Tracing the introduction history of the brown seaweed *Dictyota cyanoloma* (Phaeophyta, Dictyotales) in Europe

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Abstract

Dictyota cyanoloma has recently been described from the Mediterranean Sea and Macaronesia but doubt had arisen as to whether this species was truly native in Europe. The species is mainly found on non-natural substrata (harbour walls, marinas, boat hulls, etc.), strongly suggesting that *D. cyanoloma* is an introduction. Sequence information from historical herbarium samples proves the presence of *D. cyanoloma* within the Adriatic Sea as early as 1935. Since approximately the year 2000, however, the number of records as well as the geographic range of the species has expanded significantly. The present-day distribution of *D. cyanoloma* occupies most of the Mediterranean Sea, Macaronesia, NW Africa and southern Portugal, but recent records from Galicia and SW England (Falmouth, Cornwall) indicate that the species is rapidly expanding northward. Collections from Australia demonstrated that the species is also present from Perth in Western Australia, over much of the southern Australian coastline up to Minnie Water in New South Wales. Phylogenetic analyses resolve *D. cyanoloma* in a clade sister to a previously unreported Australian *Dictyota* species. Analysis of genetic diversity of the mitochondrial markers (*nad*6 - *nad*11 and *atp*9 – *orf*11) reveals that even though Australia contains a much higher haplotype richness, European populations are also fairly diverse. Furthermore, only two out of 25 haplotypes are shared between both regions. These somewhat counterintuitive results could be indicative of a more complicated introduction history.

Keywords: *alien species, cryptogenic species, Dictyota cyanoloma, herbarium species, mitochondrial DNA*

Introduction

Invasive species are widely recognized as a major threat to marine biodiversity. By changing the relative abundance of native species, invasive species may profoundly affect the structure and functioning of native communities, thereby often negatively impacting local economies (Molnar *et al.*, 2008; Simberloff, 2011). Even though only a minority of introduced species can be considered invasive, their impact can be devastating. Hence there is the necessity to document introductions of non-native species, and to assess the possible risk they impose on the invaded ecosystem (Molnar *et al*., 2008). The Mediterranean Sea and the Atlantic coasts of Europe are considered hotspots of marine species introductions (Galil *et al.*, 2014; Mineur *et al.*, 2015). A total of 986 alien species have been reported for the Mediterranean Sea, of which 128 are macroalgae (Zenetos *et al.*, 2012). This number, however, is likely an underestimation of the total number of introduced species owing to the difficulties surrounding morphology-based algal identification (Leliaert *et al.*, 2014; Verbruggen, 2014). A combination of a limited set of morphological, and potentially diagnostic characters (the 'low morphology problem' (Van Oppen *et al.*, 1996)) and considerable morphological plasticity that characterizes many algal species, hampers species identification based on morphological characteristics in algae. As a result, distinguishing native from non-native species becomes difficult (Grosholz, 2002). This taxonomic uncertainty also reflects on the biogeography of the species, which is often insufficiently characterized. In a context of introduced species, uncertainty regarding native and introduced distributions led Carlton (1996) to coin the term 'cryptogenic species', i.e. species that are not demonstrably native or introduced.

Here we aim to ascertain the origins of *D. cyanoloma*, which was recently described from the Mediterranean Sea in Tronholm *et al.* (2010). The species was first reported from the Iberian peninsula as *D. ciliolata* by Rull Lluch *et al*. (2007). Sequence data, however,

demonstrated unequivocally that the Iberian specimens were clearly distinct from *D. ciliolata* (Tronholm *et al.*, 2010). Because the species did not correspond to the type material of any *Dictyota* of Mediterranean or Macaronesian origin and in the absence of evidence for it to be present outside of Europe, *D. cyanoloma* was described as a new species native to Europe. This study also significantly expanded the known distribution range of the species to include the Adriatic Sea as well as Macaronesia (Tronholm *et al.* 2010). Nevertheless, some aspects relating to the ecology and morphology of the species cast doubt on its status as a native species. First, historical interest in the diversity of *Dictyota* in Europe (e.g. Hamel, 1931-1939; Weberpeukert, 1986; Schnetter *et al.*, 1987; Hornig & Schnetter, 1988; Hornig *et al.*, 1992a; Hornig *et al.*, 1992b), and the fact that the species is easily discernible by its blue iridescent margins, raises the question why *D. cyanoloma* had gone unnoticed for so long. Second, the specimens of *D. cyanoloma* are often collected from non-natural habitats such as marinas (Rull Lluch *et al.*, 2007; Aragay Soler *et al.*, 2014). Lastly, a recent sampling campaign recovered what appears to be the same species from the South of Australia (De Clerck and Verbruggen, unpublished). The combination of these factors challenges the status of *D. cyanoloma* as an indigenous European species. However, to date it remains unknown whether *D. cyanoloma* is native to Europe and introduced to Australia, or vice versa.

The main objective of this study was to provide molecular support for the origins of this cryptogenic species. Therefore, we first applied a phylogenetic approach to determine the affinities of *D. cyanoloma* with Australian species of the genus. We then compared the diversity and genetic structure of Australian and European populations based on two variable mitochondrial loci (*nad*6 - *nad*11 and *atp*9 - *orf*11). Last, the current and historical geographical range of the species within Europe was assessed employing both historical and recent records.

Material and methods

DNA extraction, amplification and sequencing

Dictyota cyanoloma Tronholm, De Clerck, Gómez Garreta & Rull Lluch was sampled from Australia, the North East Atlantic, the Mediterranean and Macaronesia (Table 1). Specimens were taken fresh from the field and apical tips were dried in silica gel for rapid dehydration and storage. In addition, the Ghent and the Zagreb herbaria were screened for *D. cyanoloma* vouchers and subsampled for DNA-extraction. DNA was extracted employing a cetyltrimethyl ammonium bromide extraction method as outlined in Steen *et al.* (2015). We amplified and sequenced two variable intergenic spacer regions of the mitochondrial genome, the *nad*6 - *nad*11 and *atp*9 - *orf*11 regions. Primers were designed in the flanking coding region of both markers, using PRIMER3 software (Untergasser *et al.*, 2012). Primer design was aided by the availability of the mitochondrial genome of *D. dichotoma* (Secq *et al.*, 2006) and a draft mitochondrial genome of *D. cyanoloma* (De Clerck & Steen, unpublished). Primer sequences are displayed in Table 2. Plastid-encoded PSII reaction center protein D1 (*psb*A) and RUBISCO large subunit (*rbc*L), mitochondrial-encoded cytochrome oxidase subunit 1 and 3 (*cox*1, *cox*3) and NADH dehydrogenase subunit 1 (*nad*1), and partial nuclear ribosomal LSU rDNA genes were amplified and sequenced following De Clerck et al. (2006), Hwang et al. (2009), and Silberfeld et al. (2010).

