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WIDELY DISTRIBUTED RED ALGAE OFTEN REPRESENT HIDDEN INTRODUCTIONS, COMPLEXES OF CRYPTIC SPECIES OR SPECIES WITH STRONG PHYLOGEOGRAPHIC STRUCTURE

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ABSTRACT

Despite studies suggesting that most seaweeds are poor dispersers, many red algal species are reported to have circumglobal distributions. Such distributions have mostly been based on morphological identifications, but molecular data have revealed a range of issues with morphologically defined species boundaries. Consequently, the real distribution of such reportedly circumglobal species must be questioned. In this study, we analysed molecular datasets (*rbc*L gene) of nine species in the Rhodomelaceae for which samples were available from widely spaced geographical locations. Three overall patterns were identified: 1) species showing strong phylogeographic structure (i.e. phylogenetic ~~structure~~ similarity correlates with geographical provenance), often to the point that populations from different locations could be considered as different species (*Lophosiphonia obscura, Ophidocladus simpliciusculus*, *Polysiphonia villum* and *Xiphosiphonia pinnulata*); 2)~~ 3)~~ species with a broad distribution that is explained, in part, by putative human-mediated transport (*Symphyocladia*~~.~~ *dendroidea* and~~ .~~ *Polysiphonia*~~.~~ *devoniensis*); and 3) non-monophyletic complexes of cryptic species, most with a more restricted distribution than previously thought (*Herposiphonia tenella, S*~~*ymphyocladia*~~*. dendroidea* and the *X. pennata* complex that includes the species *X. pinnulata* and *S. spinifera*)~~; 3) species with a broad distribution that is explained, in part, by putative human-mediated transport (*S. dendroidea* and . *P. devoniensis*)~~. This study shows that widely distributed species are the exception in marine red algae, unless they have been spread by humans.

Key words: introductions, new record, phylogeography, Rhodomelaceae, Polysiphonieae, Pterosiphonieae, Herposiphonieae, *rbc*L, species boundaries, species complexes

INTRODUCTION

Phylogeography of marine organisms is influenced by barriers to dispersal and geographical distance, as well as by aspects of their life-history, physiology and ecology (Jackson 1974, Palumbi 1994, Riginos et al. 2011). The dispersal ability of seaweeds is generally very limited, of the order of tens of meters or less (Santelices 1990, Kinlan and Gaines 2003, Destombe et al. 2009). However, long-distance dispersal is known in brown seaweeds with buoyant structures (Fraser et al. 2009, Macaya and Zuccarello 2010), which can act as rafts promoting in turn the dispersal of the epiphytic species that they host (Fraser et al. 2013, Macaya et al. 2016, López et al. 2017, 2018). Still, a large proportion of macroalgae are epilithic, so their expected dispersal ability is very limited and consequently their distribution range is expected to be relatively small. Paradoxically, many macroalgal species are reported to be very widely or even globally distributed.

Records are usually based only on morphological identification, which can be inaccurate due to morphological plasticity within species as well as similarity between cryptic species (e.g. Verbruggen 2014, Schneider et al. 2017). Closer investigation of material from distant regions using DNA data commonly leads to the discovery of cryptic species (e.g. Won et al. 2009, Bustamante et al. 2014, Schneider et al. 2017). Even though studies combining morphological and molecular data are increasing, DNA databases are still very limited for most algal groups and molecular data are often available only for some regions. As a consequence, the true distribution of many seaweed species should be regarded as uncertain. Few studies have reassessed the distribution of widely reported red algal species using molecular data from a broad sampling area. -Complexes of look-alike species, as well as widely distributed species, have been detected (Zuccarello et al. 1999, Zuccarello et al. 2002a, Zuccarello & West

2003, Won et al. 2009). Among the widely distributed species, some exhibit high genetic variability and strong phylogeographic structure that often distinguishes populations from different basins (Zuccarello et al. 2002a, b, Won et al. 2009). Other widely distributed species lack phylogeographic signal, suggesting long-distance dispersal processes by unknown mechanisms (Zuccarello et al. 2002a, Fraser et al. 2013). Therefore, red algal phylogeographic patterns are highly heterogeneous and depend on evolutionary histories and dispersal abilities.

In addition to natural dispersal mechanisms, human-mediated vectors can transport seaweeds from native areas to other world regions and rapidly alter distribution patterns (Straub et al. 2016). More than 208 red algal species have been considered as introduced or cryptogenic in one or several regions (Thomsen et al. 2016). Cryptic introductions are common in the red algae and non-native species often remain unnoticed until diversity surveys use molecular tools (McIvor et al. 2001, Zuccarello et al. 2002b, Díaz-Tapia et al. 2013b, 2017a). Considering the low dispersal ability of non-buoyant epilithic red algae, we hypothesize that the distribution of most truly cosmopolitan species can be explained by human-mediated transport – which is frequently provided as a potential explanation for wide distributions of species (Zuccarello et al. 2002a,b, Fraser et al. 2013).

The Rhodomelaceae, with >1,000 recognized species, is the most diverse red algal family (Guiry and Guiry 2018). It includes numerous examples of widely reported species and, as in most red algal groups, cryptic diversity is common (e.g. Zuccarello et al. 2002a, Díaz-Tapia and Bárbara 2013, Bustamante et al. 2014, Savoie and Saunders 2016, Zuccarello et al. 2018). ~~Furthermore, a~~Among the red algae the Rhodomelaceae accounts for the largest number of introduced species (Williams and Smith 2007). Members of this family are often major components of algal turfs where canopyforming brown algae with buoyant structures are rare as a consequence of the stressful conditions imposed by the presence of sediment (Airoldi 1998, Díaz-Tapia et al. 2013a). This makes the family a good candidate to test hypotheses about species distributions and phylogeographic patterns.

The objective of this paper is to reassess the wide reported distributions of nine turf-forming species of the family Rhodomelaceae using DNA sequences. Using molecular data from distant locations within each species' reported distribution range, we evaluate whether these are indeed widely distributed species, analyse the observed phylogeographic patterns, and consider whether these species may have been introduced into one or several regions by human activities.

MATERIALS AND METHODS

Material of *Herposiphonia tenella*, *Lophosiphonia obscura*, *Ophidocladus simpliciusculus*, *Polysiphonia villum*, *P. devoniensis*, *Symphyocladia spinifera*, *S. dendroidea*, *Xiphosiphonia pennata* and *X. pinnulata* was collected in Norway, United Kingdom, France, Spain, Portugal, Italy, Brazil, Chile, Australia and South Africa during general sampling surveys of the family Rhodomelaceae (Table S1). All these species form epilithic turfs, most of them on intertidal sand-covered rocks (Womersley 2003, Díaz-Tapia & Bárbara 2013). *Lophosiphonia obscura* was found in North Atlantic brackish water coastal lagoons or estuaries, and *Symphyocladia dendroidea* was collected in Australian and Chilean shallow subtidal turfs. Distribution maps of records for these species (Figs 1-3, lines) were drawn up based on information available in AlgaeBase and references therein (Guiry and Guiry 2018).

DNA was extracted from silica gel-dried material following Saunders and McDevit (2012), using the Qiagen DNeasy Plant Mini Kit (Qiagen GmbH, Hilden, Germany) or the Promega Wizard Magnetic 96 DNA Plant System kit (Promega Corporation, Madison, USA), following the manufacturer's instructions. PCR amplification was carried out for the *rbc*L gene using primers F7/RrbcStart, F7/R893 or F57/rbcLrevNEW (Freshwater and Rueness 1994, Mamoozadeh and Freshwater 2011, Saunders and Moore 2013), as well as the newly designed primers F2 (TGTCTAACTCTGTAGAACAACGGA), F8 (ACTCTGTAGAASAACGGACAMG), R1008 (AACTACTACAGTACCAGCATG), R1464 (AACATTAGCTGTTGGAGTTTCYAC) and R1452 (TGGAGTTTCYACRAAGTCAGCTGT). Names of these primers indicate their position in the *rbc*L gene (e.g. first base of F2 primer corresponds with the second base of the *rbc*L gene). PCR reactions were performed in a total volume of 25 µl~~, consisting~~ containing ~~of 5 µl 5~~1× MyTaqTM reaction buffer, ~~0.7 µl 10~~0.28 µM of forward and reverse primers, 0.125 ~~µl 1U/µl~~units My TaqTM DNA Polymerase (Bioline, London, UK)~~, 17.475 µl MilliQ® water~~ and 1 µl template DNA. The PCR profile consisted of initial denaturation (93ºC for 3 min), 35 cycles of denaturation (94ºC for 30 s), primer annealing (45ºC for 30 s), and extension (74ºC for 90 s) and final extension (74ºC for 5 min). The PCR products were purified and sequenced at Queen's University of Belfast on an AB3730xl DNA Analyzer (Applied Biosystems, Foster City, CA, USA) or commercially by Macrogen or the sequencing service of the University of A Coruña.

A total of 128 new *rbc*L sequences were generated in this study and an additional 91 sequences were downloaded from GenBank (Table S1). Length of sequences ranged from 585 to 1467 (Table S1). Sequences were aligned using Muscle in Geneious 6.1.8 (Kearse et al. 2012). As a first stage, we analysed these sequences in taxon-rich datasets for the tribes Herposiphonieae, Pterosiphonieae, Polysiphonieae and Streblocladieae to verify that the target species were monophyletic. Based on the resulting trees, we selected all sequences corresponding to the species (or group of closely related species) that are the focus of this paper. These datasets were analyzed species by species using the unweighted pair group method with arithmetic mean (UPGMA). For two complexes of ~~unrelated~~ non-sister species in our initial taxon-rich trees (*Symphyocladia dendroidea* and *Herposiphonia tenella*), we included wider species sampling considering the available data for the respective genera (Table S1). We performed maximum likelihood (ML) analyses separately for each of the two genera using RAxML 8.1.X (Stamatakis 2014). GTR-Gamma was used as the nucleotide model and branch support was estimated with 1000 bootstrap replicates. Three species of *Xiphosiphonia* and *Dipterosiphonia* were selected as the respective outgroups for the *Symphyocladia* and *Herposiphonia* trees based on our phylogenomic analyses of the major lineages of the Rhodomelaceae (Díaz-Tapia et al. 2017b).

RESULTS

The taxonomy of several of the studied species is complex and details are provided in Supplement 1.

Ophidocladus simpliciusculus

Ophidocladus simpliciusculus was collected in four out of the six world regions where it has been reported (Fig. 1a). ~~In Australia, its previously known distribution included South and Western Australia and our collections from Tasmania and Victoria (Table S1) are new records for these states.~~ The UPGMA analyses included 15 newly determined *rbc*L sequences and two downloaded from GenBank (Table S1). Sequences comprised four haplotypes (Fig. 1b): haplotype 1, seven samples from Europe (Atlantic and Mediterranean); haplotype 2, six samples from Australia; haplotype 3, one sample from South Africa; and haplotype 4, three samples from Brazil. The South African sample differed by only 0.1% (1 bp) from the Australian samples, while Brazilian samples were the most divergent (up to 0.8% and 11 bp) from samples from other regions. Our results indicate that *O. simpliciusculus* has a unique *rbc*L haplotype in each region, but it has a strong phylogeographic structure.

Lophosiphonia obscura

Lophosiphonia obscura has been reported in the Atlantic and Indo-Pacific and sequences are available from Europe and Australia (Fig. 1c). ~~In Australia, it had been previously recorded only in Southern Australia and our collection from Victoria is a new record for this state.~~ Furthermore, our dataset also included *Polysiphonia hemisphaerica* from Norway and *P. boldii* from Texas, USA which may be conspecific as suggested by the low *rbc*L divergence with *L. obscura* (see Supplement 1). We analysed six newly determined *rbc*L sequences and two downloaded from GenBank for *Lophosiphonia obscura, Polysiphonia hemisphaerica* and *P. boldii* (Table S1). Four haplotypes were found (Fig. 1d): 1) four samples from Spain (Atlantic and Mediterranean) and Norway; 2) a sample from the United Kingdom; 3) a sample from USA; and 4) two samples from Australia. Atlantic samples differed by 0.1-0.2% (1-2 bp), while Australian samples were 0.7-0.9% (8-11) divergent from the Atlantic samples. Our results indicate that the lineage formed by these three taxa is moderately variable in the North Atlantic, and is clearly separated from the Australian ~~haplotype~~populations.

