 6, 7) showed clear overlap. The diameter of cells in the
279 erect axis (EAXcytdia) is most strongly correlated with the x-axis, suggesting this is a key
280 trait in which some species could be recognised. A second overall dimension along which
281 some candidate species appear to be separated runs from the bottom left to the top right of the
282 graph and is correlated with the diameters of axes and rhizoids (EAXsegdia, RHdia,
283 PAXsegdia).

284 Because separation between *Polysiphonia scopulorum* 4, 6 and 7 appears particularly
285 problematic, we ran a second discriminant analysis just on the samples of those three species.

286 The biplot of that analysis (Fig. 7 A) represents nearly all the variation in the dataset but still
287 fails to separate *P. scopulorum* 4 (yellow) from *P. scopulorum* 6 (navy), indicating that these
288 species are indistinguishable. *Polysiphonia scopulorum* 7 samples are separated from the
289 other two species along the first axis, suggesting that characters with a high score against that
290 axis may help in identifying that species. The positive correlation with EAXsegdia, RHdia
291 suggests that *P. scopulorum* 7 has wider erect axes and rhizoids, and the negative correlation
292 with EAXcytlen suggests shorter cells. However, density plots – a smoothed version of
293 histograms – show significant overlap between the three species for all of these candidate
294 variables, a clear testament that for practical taxonomic purposes, these candidate species are
295 entirely indistinguishable based on these morphometric traits (Fig 7 B-D).

296

297 3.5. Tetrasporangial cover cells

298 Our examinations of the morphology of the studied specimens also revealed a qualitative
299 character useful for distinguishing some groups of candidate species. *Polysiphonia*
300 *scopulorum* 3-6, 8, 9 and 11 had tetrasporangia with three cover cells (Figs. S1 A-D, F-H),
301 while *P. scopulorum* 7 had tetrasporangia with two cover cells (Fig. S1 E). Tetrasporangia
302 were not observed in *P. scopulorum* 1, 2, 10, 12. According to Huisman et al. (2017), *P.*
303 *scopulorum* 1 has tetrasporangia with two cover cells.

304

305 4. Discussion

306 This study revealed the existence of extensive cryptic diversity among specimens
307 morphologically identified as *Polysiphonia scopulorum*. The combination of analyses of two
308 molecular markers, *rbcL* and *cox1*, and three methods for species boundaries delineation led
309 us to a consensus of 12 candidate species within the allegedly widely distributed species (Fig.

310 3A; Guiry and Guiry, 2020). Distribution patterns and frequency of these candidate species
311 were highly variable, ranging from rare species only known from one site to widely
312 distributed species including three continents. Morphometric analyses revealed that while
313 some species may be distinguishable based on combinations of quantitative traits,
314 morphological overlap between species is prevalent.

315

316 *4.1 Species delimitation*

317 The use of the *rbcL* molecular marker was more decisive for establishing boundaries between
318 candidate species in our dataset than *cox1*. Results obtained with the analysis of the *rbcL*
319 gene were totally congruent among the three used methods. By contrast, each of the three
320 methods applied to the *cox1* dataset resolved a different number of species and slightly
321 differed in the clades resolved as candidate species. This is in line with the high variability
322 observed in the performance between markers and methods in other red algal datasets (e.g.
323 Payo et al., 2013; Liu et al., 2015; Guillemin et al., 2016; Jesús et al., 2019) and further
324 supports the importance of using multi-locus approaches in species diversity assessments
325 (Leliaert et al., 2014). An advantage of using *cox1* is that sequence divergences among
326 candidate species is higher, producing a clearer barcoding gap than *rbcL* (Guillemin et al.,
327 2016). However, in our dataset, even though the intra- and interspecific divergences were
328 lower in the *rbcL* gene, they did not overlap. A recurrent problem with the use of *cox1* for
329 algae is the failure of PCR reactions as a consequence of primer mismatches (Sherwood et
330 al., 2010; Saunders and McDevit, 2012; Díaz-Tapia et al., 2017a) and large introns in the
331 gene in green seaweeds (Repetti et al., 2020). In this study we used an alignment of complete
332 *cox1* sequences for representative species of the family Rhodomelaceae in order to design
333 new primers for an amplicon of about 850 bp. This amplicon did not correspond to the

334 previously used COI5P region (Saunders and McDevit, 2012), but overlapped it by 540 bp.
335 Even with these custom-designed primers in more conserved regions than previously used
336 primer sets, we were unable to obtain PCR products for three of the studied species
337 (*Polysiphonia scopulorum* 2, 10 and 12).

338 Among the 12 consensus candidate species resolved within the *Polysiphonia*
339 *scopulorum* complex based on the molecular data, only five were resolved in a highly
340 supported clade (species 2-6) while the other seven were interspersed between other
341 taxonomically accepted species. Our *rbcL* phylogeny lacks resolution along the backbone of
342 the tree, a common problem in algal phylogenies constructed based on a single molecular
343 marker (Oliveira et al., 2018), and it is possible that a better resolved phylogeny would reveal
344 that some of these candidate species would cluster together into larger lineages. But even if
345 considering the possibility that some candidate species are sister lineages of one another, the
346 high sequence divergence among them (≥ 5.4 and 4.4% in the *cox1* and *rbcL* genes,
347 respectively) leave no doubt that *P. scopulorum* 1, 7, 8-12 represent distinct species.

348 Five of the candidate species resolved by the molecular delineation of species
349 boundaries were placed in a highly supported clade in the *rbcL* phylogenetic tree
350 (*Polysiphonia scopulorum* 2-6). All the analyses support their separation based on molecular
351 data, and even GMYC and PTP for the *cox1* gene resolved one additional species. A
352 consensus among methods and molecular markers is often used as the major argument for
353 establishing species delineation in monophyletic groups. However, additional evidence
354 provided by morphological or distributional information should be also critically considered
355 before adopting taxonomic decisions (Puillandre et al., 2012b; Kekkonen and Hebert, 2014;
356 Guillemin et al., 2016; Jesús et al., 2019). Two pairs of species were found to cohabit in the
357 same sampling sites; *P. scopulorum* 2 and 4 in the French Riviera and *P. scopulorum* 4 and 6
358 in South Australia. The finding of two sympatric candidate species is an indication of genetic

359 isolation among them and used as an argument for supporting species separation (Kekkonen
360 and Hebert, 2014).

361

362 4.2. Biogeographic patterns

363 Distribution patterns of the putative species were variable, ranging from species only known
364 in a single site to species with a wide distribution that covers three continents. Such
365 variability is unsurprising and similar results were observed in other red algal studies that
366 included molecular data from sampling wide geographical areas (Zuccarello et al., 2002a, b;
367 Won et al., 2009; Díaz-Tapia et al., 2018b).

368 Six species were only found once and each in a single locality, suggesting a high
369 endemism and rarity of many of the discovered species. High levels of endemism have been
370 found in other cryptic seaweed species (Tronholm et al., 2012; Payo et al., 2013; Pardo et al.,
371 2014; Leliaert et al., 2018; Guillemain et al., 2016; Díaz-Tapia et al., 2018b) and these results
372 are concordant with the limited dispersal ability of the red algae (Santelices, 1990; Kinlan
373 and Gaines, 2003). However, the distribution of the rare species could be wider but was not
374 detected in our collections because several regions where *Polysiphonia scopulorum* was
375 reported remain unexplored (Fig. 3). Pacific North America was not sampled in this study,
376 but species here included in the *P. scopulorum* complex were not found in a recent extensive
377 survey of *Polysiphonia* spp in this region using molecular tools (Savoie and Saunders, 2019).
378 Most probably, records of *P. scopulorum* from this region actually correspond to *P. villum*,
379 congruent with results by Savoie and Saunders (2019, as *P. scopulorum* var. *villum*). By
380 contrast, molecular data of *P. scopulorum* from tropical regions are completely absent and the
381 potential presence of the putative species here identified is uncertain. Besides potentially
382 broadening the distribution of some of the cryptic species detected here, it is highly likely that

383 a further sampling would result in the discovery of additional cryptic species. This is
384 particularly likely to be the case in tropical regions, where algal turfs are extremely common
385 (Price and Scott, 1992; Littler and Littler, 2013) and less intensively studied than in the
386 warm-temperate regions that form the focus of our work. Tropical turfs have scarcely been
387 studied using molecular tools and we predict that they will turn out to be a treasure trove of
388 new species and cryptic diversity, including but certainly not limited to the *P. scopulorum*
389 complex.

390 Interestingly, two of the three putative species identified in Rottnest Island, the type
391 locality of *Polysiphonia scopulorum*, were only found in Western Australia, while one of
392 them was also collected in a marina in Queensland and further collections are required to
393 clarify whether it is native or introduced in this state. Thus, according to our data the genuine
394 *P. scopulorum* is endemic to Australia, congruent with conclusions in previous studies
395 (Huisman et al., 2017), and *P. scopulorum* has a narrow distribution rather than the wide
396 distribution reported based on morphological identifications (Fig. 3A; Guiry and Guiry,
397 2020).

398 *Polysiphonia scopulorum* 4 has a wide distribution that comprises South Africa,
399 southern Europe and Australia and this is the only species of the complex that we detected in
400 South Africa, the type locality of *P. caespitosa*. This is one of the few examples in which the
401 wide distribution of a seaweed species, encompassing at least three continents without a clear
402 human-mediated dispersal, has been demonstrated using molecular data (but see Zuccarello et
403 al., 2002a; Won et al., 2009; Díaz-Tapia et al., 2018b). Within *P. scopulorum* 4 we identified
404 multiple *cox1* and *rbcL* haplogroups with a strong phylogeographic structure, so that each
405 haplogroup was only present in a particular region (Fig. 4). This structure is congruent with
406 the occurrence of rare dispersal events followed by genetic divergence of the resulting
407 populations isolated by distance. Similar processes have been suggested to explain the

408 genetic structure of other macroalgae and marine organisms (Palumbi, 1994; Tronholm et al.,
409 2012; Díaz-Tapia et al., 2018b). *Polysiphonia scopulorum* 4 was abundantly collected in
410 several sites from South Africa and Europe, while a single specimen was detected in South
411 Australia. This finding might correspond to a relatively recent dispersal event, and we cannot
412 rule out that it could be human mediated. There are several examples of algal introductions in
413 Australia, and *Polysiphonia* spp are among the most frequently introduced seaweeds
414 (Williams and Smith, 2007; Piñeiro-Corbeira et al., 2019). However, the South Australian
415 specimen was collected in a National Park, more than 60 km away from potential vectors for
416 marine species introductions such as harbours or aquaculture facilities (PIRSA, 2017).

417 *Polysiphonia scopulorum* 3, 6 and 7 were regionally abundant and represent
418 intermediate examples between rare species with narrow distributions and widely spread
419 species. *Polysiphonia scopulorum* 6 and 7 share the same range and were abundantly found
420 in South Australia, Victoria and Tasmania. Likewise, *P. scopulorum* 3 was abundantly
421 collected in the Canary Islands and our results suggest that it is endemic to this volcanic
422 archipelago. This is the most common scenario found when cryptic diversity is detected in
423 seaweed species (Won et al., 2009; Pardo et al., 2014; Guillemín et al., 2016; Pezsolesi et al.,
424 2019; Jesús et al., 2019).