Phylogenetic position of Dictyota cyanoloma *within the genus* Dictyota

A phylogenetic tree was constructed from a multigene alignment, using one representative per species, sequenced for 6 markers (*psb*A, *rbc*L, *cox*1, *cox*3, *nad*1, LSU rDNA) (Table 1S). All *Dictyota* species native to the North-East Atlantic, the Mediterranean and Macaronesia were included (Tronholm *et al*., 2010) as well as species closely related to *D. cyanoloma*, selected based on a preliminary *psb*A NJ phylogeny (data not shown). Partitioning strategies were

selected with Partitionfinder (Lanfear *et al.*, 2012). A partitioning scheme with seven partitions organized by codon position and organelle and a GTR+G model of sequence evolution was adapted in a subsequent Bayesian analysis with MrBayes 3.2 (Ronquist *et al.*, 2012). Two parallel runs, consisting of 3 heated chains and one cold chain each, were run for 9 million generations, using default priors and chain temperature settings. The cold chain was sampled every 1000 generations. Tracer 1.4 was used to assess stationarity of log-likelihoods and parameter values (Drummond & Rambaut, 2007). A burn-in sample of 1000 trees was removed before construction of a majority rule consensus tree.

The ML analysis, using the same partitioning strategy, was conducted employing RAxML v.8.1.11 under a GTRCAT substitution model. The robustness of the resulting phylogenies was tested using 1,000 replicates of a rapid bootstrap heuristic (Stamatakis *et al.*, 2008).

Geographical distribution of Dictyota cyanoloma

Geographical data from a global Dictyotales dataset (link), summarizing taxonomic and geographic data of more than 4400 specimens, are plotted on a global map, highlighting the occurrences of *D. cyanoloma*. Additional maps of the presumed introduced and native range are constructed indicating the localities of all samples. A distinction is made between earlier published records, records confirmed within this study, records obtained from historical herbarium specimens and unconfirmed records based on photographic evidence. Annual mean minimum and maximum sea surface temperature isotherms obtained from Bio-ORACLE (Tyberghein *et al.*, 2012), flanking the inferred species range in both hemispheres are indicated.

Genetic diversity and haplotype network construction

Concatenated *nad*6 - *nad*11 and *atp*9 - *orf*11 sequences (1235bp), corrected for indels following Simmons & Ochoterana (2000), were collapsed into haplotypes. Haplotype networks were constructed based on traditional phylogenetic algorithms, an approach which has been demonstrated to outperform widespread network constructing methods (Salzburger *et al.*, 2011). Parsimony- and maximum likelihood phylogenies were estimated in MEGA6 (Tamura *et al.*, 2013) and RaxML v.8.1.11 (Stamatakis *et al*., 2008), respectively, and converted into haplotype networks using Haploviewer (available at http://www.cibiv.at/~greg/haploviewer).

Levels of genetic variation (haplotype diversity, nucleotide diversity and haplotype richness) in European and Australian populations were estimated in Arlequin 3.5 (Excoffier & Lischer, 2010). Estimates of haplotype richness after rarefaction were obtained with a rarefaction calculator based on the program HP-RARE (Kalinowski, 2005). Haplotype richness was standardized to the smallest population size (32) to obtain an unbiased estimate of the haplotype richness for inter-population comparisons (Leberg, 2002).

Results

Phylogenetic position of D. cyanoloma *within the genus* Dictyota

Bayesian and maximum likelihood analyses of a multilocus dataset based on 6 markers (*psb*A, *rbc*L, *cox*1, *cox*3, *nad*1, LSU rDNA) resulted in highly congruent and reasonably well supported phylogenetic trees (Fig. 1). *Dictyota cyanoloma* was resolved (BS-values = 100; BPP = 1.0) as the sister taxon to an unidentified *Dictyota* species from Western Australia (*Dictyota* sp8, HV2563). The larger clade to which *D. cyanoloma* belongs, contains several other Australian species (*D. alternifida*, *D. dichotoma3*, *D. diemensis*, *D. intermedia*) next to species of which the actual distribution is hitherto unclear (*D.* sp7, sp21, *D. liturata, D. stolonifera*) due to a restricted taxon sampling.

Geographical distribution of Dictyota cyanoloma

A map displaying the distributions of more than 4400 Dictyotales specimens indicates that *D. cyanoloma* is present both in Europe and South-Australia, but presumably absent elsewhere (Fig. 2). European records stretch from Cornwall, England to the Canary Islands and Northwest Africa in the South and the Gulf of Izmir in the eastern Mediterranean Sea. This range is bordered by a 9°C minimum sea surface temperature (SSTmin) and a 27°C maximum sea surface temperature (SSTmax) (Fig. 3A). No samples from the southern hemisphere were found outside a thermal range bordered by the 12°C SSTmin and 26°C SSTmax (Fig. 3B).

The earliest *D. cyanoloma* records in Europe are from the Adriatic Sea (Split), collected in 1935. Additional records from 1947, 1958 and 1976 (herbarium), 2009 (Tronholm *et al*. 2010) and 2014 (this study) form circumstantial evidence of its intermittent presence in the Adriatic Sea. The first published record of *D. cyanoloma* appeared in 2007 by Rull Lluch *et al*. (2007) and was incorrectly identified as *D. ciliolata*. Herbarium species sequenced in this study from Cannes (1999) and Barcelona (2005) precede this record. Records within the NE-Atlantic are noted for Aveiro (Barbara *et al.*, 2014), and A Coruña (Barbara *et al.*, 2014; Peña *et al.*, 2014) and SW Britain (2014) (Table 1). More southern records were sampled in the Canary Islands (2009) and Morocco (2010) (Table 1). A single record is reported for the Aegean Sea, in the Gulf of Izmir in Turkey (Taskin, 2013). Next to these published records, evidence based on photographs searchable on the internet indicates the presence of *D. cyanoloma* in Greece and Sicily (Table 2S). All records were confirmed genetically except the specimens from Turkey, Galicia, Greece and Sicily.