Polysiphonia villum

Molecular data were obtained from two regions where *Polysiphonia villum* (as *P. scopulorum* var. *villum*, see Supplement 1) had previously been reported (Fig. 1e). Furthermore, it was also sampled in Spain, the French Mediterranean and Australia, where it is here newly recorded. The 13 sequences determined for *P. villum* and the two downloaded from GenBank (Table S1) belong to three haplotypes (Fig. 1f): 1) four samples from Australia, 2) three samples from Brazil and 3) eight samples from the North Atlantic (North Carolina, Spain and France). Australian samples were 0.5-0.6% (4-7 bp) divergent from the Atlantic samples and the Brazilian sequences differed by 0.2% (2 bp) from the North Atlantic samples. Thus, *P. villum* shows a clear phylogeographic structure.

Polysiphonia devoniensis

Our dataset included samples from the previously recorded distribution in Atlantic Europe, as well as from the northwestern Mediterranean (Italy and France), the Adriatic Sea (Italy) and Victoria (Australia), from where *P. devoniensis* is here recorded for the first time (Fig. 2a, Table S1). Furthermore, sequences of *P. kapraunii* from North Carolina were also included in our dataset (see Supplement 1). Analyses including an *rbc*L sequence of *P. kapraunii* from GenBank and 21 newly determined sequences of *P. devoniensis* (Table S1) showed eight haplotypes (Fig. 2b). One haplotype was found in the northwestern Mediterranean, Atlantic Spain and Australia; one occurred in the Adriatic Sea and the northwestern Mediterranean; and six haplotypes were each represented by a single sample (two from Wales, two from the Adriatic Sea, one from the northwestern Mediterranean and one from North Carolina). The North Carolina sample identified as *P. kapraunii* was 0.2-0.3% (3-4 bp) divergent from two of the European samples (PD301 and PD2430). These three samples differ from the others by sequence divergences of 1-1.4% (12-18 bp), while divergence between the other five haplotypes is 0.1-1% (1-9 bp). The lineage formed by samples assigned to *P. devoniensis* and *P. kapraunii* has a high genetic diversity and the distribution of haplotypes lacks geographic structure. ~~The discovery of *P. devoniensis* in Victoria (Australia), exhibiting a single haplotype that is also present in Europe, suggests that this species has been introduced into this country from Europe, possibly Atlantic Spain or the NW Mediterranean.~~

Symphyocladia dendroidea complex

Sequences of *Symphyocladia dendroidea* are available from most of the previously known distribution (British Columbia, California, Chile, Peru, Japan and the Mediterranean). Some of these sequences were labelled as *Pterosiphonia tanakae* (see Supplement 1). Furthermore, we collected this species in a Galician marina (northwestern Spain) and in Australia (Victoria), where it is here recorded for the first time (Fig. 2c).

The *rbc*L data for *Symphyocladia dendroidea* reveal cryptic diversity in the Americas, as specimens from Peru and Chile and specimens from British Columbia (here referred as *S. dendroidea* 2) do not constitute a clade (Fig. S1, Table S1). In addition to these regions, both were recorded in California. *S. dendroidea* is resolved as sister to *S. parasitica* with high support, while *S. dendroidea* 2 is placed in a moderately supported clade together with *S. brevicaulis* and *S. baileyi* (Fig. S1). Molecular data show that *S. dendroidea* has a wide distribution in the Pacific and occurs in some

European locations, while *S. dendroidea* 2 is apparently restricted to Pacific North America.

In total, 28 *rbc*L sequences were analysed for *Symphocladia dendroidea* (some sequences labelled as *S. tanakae*, see Supplement 1) including 13 newly determined and 15 downloaded from GenBank (Table S1). The UPGMA dendrogram shows seven haplotypes (Fig. 2d) of which five comprise samples from Pacific South America, one includes samples from Australia and Japan, and the other consists of samples from California and Europe. Maximum variability between South American haplotypes is 0.6% (8 bp), and sequence divergence between them and the two other clades is 0.4-1% (3-9 bp). These levels of *rbc*L variation suggest that this entity may consist of multiple species or highly differentiated populations.

~~*Symphyocladia dendroidea* was recorded as an introduced species in the French Mediterranean in 2005 (as *P. tanakae*) and our recent discovery of the same haplotype in a marina in Atlantic Spain probably represents a secondary introduction and suggests that the species is spreading in Europe via hull fouling. The presence of several genetically separated lineages in Pacific South America contrasts with the occurrence of a single haplotype in Japan, Australia and California. Furthermore, Japan and Australia have the same haplotype, suggesting that one or both populations could be introduced.~~

Xiphosiphonia pennata complex, including *X. pinnulata* and *Symphyocladia spinifera*

Xiphosiphonia pennata has been reported in the Atlantic and Indo-Pacific (Fig 2e) and this morphological species is a complex of at least three ~~unrelated~~ non-sister species. Their taxonomy has been resolved with the clarification of the identity of ~~including~~ *X.*

pinnulata and *S. spinifera* that have been misidentified as *X. pennata* (see Supplement 1).

At present, 39 *rbc*L sequences (16 newly determined and 23 downloaded from GenBank) are available for *Symphyocladia spinifera* from California, Pacific South America, Australia and Korea (Fig. 2f). The UPGMA shows 10 haplotypes of which four correspond to Korean samples, four to Peruvian samples, one to Australian samples and one to a Washingtonian sample (Fig. 2f). Sequence divergence among haplotypes is up to 0.9% (7 bp). Australian samples match the morphological concept of *Xiphosiphonia pennata*, but our molecular data reveal that none of them grouped with the European *X. pennata* but instead are mostly closely related to *S. spinifera*. Therefore, *X. pennata* should be excluded from the recorded Australian flora and replaced by *S. spinifera*. Interestingly, all the Australian samples belong to a single haplotype, which contrasts with the four haplotypes found in both Peru and Korea.

Xiphosiphonia pinnulata sequences were resolved as three haplotypes of which two were found in European samples and one in Brazilian samples (Fig. 2g). Sequence divergence among them is up to 0.7% (9 bp) and between the two European clades is up to 0.3% (3 bp). *X. pennata* was only found in the Atlantic Iberian Peninsula. Therefore, the widely reported *X. pennata* (as *Pterosiphonia pennata*) is apparently restricted to European shores. *X. pinnulata* is restricted to the Atlantic, where it has a strong phylogeographic structure with divergences that may even suggest they are separate species. *S. spinifera* is restricted to the Pacific and it has a high genetic variability between regions and within regions in Korea and South America.

Herposiphonia tenella complex

In total, 27 *rbc*L sequences were obtained for samples morphologically identified as *Herposiphonia tenella* from Europe, North America and Queensland (Australia) (Fig. 3). They were analysed together with the available *rbc*L data for the genus (15 species). The phylogeny ~~(Fig. 4)~~ resolved *H. tenella* in seven ~~clades~~lineages, four from the Atlantic and three from Queensland (Fig. 4). Sequence divergence among the lineages was at least 1.9%, while divergence within them was up to 0.7%. Only two of these ~~clades~~ lineages were resolved as sisters (1.9-2.1% sequence divergence), while the others, despite morphological similarities, were more closely related to other ~~clades~~lineages. Thus, *Herposiphonia tenella* is a large species complex that requires taxonomic revision to better understand its cryptic diversity and the distribution of the resulting new species. Its type locality is in the Mediterranean, where three of the four European ~~species~~ lineages were collected.

DISCUSSION

Species complexes

In this work we ~~distinguish between~~detected several complexes of non-sister species (*Xiphosiphonia pennata*, *Symphyocladia dendroidea* and *Herposiphonia tenella*).~~,~~ Also, we found ~~and~~ species-level taxa that represent monophyletic lineages containing several haplotypes that in most cases are distributed in accordance with geographic~~al patterns~~ regions. ~~The second group~~They could also be classified as species complexes, as sequence divergences between haplotypes are often large (up to 1.4%), possible evidence for multiple species. Interpretations of genetic divergences when delineating species boundaries vary among authors. For example, *Melanothamnus harveyi/japonicus* and other closely related species have been interpreted as a single species with an intraspecific variability in the *rbc*L gene ≤ 2.1 % (McIvor et al. 2001, as *Polysiphonia*) or as a species complex in which interspecific variability in the *rbc*L gene is 0.3-0.7 % (Savoie and Saunders 2015, as *Neosiphonia*). The species concept has been hotly debated, but there is a general consensus that speciation is a process that takes place when gene flow is interrupted as a consequence of isolation of populations (Coyne et al. 1988, Leliaert et al. 2014). In the present work, assessing species boundaries was not always straightforward, and we used information based on genetic divergences, species distribution and, in one lineage, interbreeding experiments described by Rueness (1973). The first scenario we encountered consists of species with a variety of haplotypes ~~separated by large geographical distances~~found in distant locations. Genetic isolation by distance seems obvious considering our data and, in some cases, where the divergences between distant populations are ~~particularly~~ relatively large (≤~~up to~~ 0.9%), one might consider them different species (*Ophidocladus simpliciusculus* from Europe *vs.* Brazil *vs.* Australia/South Africa, *Lophosiphonia obscura* from the North Atlantic *vs.* Australia, *Polysiphonia villum* from the Atlantic *vs.* Australia, and *Xiphosiphonia pinnulata* from Brazil *vs.* Europe). However, the low number of samples in some regions or species, as well as the lack of sampling in other regions where these species were recorded or may be still unknown precludes a definitive conclusion. Perhaps the observed large sequence divergences between the lineages within these species would be less evident with larger datasets. A second scenario is similar to the former, as it consists of species with a variety of haplotypes, but in this case several haplotypes share the same distribution (*P. devoniensis*, *Symphyocladia dendroidea, S. spinifera*). Thus, despite *rbc*L divergences among some haplotypes (≤~~up to~~ 1.4%) being even larger than in the previous group (≤~~up to~~ 0.9%), whether they are at present reproductively isolated and should be considered as distinct species is uncertain. Interbreeding experiments may assist to clarify if these species should be considered as distinct or not. While successful reproduction may have multiple interpretations (Leliaert et al. 2014), unsuccessful reproduction indicates reproductive incompatibility. The third scenario we found in this work is represented by *Lophosiphonia obscura* whose eastern and western Atlantic populations have low genetic distances (0.1-0.2 %) in the *rbc*L gene, and also in the more variable *cox*1 marker (0.6-1.2 %, HQ412544-5 as *P. hemisphaerica* and *P. boldii*, MF094025). Despite this, crossing experiments demonstrate that isolates from Texas and from Norway fail to produce fully fertile progeny (Rueness 1973, as *P. hemisphaerica* and *P. boldii*). This suggests that these two populations are reproductively isolated, and that divergent selection may be acting on these populations but *rbc*L and *cox*1 gene sequences do not reflect this isolation (Nosil et al. 2009). These three scenarios show different evolutionary patterns even among closely related species (e.g. *P. villum vs. P. devoniensis*). Therefore, application of genetic distances in delineating species boundaries should be evaluated on a case by case basis. While these are very interesting issues from a taxonomic perspective, they are not the focus of this paper. From a phylogeographic point of view, whether these closely related monophyletic lineages are different species or not is of minor importance, because either way they share a common ancestor from which several genetic entities evolved.