425

426 4.3 A case of true cryptic diversity

427 The 12 species resolved based on molecular data share the full set of qualitative traits
428 available for species identification and delimitation in *Polysiphonia* and related genera
429 (Stuercke and Freshwater, 2008). However, a detailed study of additional morphological
430 characters allowed us to find one qualitative trait that distinguishes two groups of species. *P.*
431 *scopulorum* 7 and 1 have tetrasporangia with two cover cells (this work; Huisman et al.,

432 2017), while all the other species in which tetrasporangia were observed had three cover cells
433 (*P. scopulorum* 3-6, 8, 9 and 11). This appears to be a consistent character that varies among
434 species of the tribe Polysiphonieae and can be used for species identification (Díaz-Tapia and
435 Bárbara, 2013; Díaz-Tapia et al., 2017c, 2018a), but its utility hinges on the studied plants
436 being reproductive tetrasporophytes, which will not always be the case, and we were unable
437 to score this trait for *P. scopulorum* 1, 2, 10 and 12 for this reason.

438 Considering that qualitative characters clearly cannot distinguish between the 12
439 species in the complex, morphometric analyses of quantitative traits might provide a proxy
440 for morphological species recognition. This approach has been successfully applied in
441 previous algal studies, allowing the delineation of morphologically similar species in genera
442 of the green and red algae (Verbruggen et al. 2005a,b; Meynard et al. 2019). The term
443 “cryptic diversity” has been often applied to groups of morphologically similar seaweed
444 species unmasked when applying molecular tools. However, more detailed morphological
445 investigation often finds previously overlooked traits in which they differ, making them
446 pseudo-cryptic species (e.g. Camacho et al., 2019; Jesús et al., 2019; Meynard et al., 2019).
447 In the case of the *Polysiphonia scopulorum* complex, however, morphometric analyses of
448 cells, segments and rhizoids showed a morphological continuum across the candidate species,
449 demonstrating that the complex is an example of true cryptic diversity, where species cannot
450 be distinguished despite detailed morphometric and statistical analysis. While some of the
451 species may be distinguishable using complex combinations of variables in discriminant
452 analyses (e.g. *P. scopulorum* 7 in Fig. 7A), this does not enable us to identify these species in
453 a practical taxonomic sense, as the species show significant overlap in all relevant variables
454 (Fig. 7B-E).

455

456 **Conclusions**

457 This work demonstrates that the turf-forming algae *Polysiphonia scopulorum* is actually a
458 complex in which 12 putative species were resolved based on molecular data. Most of them
459 are morphologically indistinguishable and this is, to our knowledge, the first example of
460 cryptic diversity of seaweeds demonstrated by a detailed study of qualitative characters and
461 morphometric traits analysed statistically. Biogeographic patterns greatly differed among
462 species, suggesting that they displayed different evolutionary histories despite they being
463 highly similar in habitat and morphology. Our work evidenced that the *P. scopulorum*
464 complex requires taxonomic revision, including an assessment of how the discovered
465 molecular entities map to available names (i.e. *P. scopulorum* and *P. caespitosa*), the
466 recognition of new species for the non-monophyletic lineages, and a critical assessment of the
467 species delineation in the clade that groups *P. scopulorum* 2-6. Our study also is a clear
468 testament to the need to improve our understanding of the species diversity in algal turfs, a
469 type of community that is commonly neglected in general diversity surveys because working
470 with intermixed small-sized species is tedious. But it is very timely to develop a better
471 knowledge of the diversity in algal turfs, as this type of community is replacing kelp forests
472 in temperate ecosystems and corals in tropical regions as a consequence of global change
473 (Filbee-Dexter and Wernberg, 2018; O'Brien and Scheibling, 2018).

474

475 **Acknowledgements**

476 We warmly thank the members of the Verbruggen lab (J. Costa, V. Marcelino, M. Brookes,
477 C. Cremen, G. Bribiesca-Contreras and C. Jackson), as well as other colleagues (I. Bárbara,
478 K. Dixon, L. Le Gall, M. Verlaque, L. Muñoz, A. Neto) for providing assistance during field
479 and lab work. We also thanks to the Parks Victoria and Bush Blitz teams for assistance in the

480 field. This research was supported by computational facilities of Centro de Supercomputación
481 de Galicia (CESGA).

482

483 **Funding**

484 This work was supported by Xunta de Galicia [“Axudas de apoio á etapa de formación
485 posdoutoral” (grant ED481D/2017/011) and “Talento Senior” (grant 03IN858A2019-
486 1630129) to PDT] and the Australian Biological Resources Study (ABRS) [TTC216-03 and
487 RFL213-08]. Funding for the field and molecular work was provided by the Australian
488 Biological Resources Study, including participation in a Bush Blitz expedition, a Bush Blitz
489 Strategic Taxonomy Grant (TTC216-03) and a National Taxonomy Research Grant
490 (RFL213-08). Field work in Western Australia, Queensland and Tasmania was made possible
491 through funding from the Holsworth Wildlife Research Endowment. Sampling in the
492 Mediterranean was made possible through funding from the British Phycological Society.

493

494 **Appendix A. Supplementary material**

495 Supplementary material

496 **Fig. S1.** Tetrasporangia cover cells in the *Polysiphonia scopulorum* complex. A-G and H: *P.*
497 *scopulorum* 3-9 and 11, respectively. Detail of erect axes showing tetrasporangia (t), with two
498 presporangial cover cells (pr), a postsporangial cover cell (po) and a scar cells of trichoblasts
499 (sc). Tetrasporangia not shown in A, E and H because they are in a lower focal plane. The
500 postsporangial cover cell is absent in E, and scar cells are absent in G. Scale bars: 40 µm.

501 **Table S1.** Specimens collection information indicating the ones used in morphometric
502 analyses (M), GenBank accession numbers and length of the sequences.

503 **Table S2.** Percentage (above) and number (down) of bases that differ among species *rbcL*
504 sequences included in our alignment.

505 **Table S3.** Percentage (above) and number (down) of bases that differ among species *cox1*
506 sequences included in our alignment.

507

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716

717

718 **Figure legends**

719 **Fig. 1.** A: Thallus of *Polysiphonia scopulorum* consisting on prostrate axes (pa) with rhizoids
720 (r) and erect axes (ea). Quantitative variables measured for morphometric data analysis are
721 indicated on erect (B) and prostrate (C) axes. Their legend includes the abbreviations used in
722 Figs 5-7. Scale bars: 1 mm (A); 120 μ m (B, C).

723 **Fig. 2.** RAxML tree inferred using *rbcL* sequence data. Results of analyses of molecular data
724 using GMYC, PTP and ABGD for the *Polysiphonia scopulorum* complex were mapped in
725 this tree and are indicated by vertical bars on the right. Values at nodes indicate bootstrap
726 support (BP) when >70 .

727 **Fig. 3.** Distribution of *Polysiphonia scopulorum*. (A) Distribution of *P. scopulorum* according
728 to morphological identifications indicated with red lines (Guiry and Guiry, 2020; and
729 references therein). (B-D) Maps of southern Europe, South Africa and Australia and showing
730 distribution of the putative species in the *P. scopulorum* complex resolved in the analyses of
731 molecular data. Numbers in the legend correspond to the numbers of the 12 *P. scopulorum*
732 species identified in the tree (Fig. 2). The red and blue stars indicate the type localities of *P.*
733 *scopulorum* and *P. caespitosa*, respectively.

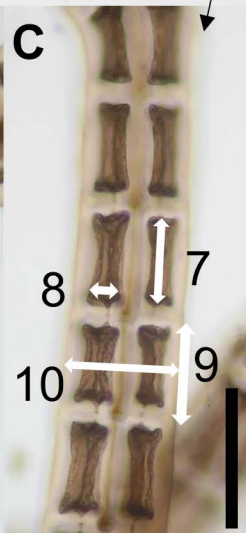
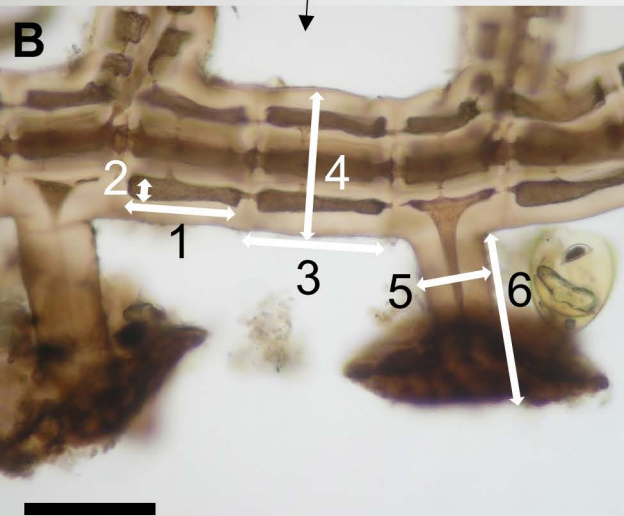
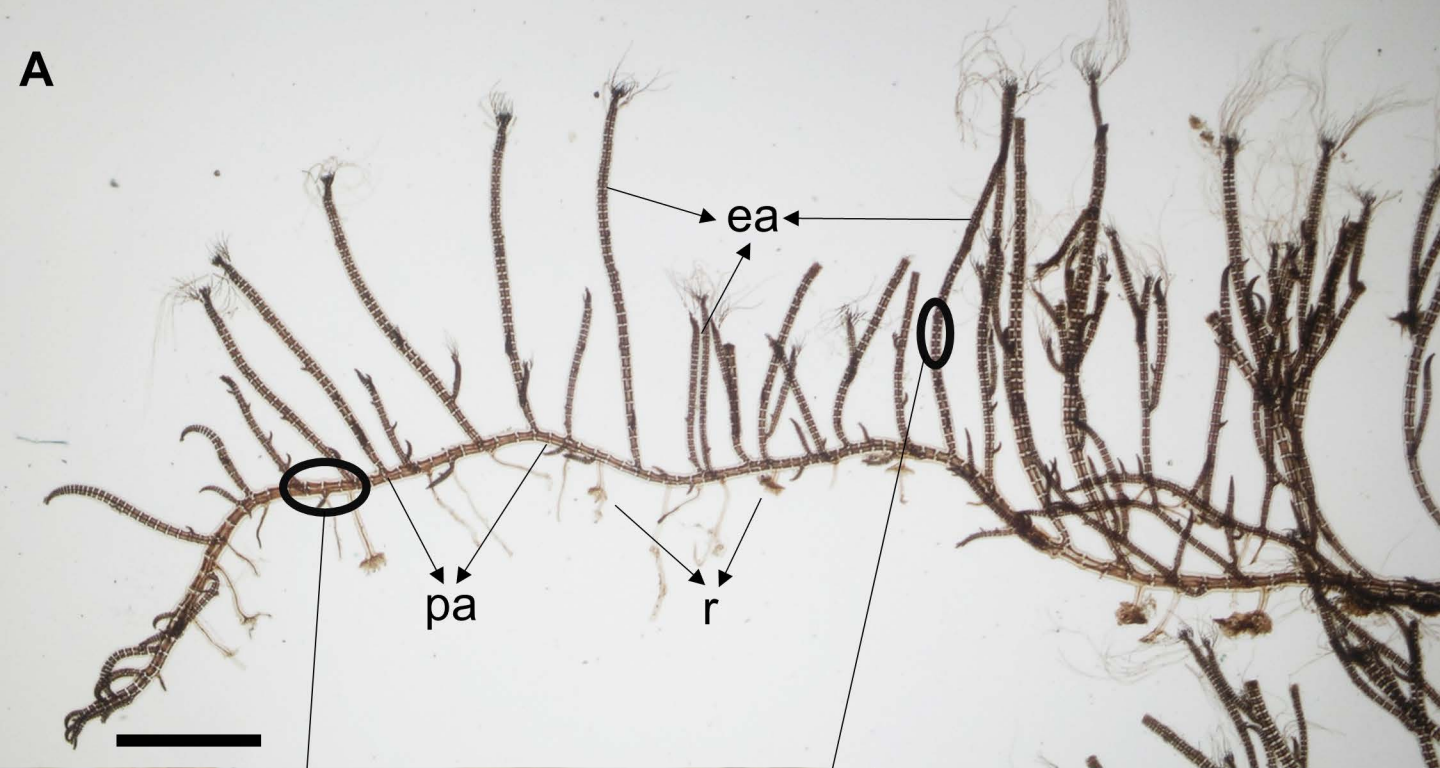
734 **Fig. 4.** Phylogenetic relationships among haplotypes of *Polysiphonia scopulorum* 3-6 and
735 their geographic distribution based on *cox1* data set. Each circle represents a haplotype and
736 its size is proportional to the frequency in which the haplotype was found. Black circles
737 represent hypothetical un-sampled haplotypes. The number of base pares that differ among
738 haplotypes is indicated by a number when it is >1 .