Genetic diversity and haplotype networks

A total of 25 haplotypes were found among 93 *D. cyanoloma* samples. In the haplotype network a 37 bp gap separates three Australian specimens (LT0030, LT0384, HV2123) from the remainder of the specimens. The *cox*1 gene sequences of the two clusters, however, differed by no more than 1.6%. Compared to typical interspecific distances in *Dictyota* (~ 20-30%) this is a low value that persuaded us to treat both clusters as the same species. Australian samples contained 16 haplotypes (32 samples), including 12 singletons, while in Europe 11 haplotypes are recorded for 61 samples, including 4 singletons. Only 2 haplotypes, however, are shared between Australia and Europe. One of the shared haplotypes is from a Croatian herbarium sample from 1958. Haplotype networks based on ML- (Fig. 4) or MP-trees (Fig. 1S) are generally consistent in the patterns they reveal, except in the reciprocal positioning of the singleton haplotypes from three out of four of the herbarium specimens and in the position of haplotype 15. These minor differences do not, however, alter the general phylogeographic pattern.

For the calculation of the genetic diversity indices, haplotypes of 4 European specimens collected in 1935 and 1958 in Split respectively (D3815, D3815b, D3818, D3819) were removed as these are not representative of the current genetic diversity within the introduced range. The corresponding haplotype diversity for Australia and Europe were 0.8931 ± 0.0370 and 0.7713 ± 0.0327 respectively. The nucleotide diversities were 0.008967 ± 0.004653 for Australia compared to 0.002904 ± 0.001660 for Europe. Haplotype richness after rarefaction brings the total number of Australian haplotypes to 16 compared to 7 for Europe.

Discussion

Using a combination of phylogenetic and phylogeographic analyses, we have demonstrated that the *Dictyota cyanoloma*, recently described from Europe (Tronholm *et al*. 2010) is present also in large parts of Australia. Below we discuss the plausibility of a number of alternative hypothesis that could potentially account for this pattern.

Alternative hypotheses for the disjunct distribution of Dictyota cyanoloma

A first hypothesis, that Australian and European specimens belong to different species, is not supported by the genetic data. Genetic divergence between Australian and European populations of typical barcoding markers such as the *cox*1 gene is very close to 0%. As a comparison, interspecific p-distances among *Dictyota* species vary from 7-8% to about 25%. In addition, a haplotype network based on mitochondrial *nad*6 - *nad*11 and *atp*9 - *orf*11 regions fails to illustrate two clusters corresponding to European and Australian samples. Haplotypes between both regions are interspersed.

It is also rather unlikely that *D. cyanoloma* is characterized by a continuous biogeographic range extending from Europe to Australia. First, seaweeds are predominantly characterized by relatively narrow thermal tolerances (Santelices, 1980; Van den Hoek, 1982; Eggert, 2012) making exceptionally wide latitudinal ranges spanning tropical as well as temperate regions uncommon. Second, no specimens were sampled in tropical latitudes or in other temperate areas (e.g. Southern Africa) as shown by our global Dictyotales dataset (Fig. 2). It is therefore most likely that *D. cyanoloma* has a truly disjunct distribution, with established populations in Europe and Australia. In the light of our present knowledge of natural seaweed distributions and cases on anthropogenic introductions of non-native species through maritime traffic and aquaculture, a discontinuous distribution pattern as demonstrated by *Dictyota cyanoloma* is highly indicative for an introduction history.

Evidence supporting an Australian native range of Dictyota cyanoloma

Under the hypothesis that the current biogeographic range of *Dictyota cyanoloma* involves an introduction, the question remains as to which area should be considered the native range. Several lines of evidence supports the hypothesis that *D. cyanoloma* has been introduced in Europe from Australia. First, a phylogenetic analysis shows that *D. cyanoloma* belongs to a clade consisting of species with a mainly South Pacific distribution, many of them restricted to Australia. Furthermore, the fact that *D. sp8*, the sister species of *D. cyanoloma*, is recorded only from Australia is additional evidence for an Australian native range. Australasia is known as one of the main three regions from which species are introduced into the Mediterranean, next to the Red Sea and the North Western Pacific (Mineur *et al*., 2015). While Lessepsian migration and the transport of live shellfish, especially oysters, are the main introduction pathways and vectors from the latter two regions respectively, it hasn't been demonstrated what caused the introductions of Australasian species into the Mediterranean (Mineur *et al*., 2015), except for aquarium trade in the case of *Caulerpa taxifolia* (Jousson *et al.*, 1998).

The general trend is that invaded regions generally contain a reduced genetic diversity through founder effects and genetic drift (Roman & Darling, 2007; Dlugosch & Parker, 2008).

Frederique: I would like to see this rewritten a little. A recent meta-analysis by Ruis et al. (2015) om marine invasion genetics concludes that "The results strongly favour the notion that genetic diversity is not generally impaired when species are introduced. Of the ca. 54% of studies that did compare genetic diversity in both native and introduced populations, the majority of them (ca. 74%) found similar diversity in some or all introduced populations.

Only ca. 23% of the studies reported lower genetic diversity in introduced populations, with one study (ca. 2%) reporting higher diversity in the introduced range (Fig. 1D)."

Rius, M., Turon, X., Bernardi, G., Volckaert, F. A. & Viard, F. 2015. Marine invasion genetics: from spatio-temporal patterns to evolutionary outcomes. *Biol. Invasions* **17**:869-85.

The above statement makes that the typical algal examples (Codium – Sargassum) are exceptions rather than the rule.

A reduction of genetic diversity is documented for the invasive species *Codium fragile* ssp. *fragile* for chloroplast microsatellite markers (Provan *et al.*, 2005) and for *Sargassum muticum* for a concatenated dataset of *cox*3 and *trn*W-I markers (Bae *et al.*, 2013) and for plastidial RUBISCO, *trn*W-I and ITS2 (Cheang *et al.*, 2010).