Phylogeographic patterns

The paradox between expected dispersal limitation (Santelices 1990, Kilan and Gaines 2003) and wide reported species distributions led us to hypothesize that such widely distributed species would either have strong phylogeographic structure or were spread by humans. Our results confirmed these hypotheses and exposed a third ~~option~~scenario, where the morphologically defined species was in fact a complex of non-sister cryptic species.

Three of the species ~~or groups of species form monophyletic lineages and~~ exhibit genetic variability with clear phylogeographic structure in Australia, and the North and South Atlantic (*Ophidocladus simpliciusculus*, *Lophosiphonia obscura* and *Polysiphonia villum*). ~~Genetic divergences of sequences of these species from Australia, North and South Atlantic reflect geographical separation.~~ This result is not unexpected considering that genetic divergence is promoted by the isolation among populations separated by large geographic distances (Palumbi 1994). However, the observed genetic divergence is relatively low (≤~~up to~~ 0.9%) considering that Australia and the North and South Atlantic~~these regions~~ have been separated since about 80 My (Jordan et al. 2016). Therefore, rather than this genetic divergence resulting from an 80 My old vicariant evolution, long-distance dispersal processes acting on a common ancestor and subsequent divergence into differentiated populations are invoked to explain the observed patterns. Mechanisms responsible for this long-distance dispersal are obscure considering that these species either occur in coastal lagoons/estuaries or on sand-covered rocks where buoyant macroalgae that can act as rafts are rare (Airoldi 1998, Díaz-Tapia et al. 2013a). Molecular data have provided evidence for long-distance dispersal in other red algal species but mechanisms remain unknown (Zuccarello et al. 2002a, Fraser et al. 2013). The genetic separation among geographically distant lineages may indicate that long-distance dispersal occurs at a low rate. Alternatively, density-dependent processes are involved and once a population colonizes a new region it prevents the establishment of latecomers (Waters et al. 2013). Furthermore, available data for the three species mentioned above indicate different evolutionary histories and/or dispersal paths. For instance, in *L. obscura* and *P. villum* the largest sequence divergences are between Australian and Atlantic populations, whereas in *O. simpliciusculus* the Australian haplotype is relatively close to South African and European haplotypes but the divergence across the Atlantic (Brazil *vs.* Europe) is much larger.

Several species showed a diversity of haplotypes sharing the same region: the Pacific *Symphyocladia spinifera* and *S. dendroidea*, as well as the Atlantic *Polysiphonia devoniensis*. The origin of this diversity must be related to processes of isolation that led to genetic differentiation, followed by local dispersal events. As ~~in~~ for *Ophidocladus simpliciusculus*, *Lophosiphonia obscura* and *Polysiphonia villum*~~the examples mentioned above~~, dispersal mechanisms for *S. spinifera* and *P. devoniensis* are unknown. In contrast, *S. dendroidea* has been reported growing on stranded holdfasts of the floating alga *Durvillaea antarctica* (Macaya et al. 2016, López et al. 2017, 2018), which could contribute to dispersal after genetic differentiation ~~influencing~~ influenced its genetic structure.

The disjunct distribution of a second group of species (*Polysiphonia devoniensis* and *Symphyocladia dendroidea*) can be explained by human-mediated introduction events. The human transport of species from native (donor) to introduction (recipient) regions causes the rapid expansion of species' distribution and alters natural phylogeographic patterns (Straub et al. 2016). The discovery of *P. devoniensis* in Victoria (Australia), exhibiting a single haplotype that is also present in Europe, suggests that this species has been introduced into this country from Europe, possibly Atlantic Spain or the NW Mediterranean. *Symphyocladia dendroidea* was recorded as an introduced species in the French Mediterranean in 2005 (Boudouresque and Verlaque 2008, as *P. tanakae*) and our recent discovery of the same haplotype in a marina in Atlantic Spain probably represents a secondary introduction and suggests that the species is spreading in Europe via hull fouling. The presence of several genetically separated lineages of *S. dendroidea* in Pacific South America contrasts with the occurrence of a single haplotype in Japan, Australia and California. Japan and Australia have the same haplotype, suggesting that one or both populations could be introduced. Genetic diversity of seaweeds in the introduced regions is either similar or reduced relative to the native area (McIvor et al. 2001, Provan et al. 2008, Voisin et al. 2005, Geoffroy et al. 2016). The finding of diverse haplotypes in the introduced region is indicative of an introduction involving several haplotypes or multiple introductions, depending on the phylogeographic structure in the native area (McIvor et al. 2001, Voisin et al. 2005, Geoffroy et al. 2016). A single haplotype of both *S. dendroidea* and *P. devoniensis* has been detected in the areas where the introduction of these species is certain, suggesting that their introduction is the result of a single event in which a single haplotype was involved. However, much more complex scenarios could explain the observed patterns and a better understanding of the phylogeographic patterns in native and introduced areas would be needed to elucidate the introduction dynamics.

~~*P. devoniensis* in Australia is represented by only one haplotype, compared to eight in the North Atlantic, suggesting that the introduction could be the result of a single event in which a single haplotype was involved.*Symphyocladia dendroidea* was recorded as an introduced species in the French Mediterranean in 2005 (as *P. tanakae*) and our recent discovery of the same haplotype in a marina in Atlantic Spain probably represents a secondary introduction and suggests that the species is spreading in Europe via hull fouling. The presence of several genetically separated lineages in Pacific South America contrasts with the occurrence of a single haplotype in Japan, Australia and California. Furthermore, Japan and Australia have the same haplotype, suggesting that one or both populations could be introduced.~~

~~Our study showed that in the regions where *S. dendroidea* (Europe) and *P. devoniensis* (Australia) are known to be introduced, each species is represented by a single *rbc*L haplotype.~~ ~~Genetic diversity of seaweeds in the introduced regions is either similar or reduced relative to the native area (McIvor et al. 2001, Provan et al. 2008, Voisin et al. 2005, Geoffroy et al. 2016). The finding of diverse haplotypes in the introduced region is indicative of an introduction involving several haplotypes or multiple introductions, depending on the phylogeographic structure in the native area (McIvor et al. 2001, Voisin et al. 2005, Geoffroy et al. 2016). *P. devoniensis* in Australia is represented by only one haplotype, compared to eight in the North Atlantic, suggesting that the introduction could be the result of a single event in which a single haplotype was involved.~~ ~~Likewise, only one haplotype was found in Europe for *S. dendroidea*, showing reduction of genetic diversity if South America were the native area, but this is uncertain and much more complex scenarios could explain the observed patterns. An alternative hypothesis is that South America is a centre of diversification of lineages and that two of them established naturally in other Pacific regions, where the genetic diversity of the *rbc*L gene remains low, and that it has been introduced in Europe from one of these locations. Thus, a better understanding of the phylogeographic patterns in native and introduced areas would be needed to elucidate the introduction dynamics.~~

The third group of species analyzed here involved species complexes of non-sister cryptic species (*Xiphosiphonia pennata* including *X. pinnulata* and *Symphyocladia spinifera*; *S. dendroidea;* and *Herposiphonia tenella*)~~ in which specimens morphologically identified as a single species were resolved as complexes of non-sister cryptic species~~. In both cases species found in the Atlantic and Pacific basins differ, but in addition several species were found with overlapping distributions in some regions of each basin. Therefore, the distribution of these widely reported species is much narrower than previously thought. Cryptic algal species often involve a group of morphologically similar species that are genetically differentiated, but resolve as a monophyletic group (Zuccarello et al. 2002a, Won et al. 2009, Payo et al. 2013). However, examples of non-monophyletic cryptic "species" have also been documented in the red algae (Zuccarello et al. 2018). Morphological similarity among non-monophyletic groups of cryptic species can be explained by evolutionary convergence, morphological stasis or developmental constraints (Leliaert et al. 2014, Zuccarello et al. 2018). *X. pennata, S. spinifera* and *S. dendroidea* are placed in a tribe (Pterosiphonieae) with high morphological variation ranging from filiform to foliose species (Díaz-Tapia et al. 2017b). The body plan of both species is filiform, among the simplest observed in the tribe, and morphological stasis is a plausible explanation for their similarity. In the tribe Herposiphonieae all species are very similar in morphology, with limited differences in their body plans (Díaz-Tapia et al. 2017b) and the cryptic diversity in *Herposiphonia tenella* might result from morphological stasis or developmental constraints.

Understanding the processes underlying phylogeographic patterns requires the study of numerous specimens from across the entire distribution of the species. In this regard, we recognize important limitations in our work that prevent us from fully elucidating causes of the observed phylogeographic patterns, leading to some tentative conclusions about the potentially introduced status of some of the analysed populations. However, most of the species treated here are rare in all or part of their known distribution range so improving the datasets would be very difficult. For example, *Lophosiphonia obscura*, despite being widely reported, is very rare in the regions here studied: the sample from the UK used in this study is the first one collected since 1970

(Maggs and Hommersand 1993). In Spain, we found it only once in the Atlantic and once in the Mediterranean, and the species is here recorded for only the third time in Australia. Our work should thus be interpreted as one of the first attempts to understand phylogeographic patterns of widely distributed red algal species. Even though ~~some of the nuances of~~ their evolutionary history ~~remain unknown~~is not well known, our analyses provide clear examples of 1) species with wide distributions and strong phylogeographic structure that reflects the geographical distance~~species complexes in which non-monophyletic cryptic diversity has been found~~; 2) species with a broad distribution that can be only explained by human-mediated transport; and 3) -species complexes in which non-monophyletic cryptic diversity has been found ~~species with wide distributions and strong phylogeographic structure that reflects the geographical distance~~. This study indicates that widely distributed species are the exception in red algae, except when they have been spread by humans.

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Figure legends

Figure 1 Distribution and UPGMA unrooted distance phylogram based on *rbc*L sequences of *Ophidocladus simpliciusculus* (a, b), *Lophosiphonia obscura* (as *Polysiphonia hemisphaerica* and *P. boldii* in Norway and Texas, respectively, see Supplement 1) (c, d) and *P. villum* (e, f). In figures a, c and e, circles indicate the regions from which sequences are available and their colors indicate the distribution of haplotypes. Areas outlined in red are regions where the species is recorded for the first time. Coastline in black shows the reported distribution (Guiry and Guiry 2018). In figure c, black coastlines represent the recorded distribution of *Lophosiphonia obscura,* red line *P. hemisphaerica* and yellow line *P. boldii*. Scale bars: 5 mm in (a), 8 mm in (c), 6 mm in (e).

Figure 2 Distribution and UPGMA unrooted distance phylogram based on *rbc*L sequences of *Polysiphonia devoniensis* (as *P. kaprauni* in North Carolina) (a, b), *Symphyocladia dendroidea* (c, d) and *S. spinifera/Xiphosiphonia pennata/X. pinnulata* (e, f, g). Symbols are as in Figure 1, and pie divisions in Figures a, c and e indicate proportions of each haplotype when multiple haplotypes were present. In figure e, circles with white border correspond to *S. spinifera* and the ones with black border to *X. pinnulata*. Encircled areas marked with red color are regions where the species are here recorded for the first time. In figure a, black lines represent the recorded distribution of *P. devoniensis* and red line the distribution of *P. kapraunii*. In figure c, black lines represent the recorded distribution of *S. dendroidea*, blue lines the regions where it was recorded as *S. tanakae*, red line the region where molecular data demonstrated that *S. dendroidea* 2 is present, the asterisk indicates the area where both *S. dendroidea* 2 and *S. tanakae* were reported based on molecular data, and plus symbols the regions from which sequences of *S. dendroidea* 2 are available. In figure e, black lines represent the recorded distribution of *X. pennata*; yellow lines the regions where molecular data showed the presence of *S. spinifera* instead *X. pennata*, red lines regions where only *X. pinnulata* has been recorded based on molecular data and blue line the region where both *X. pinnulata* and *X. pennata* have been recorded based on molecular data. Scale bars: 6 mm in (a), 7 mm in (c), 4 mm in (e).