739 **Fig. 5.** Biplot of a Principal Components Analysis of morphometric data, representing ca.
740 70% of the variation between the first two dimensions. For species where multiple samples

741 were included in morphometric analyses, a polygon was drawn around them to better show
742 their spread. Abbreviations follow Fig. 1.

743 **Fig. 6.** Biplot of the main discriminant analysis of morphometric data, representing ca. 70%
744 of the variation between the first two dimensions. Annotations follow Fig. 1.

745 **Fig. 7.** Detailed analysis of morphological differences between *Polysiphonia scopulorum* 4
746 (yellow), 6 (navy) and 7 (brown). (A) Biplot of discriminant analysis, with annotations
747 following Fig. 1. (B-E) Density plots of indicated morphometric variables.

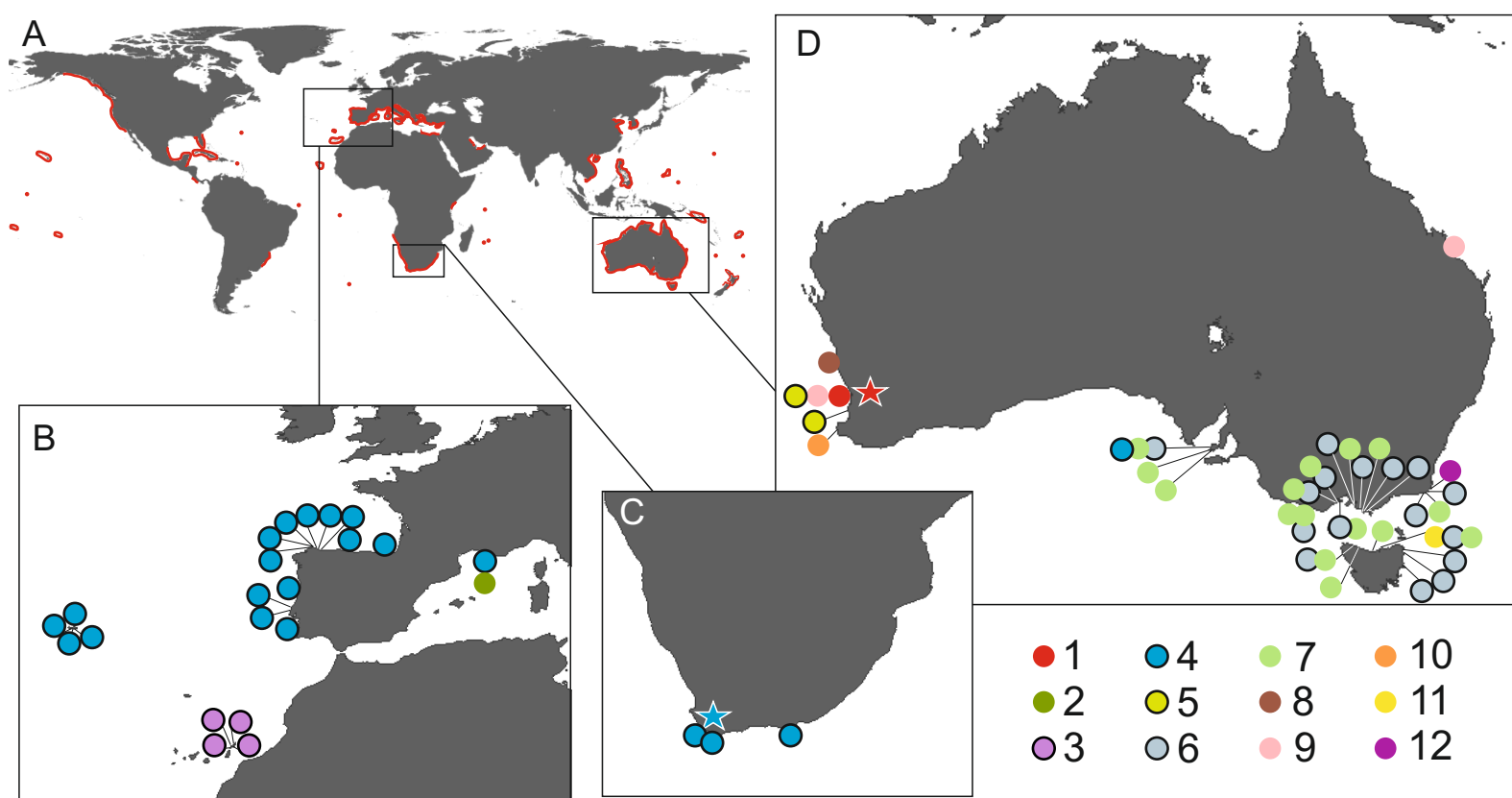


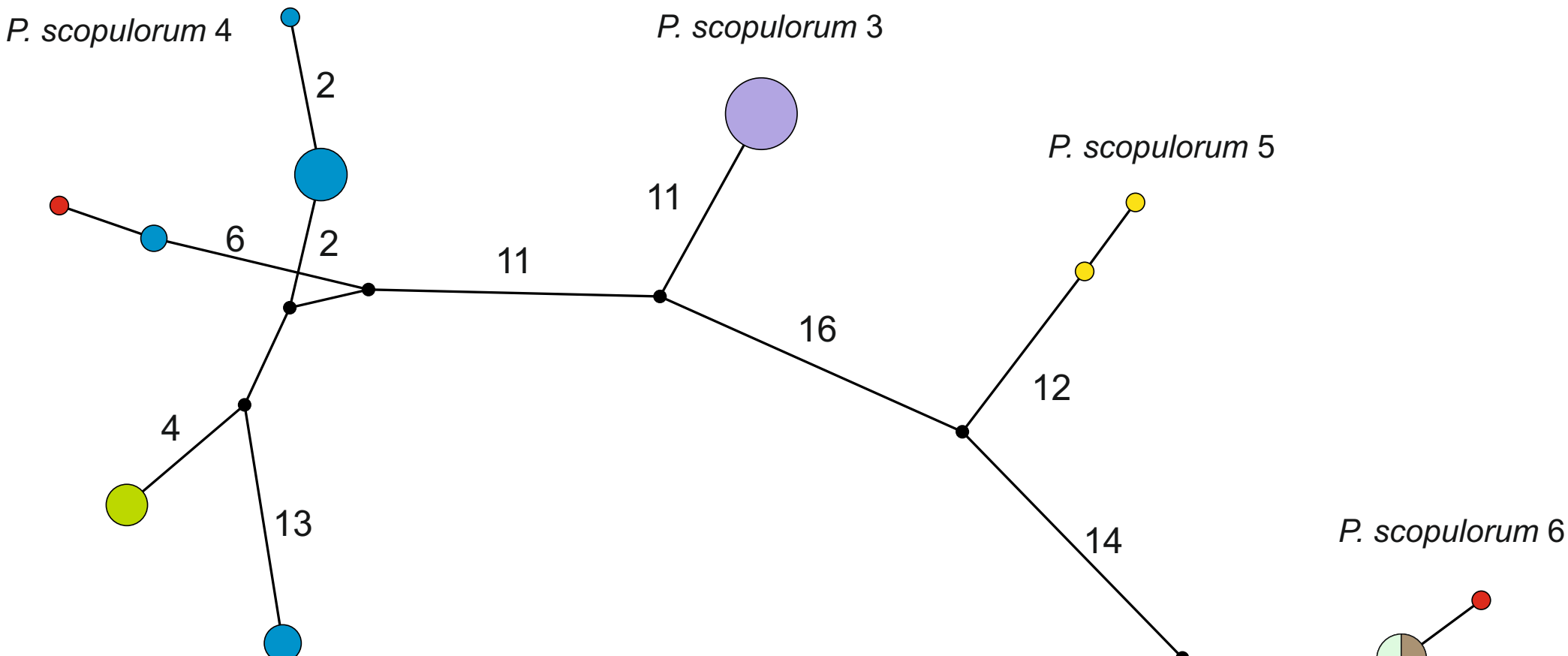
Prostrate axes (Fig. B)

1. Length of cytoplasm (PAXcytlen)
2. Diameter of cytoplasm (PAXcytdia)
3. Length of segment (PAXseglen)
4. Diameter of segment (PAXsegdia)
5. Diameter of rhizoid (RHdia)
6. Length of rhizoid (RHlen)

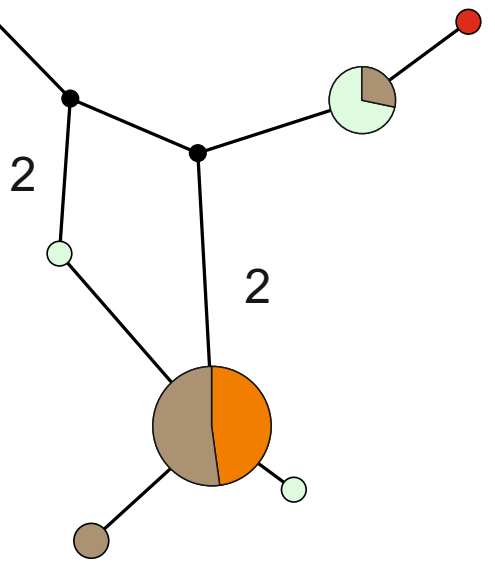
Erect axes (Fig. C)