Even though allelic richness is higher in Australia than in Europe, haplotype and nucleotide diversities indicate that Australian as well as European populations harbour a high level of genetic diversity. Australian haplotype diversities are only slightly higher than in Europe, but the nucleotide diversities differ significantly. This discrepancy can be indicative of a bias in calculated diversity measures (Goodall-Copestake *et al.*, 2012). Diverging haplotypes within a sample suggest an undersampling and inflate estimates of nucleotide diversity, as is the case for the Australian population. As a matter of fact, the high proportion of singleton haplotypes (12 out of 16) together with the large genetic gap for Australian specimens suggest that this region is undersampled, and thus might inflate nucleotide diversities. Allelic richness is higher for Australia (16 versus 7 haplotypes)

Recent insights, however, claim that genetic diversity is not necessarily depauperate after an aquatic invasion. In many cases, large inocula and multiple introductions boost the genetic diversity in the introduced range (Roman & Darling, 2007). Introduced populations of *Undaria pinnatifida* clearly illustrate the importance of above factors. While Australasian

introduced populations show a high genetic diversity, European introduced populations have a much lower diversity in comparison to the Asian source populations. This disparity stems from the fact that the European introduction was the consequence of an intentional introduction for aquaculture, while the Australasian populations were the consequence of recurrent introductions by accidental translocations associated with maritime traffic (Voisin *et al.*, 2005). Multiple introductions, or great genetic diversity within the inocula together with beneficial life history characteristics as clonal propagation could have enabled *D. cyanoloma* to by-pass successfully a bottleneck associated with the founder event and to establish a genetically diverse introduced population.

Within Europe, *D. cyanoloma* is thriving in non-natural environments such as ports, marinas and yachting clubs (Table 1), and artificial substrata as pontoons, jetties and neglected ship hulls are often fouled by the species (Fig. 5A). Along the Iberian peninsula and the NW Moroccan coast, some natural habitats harbour populations of the species. In comparison sampling localities within Australia are almost strictly natural environments. This observation is concurrent with the idea of Europe being the introduced range, as marine invaders are often growing on artificial substrata.

The combination of these findings offers support for the hypothesis of an introduction of *D. cyanoloma* from the southern hemisphere into the Mediterranean and Europe.

Introduction and potential spread within Europe

Molecular data demonstrated that the species was at least present in the Adriatic Sea as early as 1935. Its presence in the Split area is confirmed by molecular data obtained from herbarium samples collected in 1947, 1958 and 1976. Other herbarium records from Cannes (1999) and Barcelona (2005) were confirmed to be genuine *D. cyanoloma* and all predate the finding of Rull Lluch (2007). Since the publication of Tronholm *et al.* (2010), species

observations (UK, Greece, Sicily) and published records (Taskin, 2013; Barbara *et al.*, 2014; Peña *et al.*, 2014) increased steadily, with reports for the North-East Atlantic until the eastern Mediterranean and Macaronesia. The question remains as to whether *D. cyanoloma* remained unreported until about a decade ago despite being widespread in southern Europe or whether the species only spread recently despite being locally present in the Mediterranean Sea for several decades. Accepting the historical records in the Adriatic as evidence for a species introduction within this area would be premature, as no other than the Ghent and Zagreb herbarium were screened for this species. In this respect and based on our data, we cannot exclude the hypothesis that *D. cyanoloma* was present along most European coastlines throughout most of the 20th century. The same was for *Codium fragile*, which had been colonizing habitats across the world in some cases nearly 100 years before it was noticed and remaining cryptically present (Provan *et al.*, 2005).

The occurrence of populations of *D. cyanoloma* in marinas and yachting clubs suggest an important role of recreational boating as a secondary dispersal vector. This could explain the presence of *D. cyanoloma* in the Falmouth marina in Cornwall. This marina is one of the most famous and well-visited yachting marinas in the south of the UK, often used as a stop-over point for yachts returning from southern Europe.

Comparison of the thermal boundaries of the native and introduced ranges shows that these are similar, except that *D. cyanoloma* has established sustainable populations in significantly lower temperatures in its introduced range than in its native range. The most southern sample from Tasmania does not go below a mean minimum temperature of 12°C, while in Europe, populations are established in the South West of Britain (UK), where mean minimum temperatures are as low as 9°C. This could indicate that the climatic tolerance for the species is wider than the conditions to which it is subjected in its native range. The same has been noted for several invasive tropical algae in the Mediterranean, which thrive in

temperatures lower than the limit of tropical temperatures (Boudouresque & Verlaque, 2002). Extreme mean maximum temperatures isotherms for the species are comparable in both the native and introduced range (26 and 27° C, respectively). Due to this northward extension of the minimum thermal boundary in Europe, *D. cyanoloma* has been able to establish itself in a geographical range exceeding the size of its presumed potential range.

Conclusions and future prospects

Using gene sequence data we provide ample evidence for the introduced nature of *D. cyanoloma* in Europe. However, several questions remain unanswered to date. The chief question is whether *D. cyanoloma* was ubiquitous but unrecognized within the Mediterranean throughout the 20th century, or whether we could speak of an introduction that remained contained during a lag phase of several decades before expanding its range (Crooks *et al.*, 1999; Mack *et al.*, 2000; Sakai *et al.*, 2001). A first step in being conclusive about this matter would be to screen other European herbaria for historical records. Additionally, a population genetic study including elaborate sampling of both the introduced and native range, together with the use of more variable multilocus molecular markers such as microsatellites, could shed a light on different ecological processes as colonization and dispersal. Contrasting the multilocus genetic diversity of both native and introduced populations could pinpoint source populations and allow us to infer whether there was a single or multiple successive introductions within Europe. This approach might answer important questions regarding pathways and dynamics of secondary spread within the introduced range. There are indications that recreational boating acts as a secondary vector since *D. cyanoloma* is growing abundantly in marinas and harbours, where polluted conditions hamper the growth of native species. Recent reports of populations in natural environments raise suspicion that they might spread from these marina populations. These patterns should be monitored, as well as the

ecological impact of the species on the native communities. Last, it seems evident that *D. cyanoloma* is still spreading north. Predicting the eventual range in Europe therefore is important. Regarding the extent to which the species has spread, it is important to assess what exactly the potential range within Europe could be.

References

ARAGAY SOLER, J. GOMEZ GARRETA, A. RIBERA SIGUAN, M.A. & RULL LLUCH, J. (2014). New data about the phenology and the distribution of *Dictyota cyanoloma* Tronholm et al. in the Mediterranean Iberian coasts. In *Proceedings of the 5th Mediterranean Symposium on Marine vegetation. Portoroz, Slovenia*, 194-195.