Figure 3 Distribution of *Herposiphonia tenella*. Asterisks indicate the regions from which sequences are available. Scale bar: 1 mm.

Figure 4 RAxML tree based on *rbc*L sequences of the genus *Herposiphonia*. Samples that morphologically correspond with *Herposiphonia tenella* are in bold. Bootstrap values are indicated on the nodes when > 80. BE (Belize), CA (Canada), CI (Canary Islands), FR (France), IN (India), IT (Italy), KO (Korea), NC (North Carolina), PO (Portugal), QL (Queensland), SP (Spain), WA (Western Australia), VIC (Victoria).

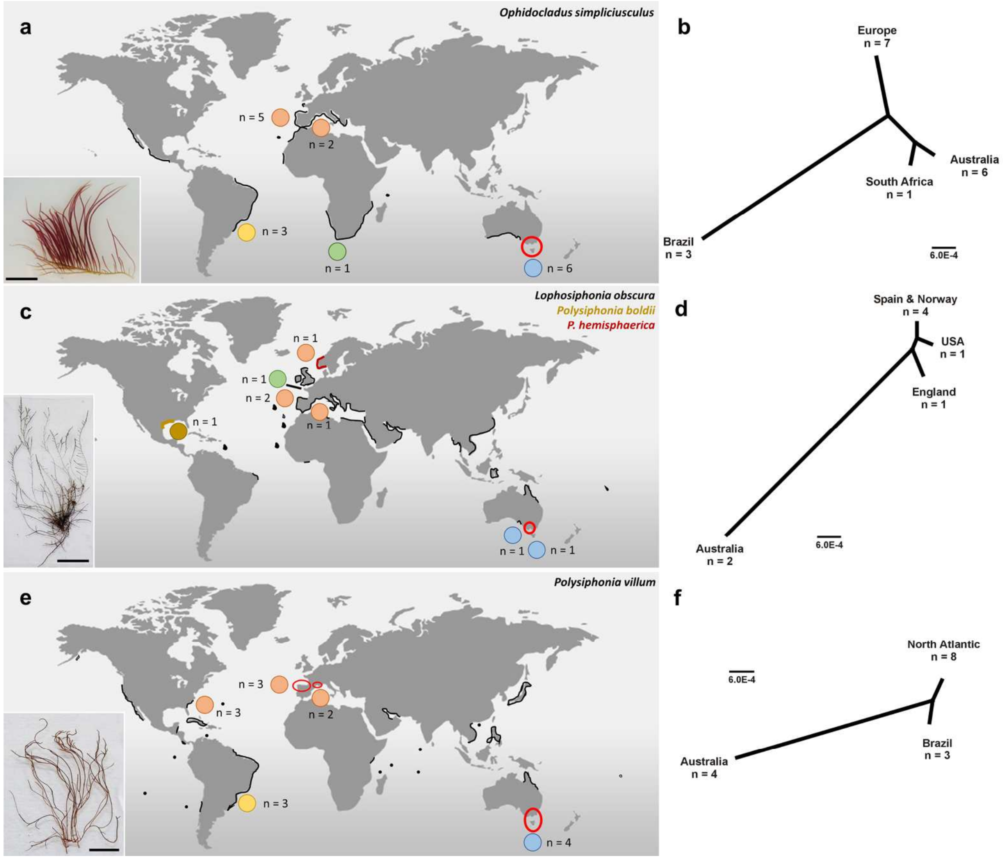


Figure 1 Distribution and UPGMA unrooted distance phylogram based on rbcL sequences of Ophidocladus simpliciusculus (a, b), Lophosiphonia obscura (as Polysiphonia hemisphaerica and P. boldii in Norway and Texas, respectively, see Supplement 1) (c, d) and P. villum (e, f). In figures a, c and e, circles indicate the regions from which sequences are available and their colors indicate the distribution of haplotypes. Areas outlined in red are regions where the species is recorded for the first time. Coastline in black shows the reported distribution (Guiry and Guiry 2018). In figure c, black coastlines represent the recorded distribution of Lophosiphonia obscura, red line P. hemisphaerica and yellow line P. boldii. Scale bars: 5 mm in (a), 8 mm in (c), 6 mm in (e).

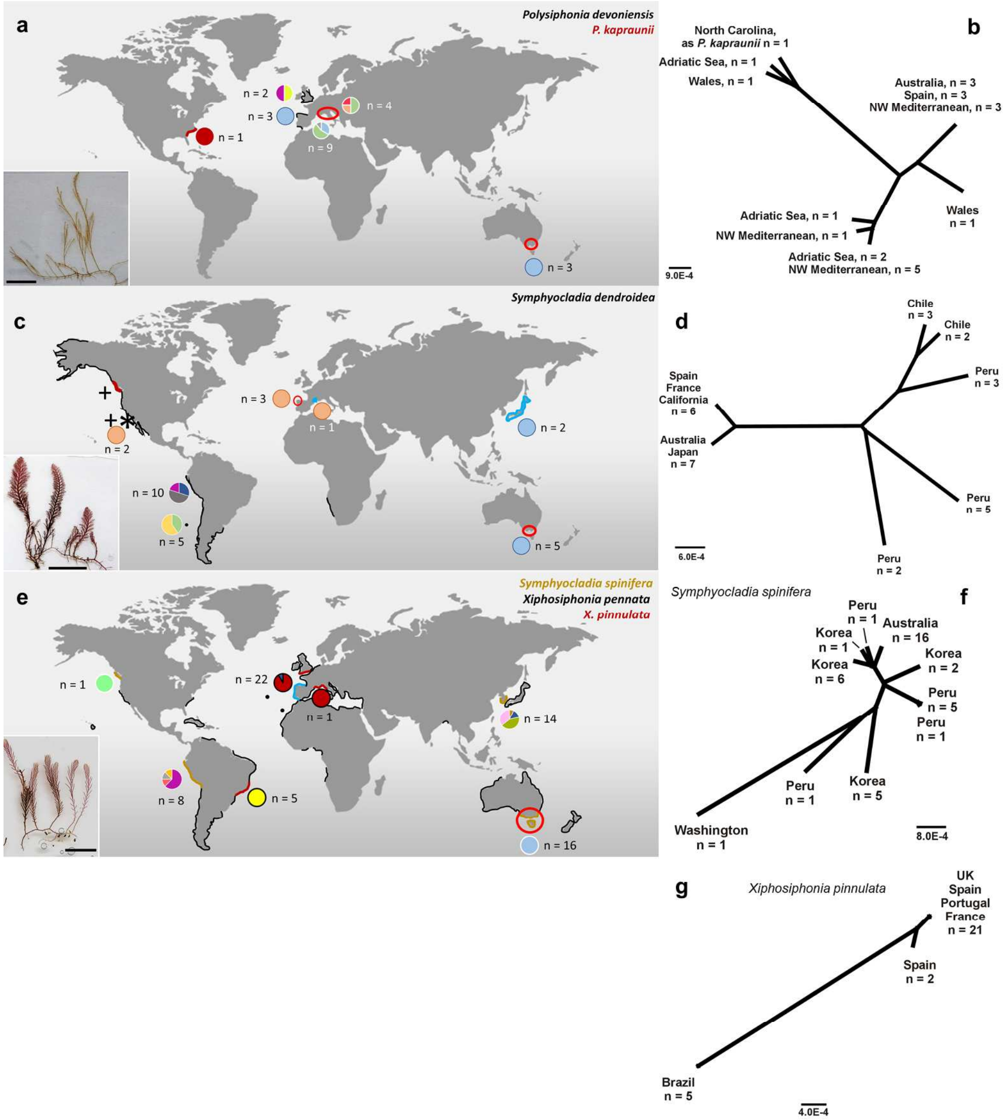


Figure 2 Distribution and UPGMA unrooted distance phylogram based on rbcL sequences of Polysiphonia devoniensis (as P. kaprauni in North Carolina) (a, b), Symphyocladia dendroidea (c, d) and S. spinifera/Xiphosiphonia pennata/X. pinnulata (e, f, g). Symbols are as in Figure 1, and pie divisions in Figures a, c and e indicate proportions of each haplotype when multiple haplotypes were present. In figure e, circles with white border correspond to S. spinifera and the ones with black border to X. pinnulata. Encircled areas marked with red color are regions where the species are here recorded for the first time. In figure a, black lines represent the recorded distribution of P. devoniensis and red line the distribution of P. kapraunii. In figure c, black lines represent the recorded distribution of S. dendroidea, blue lines the regions where it was recorded as S. tanakae, red line the region where molecular data demonstrated that S. dendroidea 2 is present, the asterisk indicates the area where both S. dendroidea 2 and S. tanakae were reported based on molecular data, and plus symbols the regions from which sequences of S. dendroidea 2 are available. In figure e, black lines represent the recorded distribution of X. pennata; yellow lines the regions where molecular data showed the presence of S. spinifera instead X. pennata, red lines regions where only X. pinnulata has been recorded based on molecular data and blue line the region where both X. pinnulata and X. pennata have been recorded based on molecular data. Scale bars: 6 mm in (a), 7 mm in (c), 4 mm in (e).