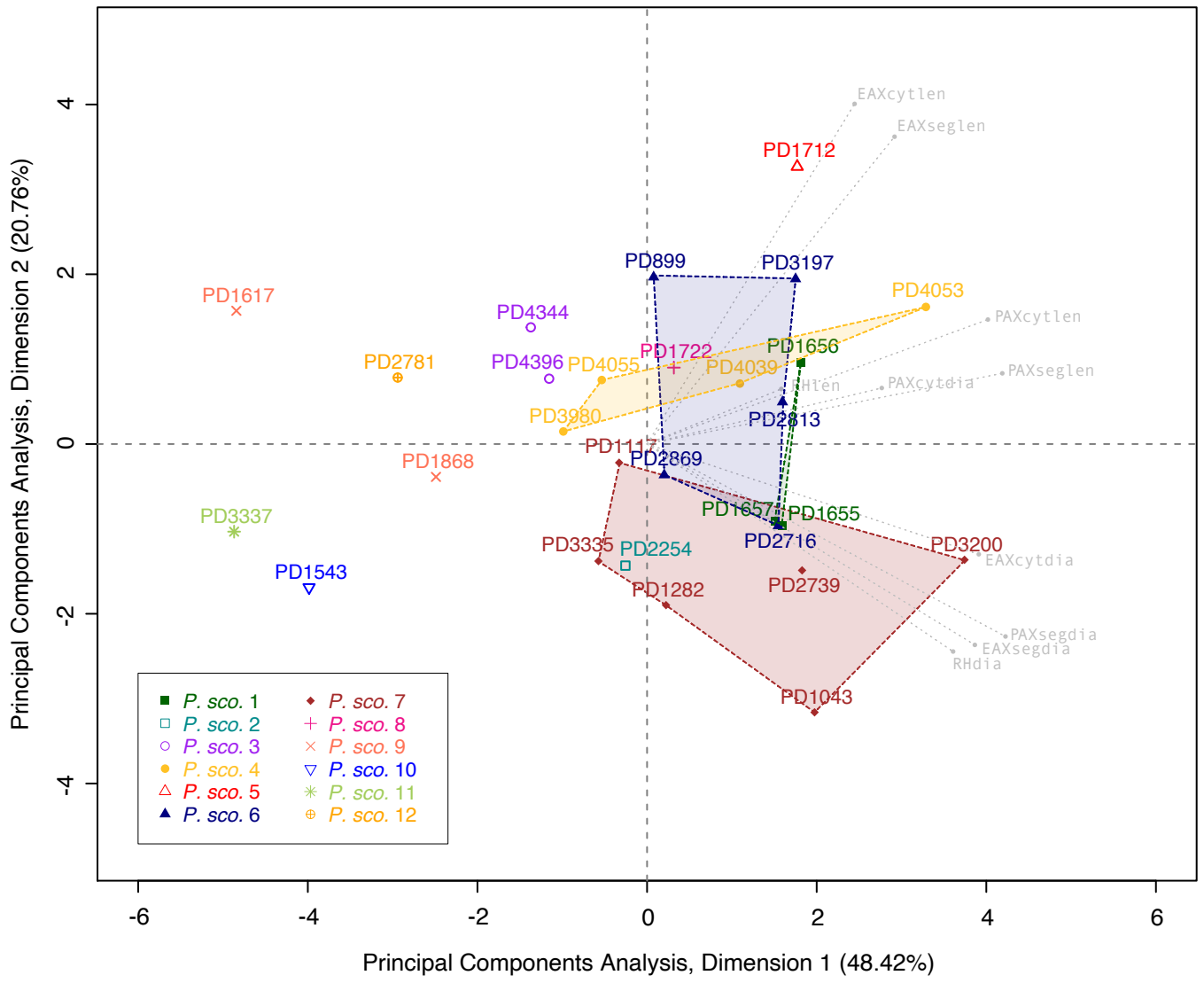
7. Length of cytoplasm (EAXcytlen)
8. Diameter of cytoplasm (EAXcytdia)
9. Length of segment (EAXseglen)
10. Diameter of segment (EAXsegdia)

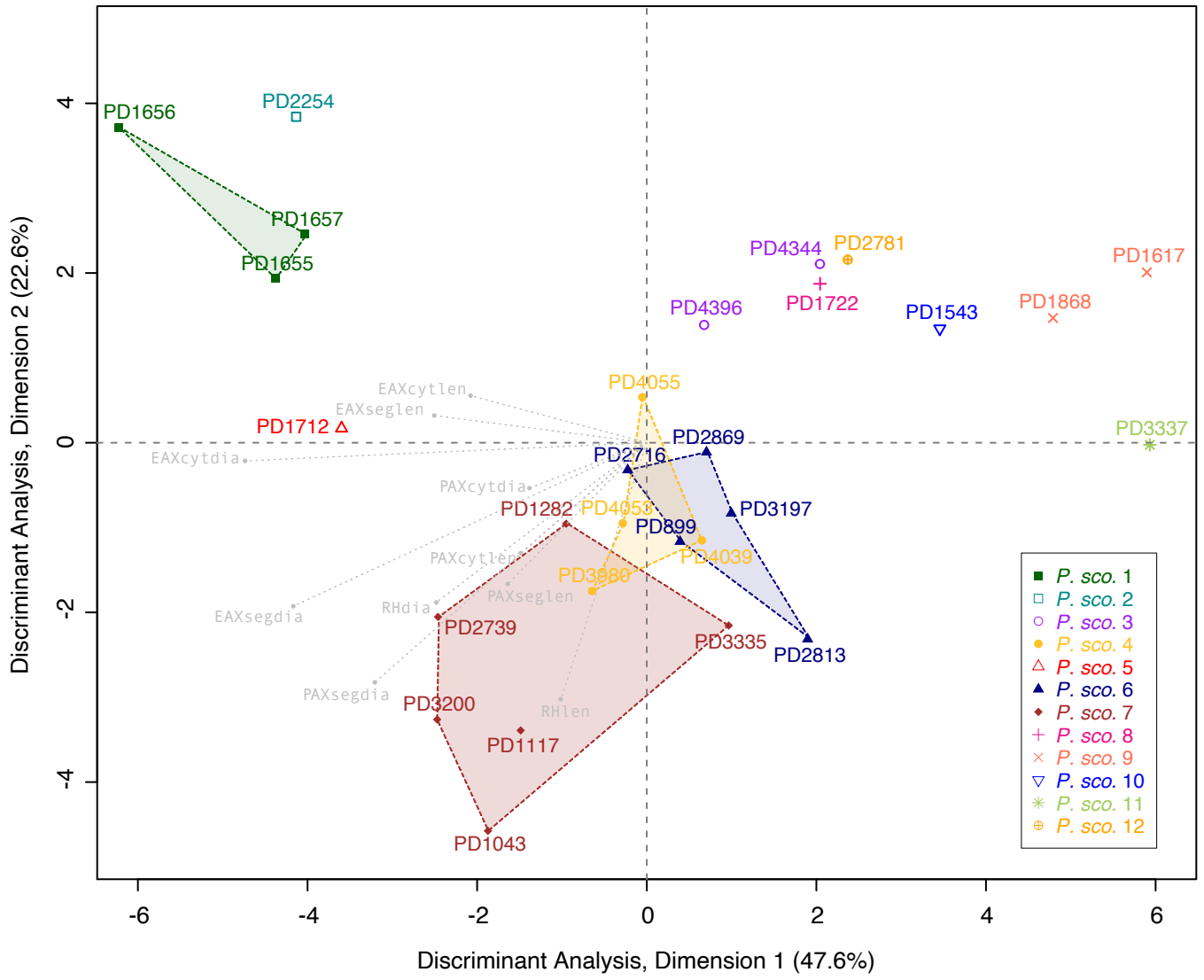




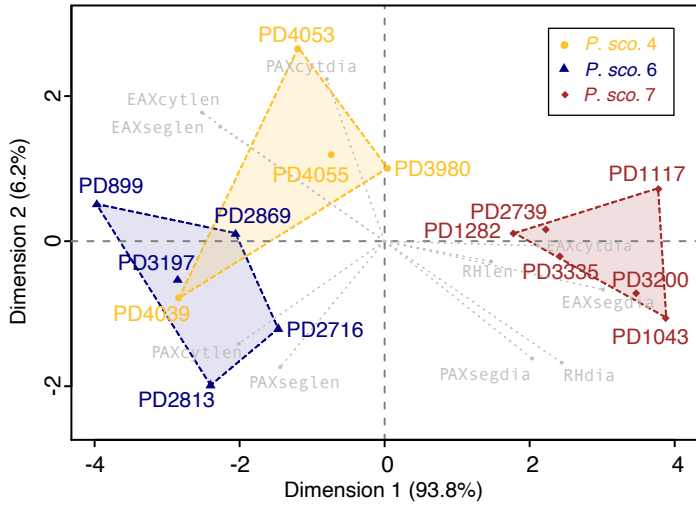
- South Africa
- Azores
- South Australia
- Canary Islands
- Western Australia
- Tasmania
- Western Victoria
- Eastern Victoria