BAE, D.Y. ANG JR, P.O. & BOO, S.M. (2013). Mitochondrial cox3 and trnW-I sequence diversity of Sargassum muticum. *Aquatic Botany* **104**: 220-223.

BARBARA, I. PETEIRO, C. PEÑA, V. ALTAMIRANO, M. PIÑEIRO-CORBEIRA, C. SANCHEZ, N. DIAZ-TAPIA, P. GARCIA-REDONDO, V. GARCIA-FERNANDEZ, A. & ZANOLLA, M. (2014). Fragmentos taxonomicos, corologicos, nomenclaturales y fitocenologicos. *Acta Botanica Malacitana* **39**: 207-239.

BOUDOURESQUE, C.F. & VERLAQUE, M. (2002). Biological pollution in the Mediterranean Sea: invasive versus introduced macrophytes. *Marine Pollution Bulletin* **44**: 32-38.

CARLTON, J.T. (1996). Biological Invasions and Cryptogenic Species. *Ecology* **77**: 1653-1655.

CHEANG, C.C. CHU, K.H. FUJITA, D. YOSHIDA, G. HIRAOKA, M. CRITCHLEY, A. CHOI, H.G. DUAN, D. SERISAWA, Y. & ANG, P.O. (2010). Low genetic variability of *Sargassum muticum* (Phaeophyceae) revealed by a global analysis of native and introduced populations. *Journal of Phycology* **46**: 1063-1074.

CROOKS, J.A. SOULÉ, M.E. & SANDLUND, O. (1999). Lag times in population explosions of invasive species: causes and implications. *Invasive species and biodiversity management*: 103-125.

DE CLERCK, O. LELIAERT, F. VERBRUGGEN, H. LANE, C.E. DE PAULA, J.C. PAYO, D.A. & COPPEJANS, E. (2006). A revised classification of the Dictyoteae (Dictyotales, Phaeophyceae) based on *rbc*L and 26S ribosomal DNA sequence analyses. *Journal of Phycology* **42**: 1271-1288.

DLUGOSCH, K. & PARKER, I. (2008). Founding events in species invasions: genetic variation, adaptive evolution, and the role of multiple introductions. *Molecular Ecology* **17**: 431-449.

DRUMMOND, A.J. & RAMBAUT, A. (2007). BEAST: Bayesian evolutionary analysis by sampling trees. *Bmc Evolutionary Biology* **7**.

EGGERT, A. (2012). Seaweed responses to temperature. In *Seaweed biology*, 47-66. Springer.

EXCOFFIER, L. & LISCHER, H.E.L. (2010). Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. *Molecular Ecology Resources* **10**: 564-567.

GALIL, B.S. MARCHINI, A. OCCHIPINTI-AMBROGI, A. MINCHIN, D. NARSCIUS, A. OJAVEER, H. & OLENIN, S. (2014). International arrivals: widespread bioinvasions in European Seas. *Ethology, Ecology and. Evolution.* **26**: 152-171.

GOODALL-COPESTAKE, W.P. TARLING, G.A. & MURPHY, E.J. (2012). On the comparison of population-level estimates of haplotype and nucleotide diversity: a case study using the gene cox1 in animals. *Heredity* **109**: 50-56.

GROSHOLZ, E. (2002). Ecological and evolutionary consequences of coastal invasions. *Trends in Ecology & Evolution* **17**: 22-27.

HAMEL, G. (1931-1939). Phéophycées de France. *Fascicules 1-3*: 432.

HÖRNIG, I. & SCHNETTER, R. (1988). Notes on Dictyota-Dichotoma, Dictyota-Menstrualis, Dictyota-Indica and Dictyota-Pulchella Spec-Nova (Phaeophyta). *Phyton-Annales Rei Botanicae* **28**: 277-291.

HÖRNIG, I. SCHNETTER, R. & VANREINE, W.F.P. (1992a). The Genus *Dictyota* (Phaeophyceae) in the North-Atlantic. 2. Key to the Species. *Nova Hedwigia* **54**: 397-402.

HÖRNIG, I. SCHNETTER, R. VANREINE, W.F.P. COPPEJANS, E. ACHENBACHWEGE, K. & OVER, J.M. (1992b). The Genus *Dictyota* (Phaeophyceae) in the North-Atlantic .1. a New Generic Concept and New Species. *Nova Hedwigia* **54**: 45-62.

HWANG, I.-K. LEE, W.J. KIM, H.-S. & DE CLERCK, O. (2009). Taxonomic reappraisal of *Dilophus okamurae* (Dictyotales, Phaeophyta) from the western Pacific Ocean. *Phycologia* **48**: 1-12.

JOUSSON, O. PAWLOWSKI, J. ZANINETTI, L. MEINESZ, A. & BOUDOURESQUE, C.-F. (1998). Molecular evidence for the aquarium origin of the green alga *Caulerpa taxifolia* introduced to the Mediterranean Sea. *Marine Ecology Progress Series* **172**: 275-280.

KALINOWSKI, S.T. (2005). HP-RARE 1.0: a computer program for performing rarefaction on measures of allelic richness. *Molecular Ecology Notes* **5**: 187-189.

LANFEAR, R. CALCOTT, B. HO, S.Y.W. & GUINDON, S. (2012). PartitionFinder: Combined Selection of Partitioning Schemes and Substitution Models for Phylogenetic Analyses. *Molecular Biology and Evolution* **29**: 1695-1701.

LEBERG, P.L. (2002). Estimating allelic richness: Effects of sample size and bottlenecks. *Molecular Ecology* **11**: 2445-2449.

LELIAERT, F. VERBRUGGEN, H. VANORMELINGEN, P. STEEN, F. LÓPEZ-BAUTISTA, J.M. ZUCCARELLO, G.C. & DE CLERCK, O. (2014). DNA-based species delimitation in algae. *European Journal of Phycology* **49**: 179-196.

MACK, R.N. SIMBERLOFF, D. MARK LONSDALE, W. EVANS, H. CLOUT, M. & BAZZAZ, F.A. (2000). Biotic invasions: causes, epidemiology, global consequences, and control. *Ecological Applications* **10**: 689-710.