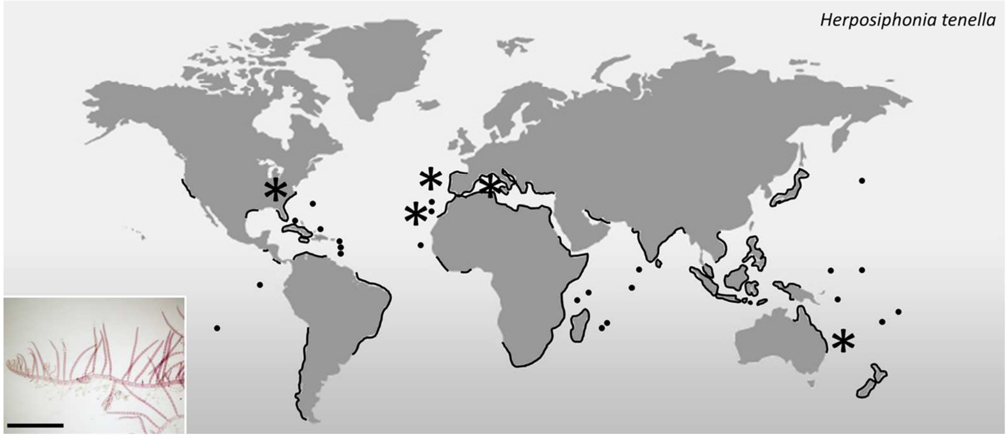
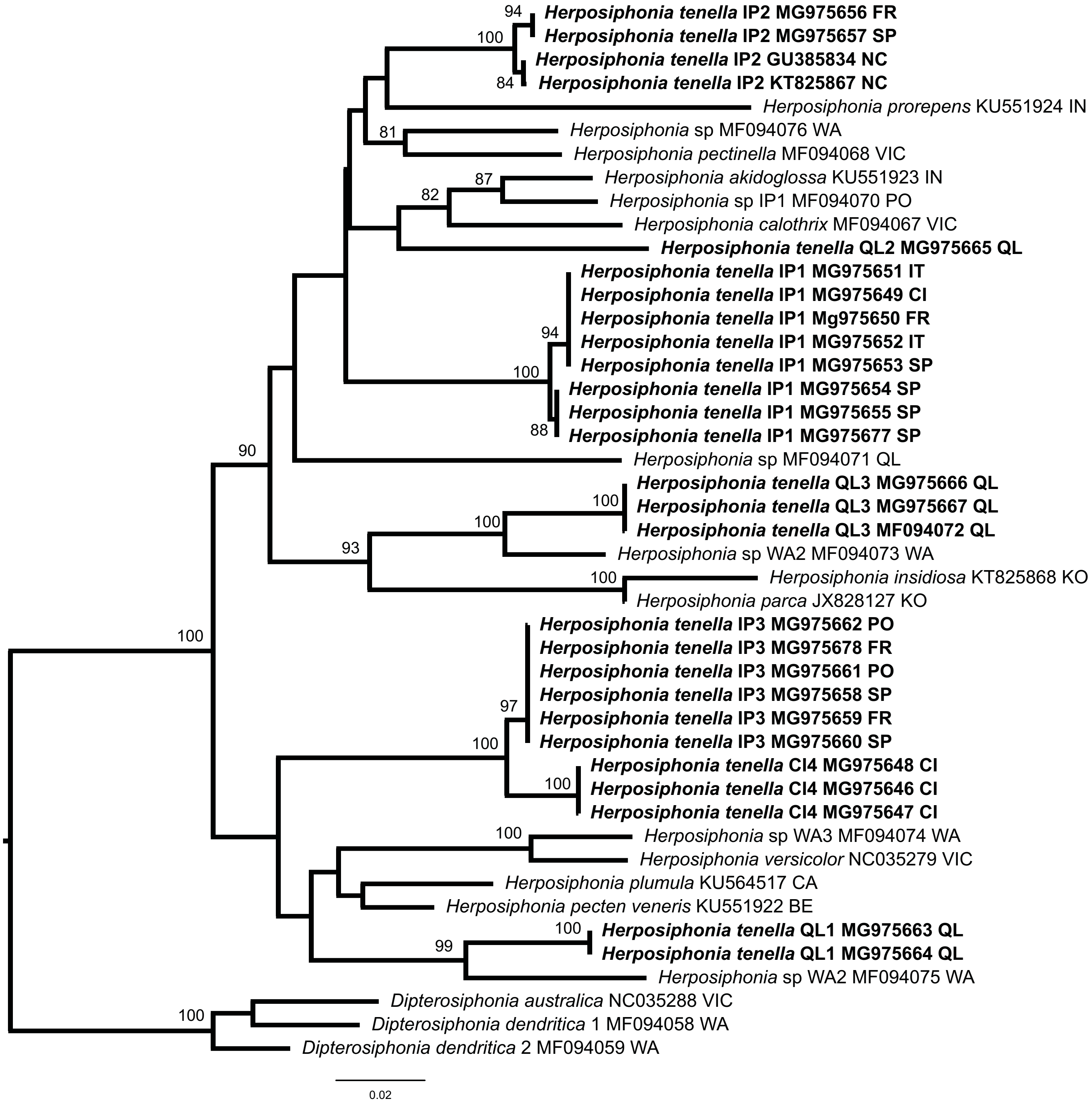


Figure 3 Distribution of Herposiphonia tenella. Asterisks indicate the regions from which sequences are available. Scale bar: 1 mm.


94
100
84
Herposiphonia tenella IP2 MG975656 FR
Herposiphonia tenella IP2 MG975657 SP
Herposiphonia tenella IP2 GU385834 NC
Herposiphonia tenella IP2 KT825867 NC
Herposiphonia prorepens KU551924 IN
81
Herposiphonia sp MF094076 WA
Herposiphonia pectinella MF094068 VIC
87
82
Herposiphonia akidoglossa KU551923 IN
Herposiphonia sp IP1 MF094070 PO
Herposiphonia calothrix MF094067 VIC
Herposiphonia tenella QL2 MG975665 QL
94
100
88
Herposiphonia tenella IP1 MG975651 IT
Herposiphonia tenella IP1 MG975649 CI
Herposiphonia tenella IP1 Mg975650 FR
Herposiphonia tenella IP1 MG975652 IT
Herposiphonia tenella IP1 MG975653 SP
Herposiphonia tenella IP1 MG975654 SP
Herposiphonia tenella IP1 MG975655 SP
Herposiphonia tenella IP1 MG975677 SP
90
Herposiphonia sp MF094071 QL
100
100
93
Herposiphonia tenella QL3 MG975666 QL
Herposiphonia tenella QL3 MG975667 QL
Herposiphonia tenella QL3 MF094072 QL
Herposiphonia sp WA2 MF094073 WA
100
Herposiphonia insidiosa KT825868 KO
Herposiphonia parca JX828127 KO
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97
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Herposiphonia tenella IP3 MG975662 PO
Herposiphonia tenella IP3 MG975678 FR
Herposiphonia tenella IP3 MG975661 PO
Herposiphonia tenella IP3 MG975658 SP
Herposiphonia tenella IP3 MG975659 FR
Herposiphonia tenella IP3 MG975660 SP
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Herposiphonia tenella CI4 MG975648 CI
Herposiphonia tenella CI4 MG975646 CI
Herposiphonia tenella CI4 MG975647 CI
100
Herposiphonia sp WA3 MF094074 WA
Herposiphonia versicolor NC035279 VIC
Herposiphonia plumula KU564517 CA
Herposiphonia pecten veneris KU551922 BE
100
99
Herposiphonia tenella QL1 MG975663 QL
Herposiphonia tenella QL1 MG975664 QL
Herposiphonia sp WA2 MF094075 WA
100
Dipterosiphonia australica NC035288 VIC
Dipterosiphonia dendritica 1 MF094058 WA
Dipterosiphonia dendritica 2 MF094059 WA
0.02

Supplement S1. Taxonomic notes.

Lophosiphonia obscura, Polysiphonia hemisphaerica and P. boldii

The taxonomic history of *Lophosiphonia obscura* is complex (Silva et al. 1996, Díaz-Tapia and Bárbara 2013), involving several names that have been proposed in different regions. Among these names are *Polysiphonia hemisphaerica* from Scandinavia (Rueness 1971) and *P. boldii* from USA (Wynne and Edwards 1970). Rueness (1973) showed that male and female gametophytes of these two species successfully interbreed, producing carpospores from which tetrasporophytes germinate. However, the viability of tetraspores obtained from these tetrasporophytes was reduced. Thus, despite their high *cox*1 similarity, *P. boldii* and *P. hemisphaerica* failed to produce fully fertile progeny and the taxonomic status of these two species remained unresolved (Rueness 1973, 2010). We obtained *rbc*L sequences for the three taxa and our phylogenetic analysis revealed that they form a clade, are closely related (tree not shown), and whether they should be considered a single species is unclear. For simplicity, we are including these three currently recognized taxonomic species under the heading "*Lophosiphonia obscura*" but a taxonomic revision is required to clarify their taxonomic status.

Polysiphonia villum

Polysiphonia villum was originally described based on Mexican material (Agardh 1863) and its taxonomic status with regard to the Australian *P. scopulorum* was questioned (Cribb 1956). Based on its morphology, Hollenberg (1968) proposed to retain *P. villum* as a variety of *P. scopulorum*. However, molecular data showed that material attributed to these two taxa represents two different, non-monophyletic, molecular entities (Huisman et al. 2017). Consequently, here we apply the name *P. villum* to the molecular entity that matches American specimens (Stuercke and Freshwater 2008) and differs from Australian specimens (Huisman et al. 2017). Assessment of the correspondence of both *P. scopulorum* and *P. villum* with their respective type material has not been studied.

Polysiphonia devoniensis and P. kapraunii

Polysiphonia devoniensis was originally described from southern England (Maggs and Hommersand 1993) and subsequently recorded at other locations in Atlantic Europe (Díaz-Tapia and Bárbara 2013). More recently, *P. kapraunii* was described from North Carolina (Stuercke and Freshwater 2010). Our phylogenetic analysis revealed that these two entities form a clade, are closely related (tree not shown), and whether they should be considered a single species is unclear.

Symphyocladia dendroidea

Symphyocladia dendroidea was originally described from Peru and subsequently recorded from other locations in Pacific America, Argentina and Namibia (Fig. 2c). More recently, *S. tanakae* was described from Japan (Uwai and Masuda 1999, as *Pterosiphonia tanakae*) and it was recorded as an introduced species in the Mediterranean (Verlaque et al. 2015). The synonymy between these two species was proposed based on similarity of sequence data from their type localities (Bustamante et al. 2016a).

Xiphosiphonia pennata, X. pinnulata and Symphyocladia spinifera

Xiphosiphonia pennata was widely reported on Atlantic and Pacific coasts (Fig. 2e, as *Pterosiphonia pennata*) and successive publications have unmasked cryptic diversity in this taxon, resolving a Pacific and two Atlantic species. Maggs and Hommersand (1993) noted that the smaller, less robust European forms of this species should be assigned to *X. pinnulata* (as *P. pinnulata*). This distinction was later supported by molecular data (Díaz-Tapia and Bárbara 2013). Kim et al. (2012) revealed that Korean specimens previously regarded as *X. pennata* represented a distinct molecular species compared to European specimens and *P. arenosa* was described. Recently, the synonymy of *P. arenosa* with *Symphyocladia spinifera* (as *P. spinifera*; type locality Peru) was proposed (Bustamante et al. 2016b). A taxonomic revision of the tribe Pterosiphonieae demonstrated that, despite the high morphological similarity among *X. pennata*, *X. pinnulata* and *S. spinifera,* they do not form a clade (Savoie and Saunders 2016). In fact, they are placed in two distinct lineages and accordingly, the Pacific entities *P. arenosa* and *P. spinifera* were transferred to the genus *Symphyocladia*, while the Atlantic entities *P. pennata* and *P. pinnulata* were placed in the new genus *Xiphosiphonia* (Savoie and Saunders 2016).

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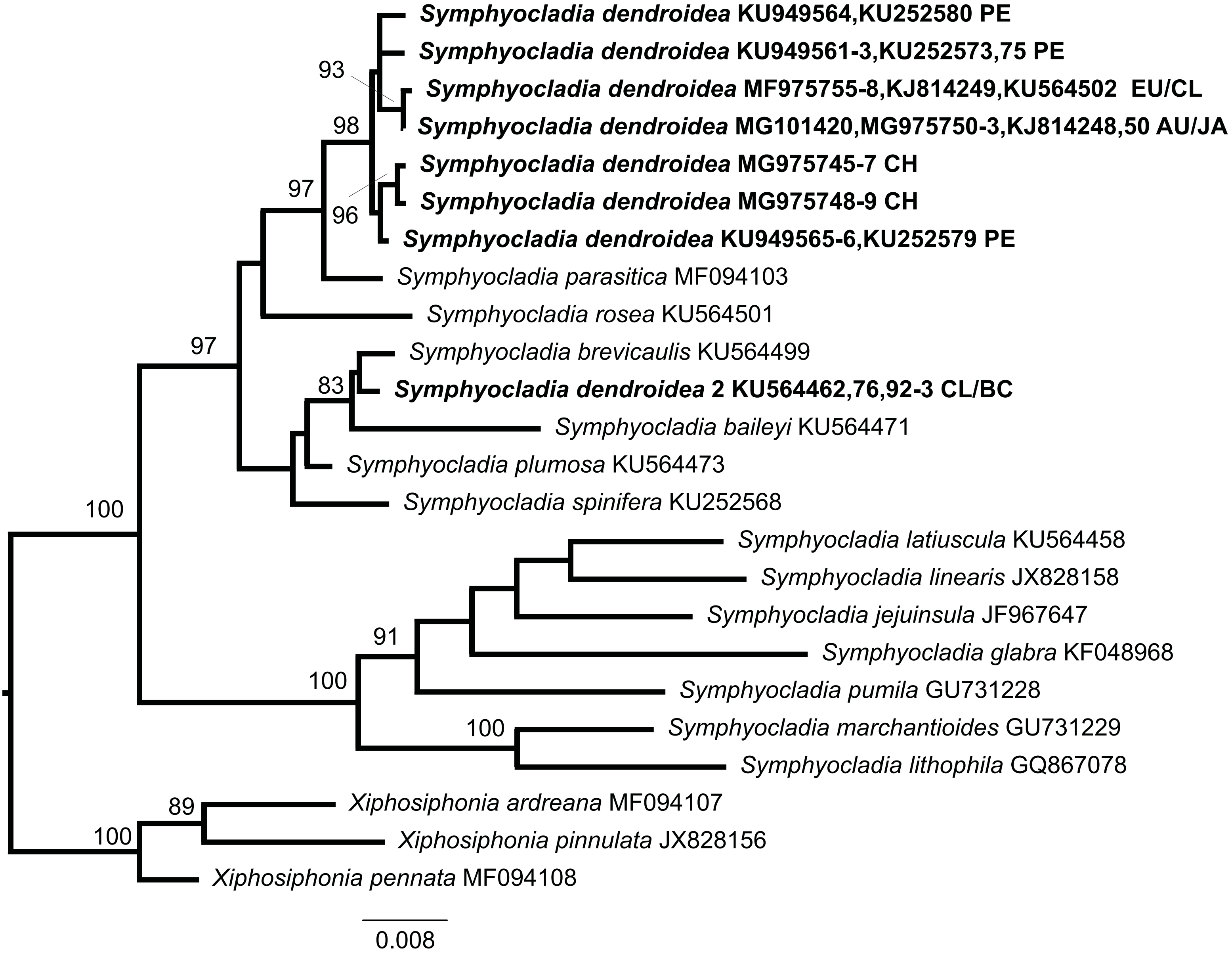