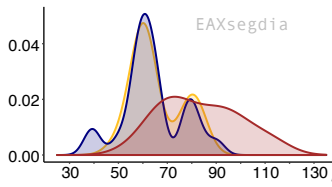




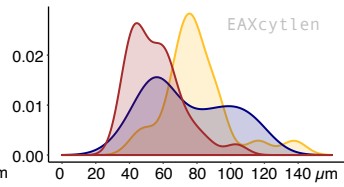
A. Discriminant analysis



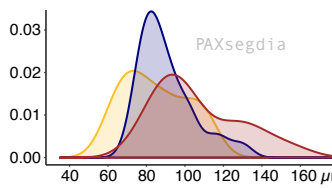
B. Erect axis diameter



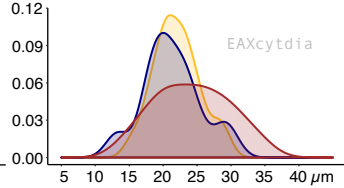
D. Erect axis cytoplasm length



C. Prostrate axis diameter



E. Erect axis cytoplasm diameter



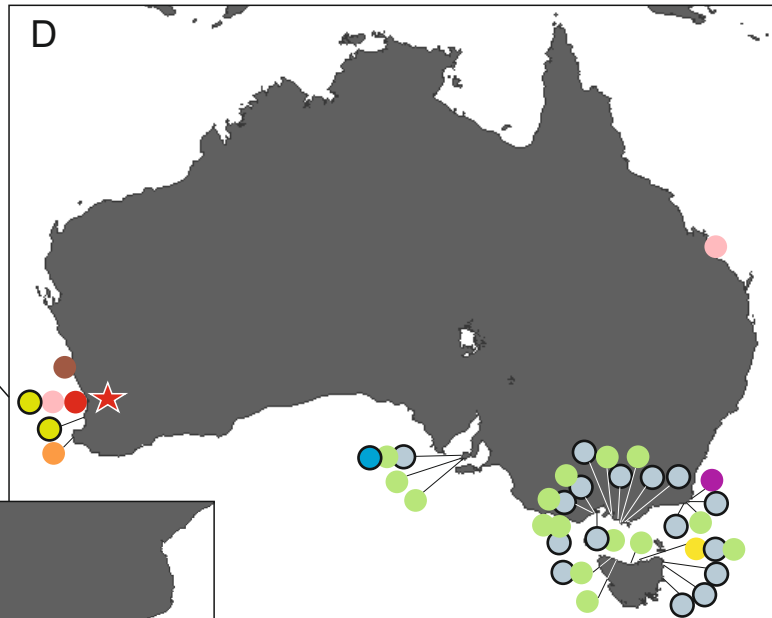
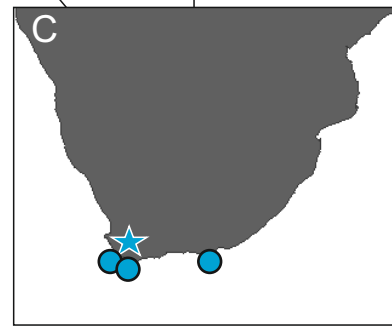
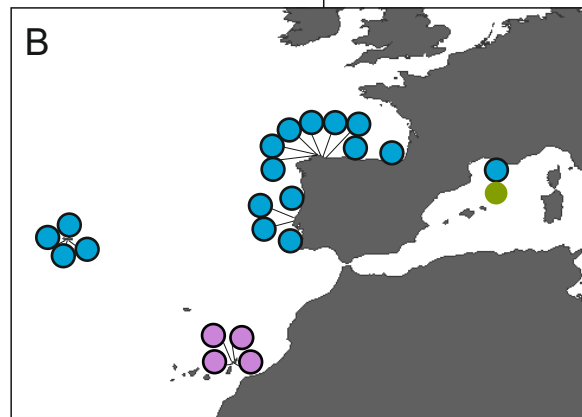
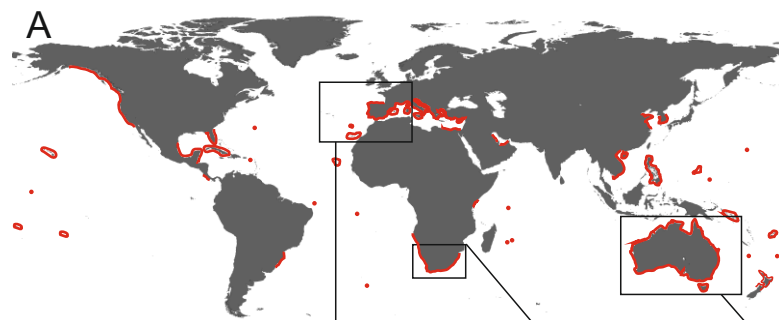
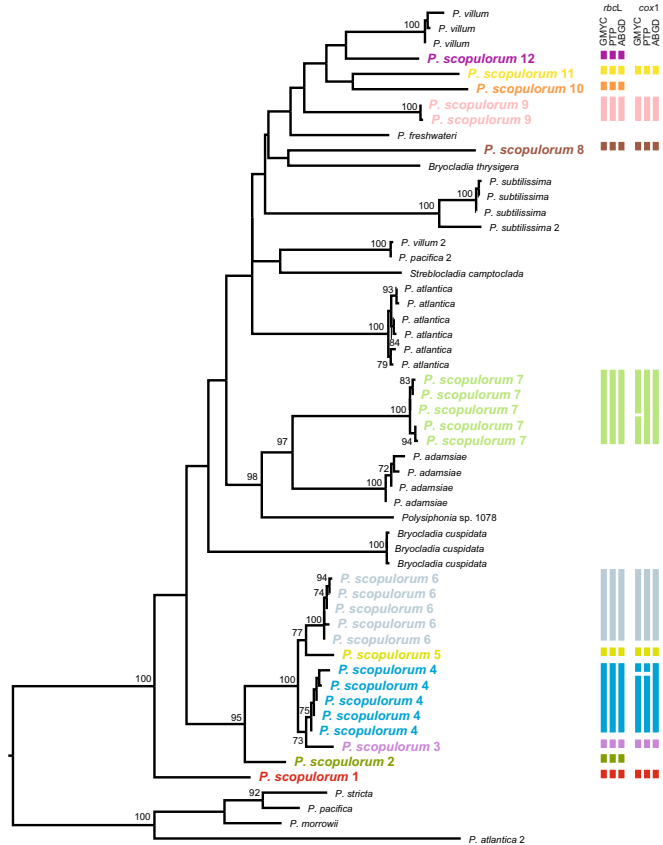


Fig. S1. Tetrasporangia cover cells in the *Polysiphonia scopulorum* complex. A-G and H: *P. scopulorum* 3-9 and 11, respectively. Detail of erect axes showing tetrasporangia (t), with two presporangial cover cells (pr), a postsporangial cover cell (po) and a scar cells of trichoblasts (sc). Tetrasporangia not shown in A, E and H because they are in a lower focal plane. The postsporangial cover cell is absent in E, and scar cells are absent in G. Scale bars = 40 μ m.

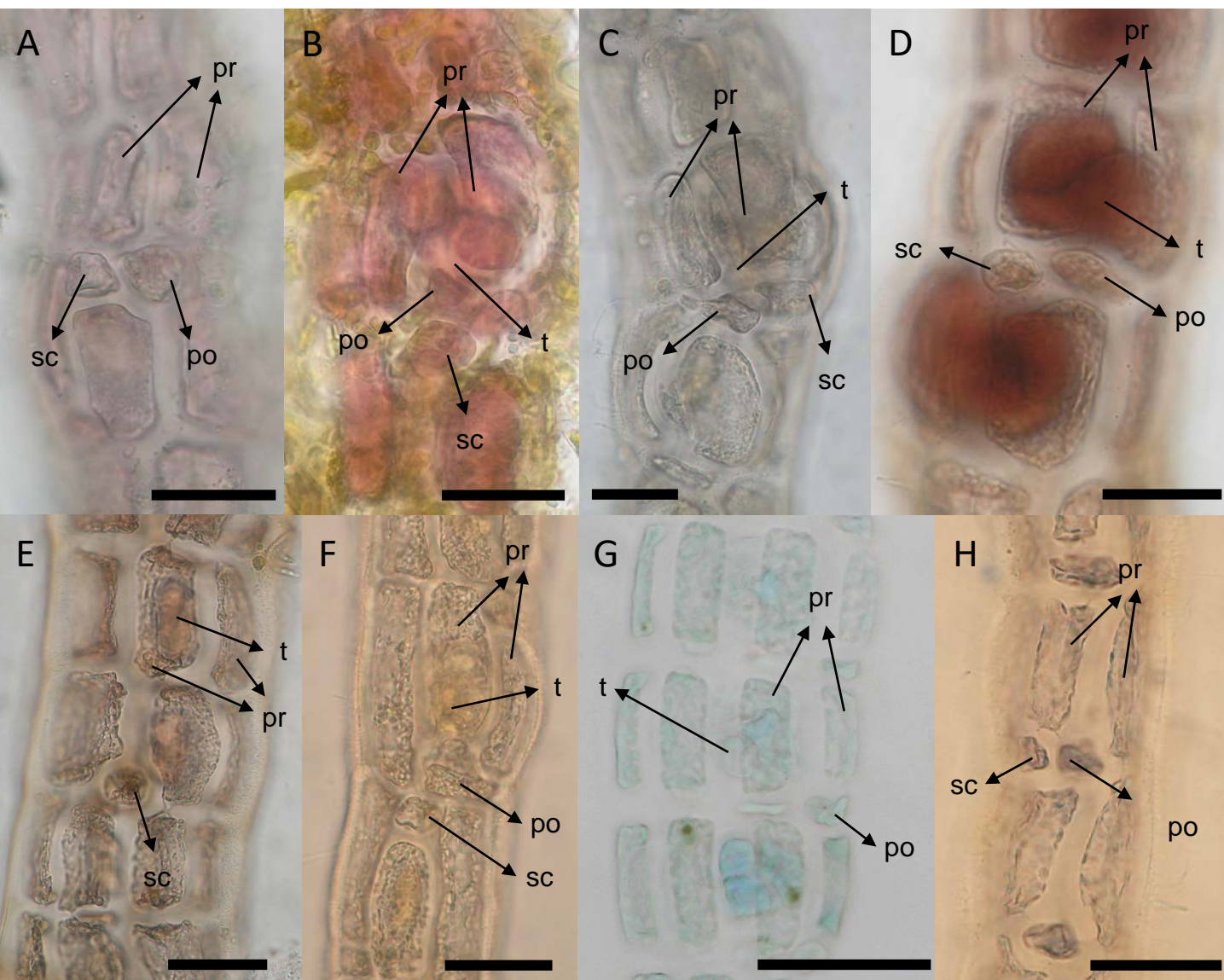


Table S1. Specimens collection information indicating the ones used in morphometric analyses (M), GenBank accession numbers and length of sequences.

Species	Specimen	Collection information	M	rbc L	length	cox 1	length
<i>P. scopulorum</i> 1	PD1637	Parakeet Beach, Rottnest Island, Western Australia; 17.03.2015		MT676284	702	-	-
	PD1655	Parakeet Beach, Rottnest Island, Western Australia; 17.03.2015	1	MT676285	1367	MT676017	847
	PD1656	Parakeet Beach, Rottnest Island, Western Australia; 17.03.2015	1	MT676286	1096	MT676015	868
	PD1657	Parakeet Beach, Rottnest Island, Western Australia; 17.03.2015	1	MT676287	1379	MT676016	847
	15Psc101	Fays Bay, Rottnest Island, Western Australia (Huisman et al. 2017)		MF139308	1250	-	-
	15Psc102	Fays Bay, Rottnest Island, Western Australia (Huisman et al. 2017)		MF139309	1250	-	-
	15Psc103	Fays Bay, Rottnest Island, Western Australia (Huisman et al. 2017)		MF139310	1250	-	-
<i>P. scopulorum</i> 2	PD2254	Calanque du Sormiou, France; 23.05.2016	1	MT676277	1279	-	-
<i>P. scopulorum</i> 3	PD4124	Puerto del Carmen, Canary Islands; 11.06.2018		MT676159	1337	MT676018	819
	PD4136	Puerto del Carmen, Canary Islands; 11.06.2018		MT676160	1354	MT676019	819
	PD4233	El Golfo, Canary Islands; 12.06.2018		MT676161	1238	-	-
	PD4296	Caleta de Famara, Canary Islands; 13.06.2018		MT676162	1339	MT676020	819
	PD4300	Caleta de Famara, Canary Islands; 13.06.2018		MT676163	1339	MT676021	819
	PD4308	Caleta de Famara, Canary Islands; 13.06.2018		MT676164	1356	MT676022	819
	PD4322	Caleta de Famara, Canary Islands; 13.06.2018		MT676165	1349	MT676023	819
	PD4332	Caleta de Famara, Canary Islands; 13.06.2018		MT676166	1339	MT676024	819
	PD4334	Caleta de Famara, Canary Islands; 13.06.2018		MT676167	1363	MT676025	819
	PD4339	Castillo de Águila, Canary Islands; 14.06.2018		MT676168	1365	MT676026	819
	PD4344	Castillo de Águila, Canary Islands; 14.06.2018	1	MT676169	1346	MT676027	819
	PD4347	Castillo de Águila, Canary Islands; 14.06.2018		MT676170	1336	MT676028	819
	PD4349	Castillo de Águila, Canary Islands; 14.06.2018		MT676171	1346	-	-
	PD4354	Castillo de Águila, Canary Islands; 14.06.2018		MT676172	1362	MT676031	740
	PD4396	Puerto del Carmen, Canary Islands; 15.06.2018	1	MT676173	1369	MT676029	819
	PD4398	Puerto del Carmen, Canary Islands; 15.06.2018		MT676174	1358	MT676030	819
	<i>P. scopulorum</i> 4	PD4553	Gym Beach, South Australia; 27.10.2018		MT676191	1363	MT676036
CH1290		Spain (Bárbara et al. 2013)		JX828149	1467	-	-
SANT.A.24676		Almograve, Portugal; 22.02.2011		MT676205	1457	KF648510	614
SANT.A.25144		Zumaia, Spain; 18.03.2011		MT676206	1449	KF648509	614
PD2245		Calanque du Sormiou, France; 23.05.2016		MT676207	744	-	-