MINEUR, F. ARENAS, F. ASSIS, J. DAVIES, A.J. ENGELEN, A.H. FERNANDES, F. MALTA, E.-J. THIBAUT, T. VAN NGUYEN, T. VAZ-PINTO, F. VRANKEN, S. SERRÃO, E.A. & DE CLERCK, O. (2015). European seaweeds under pressure: Consequences for communities and ecosystem functioning. *Journal of Sea Research* **98**.

MOLNAR, J.L. GAMBOA, R.L. REVENGA, C. & SPALDING, M.D. (2008). Assessing the global threat of invasive species to marine biodiversity. *Frontiers in Ecology and the Environment* **6**: 485-492.

PEÑA, V. BÁRBARA, I. GRALL, J. MAGGS, C.A. & HALL-SPENCER, J. (2014). The diversity of seaweeds on maerl in the NE Atlantic. *Marine Biodiversity* **44**: 533-551.

PROVAN, J. MURPHY, S. & MAGGS, C.A. (2005). Tracking the invasive history of the green alga *Codium fragile* ssp. *tomentosoides*. *Molecular Ecology* **14**: 189-194.

ROMAN, J. & DARLING, J.A. (2007). Paradox lost: genetic diversity and the success of aquatic invasions. *Trends in Ecology & Evolution* **22**: 454-464.

RONQUIST, F. TESLENKO, M. VAN DER MARK, P. AYRES, D.L. DARLING, A. HOHNA, S. LARGET, B. LIU, L. SUCHARD, M.A. & HUELSENBECK, J.P. (2012). MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space. *Systematic Biology* **61**: 539-542.

RULL LLUCH, J.R. BALLESTEROS, E. BARCELO, M.C. GARRETA, A.G. & SIGUAN, M.A.R. (2007). *Dictyota ciliolata* sonder ex Kutzing (Phaeophyceae, Dictyotales) in the Mediterranean Sea. *Cryptogamie Algologie:* **28**: 89-97.

SAKAI, A.K. ALLENDORF, F.W. HOLT, J.S. LODGE, D.M. MOLOFSKY, J. WITH, K.A. BAUGHMAN, S. CABIN, R.J. COHEN, J.E. & ELLSTRAND, N.C. (2001). The population biology of invasive species. *Annual Review of Ecology and Systematics*: 305-332.

SALZBURGER, W. EWING, G.B. & VON HAESELER, A. (2011). The performance of phylogenetic algorithms in estimating haplotype genealogies with migration. *Molecular Ecology* **20**: 1952-1963.

SANTELICES, B. (1980). Phytogeographic characterization of the temperate coast of Pacific South America. *Phycologia* **19**: 1-12.

SCHNETTER, R. HORNIG, I. & WEBERPEUKERT, G. (1987). Taxonomy of Some North-Atlantic *Dictyota* Species (Phaeophyta). *Hydrobiologia* **151**: 193-197.

SECQ, M.P.O. GOER, S.L. STAM, W.T. & OLSEN, J.L. (2006). Complete mitochondrial genomes of the three brown algae (Heterokonta : Phaeophyceae) *Dictyota dichotoma*, *Fucus vesiculosus* and *Desmarestia viridis*. *Current Genetics* **49**: 47-58.

SILBERFELD, T. LEIGH, J.W. VERBRUGGEN, H. CRUAUD, C. DE REVIERS, B. & ROUSSEAU, F. (2010). A multi-locus time-calibrated phylogeny of the brown algae (Heterokonta, Ochrophyta, Phaeophyceae): Investigating the evolutionary nature of the "brown algal crown radiation". *Molecular Phylogenetics and Evolution* **56**: 659-674.

SIMBERLOFF, D. (2011). How common are invasion-induced ecosystem impacts? *Biological Invasions* **13**: 1255-1268.

SIMMONS, M.P. & OCHOTERENA, H. (2000). Gaps as characters in sequence-based phylogenetic analyses. *Systematic Biology* **49**: 369-381.

STAMATAKIS, A. HOOVER, P. & ROUGEMONT, J. (2008). A Rapid Bootstrap Algorithm for the RAxML Web Servers. *Systematic Biology* **57**: 758-771.

STEEN, F. VIEIRA, C. LELIAERT, F. PAYRI, E.C. & CLERCK, O.D. (2015). Biogeographic Affinities of Dictyotales from Madagascar: A Phylogenetic Approach. *Cryptogamie Algologie* **36**: 129-141.

TAMURA, K. STECHER, G. PETERSON, D. FILIPSKI, A. & KUMAR, S. (2013). MEGA6: molecular evolutionary genetics analysis version 6.0. *Molecular Biology and Evolution* **30**: 2725-2729.

TASKIN, E. (2013). New records of three dictyotalean brown algae for Turkey. *Botanica Marina* **56**: 299-302.

TRONHOLM, A. STEEN, F. TYBERGHEIN, L. LELIAERT, F. VERBRUGGEN, H. SIGUAN, M.A.R. & DE CLERCK, O. (2010). Species Delimitation, Taxonomy, and Biogeography of *Dictyota* in Europe (Dictyotales, Phaeophyceae). *Journal of Phycology* **46**: 1301-1321.

TYBERGHEIN, L. VERBRUGGEN, H. PAULY, K. TROUPIN, C. MINEUR, F. & DE CLERCK, O. (2012). Bio-ORACLE: a global environmental dataset for marine species distribution modelling. *Global Ecology and Biogeography* **21**: 272-281.

UNTERGASSER, A. CUTCUTACHE, I. KORESSAAR, T. YE, J. FAIRCLOTH, B.C. REMM, M. & ROZEN, S.G. (2012). Primer3-new capabilities and interfaces. *Nucleic Acids Research* **40**.

VAN DEN HOEK, C. (1982). The distribution of benthic marine algae in relation to the temperature regulation of their life histories. *Biological Journal of the Linnean Society* **18**: 81-144.

VAN OPPEN, M.J. KLERK, H. OLSEN, J.L. & STAM, W.T. (1996). Hidden diversity in marine algae: some examples of genetic variation below the species level. *Journal of the Marine Biological Association of the United Kingdom* **76**: 239-242.

VERBRUGGEN, H. (2014). Morphological complexity, plasticity, and species diagnosability in the application of old species names in DNA-based taxonomies. *Journal of Phycology* **50**: 26-31.