Figure S1 RAxML tree based on *rbc*L sequences of the genus *Symphyocladia. S. dendroidea* and *S. dendroidea* 2 are marked in bold. Bootstrap values are indicated on the nodes when > 80. AU (Australia), BC (British Columbia), CL (California), CH (Chile), EU (Europe), JA (Japan), PE (Peru).

Table S1. GenBank accession numbers of the *rbc* L sequences included in the UPGMA and phylogenetic analysis.

	GenBank	Sample ID	Length	Collection site; habitat; date; collectors	Reference
Ophidocladus simpliciusculus (P.Crouan & H.Crouan) Falkenberg	MG975673	JF1003	1291	Elandsbaai point, Western Cape, South Africa; intertidal; 29.xi.2014; KD & JFC	This work
	MG975674	PD625	1340	Praia de Parati, Ubu, Espirito Santo,Brazil; intertidal; 8.ix.2014; PD & MTF	This work
	MG975675	PD634	1341	Ponta Castelhanos, Espirito Santo,Brazil; intertidal; 9.ix.2014; PD & MTF	This work
	MG975676	PD664	1407	Praia de Santa Cruz, Espirito Santo,Brazil; intertidal; 10.ix.2014; PD & MTF	This work
	NC035284	PD949	1467	Queenscliff, Victoria, Australia; intertidal; 2.xii.2014; PD	Díaz-Tapia et al. 2017
	MG975677	PD1256	833	Inverloch, Victoria, Australia; intertidal; 18.i.2015; PD & MB	This work
	MG975678	PD1283	1377	Twen Reef, Victoria, Australia; intertidal; 19.i.2015; PD & MB	This work
	MG975679	PD1331	830	Walkerville, Victoria, Australia; intertidal; 20.i.2015; PD & MB	This work
	MG975680	PD1409	806	Lighthouse Reef, Victoria, Australia; intertidal; 29.i.2015; PD	This work
	MG975683	PD3342	1357	Georgetown, Tasmania, Australia; intertidal; 5.xi.2017; PD & JC	This work
	MG975684	SANT-A 25413	1443	Biarritz, French Atlantic; intertidal; 19.iii.2011; PD & IB	This work
	MG975672	CAM1032	1245	Biarritz, French Atlantic; intertidal; 9.ix.1999; CAM	This work
	MG975685	SANT-A 26249	1445	Peinzás, Foz, Galicia, Spain; intertidal; 19.iv.2011; PD	This work
	JX828139	CH827	1467	Linorsa, San Cibrao, Galicia, Spain; intertidal; 25.iv.2005; PD & IB	Bárbara et al. 2013
	MG975686	SANT-A 26460	1354	Olhos d´Agua, Algarve, Portugal; intertidal; 20.ii.2011; PD & IB	This work
	MG975681	PD2562	1355	Rochelonga, Adge, French Mediterranean; intertidal; 9.vi.2016; PD	This work
	MG975682	PD2585	1330	Rochelonga, Adge, French Mediterranean; intertidal; 9.vi.2016; PD	This work
Polysiphonia hemisphaerica Areschoug	MG975709	PD300	1303	Culture strain mantained by Jan Rueness and initiated from samples collected in Oslofjord, Norway	This work
Polysiphonia boldii M.J.Wynne & P.Edwards	MG975687	PD348	1287	Culture strain mantained by Jan Rueness and initiated from samples collected in Port Aransas, Texas, USA	This work
Lophosiphonia obscura (C.Agardh) Falkenberg	KT825865	CUK11188	1435	Wallaroo, Adelaide, Australia; 26.iii.2014	Bustamante et al. 2017
	MG975670	PD1352	1290	Eagle Nets Reef, Victoria, Australia; intertidal; 21.i.2015; PD & MB	This work
	MG975671	PD3007	1311	The Fleet, Weymouth, England; intertidal; 10.v.2017; CAM	This work
	MG975669	PD349	1316	Vilalonga, A Coruña, Spain; lagoon, intertidal; 9.vi.2011; RC	This work
	MF094086	SANT-A 26325	1345	Vilalonga, Galicia, Spain; lagoon with low salinity; 9.vi.2011; RC	Díaz-Tapia et al. 2017
	MG975668	PD326	1305	Fondo de Son Bauló, Palma de Mallorca, Spain; intertidal; 30.v.2013; IC	This work
Polysiphonia villum J.Agardh	MG975710	SANT-A 25434	1356	Biarritz, Atlantic France; intertidal; 19.iii.2011; PD & IB	This work
	MG975711	SANT-A 25665	1350	La Arena, Basque Country, Spain; intertidal; 22.ii.2011; PD & IB	This work
	MG975716	SANT-A 28109	1357	Gandarío, Galicia, Spain; intertidal; 25.iv.2013; PD, VG, CP & FC	This work
	MG975721	PD2249	1231	Calanque du Sormiou, Marseille, France; intertidal; 23.v.2016; PD, LLG & MV	This work
	MG975722	PD2250	1281	Calanque du Sormiou, Marseille, France; intertidal; 23.v.2016; PD, LLG & MV	This work
	MG975712	PD3058	1318	Wrightsville Beach, North Carolina, USA; v.1996; MH	This work
	EU492915	NC.33	1341	Masonboro Inlet, New Hanover, North Carolina, USA; -; 22.vii.2005	Stuercke & Freshwater 2008, as *P. scopulorum* var. *villum*
	EU492915	NC.09	1341	Masonboro Inlet, New Hanover, North Carolina, USA; -; 4.v.2005	Stuercke & Freshwater 2008, as *P. scopulorum* var. *villum*

	MG975717	PD603	837	Praia de Parati, Ubu, Espirito Santo,Brazil; intertidal; 8.ix.2014; PD & MTF	This work
	MG975718	PD614	1327	Praia de Parati, Ubu, Espirito Santo,Brazil; intertidal; 8.ix.2014; PD & MTF	This work
	MG975719	PD631	1297	Ponta Castelhanos, Espirito Santo,Brazil; intertidal; 9.ix.2014; PD & MTF	This work
	MG975720	PD967	1341	13th Beach, Victoria, Australia; intertidal; 4.xii.2014; PD	This work
	MG975715	PD3194	1346	Boat Harbour, Tasmania, Australia; intertidal; 2.xi.2017; PD & JFC	This work
	MG975713	PD3198	1327	Boat Harbour, Tasmania, Australia; intertidal; 2.xi.2017; PD & JFC	This work
	MG975714	PD3208	1319	Boat Harbour, Tasmania, Australia; intertidal; 2.xi.2017; PD & JFC	This work
Polysiphonia devoniensis Maggs & Hommersand	MG975689	CAM467	1245	Sarn Badrig, Pembs, Wales, UK; 15.viii.1998; CAM	This work
	MG975690	PD301	1348	Pwllheli, Wales, UK; 27.vi.2014; FB	This work
	MG975706	SANT-A 25664	1439	La Arena, Basque Country, Spain; intertidal; 22.ii.2011; PD & IB	This work
	MG975707	SANT-A 26229	1439	Llas, Foz, Galicia, Spain; intertidal; 19.iv.2011; PD, VP & AS	This work
	MG975708	SANT-A 28087	711	Miño, Galicia, Spain; intertidal; 25.v.2013; PD	This work
	MG975700	PD2445	926	Tirrenia, Pisa, Italy; intertidal; 3.vi.2016; PD & FR	This work
	MG975701	PD2604	1284	Adge, French Mediterranean; intertidal; 10.vi.2016 ; PD	This work
	MG975702	PD2627	1292	Setè, French Mediterranean; intertidal; 11.vi.2016; PD	This work
	MG975703	PD2658	1285	Mèze, French Mediterranean; intertidal; 12.vi.2016; PD	This work
	MG975704	PD2659	1290	Mèze, French Mediterranean; intertidal; 12.vi.2016; PD	This work
	MG975705	PD2660	1288	Mèze, French Mediterranean; intertidal; 12.vi.2016; PD	This work
	MG975694	PD2245	943	Calanque du Sormiou, Marseille, France; intertidal; 23.v.2016; PD, LLG & MV	This work
	MG975695	PD2251	922	Calanque du Sormiou, Marseille, France; intertidal; 23.v.2016; PD, LLG & MV	This work
	MG975696	PD2255	926	Calanque du Sormiou, Marseille, France; intertidal; 23.v.2016; PD, LLG & MV	This work
	MG975688	PD2017	1314	Passeto, Ancona, Italy; intertidal; 8.v.2013; FR	This work
	MG975697	PD2384	712	Passeto, Ancona, Italy; intertidal; 8.v.2016; PD & FR	This work
	MG975698	PD2430	1352	Due Sorelle, Ancona, Italy; intertidal; 1.vi.2016; PD & FR	This work
	MG975699	PD2434	1248	Due Sorelle, Ancona, Italy; intertidal; 1.vi.2016; PD & FR	This work
	MG975691	PD766	761	13th Beach, Victoria, Australia; intertidal; 9.xi.2014; PD	This work
	MG975692	PD1255	1391	Inverloch, Victoria, Australia; intertidal; 18.i.2015; PD & MB	This work
	MG975693	PD1259	1404	Inverloch, Victoria, Australia; intertidal; 18.i.2015; PD & MB	This work
Polysiphonia kapraunii B.Stuercke & D.W.Freshwater	EU492920	NC11	1341	Masonboro Inlet, New Hanover, North Carolina, USA; 4.v.2005	Sturcke & Freshwater 2008
Symphyocladia dendroidea (Montagne) Savoie & G.W.Saunders	KU949561	CUK6528	1372	Lagunillas, Pisco, Peru	Bustamante et al. 2016b, as *Pterosiphonia spinifera*
	KU252575	CUK6615	1378	Yacila, Paita, Peru; 2.ix.2008	Bustamante et al. 2016b, as *Pterosiphonia spinifera*
	KU949563	CUK8208	1372	Yacila, Paita, Peru	Bustamante et al. 2016b, as *Pterosiphonia spinifera*
	KU252573	CUK8268	1377	Lagunillas, Pisco, Peru; 7.vii.2012	Bustamante et al. 2016b, as *Pterosiphonia spinifera*
	KU949562	CUK8290	1372	Medieta, Pisco, Peru	Bustamante et al. 2016b, as *Pterosiphonia spinifera*
	KU252580	CUK15435	1313	Yacila, Paita, Peru; 14.ii.2012	Bustamante et al. 2016b, as *Pterosiphonia spinifera*