PD3684	Praia do Populo, Azores; 12.04.2018	MT676193	1376	MT676039	833
PD3691	Praia do Populo, Azores; 12.04.2018	MT676194	1376	MT676040	833
PD3759	Maia, Azores; 13.04.2018	MT676195	1376	MT676044	752
PD3760	Maia, Azores; 13.04.2018	MT676196	1376	MT676046	712
PD3767	Maia, Azores; 13.04.2018	MT676203	1383	MT676045	752
PD3775	Maia, Azores; 13.04.2018	MT676197	1376	MT676047	698
PD3778	Maia, Azores; 13.04.2018	MT676204	1365	-	-
PD3820	Praia San Roque, Azores; 15.04.2018	MT676198	1376	MT676048	722
PD3822	Praia San Roque, Azores; 15.04.2018	MT676199	1376	MT676049	684
PD3824	Praia San Roque, Azores; 15.04.2018	MT676200	1376	MT676050	747
PD3963	Pau d'Água, Azores; 19.04.2018	MT676201	1376	MT676041	833
PD3968	Pau d'Água, Azores; 19.04.2018	MT676202	1376	MT676042	833
PD3980	Pau d'Água, Azores; 19.04.2018	1 MT676192	1377	MT676043	833
PD4009	Hermanaus, South Africa	MT676189	1297	MT676037	850
PD4015	Hermanaus, South Africa	MT676190	1338	MT676038	849
PD4026	Jeffrey's Bay, South Africa	MT676179	1323	MT676052	850
PD4030	Jeffrey's Bay, South Africa	MT676180	1031	MT676051	850
PD4032	Jeffrey's Bay, South Africa	MT676181	1337	MT676059	867
PD4033	Jeffrey's Bay, South Africa	MT676182	1349	MT676053	850
PD4035	Jeffrey's Bay, South Africa	MT676183	1354	-	-
PD4037	Jeffrey's Bay, South Africa	MT676184	1328	MT676054	850
PD4039	Jeffrey's Bay, South Africa	1 MT676185	1351	MT676055	850
PD4042	Jeffrey's Bay, South Africa	MT676186	1351	MT676056	850
PD4044	Jeffrey's Bay, South Africa	MT676187	1356	MT676057	850
PD4045	Jeffrey's Bay, South Africa	MT676188	1345	MT676058	850
PD4048	Muizenberg Bay; South Africa	MT676175	1341	MT676032	850
PD4052	Muizenberg Bay; South Africa	MT676176	1353	MT676033	850
PD4053	Muizenberg Bay; South Africa	1 MT676177	1358	MT676035	869
PD4055	Muizenberg Bay; South Africa	1 MT676178	1222	MT676034	850
SANT.A.24420	Galicia, Spain (Díaz-Tapia & Bárbara 2013)	-	-	KF671181	614
SANT.A.24413	Galicia, Spain (Díaz-Tapia & Bárbara 2013)	-	-	KF671178	614
SANT.A.24214	Portugal (Díaz-Tapia & Bárbara 2013)	-	-	KF671177	614
SANT.A.24435	Galicia, Spain (Díaz-Tapia & Bárbara 2013)	-	-	KF671175	614

	SANT.A.24212	Portugal (Díaz-Tapia & Bárbara 2013)	-	-	KF671166	614
	SANT.A.24343	Asturias, Spain (Díaz-Tapia & Bárbara 2013)	-	-	KF671163	614
	SANT.A.24479	Galicia, Spain (Díaz-Tapia & Bárbara 2013)	-	-	KF671161	614
	SANT.A.24257	Portugal (Díaz-Tapia & Bárbara 2013)	-	-	KF671159	614
	SANT.A.24158	Asturias, Spain (Díaz-Tapia & Bárbara 2013)	-	-	KF671152	614
<i>P. scopulorum</i> 5	PD1636	Parakeet Beach, Rottneest Island, Western Australia; 17.03.2015	MT676278	1413	MT676060	850
	PD1712	Grey, Western Australia; 20.03.2015	1 MT676279	1249	MT676061	886
<i>P. scopulorum</i> 6	PD770	13th beach, Victoria, Australia; 9.11.2014	MT676239	1341	MT676069	850
	PD899	Queenscliff beach, Victoria, Australia; 01.12.2014	1 MF093999	1467	MF093999	1605
	PD984	Minya reef, Victoria, Australia; 10.12.2014	MT676233	1344	MT676065	850
	PD1120	Killornei beach, Victoria, Australia; 27.12.2014	MT676234	1407	MT676068	859
	PD1258	Inverloch, Victoria, Australia; 18.01.2015	MT676235	1375	-	-
	PD1295	Flat Rocks, Victoria, Australia; 19.01.2015	MT676241	705	MT676066	850
	PD1333	Walkerville, Victoria, Australia; 20.01.2015	MT676229	1406	MT676074	850
	PD1480	Back Beach, Sorrento, Victoria, Australia; 28.02.2015	MT676232	1045	MT676064	848
	PD2716	Bastion point, Victoria, Australia; 08.11.2016	1 MT676227	1310	MT676076	849
	PD2813	Bastion point, Victoria, Australia; 11.11.2016	1 MT676226	1315	MT676078	850
	PD2814	Bastion point, Victoria, Australia; 11.11.2016	MT676225	1103	MT676079	850
	PD2816	Bastion point, Victoria, Australia; 11.11.2016	MT676224	1314	MT676080	850
	PD2823	Bastion point, Victoria, Australia; 11.11.2016	MT676221	1320	MT676077	849
	PD2824	Bastion point, Victoria, Australia; 11.11.2016	MT676220	1305	MT676081	850
	PD2863	Shipwreck Creek, Victoria, Australia; 13.11.2016	MT676218	1295	MT676082	850
	PD2869	Shipwreck Creek, Victoria, Australia; 13.11.2017	1 MT676238	1318	MT676070	850
	PD2879	Shipwreck Creek, Victoria, Australia; 13.11.2018	MT676222	1320	MT676075	848
	PD2885	Shipwreck Creek, Victoria, Australia; 13.11.2019	MT676208	1086	MT676083	848
	PD3195	Boat Harbour, Tasmania, Australia; 02.11.2017	MT676231	1308	MT676067	850
	PD3197	Boat Harbour, Tasmania, Australia; 02.11.2017	1 MT676230	1318	MT676063	867
	PD3326	Georgetown, Tasmania, Australia; 05.11.2017	MT676237	1309	MT676071	850
	PD3386	The Gardens, Tasmania, Australia; 07.11.2017	MT676217	1308	MT676084	850
	PD3422	Binaong Bay, Tasmania, Australia; 08.11.2017	MT676236	1015	MT676072	857
	PD3430	Binaong Bay, Tasmania, Australia; 08.11.2017	MT676223	1320	MT676085	850
	PD3433	Binaong Bay, Tasmania, Australia; 08.11.2017	MT676215	1308	MT676073	850
	PD3439	Binaong Bay, Tasmania, Australia; 08.11.2017	MT676214	1320	MT676086	850

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PD3442	Binaong Bay, Tasmania, Australia; 08.11.2017		MT676213	1321	MT676087	850
PD3455	Binaong Bay, Tasmania, Australia; 08.11.2017		MT676219	1295	MT676088	850
PD3458	Bicheno, Tasmania, Australia; 09.11.2017		MT676212	1290	MT676089	850
PD3473	Bicheno, Tasmania, Australia; 09.11.2017		MT676211	1307	MT676090	850
PD3479	Bicheno, Tasmania, Australia; 09.11.2017		MT676228	1310	MT676091	850
PD3486	Bicheno, Tasmania, Australia; 09.11.2017		MT676210	1349	MT676092	850
PD3489	Bicheno, Tasmania, Australia; 09.11.2017		MT676209	1298	MT676093	850
PD3492	Bicheno, Tasmania, Australia; 09.11.2017		MT676216	1308	MT676094	850
PD4550	Gym Beach, South Australia; 27.10.2018		MT676240	1361	MT676062	850
PD762	Lighthouse reef, Victoria, Australia; 08.11.2014		MT676260	1410	MT676108	850
PD954	Galaneuse reef, Victoria, Australia; 02.12.2014		MT676261	1410	MT676109	850
PD969	13th beach, Victoria, Australia; 09.11.2014		MT676259	1038	MT676110	850
PD987	Minya reef, Victoria, Australia; 10.12.2014		MT676251	664	-	-
PD1036	Minya reef, Victoria, Australia; 10.12.2014		MT676258	1340	-	-
PD1043	Kilkunda, Victoria, Australia; 23.12.2014	1	MT676257	1409	MT676111	850
PD1052	Kilkunda, Victoria, Australia; 23.12.2014		MH101826	1413	MT676114	850
PD1117	Killornei beach, Victoria, Australia; 27.12.2014	1	MT676256	1327	MT676095	850
PD1121	Pea Soup, Victoria, Australia; 28.12.2014		MT676265	1327	MT676107	850
PD1282	Twen Reef, Victoria, Australia; 19.01.2015	1	MT676255	1411	MT676112	850
PD1477	Back Beach, Sorento, Victoria, Australia; 28.02.2015		MT676254	1385	MT676113	850
PD2739	Pebbly beach, Victoria, Australia; 09.11.2016	1	MT676253	1126	MT676115	850
PD2758	Pebbly beach, Victoria, Australia; 09.11.2016		MT676252	1324	MT676116	850
PD2765	Pebbly beach, Victoria, Australia; 09.11.2016		MT676262	1306	MT676117	850
PD3200	Boat Harbour, Tasmania, Australia; 02.11.2017	1	MT676249	1305	MT676096	850
PD3202	Boat Harbour, Tasmania, Australia; 02.11.2017		MT676243	1314	MT676097	850
PD3210	Boat Harbour, Tasmania, Australia; 02.11.2017		MT676248	1308	MT676098	850
PD3233	Devonport, Tasmania, Australia; 03.11.2017		MT676242	1038	MT676099	850
PD3241	Devonport, Tasmania, Australia; 03.11.2017		MT676263	1308	MT676105	850
PD3242	Devonport, Tasmania, Australia; 03.11.2017		MT676244	1315	MT676100	850
PD3265	Devonport, Tasmania, Australia; 03.11.2017		MT676250	1318	MT676101	850
PD3289	Wynyard, Tasmania, Australia; 04.11.2017		MT676264	1316	MT676106	850
PD3335	Georgetown, Tasmania, Australia; 05.11.2017	1	MT676247	1323	MT676102	850
PD3338	Georgetown, Tasmania, Australia; 05.11.2017		MT676245	1301	MT676103	850