VOISIN, M. ENGEL, C.R. & VIARD, F. (2005). Differential shuffling of native genetic diversity across introduced regions in a brown alga: Aquaculture vs. maritime traffic effects. *Proceedings of the National Academy of Sciences of the United States of America* **102**: 5432-5437.

WEBERPEUKERT, G. (1986). Ontogenic, autoecological and taxonomic investigations on selected species of the genus of *Dictyota* (Dictyotales, Phaeophyceae) .1. Cytological data as differentiating characteristics. *Nova Hedwigia* **42**: 123-149.

ZENETOS, A. GOFAS, S. MORRI, C. ROSSO, A. VIOLANTI, D. GARCIA RASO, J.E. CINAR, M.E. ALMOGI-LABIN, A. ATES, A.S. AZZURO, E. BALLESTEROS, E. BIANCHI, C.N. BILECENOGLU, M. GAMBI, M.C. GIANGRANDE, A. GRAVILI, C. HYAMS-KAPHZAN, O. KARACHLE, P.K. KATSANEVAKIS, S. LIPEJ, L. MASTROTOTARO, F. MINEUR, F. PANCUCCI-PAPADOPOULOU, M.A. RAMOS ESPLA, A. SALAS, C. SAN MARTIN, G. SFRISO, A. STREFTARIS, N. & VERLAQUE,

M. (2012). Alien species in the Mediterranean Sea by 2012. A contribution to the application of European Union's Marine Strategy Framework Directive (MSFD). Part 2. Introduction trends and pathways. In *2012* (13).

Tables

Table 1. Specimen of *D. cyanoloma* used for the network analysis, with indication of haplotype number (h), habitat, locality with coordinates,

year of sampling, and accession number par phylogenetic marker.

h	ID	Locality	habitat	Country	Latitude	Longitude	Sampling year	Nad6	Atp9
1	LT0030	New South Wales: Minnie Waters	natural	Australia	-29,7761	153,3021	2009	LN871845	LN871881
2	LT0384	Western Australia: Albany: Vancouver Peninsula: Whaling Cove	natural	Australia	-35,0552	117,9314	2009	LN871846	LN871882
3	HV2123	New South Wales: Minnie Waters	natural	Australia	-29,7761	153,3021	2009	LN871847	LN871883
4	HV2301	Victoria: Bellarine Peninsula: Point Lonsdale: Glaneuse Reef	natural	Australia	-38,2914	144,6078	2009	LN871848	LN871884
5	HV2335	South Australia: Port McDonnell	natural	Australia	-38,0602	140,6629	2009	LN871849	LN871885
6	HV2155	New South Wales: Newcastle	natural	Australia	-32,9277	151,7919	2009	LN871850	LN871886
7	ED138	Doukkala-Abda: Oualidia	natural	Morocco	32,7258	-9,0560	2010	LN871851	LN871887

ED141	Doukkala-Abda: Oualidia	natural	Morocco	32,7258	-9,0560	2010
ED197	Doukkala-Abda: Safi	natural	Morocco	32,3209	-9,2596	2010
ED151	Marrakech-Tensift-El Haouz: Essaouira	natural	Morocco	31,5089	-9,7757	2010
ED283	Tangier-Tétouan: Asilah	natural	Morocco	35,4647	-6,0423	2010
ED284	Tangier-Tétouan: Asilah	natural	Morocco	35,4647	-6,0423	2010
ED477	Tangier-Tétouan: Tangier: Cap Spartel	natural	Morocco	35,7607	-5,9395	2010
FS0480	Algarve: Albufeira: Olhos de Agua	natural	Portugal	37,0886	-8,1935	2009
SMG-09-01	Azores: São Miguel: Lagoa	natural	Portugal	37,7411	-25,5738	2009
HEC15777	Madeira Island: Rais Magos	natural	Portugal	32,6024	-16,8036	2006
Algecires2	Andalusia: Cádiz: Algeciras	marina	Spain	36,1173	5,4355	2014
Algecires3	Andalusia: Cádiz: Algeciras	marina	Spain	36,1173	5,4355	2014
Motril1	Andalusia: Granada: Motril	marina	Spain	36,7239	3,5260	2014
Motril2	Andalusia: Granada: Motril	marina	Spain	36,7239	3,5260	2014
D1567	Canary Islands: El Hierro	natural	Spain	27,6383	-17,9849	2009
D1568	Canary Islands: El Hierro	natural	Spain	27,6383	-17,9849	2009

	Castell5	Castelló: Castelló de la Plana	marina	Spain	39,9677	0,0220	2014		
	Castell6	Castelló: Castelló de la Plana	marina	Spain	39,9677	0,0220	2014		
	D621	Catalonia: Barcelona	marina	Spain	41,3314	2,1736	2008		
	Estartit2	Girona: Costa Brava: Estartit	marina	Spain	42,0528	3,2052	2014		
	Estartit3	Girona: Costa Brava: Estartit	marina	Spain	42,0528	3,2052	2014		
8	KD879	Victoria: Williamstown: Gloucester reserve	natural	Australia	-37,8690	144,8818	2010	LN871852	LN871888
	KD880	Victoria: Williamstown: Gloucester reserve	natural	Australia	-37,8690	144,8818	2010		
9	LT0287	South Australia: Port Noarlunga	natural	Australia	-35,1486	138,4642	2009	LN871853	LN871889
	HV2384	South Australia: Port Noarlunga	natural	Australia	-35,1491	138,4656	2009		
	HV2389	South Australia: Port Noarlunga	natural	Australia	-35,1491	138,4656	2009		
10	LT0057	New South Wales: Newcastle	natural	Australia	-32,9277	151,7919	2009	LN871854	LN871890
	FS0478	Algarve:Albufeira: Olhos de Agua	natural	Portugal	37,0886	-8,1935	2009		
	Almeria1	Andalusia: Almería	marina	Spain	36,8307	2,4671	2014		
	Almeria2	Andalusia: Almería	marina	Spain	36,8307	2,4671	2014		
	D502	Canary Islands: Gran Canaria: Arinaga: Zoco del Negro	natural	Spain	27,8661	-15,3847	2008		