	KU252579	CUK15436	1394	Yacila, Paita, Peru; 14.ii.2012	Bustamante et al. 2016b, as *Pterosiphonia spinifera*
	KU949564	CUK16791	1306	Callao, Peru	Bustamante et al. 2016b, as *Pterosiphonia spinifera*
	KU949565	CUK16792	1372	Callao, Peru	Bustamante et al. 2016b, as *Pterosiphonia spinifera*
	KU949566	CUK16794	1372	Callao, Peru	Bustamante et al. 2016b, as *Pterosiphonia spinifera*
	MG975745	JF212	1301	Pangal, Juan Fernández, Chile; intertidal; 17.ii.2014; EM	This work
	MG975748	JF353	1235	Palillo, Juan Fernández, Chile; intertidal; 27.ii.2014; EM	This work
	MG975746	JF369	1358	Palillo, Juan Fernández, Chile; intertidal; 2.iii.2014; EM	This work
	MG975749	JF370	1301	Palillo, Juan Fernández, Chile; intertidal; 2.iii.2014; EM	This work
	MG975747	JF371	1269	Palillo, Juan Fernández, Chile; intertidal; 2.iii.2014; EM	This work
	KU564502	GWS022392	1248	Monterey, California, USA; 23.v.2010	Savoie & Saunders 2016 (as *Symphyocladia tanakae*)
	KJ814249	UC1965348	672	Monterei, California, USA; intertidal boat ramp	Hughey & Uwai 2015 (as *Pterosiphonia tanakae*)
	KJ814248	UC1965349	672	Motoujina, Japan	Hughey & Uwai 2015 (as *Pterosiphonia tanakae*)
	KJ814250	UC1965350	809	Motoujina, Japan	Hughey & Uwai 2015 (as *Pterosiphonia tanakae*)
	MG975750	PD717	1307	Williamstown South, Victoria, Australia; subtidal (-1 m); 29.x.2014; HV	This work
	MG975751	PD826	662	Frankston, Victoria, Australia; subtidal (-1 m); 19.xi.2014; HV	This work
	MG975752	PD879	1313	Queenscliff Marina, Victoria, Australia; pontoons; 29.xi.2014; PD	This work
	MG975753	PD1427	1384	Geelong, Victoria, Australia; intertidal; 3.ii.2015; PD & MB	This work
	MF101420	JW3780	1467	Culture strain mantained by John West and initiated from samples collected by L. Phillips on 6.iii.1997 in Williamstown, Port Phillip Bay, Australia	Díaz-Tapia et al. 2017
	MG975755	SANT-A 25913	1309	Mèze, France; subtidal (-1 m); 17.v.2011; IB & MV	This work
	MG975756	PD2688	1298	Ribadeo, Lugo, Spain; pontoons; 28.viii.2016; PD	This work
	MG975757	PD2691	1298	Ribadeo, Lugo, Spain; pontoons; 28.viii.2016; PD	This work
	MG975758	PD2692	1298	Ribadeo, Lugo, Spain; pontoons; 28.viii.2016; PD	This work
Symphyocladia dendroidea 2 *	KU564493	GWS021879	1248	Santa Cruz, California, USA	Savoie & Saunders 2016 (as *Symphyocladia dendroidea*)
Symphyocladia brevicaulis Savoie & G.W.Saunders	KU564499	GWS019412	1248	Bamfield, British Columbia, Canada	Savoie & Saunders 2016 (as *Symphyocladia dendroidea*)
Symphyocladia baileyi (Harvey) Savoie & G.W.Saunders	KU564471	GWS022257	1363	Monterey, California, USA	Savoie & Saunders 2016 (as *Symphyocladia dendroidea*)
Symphyocladia plumosa Savoie & G.W.Saunders	KU564473	GWS014494	1363	Bamfield, British Columbia, Canada	Savoie & Saunders 2016 (as

Symphyocladia parasitica (Hudson) Savoie & G.W.Saunders	MF094103	PD2170	1448	San Felipe, Ferrol, Galicia, Spain; subtidal (-3 m); 14.x.2015	Díaz-Tapia et al. 2017
Symphyocladia rosea Savoie & G.W.Saunders	KU564501	GWS010157	1248	Tahsis, British Columbia, Canada	Savoie & Saunders 2016 (as *Symphyocladia dendroidea*)
Symphyocladia linearis (Okamura) Falkenberg	JX828158	CH419	1467	Anin, Gangwondo, Korea; intertidal; 6.xii.2002	Bárbara et al. 2013
Symphyocladia latiuscula (Harvey) Yamada	KU564458	GWS011933	1363	Hokkaido, Oshoro Bay, Japan	Savoie & Saunders 2016
Symphyocladia jejuinsula S.Y.Kim, W.Nelson & M.S.Kim	JF967647	T14	1150	Chujado, Jeju, Korea; 4.viii.2008	Kim et al. 2012b
Symphyocladia glabra J.C.Kang & M.S.Kim	KF048968	121027-27	1150	Gangneung, Korea; subtidal; 27.x.2012	Kang & Kim 2013
Symphyocladia pumila (Yendo) S.Uwai & M.Masuda	GU731228	S204	1154	Daepodong, Seogwipo, Korea; 16.xii.2009	Kim et al. 2010
Symphyocladia lithophila M.-S.Kim	GQ867078	S146	1154	Gampo, Gyeongju, Korea; 16.iii.2003	Kim et al. 2010
Symphyocladia marchantioides (Harvey) Falkenberg	GU731229		1154	Mataikona, Wairarapa, New Zealand; 5.i.2010	Kim et al. 2010
Xiphosiphonia ardreana (Maggs & Hommersand) Savoie & G.W.Saunders	MF094107	SANT-A 25640	1448	La Arena, Basque Country, Spain; intertidal; 22.iii.2011	Díaz-Tapia et al. 2017
Symphyocladia spinifera (Kützing) Savoie & G.W.Saunders	KU252578	CUK6529	1374	Lagunillas, Pisco, Peru; 27.viii.2008	Bustamante et al. 2016a
	KU252572	CUK8269	1371	Lagunillas, Pisco, Peru; 5.vii.2012	Bustamante et al. 2016a
	KU252571	CUK8293	1394	Mendieta, Pisco, Peru; 5.vii.2012	Bustamante et al. 2016a
	KU252570	CUK8320	1372	Hueco de la Zorra, Pisco, Peru; 5.vii.2012	Bustamante et al. 2016a
	KU252577	CUK6553	1333	Punta Hermosa, Lima, Peru; 30.viii.2008	Bustamante et al. 2016a
	KU252576	CUK6570	1334	Pucusana, Lima, Peru; 30.viii.2008	Bustamante et al. 2016a
	KU252569	CUK8403	1394	Barranco, Lima, Peru; 6.vii.2012	Bustamante et al. 2016a
	KU252574	CUK8236	1394	Eten Port, Chiclayo, Peru; 3.vii.2012	Bustamante et al. 2016a
	KU252568	CUK9780	1394	Gwakji, Aewoleup, Jeju, Korea; 28.iv.2013	Bustamante et al. 2016a
	KU252584	CUK12235	1394	Gwakji, Aewoleup, Jeju, Korea; 30.v.2014	Bustamante et al. 2016a
	KU252581	CUK14857	1394	Woljeongri, Gujwaeup, Jeju, Korea; 7.v.2015	Bustamante et al. 2016a
	JX857413	S105	1150	Geumneung, Jeju, Korea; 15.i.2010	Kim et al. 2012a (as *P. arenosa*)
	JX857414	12pte01	1150	Geumneung, Jeju, Korea; 21.i.2012	Kim et al. 2012a (as *P. arenosa*)
	JX857415	PT012	1150	Geumneung, Jeju, Korea; 4.iv.2012	Kim et al. 2012a (as *P. arenosa*)
	JX857422	PT03	1150	Geumneung, Jeju, Korea; 4.iv.2011	Kim et al. 2012a (as *P. arenosa*)
	JX857423	PT01	1150	Geumneung, Jeju, Korea; 7.iii.2011	Kim et al. 2012a (as *P. arenosa*)
	JX857416	PT011	1150	Gosung, Jeju, Korea; 23.iii.2012	Kim et al. 2012a (as *P. arenosa*)
	JX857417	PT08	1150	Jongdal, Jeju, Korea; 4.ii.2012	Kim et al. 2012a (as *P. arenosa*)

	JX857418	PT07	1150	Gimnyeong, Jeju, Korea; 21.i.2012	Kim et al. 2012a (as *P. arenosa*)
	JX857419	PT06	1150	Gimnyeong, Jeju, Korea; 27.xii.2011	Kim et al. 2012a (as *P. arenosa*)
	JX857420	PT05	1150	Hyeopjae, Jeju, Korea; 3.v.2011	Kim et al. 2012a (as *P. arenosa*)
	JX857421	PT04	1150	Hyeopjae, Jeju, Korea; 3.v.2011	Kim et al. 2012a (as *P. arenosa*)
	GQ252572	AC250	758	San Juan Is., Washington, USA; 2.viii.2006	Carlile 2009 (as *P. dendroidea*)
	MG975759	PD1112	660	Killorney Beach, Victoria, Australia; intertidal; 27.xii.2014; PD	This work
	MG975760	PD1174	1292	Sandringham, Victoria, Australia; intertidal; 8.i.2015; PD & MB	This work
	MG975761	PD2803	1297	Bastion Point, Victoria, Australia; intertidal; 11.xi.2016; PD	This work
	MG975762	PD2871	1307	Shipwreck Creek, Victoria, Australia; intertidal; 13.xi.2016; PD	This work
	MG975763	PD2872	1308	Shipwreck Creek, Victoria, Australia; intertidal; 13.xi.2016; PD	This work
	MG975764	PD2878	1321	Shipwreck Creek, Victoria, Australia; intertidal; 13.xi.2016; PD	This work
	MG975765	PD3341	1290	Georgetown, Tasmania, Australia; intertidal; 5.xi.2017; PD & JC	This work
	MG975766	PD3412	1292	Bianlong Bay, Tasmania, Australia; intertidal; 8.xi.2017; PD & JC	This work
	MG975767	PD3431	1306	Bianlong Bay, Tasmania, Australia; intertidal; 8.xi.2017; PD & JC	This work
	MG975768	PD3453	960	Bianlong Bay, Tasmania, Australia; intertidal; 8.xi.2017; PD & JC	This work
	MG975769	PD3472	1302	Bicheno, Tasmania, Australia; intertidal; 9.xi.2017; PD & JC	This work
	MG975770	PD3480	961	Bicheno, Tasmania, Australia; intertidal; 9.xi.2017; PD & JC	This work
	MG975771	PD3567	968	Tasman Peninsula, Tasmania, Australia; intertidal; 12.xi.2017; PD & JC	This work
	MG975772	PD3592	1350	Port Arthur, Tasmania, Australia; intertidal; 13.xi.2017; PD & JC	This work
	MG975773	PD3168	1315	Southport, Tasmania, Australia; intertidal; 1.xi.2017; PD & JC	This work
	MG975774	PD3344	1320	Georgetown, Tasmania, Australia; intertidal; 5.xi.2017; PD & JC	This work
Xiphosiphonia pennata (C.Agardh) Savoie & G.W.Saunders	MF094108	SANT-A 24618	654	Langre, Asturias, Spain; intertidal; 6.xi.2010; PD	Díaz-Tapia et al. 2017
	MG975723	SANT-A 26631	615	Cala Encendida, Cádiz, Spain; intertidal; 18.ii.2011; PD & IB	This work
	MG975724	SANT-A 28747	640	Margaritas, Galicia, Spain; intertidal; 4.xii.2013; PD	This work
Xiphosiphonia pinnulata (Kützing) Savoie & G.W.Saunders	KU252567	IBT0242	1394	Praia Domingas Dias, Ubatuba, Sao Paulo, Brazil; ix.2009	Bustamante et al. 2016a (as *P. pennata*)
	KU252566	IBT0456	1394	Praia de Cambriú, Ilha do Cardoso, Sao Paulo, Brazil; viii.2008	Bustamante et al. 2016a (as *P. pennata*)
	MG975727	PD617	1263	Praia de Parati, Ubu, Espirito Santo,Brazil; intertidal; 8.ix.2014; PD & MTF	This work
	MG975728	PD622	1280	Praia de Parati, Ubu, Espirito Santo,Brazil; intertidal; 8.ix.2014; PD & MTF	This work
	MG975729	PD655	1277	Praia de Santa Cruz, Espirito Santo,Brazil; intertidal; 10.iv.2014; PD & MTF	This work
	MG975730	PD3027	1295	Hengistbury Head, Bournemouth, Engand; intertidal; 23.vi.2017; CAM	This work
	MG975735	SANT-A 25155	660	Zumaia, Guipúzcoa, Spain; intertidal; 28.iii.2011; PD & IB	This work
	MG975736	SANT-A 25156	616	Zumaia, Guipúzcoa, Spain; intertidal; 28.iii.2011; PD & IB	This work
	MG975739	SANT-A 25647	665	Muskiz, Vizcaya, Spain; intertidal; 22.iii.2011; PD & IB	This work
	MG975740	SANT-A 25661	623	Muskiz, Vizcaya, Spain; intertidal; 22.iii.2011; PD & IB	This work