	PD3339	Georgetown, Tasmania, Australia; 05.11.2017		MT676246	1313	MT676104	850
	PD4545	Gym Beach, South Australia; 27.10.2018		MT676269	1368	MT676118	850
	PD4547	Gym Beach, South Australia; 27.10.2018		MT676271	1361	MT676119	850
	PD4638	Chinaman Hut, South Australia; 29.10.2018		MT676270	1368	MT676121	850
	PD4640	Chinaman Hut, South Australia; 29.10.2018		MT676273	1366	MT676122	850
	PD4641	Chinaman Hut, South Australia; 29.10.2018		MT676266	1368	MT676125	850
	PD4646	Chinaman Hut, South Australia; 29.10.2018		MT676268	1361	-	-
	PD4652	Chinaman Hut, South Australia; 29.10.2018		MT676267	1363	MT676123	850
	PD4653	Chinaman Hut, South Australia; 29.10.2018		MT676274	1365	MT676124	850
	PD4690	Pondalowi Bay, South Australia; 30.10.2018		MT676272	1360	MT676120	850
<i>P. scopulorum</i> 8	PD1722	Green Head, Western Australia; 21.03.2015	1	MT676281	1361	MT676132	850
<i>P. scopulorum</i> 9	PD1617	Rottnest Island, Western Australia; 15.03.2015	1	MT676275	1410	MT676126	850
	PD1868	Gladstone, Queensland; 13.05.2015	1	MT676276	1412	MT676127	850
<i>P. scopulorum</i> 10	PD1543	Channel Rocks, Western Australia; 21.03.2015	1	MT676282	704	-	-
<i>P. scopulorum</i> 11	PD3337	Georgetown, Tasmania, Australia; 05.11.2017	1	MT676280	1307	MT676133	840
<i>P. scopulorum</i> 12	PD2781	South Gabo Harbour, Victoria, Australia; 10.11.2016	1	MT676283	1320	-	-
<i>Bryocladia cuspidata</i>	GGSCSR	Venezuela (García-Soto & López-Bautista 2018)		MH388522	1057	-	-
	-	-		AF259498	1435	-	-
	PD618	Brazil (Díaz-Tapia et al. 2018a)		MH395866	1342	-	-
<i>Bryocladia thrysigera</i>	PD662	Brazil (Díaz-Tapia et al. 2018a)		MF094040	1303	-	-
	PD619	Praia de Parati, Ubu; 08.09.2014		MT676134	1301	-	-
<i>P. adamsiae</i>	PD2751	Australia (Díaz-Tapia et al. 2018a)		MH101810	1315	-	-
	PD2752	Australia (Díaz-Tapia et al. 2018a)		MH101811	1305	-	-
	PD3080	Australia (Díaz-Tapia et al. 2018a)		MH101812	1316	-	-
	PD3377	Australia (Díaz-Tapia et al. 2018a)		MH101813	1322	-	-
	PD3380	Australia (Díaz-Tapia et al. 2018a)		MH101814	1311	-	-
	PD3382	Australia (Díaz-Tapia et al. 2018a)		MH101815	1321	-	-
	PD3384	Australia (Díaz-Tapia et al. 2018a)		MH101816	1311	-	-
	PD3414	Australia (Díaz-Tapia et al. 2018a)		MH101817	1316	-	-
	PD3456	Australia (Díaz-Tapia et al. 2018a)		MH101818	1314	-	-
	PD3461	Australia (Díaz-Tapia et al. 2018a)		MH101819	1320	-	-
	PD3589	Australia (Díaz-Tapia et al. 2018a)		MH101820	1325	-	-
	PD3590	Australia (Díaz-Tapia et al. 2018a)		MH101821	1349	-	-

	PD3591	Australia (Díaz-Tapia et al. 2018a)	MH101822	1304	-	-
	PD3595	Australia (Díaz-Tapia et al. 2018a)	MH101823	1309	-	-
	PD3602	Australia (Díaz-Tapia et al. 2018a)	MH101824	1316	-	-
	PD3606	Australia (Díaz-Tapia et al. 2018a)	MH101825	1293	-	-
<i>P. atlantica</i>	CH1268	Spain (Bárbara et al. 2013)	JX828141	1467	-	-
	CH1285	Spain (Bárbara et al. 2013)	JX828142	1467	-	-
	PD4105	Baleo, A Coruña, Spain; 27.05.2018	MT676137	1320	-	-
	PD4107	Baleo, A Coruña, Spain; 27.05.2018	MT676136	1339	-	-
	PD4108	Baleo, A Coruña, Spain; 27.05.2018	MT676135	1372	-	-
	PD3677	Praia do Populo, Azores; 12.04.2018	MT676145	1311	-	-
	PD3680	Praia do Populo, Azores; 12.04.2018	MT676138	1328	-	-
	PD3681	Praia do Populo, Azores; 12.04.2018	MT676146	1336	-	-
	PD3687	Praia do Populo, Azores; 12.04.2018	MT676147	1336	-	-
	PD3724	Calhetas, Azores; 13.04.2018	MT676153	1351	-	-
	PD3774	Maia, Azores; 13.04.2018	MT676154	1334	-	-
	PD3776	Maia, Azores; 13.04.2018	MT676155	1334	-	-
	PD3830	Praia San Roque, Azores; 15.04.2018	MT676148	1375	-	-
	PD3831	Praia San Roque, Azores; 15.04.2018	MT676149	1351	-	-
	PD3845	Praia San Roque, Azores; 15.04.2018	MT676150	1379	-	-
	PD3871	Caloura, Azores; 16.04.2018	MT676143	1370	-	-
	PD3877	Vila Franca, Azores; 17.04.2018	MT676156	1375	-	-
	PD3880	Vila Franca, Azores; 17.04.2018	MT676142	1359	-	-
	PD3878	Vila Franca, Azores; 17.04.2018	MT676157	1375	-	-
	PD3879	Vila Franca, Azores; 17.04.2018	MT676151	1377	-	-
	PD3883	Vila Franca, Azores; 17.04.2018	MT676144	1370	-	-
	PD3907	Vila Franca, Azores; 18.04.2018	MT676158	1383	-	-
	PD3920	Vila Franca, Azores; 18.04.2018	MT676152	1384	-	-
	PD3966	Pau d'Água, Azores; 19.04.2018	MT676139	1374	-	-
	PD3977	Pau d'Água, Azores; 19.04.2018	MT676140	1382	-	-
	PD3981	Pau d'Água, Azores; 19.04.2018	MT676141	1383	-	-
	SANT.A.26230	Llas, Asturias, Spain; 19.iv.2011	-	-	MT676131	619
<i>P. atlantica 2</i>	NC.04	USA (Stuercke & Freshwater 2008)	EU492910	1341	-	-
<i>P. freshwateri</i>	CUK10427	Korea (Bustamante et al. 2015)	KJ957812	1395	-	-

<i>P. morrowii</i>	AC229	Korea (Carlile 2009, as <i>Polysiphonia</i> sp.)	GQ252569	1467	-	-	
<i>P. pacifica</i>	P194	USA (Kim & Yang 2005)	AY958162	1401	-	-	
<i>Polysiphonia</i> sp.	SMB-2003a	Chile (Kim et al. 2004)	AY396038	1379	-	-	
	SMB-2003a	Chile (Kim et al. 2004)	AY396037	1379	-	-	
<i>P. scopulorum</i> var <i>villum</i> sensu Savoie & Saunders (2019)	AC172	USA, (Carlile 2009, as <i>P. pacifica</i> var <i>delicatula</i>)	GQ252566	1467	-	-	
	AC181	USA (Carlile 2009, as <i>P. pacifica</i>)	GQ252565	1467	-	-	
	-	USA (Kim et al. 2004)	AY396039	1379	-	-	
	GWS006329	USA (Savoie & Saunders 2019)	MF120852	1338	HM916746	664	
	GWS006336	USA (Savoie & Saunders 2019)	MF120834	1338	HM916753	664	
	GWS002902	Canada (Savoie & Saunders 2019)	-	-	HM918528	664	
	GWS004788	Canada (Savoie & Saunders 2019)	-	-	HM918699	664	
	GWS008217	Canada (Savoie & Saunders 2019)	-	-	HM917000	664	
	GWS008218	Canada (Savoie & Saunders 2019)	-	-	HM917001	664	
	GWS008278	Canada (Savoie & Saunders 2019)	-	-	HM916554	664	
	GWS009051	Canada (Savoie & Saunders 2019)	-	-	HM916560	664	
	GWS019608	Canada (Savoie & Saunders 2019)	-	-	HQ544523	664	
	GWS019672	Canada (Savoie & Saunders 2019)	-	-	HQ544569	664	
	GWS020743	Canada (Savoie & Saunders 2019)	-	-	HQ545054	664	
	GWS020755	Canada (Savoie & Saunders 2019)	-	-	HQ545062	664	
	GWS022212	USA (Savoie & Saunders 2019)	-	-	KM254519	661	
	GWS022224	USA (Savoie & Saunders 2019)	-	-	KM254911	661	
	GWS022244	USA (Savoie & Saunders 2019)	-	-	HQ544219	661	
	GWS022266	USA (Savoie & Saunders 2019)	-	-	KM254964	604	
	GWS022301	USA (Savoie & Saunders 2019)	-	-	KM254832	661	
	GWS022390	USA (Savoie & Saunders 2019)	-	-	KM254236	664	
	GWS028437	Canada (Savoie & Saunders 2019)	-	-	MF120785	664	
	GWS034876	Canada (Savoie & Saunders 2019)	-	-	MF120768	664	
	GWS036020	Canada (Savoie & Saunders 2019)	-	-	MF120627	664	
	<i>P. stricta</i>	PD550	UK (Díaz-Tapia et al. 2017)	MF101428	1467	-	-
	<i>P. subtilissima</i>	NC.21	North Carolina, USA (Stuercke & Freshwater 2008)	EU492917	1341	-	-
		NC.24	Panama (Mamoozadeh & Freshwater 2012)	-	-	HM573529	639

	-	USA (Lam et al. 2013)	JX294917	1352	JX294915	617
	HI.01	Hawai, USA (Stuercke & Freshwater 2008)	EU492919	1341	-	-
	-	Spain (Lam et al. 2013)	JX294918	1352	JX294916	617
<i>P. subtilissima</i> 2	PHYKOS.3271	Panama (Mamoozadeh & Freshwater 2012)	HM573575	1284	-	-
<i>P. villum</i> sensu Díaz-Tapia et al. 2018b	SANT.A.25434	Spain (Díaz-Tapia et al. 2018b)	MG975710	1356	MT676128	617
	SANT.A.25665	Spain (Díaz-Tapia et al. 2018b)	MG975711	1350	MT676130	617
	SANT.A.28109	Spain (Díaz-Tapia et al. 2018b)	MG975716	1357	-	-
	SANT.A.26253	Ber, A Coruña, Spain; 17.04.2011	-	-	MT676129	617
	PD2249	France (Díaz-Tapia et al. 2018b)	MG975721	1231	-	-
	PD2250	France (Díaz-Tapia et al. 2018b)	MG975722	13281	-	-
	PD3058	North Carolina, USA (Díaz-Tapia et al. 2018b)	MG975712	1318	-	-
	NC.33	North Carolina, USA (Stuercke & Freshwater 2008, as <i>P. scopulorum</i> var. <i>villum</i>)	EU492915	1341	-	-
	NC.09	North Carolina, USA (Stuercke & Freshwater 2008, as <i>P. scopulorum</i> var. <i>villum</i>)	-	-	HM573535	673
	PD603	Brazil (Díaz-Tapia et al. 2018b)	MG975717	837	-	-
	PD614	Brazil (Díaz-Tapia et al. 2018b)	MG975718	1327	-	-
	PD631	Brazil (Díaz-Tapia et al. 2018b)	MG975719	1297	-	-
	PD967	Brazil (Díaz-Tapia et al. 2018b)	MG975720	1341	-	-
	PD3194	Australia (Díaz-Tapia et al. 2018b)	MG975715	1346	-	-
	PD3198	Australia (Díaz-Tapia et al. 2018b)	MG975713	1327	-	-
	PD3208	Australia (Díaz-Tapia et al. 2018b)	MG975714	1319	-	-
<i>Streblocladia camptoclada</i>	GWS036399	South Africa (Savoie & Saunders 2019)	MF120884	1363	MF120765	664

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Table S2. Percentage (above) and number (down) of bases that differ among species *rbc* L sequences included in our alignment.

	<i>P. scopulorum</i> 1	<i>P. scopulorum</i> 2	<i>P. scopulorum</i> 3	<i>P. scopulorum</i> 4	<i>P. scopulorum</i> 5	<i>P. scopulorum</i> 6	<i>B. cuspidata</i>	<i>Polysiphonia</i> sp.	<i>P. adamsiae</i>	<i>P. scopulorum</i> 7	<i>P. atlantica</i>	<i>S. camptoclada</i>	<i>P. villum</i> 2	<i>P. subtilissima</i> 2	<i>P. subtilissima</i>	<i>B. thrysigera</i>	<i>P. scopulorum</i> 8	<i>P. freshwateri</i>	<i>P. scopulorum</i> 9	<i>P. scopulorum</i> 10	<i>P. scopulorum</i> 11	<i>P. scopulorum</i> 12	<i>P. villum</i>
<i>P. scopulorum</i> 1	0	5	7	7.1-7.8	5.1	6.4-7.1	5.9-6.2	6.7	6.2-6.5	6.1-6.4	6.8-6.9	6.9	6.7	7.9	7.5-7.8	6.3	7.8	5.4	5.5-5.6	6	5.7	4.9	4.9-5.2
<i>P. scopulorum</i> 2	64	-	3	2.7-2.9	3.4	3-3.1	5.9-6.1	6.2	5.7-6.2	6.5-6.7	5.7-5.9	6.4	5.8-5.9	7.2	6.8-6.9	6.3	7.7	5.5	5.8	5	6.6	5.5	4.7-5.1
<i>P. scopulorum</i> 3	68	39	0	0.9-1.1	1.6	1.7-2	6.7-7.1	7.1	6.7-7.2	7.3-7.7	6.9-7.1	7.4	7-7.1	8.6	7.9-8.2	6.5	8.4	6.8	6.7	6.5	8	6.7	6.9-7.3
<i>P. scopulorum</i> 4	66-68	34-37	12-15	0.5 (6)	1.3-1.6	1-1.5	6.2-6.9	6.2-7.1	6.2-7	6.7-7.3	6.2-6.8	6.6-7	6.1-6.9	8.3-8.7	7.7-8.3	6.3-6.8	8.1-8.6	6.3-6.8	6.2-6.7	6.1-6.4	7.8-8.3	6.4-6.7	6.7-7.4
<i>P. scopulorum</i> 5	70	43	22	18-21	0	1.2-1.4	6.8-7	6.7	6.9-7.3	7.5-7.8	6.8-7.2	7	7-7.1	8.3	7.8	6.8	8.5	6.2	6.3-6.4	6.1	8.2	6.6	6.9-7.2
<i>P. scopulorum</i> 6	69-73	38-40	23-25	15-19	17-19	0.4 (5)	6.3-7.1	6.5-6.6	6.4-7	7.1-7.6	6.1-6.7	6.8-7.1	6.4-7.2	8.3	7.7-8.1	6.5-6.9	8.2-8.5	6.1-6.5	5.9-6.3	6.5-7.2	7.7-7.8	6.4-6.6	6.9-7.4
<i>B. cuspidata</i>	62-83	66-77	75-92	71-90	74-93	71-90	0.1 (2)	7-7.2	7.1-7.7	6.4-6.9	6.5-7.7	7.4-7.8	6.3-6.7	8.2-8.3	7-8.2	5.7-6.3	7.4	5.7-6	6.3-6.5	5.3-5.6	7-7.2	5.5-5.9	6-6.4
<i>Polysiphonia</i> sp.	87	79	94	84-88	93	84-88	74-97	0	5.6-5.9	5.6-5.8	6.2-6.4	5.8	6.7	8.3	7.7-7.8	7.1	7.5	6	6.9	7.8	7.7	7.6	6.8-6.9
<i>P. adamsiae</i>	81-82	73-79	91-94	84-92	93-96	86-90	75-100	74-77	0.6 (8)	4.7-5.4	6.2-6.8	6.2-6.4	6.1-6.5	8.3-8.6	8.1-8.6	7.1-7.4	8-8.3	6.2-6.6	6.4-6.9	6.6-7.3	7.2-7.4	7.2-7.5	6.8-6.3
<i>P. scopulorum</i> 7	84-88	83-85	97-102	89-96	101-106	95-101	66-90	74-77	62-71	0.3 (4)	7.1-7.6	6.8-7.2	6-6.4	8.2-8.3	8-8.4	7.2-7.4	8.7-8.4	7-7.1	7.4-7.5	6.4-7	8-8.3	7.7-7.9	6.8-7.4
<i>P. atlantica</i>	93-95	73-75	93-97	86-93	94-98	81-91	69-109	84-86	83-89	95-102	0.5 (7)	5.6-5.9	4.9-5.3	6.9-7.2	6.8-7.3	6.3-6.5	6.8-7.1	5.9-6.2	6.1-6.5	6.1-6.7	6.4-6.7	6.2-6.3	5.8-6.3
<i>S. camptoclada</i>	93	82	98	90-93	96	91-94	78-105	78	82-84	91-95	75-78	-	5.3-5.4	7.2	7-7.2	5.9	6.9	5.4	6.5	7.1	7.1	6.4	6.3-6.7
<i>P. villum</i> 2	92-93	74-75	96-97	91-93	99-100	93-96	67-96	92-93	82-86	80-88	70-74	72-73	0.1 (1)	7-7.1	6.9-7.2	5.1	7.3-7.4	5.4-5.4	6.5-6.7	6.5-7.2	4.7-5.1	4.9-5	4.9-5.3
<i>P. subtilissima</i> 2	101	90	108	106-109	107	104-107	81-106	107	105-109	105-106	88-92	93	90-91	-	2-2.2	7.5	7.7	6.1	7.5	6.9	7.9	6.9	6.8-6.3
<i>P. subtilissima</i>	101-102	87-88	105-106	103-107	105-106	102-106	82-106	103-104	107-111	102-112	92-99	93-96	93-98	26-28	0.3 (4)	7.3-7.5	7.7-8	6.2-6.5	7.5-7.8	6.8-7	7.9-8	7.4-7.5	6.3-6.9
<i>B. thrysigera</i>	80	78	81	82-85	88	85-87	56-82	92	89-92	91-96	80-82	75	66-67	95	96-98	0	6.7	5.1	5.5	6.8	6.7	5.2	5.1-5.5
<i>P. scopulorum</i> 8	108	99	114	114-117	120	110-117	78-105	104	105-110	113-119	95-98	94	104-105	99	104-108	87	-	6.7	6.4-6.5	8.2	6.7	6.7	6.1-6.5
<i>P. freshwateri</i>	80	70	91	88-91	87	82-87	63-81	83	83-87	92-97	82-84	73	76-77	78	87	67	94	-	4.4-4.5	5.3	5.4	4.8	4.6-5.1
<i>P. scopulorum</i> 9	86-87	74	90-91	88-91	89-90	82-86	69-89	95	86-91	99-105	85-89	89	78-80	99	100-105	72	91-92	62-63	0.1 (1)	5.3-5.5	5.8	5.1	5.4-5.7
<i>P. scopulorum</i> 10	42	32	46	43-46	43	44-47	35-37	52	46-48	43-46	42-47	48	44-47	42	43-48	40	58	36	37-38	-	5.6	4.4	3.5-3.9
<i>P. scopulorum</i> 11	94	85	104	102-107	107	99-102	74-91	100	93-96	104-406	84-87	93	61-66	100	102-103	84	88	71	76	36	-	4.7	4.7-5.1
<i>P. scopulorum</i> 12	79	70	87	84-87	87	84-86	57-77	100	94-99	101-103	82-83	85	65-66	88	97	65	88	63	67	29	61	-	3.6-4.1
<i>P. villum</i>	82-84	60-65	93-97	91-97	93-97	91-96	61-68	90-91	89-95	91-97	79-82	71-76	65-71	81-85	83-92	65-68	81-87	61-68	71-76	36-41	61-66	47-53	0.6 (7)

Table S3. Percentage (above) and number (down) of bases that differ among species *cox1* sequences included in our alignment.

	P. scopulorum 1	P. scopulorum 3	P. scopulorum 4	P. scopulorum 5	P. scopulorum 6	P. scopulorum 7	P. atlantica	S. camptoclada	P. villum 2	P. subtilissima	P. scopulorum 8	P. scopulorum 9	P. scopulorum 11	P. villum
P. scopulorum 1	0	6.2	6.4-7.4	5.4-5.5	6.5-6.7	8-8.3	10.4	11.4	8.5-8.8	11.7	8.8	9.1	8.1	8.9
P. scopulorum 3	51	0	3.1-3.5	4.8-4.9	5.3-5.7	8.1-8.4	8.6	10.2	6.6-7	8.9	8.5	8.7-8.8	8.4	8
P. scopulorum 4	42-58	18-28	2.6 (22)	5.1-5.9	5.5-6.8	7.8-9.3	8.3-9	10.5-11.6	8.6-10.3	9.5-10.7	8.9-9.6	8.6-9.1	8-9.5	6.6-9
P. scopulorum 5	47	39-40	31-51	0.1 (1)	3.5-3.9	7.9-8.2	9-9.3	10.4-10.5	6.1-6.4	9.9-10	8.8-8.9	9.3-9.6	7.9-8	8.8-9
P. scopulorum 6	55,-57	43-47	36-57	30-33	0.7(6)	8.7-8.1	9.4-9.7	10.4-11.1	7.6-8.3	10.5-11	8.5-9	9-9.5	8.9-9.4	9.8-10.5
P. scopulorum 7	68-70	66-69	45-79	67-70	69-74	2.6(14)	9.5-9.8	10.8-11.1	7.6-8.4	10.3-10.8	8.5-8.8	9.4-9.8	9.5-9.8	8.8-9.4
P. atlantica	59	66	40-50	49-54	52-58	57-59	-	10	6.5-6.8	11,1	9.7	9.5-9.9	9.2	10.8-11
S. camptoclada	70	57	62-71	62-65	64-69	64-66	62	-	7.5-8	11	9.3	7.6	8.2	9.2-9.4
P. villum 2	52-54	37-39	47-63	36-43	45-51	45-50	40-42	57-58	0.6 (4)	8.3-8.6	6.8-7.1	6.8-7.1	5.9-6.2	7.3-7.7
P. subtilissima	66	51	50-66	55-58	57-67	56-59	69	68	51-53	0	10.3	10.1	9.7	10.1-10.5
P. scopulorum 8	75	70	49-82	75-76	81-85	81-85	53	55	40-42	56	-	8.4	7.4	7.5
P. scopulorum 9	77	71-72	47-77	79-82	85-89	80-83	52-54	45	40-42	55	71	0.2 (2)	8.3	8.4
P. scopulorum 11	68	66	45-78	66	74-77	70-72	52	50	36-38	55	61	68	-	6.5
P. villum	56	41	38-55	48-52	54-62	48-51	67-68	57-58	45-48	64-65	41	46	37	0.2 (1)