	JX857425	SANT-A 19754	1150	La Franca, Asturias, Spain; intertidal; 6.x.2006; PD	Kim et al. 2012a (as *Pterosiphonia pennata*)
	MG975738	SANT-A 25589	649	La Franca, Asturias, Spain; intertidal; 23.iii.2011; PD & IB	This work
	MG975731	SANT-A 24615	597	Langre, Asturias, Spain; intertidal; 6.xi.2010; PD	This work
	MG975742	SANT-A 26247	642	Peinzás, Lugo, Spain; intertidal; 19.iv.2011; PD, AS & VP	This work
	MG975744	SANT-A 26660	663	Picón, A Coruña, Spain; intertidal; 28.ix.2011; PD	This work
	JX857424	SANT-A 19607	1150	Chanteiro, A Coruña, Spain; intertidal; 17.ix.2005; PD	Kim et al. 2012a (as *Pterosiphonia pennata*)
	JX828155	CH977	1467	Ber, A Coruña, spain; intertidal; 25.viii.2005; PD	Bárbara et al. 2013 (as *Pterosiphonia pennata*)
	MG975734	SANT-A 24731	625	Perbes, A Coruña, Spain; intertidal; 20.i.2011; PD & CPA	This work
	JX857426	SANT-A 20940	1150	Ártabra, A Coruña, Spain; intertidal; 6.vi.2008; PD	Kim et al. 2012a (as *Pterosiphonia pennata*)
	JX828154	CH816	1463	Nerga, Pontevedra; Spain; intertidal; 12.ii,2005; PD & IB	Bárbara et al. 2013 (as *Pterosiphonia pennata*)
	JX828156	CH1308	1467	Almograve, Baijo Alentejo, Portugal; intertidal; 25.v.2005; PD	Bárbara et al. 2013 (as *Pterosiphonia pennata*)
	MG975732	SANT-A 24668	611	Almograve, Baijo Alentejo, Portugal; intertidal; 22.ii.2011; PD & IB	This work
	MG975733	SANT-A 24669	644	Almograve, Baijo Alentejo, Portugal; intertidal; 22.ii.2011; PD & IB	This work
	MG975737	SANT-A 25472	665	Ingrina, Algarve, Portugal; intertidal; 20.ii.2011; PD & IB	This work
	MG975725	CAM462	1249	Cádiz, Spain; intertidal; 4.v.1998; CAM	This work
	MG975726	CAM478	1245	Cádiz, Spain; intertidal; 4.v.1998; CAM	This work
	MG975743	SANT-A 26533	665	Punta Plata, Cádiz, Spain; intertidal; 19.ii.2011; PD & IB	This work
	MG975741	SANT-A 25837	608	Anse de Malmosuqui, Marseille, France; intertidal; 9.v.2011; IB	This work
Herposiphonia akidoglossa R.E.Norris	KU551923	TC13944	1380	Puducherry, Tamil Nadu, India; 8.ii.2015	Bustamante et al. 2017
Herposiphonia calothrix (Harvey) Womersley	MF094067	PD1478	1417	Sorento, Victoria, Australia; intertidal; 28.ii.2015; PD, MB & VRM	Díaz-Tapia et al. 2017
Herposiphonia insidiosa (Greville ex J.Agardh) Falkenberg	KT825868	CUK10410	1373	Yeonji-ri, Gyeonsangbuk-do, Korea; 5.x.2013	Bustamante et al. 2017
Herposiphonia parca Setchell	JX828127	CH426	1467	Jukbyun, Gyeongbuk, Korea; 18.xii.2002	Bárbara et al. 2013
Herposiphonia pectinella (Harvey) Falkenberg	MF094068	PD1415	1415	Geelong, Victoria, Australia; intertidal; 3.ii.2015; PD & MB	Díaz-Tapia et al. 2017
Herposiphonia plumula (J.Agardh) Falkenberg	KU564517	GWS027411	1363	Panther Pt., Wallace I., British Columbia, Canada	Savoie & Saunders 2016
Herposiphonia prorepens (Harvey) F.Schmitz	KU551924	TC6194	1395	Puducherry, Tamil Nadu, India; 12.ii.2015	Bustamante et al. 2017
Herposiphonia versicolor (Hooker & Harvey) Reinbold	NC035279	PD852	1467	Sant Leonards, Victoria, Australia; subtidal (-2 m); 27.xi.2014; HV	Díaz-Tapia et al. 2017
Herposiphonia sp QL2	MF094071	PD1910	1410	Heron Island, Queensland, Australia; intertidal; 15.v.2015; PD, HV, VRM & CC	Díaz-Tapia et al. 2017
Herposiphonia sp IP1	MF094070	SANT-A 24671	1437	Almograve, Portugal; intertidal; 22.ii.2011; PD & IB	Díaz-Tapia et al. 2017
Herposiphonia sp WA2	MF094073	PD1757	1416	Coral Bay, Western Australia; subtidal (-15 m); 24.iii.2015; PD & JFC	Díaz-Tapia et al. 2017
Herposiphonia sp WA3	MF1094074	PD1757	1073	Channel Rocks, Western Australia; subtidal (-2 m); 13.iii.2015; PD & JFC	Díaz-Tapia et al. 2017
Herposiphonia sp WA4	MF094075	PD1650	1217	Rottnest Island, Western Australia; subtidal (-2 m); 17.iii.2015; PD & JFC	Díaz-Tapia et al. 2017
Herposiphonia sp WA5	MF094076	PD1781	1415	Geraldton, Western Australia; drift; 26.iii.2015; PD & JFC	Díaz-Tapia et al. 2017

Herposiphonia pecten veneris (Harvey) Falkenberg	KU551922	TC13698	1395	Pelican Beach, Belize; 15.v.2015	Bustamante et al. 2017
Herposiphonia tenella CI4	MG975648	PD323	790	Tufia, Gran Canaria, Canary Islands, Spain; intertidal; 24.vi.2013; PD	This work
	MG975646	PD317	652	Tufia, Gran Canaria, Canary Islands, Spain; intertidal; 24.vi.2013; PD	This work
	MG975647	PD321	715	Tufia, Gran Canaria, Canary Islands, Spain; intertidal; 24.vi.2013; PD	This work
Herposiphonia tenella IP1	MF094077	PD322	788	Virgen del Mar, Cantabria, Spain; intertidal; 7.xi.2010; PD	Díaz-Tapia et al. 2017
	MG975649	PD183	585	Ojos de Garza, Gran Canaria, Canary Islands, Spain; intertidal; 24.vi.2013; PD	This work
	MG975650	PD2338	711	Marseille, France; intertidal; 27.v.2016; PD	This work
	MG975651	PD2488	715	Alassio, Italy; intertidal; 5.vi.2016	This work
	MG975652	PD2496	711	Alassio, Italy; intertidal; 5.vi.2016	This work
	MG975653	SANT-A 26526	745	Punta Plata, Cádiz, Spain; intertidal; 19.i.2011; PD & IB	This work
	MG975654	SANT-A 26810	660	Bastiagueiro Pequeño, A Coruña, Spain; intertidal; 30.ix.2011; IB	This work
	MG975655	SANT-A 27354	723	Camelle, A Coruña, Spain; intertidal; 13.i.2012; IB	This work
Herposiphonia tenella IP2	KT825867	CUK910	1450	Beaufort, North Carolina, USA; 26.x.2003	Bustamante et al. 2017
	MG975656	PD2655	708	Mèze, France; 12.vi.2016; PD	This work
	GU385834	NC.1	1353	Pender Co., North Carolina, USA	Stuercke & Freshwater 2010
	MG975657	SANT-A 25620	771	La Franca, Asturias, Spain; intertidal; 23.iii.2011; PD & IB	This work
Herposiphonia tenella IP3	MG975661	SANT-A 25480	634	Ingrina, Algarve, Portugal; intertidal; 20.ii.2011; PD & IB	This work
	MG975662	SANT-A 25481	790	Ingrina, Algarve, Portugal; intertidal; 20.ii.2011; PD & IB	This work
	MG975658	CAM463	887	San Sebastián, Cádiz, Spain; 4.v.1998; CAM	This work
	MF094078	SANT-A 25835	1439	Marseille, France; subtidal (-2 m); 9.v.2015; IB	Díaz-Tapia et al. 2017
	MG975659	PD2333	701	Marseille, France; intertidal; 27.v.2016; PD	This work
	MG975660	PD2554	695	Menton, France; intertidal; 8.vi.2016; PD	This work
Herposiphonia tenella QL1	MG975663	PD1908	704	Heron Island, Queensland, Australia; intertidal; 15.v.2015; PD, HV, VRM & CC	This work
	MG975664	PD1975	701	Heron Island, Queensland, Australia; subtidal (-3 m); 15.v.2015; PD & CC	This work
Herposiphonia tenella QL2	MG975665	PD1986	695	Heron Island, Queensland, Australia; intertidal; 19.v.2015; PD, HV, VRM & CC	This work
Herposiphonia tenella QL3	MF094072	PD1933	1413	Heron Island, Queensland, Australia; intertidal; 15.v.2015; PD, HV, VRM & CC	Díaz-Tapia et al. 2017
	MG975666	PD1887	702	Heron Island, Queensland, Australia; intertidal; 15.v.2015; PD, HV, VRM & CC	This work
	MG975667	PD1890	1406	Heron Island, Queensland, Australia; intertidal; 14.v.2015; PD, HV, VRM & CC	This work
Dipterosiphonia australica Womersley	NC035288	PD1107	1467	Killornei, Victoria, Australia; intertidal; 27.xii.2014; PD	Díaz-Tapia et al. 2017
Dipterosiphonia dendritica 1	MF094058	PD1654	1417	Rottnest Island, Western Australia; subtidal (-2 m); 17.iii.2015; PD & JFC	Díaz-Tapia et al. 2017
Dipterosiphonia dendritica 2	MF094059	PD1799	1413	Drummonde Cove, Western Australia; drift; 27.iii.2015; PD & JFC	Díaz-Tapia et al. 2017

* Only one *rbc* L sequence of *Symphyocladia dendroidea* 2 was included in our phylogeny. However, six *rbc* L sequences and 22 *cox* 1 sequences were generated for this species (Savoie & Saunders 2016)

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