	LLan2	Girona: Llançà	marina	Spain	42,3738	3,1631	2014		
	LLan3	Girona: Llançà	marina	Spain	42,3738	3,1631	2014		
	FS0715	Huelva: Chipiona: marina	marina	Spain	36,7240	-6,4391	2009		
	FS0734	Huelva: Zahara de los Atunes: Playa de los Alemanes	natural	Spain	36,1028	-5,8247	2009		
11	FS0405	Dalmatia: Split: Bacvice	natural	Croatia	43,5003	16,4461	2009	LN871855	LN87189 A
	ED199	Doukkala-Abda: Doukkala-Abda: Safi	natural	Morocco	32,3209	-9,2596	2010		
	ED079	Doukkala-Abda: El Jadida: Sidi Bouzid	natural	Morocco	33,2314	-8,5541	2010		
	ED389	Tangier-Tétouan: Ben Younech	natural	Morocco	35,9116	-5,3846	2010		
	ED408	Tangier-Tétouan: Ben Younech	natural	Morocco	35,9116	-5,3846	2010		
	ED014	Tangier-Tétouan: Larache: Port Lixus	natural	Morocco	35,2042	-6,1465	2010		
	ED018	Tangier-Tétouan: Larache: Port Lixus	natural	Morocco	35,2042	-6,1465	2010		
	FS0547	Algarve: Lagos: Praia da Dona Ana	natural	Portugal	37,0908	-8,6693	2009		
	Estepona1	Andalusia: Málaga: Estepona	marina	Spain	36,4149	5,1597	2014		
	Estepona2	Andalusia: Málaga: Estepona	marina	Spain	36,4149	5,1597	2014		

	Palamos3	Girona: Palamós	marina	Spain	41,8455	3,1276	2014		
	Palamos4	Girona: Palamós	marina	Spain	41,8455	3,1276	2014		
	FS0733	Huelva: Zahara de los Atunes: Playa de los Alemanes	natural	Spain	36,1028	-5,8247	2009		
	Cartagena1	Murcia: Cartagena	marina	Spain	37,5847	0,9849	2014		
	Cartagena2	Murcia: Cartagena	marina	Spain	37,5847	0,9849	2014		
12	FS0429	Alentejo: Sines: Porto Covo	natural	Portugal	37,8272	-8,7922	2009	LN871856	LN871892
	FS0716	Huelva: Chipiona: marina	marina	Spain	36,7240	-6,4391	2009		
13	LT0095	New South Wales: Jervis Bay: Bowen Island	natural	Australia	-35,1118	150,7688	2009	LN871857	LN871893
14	HV2182	New South Wales: Jervis Bay: Bowen Island	natural	Australia	-35,1118	150,7688	2009	LN871858	LN871894
15	D3814	Dalmatia: Split	harbour	Croatia	43,5037	16,4298	2013	LN871859	LN871895
	D4009	Istria: Rovinj	natural	Croatia	45,0769	13,6336	2014		
	D4010	Istria: Rovinj	natural	Croatia	45,0769	13,6336	2014		
	D4011	Istria: Rovinj	natural	Croatia	45,0769	13,6336	2014		
	D3813	Catalonia: Barcelona	marina	Spain	41,3538	2,1780	2005		
	D4006	Galicia: Oleiros: Ría de A Coruña	natural	Spain	43,3472	-8,3794	2014		

16	HV2387	South Australia: Port Noarlunga	natural	Australia	-35,1491	138,4656	2009	LN871860	LN871896
17	FS1752	West Australia: Perth: Port of Fremantle	harbour	Australia	-32,0558	115,7333	2014	LN871861	LN871897
	FS1739	Victoria: Portarlington	natural	Australia	-38,1109	144,6529	2014		
	FS1740	Victoria: Portarlington	natural	Australia	-38,1109	144,6529	2014		
	FS1746	Victoria: Portarlington	natural	Australia	-38,1109	144,6529	2014		
	FS1728	Victoria: Williamstown: South	natural	Australia	-37,8690	144,8818	2014		
	FS1729	Victoria: Williamstown: South	natural	Australia	-37,8690	144,8818	2014		
	FS1732	Victoria: Williamstown: South	natural	Australia	-37,8690	144,8818	2014		
18	FS1733	Victoria: Williamstown: South	natural	Australia	-37,8690	144,8818	2009	LN871862	LN871898
19	FS1748	West Australia: Perth: Port of Fremantle	harbour	Australia	-38,1453	115,7333	2014	LN871863	LN871999
	HV5285	Victoria: Frankston	natural	Australia	-38,1453	145,1141	2014		
	FS1738	Victoria: Portarlington	natural	Australia	-38,1109	144,6529	2014		
	FS1742	Victoria: Portarlington	natural	Australia	-38,1109	144,6529	2014		
	FS1744	Victoria: Portarlington	natural	Australia	-38,1109	144,6529	2014		
	FS1747	Victoria: Portarlington	natural	Australia	-38,1109	144,6529	2014		
	FS1734	Victoria: Williamstown: South	natural	Australia	-37,8690	144,8818	2014		

	FS1731	Victoria: Williamstown: South	natural	Australia	-37,8690	144,8818	2014			
	D3819	Dalmatia: Split (Zagreb herbarium)	harbour	Croatia	43,5037	16,4298	1958			
20	FS1735	Victoria: Williamstown: South	natural	Australia	-37,8690	144,8818	2014	LN871864	LN871900	
21	D3936A	Cornwall: Falmouth	marina	UK	50,1653	-5,0845	2014	LN871865	LN871901	
	D3936B	Cornwall: Falmouth	marina	UK	50,1653	-5,0845	2014			
	D3936C	Cornwall: Falmouth	marina	UK	50,1653	-5,0845	2014			
	D3936D	Cornwall: Falmouth	marina	UK	50,1653	-5,0845	2014			
22	D3817	Côte d'Azur: Cannes	marina	France	43,5494	7,0149	1999	LN871866	LN871902	
23	D3818	Dalmatia: Split (Zagreb herbarium)	harbour	Croatia	43,5037	16,4298	1935	LN871867	LN871903	
24	D3815b	Dalmatia: Split (Zagreb herbarium)	harbour	Croatia	43,5037	16,4298	1935	LN871868	LN871904	
25	D3815	Dalmatia: Split (Zagreb herbarium)	harbour	Croatia	43,5037	16,4298	1935	LN871869	LN871905	

Table 2. Primer sequence for the mitochondrial markers *nad*6 - *nad*11 and *atp*9 - *orf*11

Marker	Forward primer	Reverse Primer
*nad*6 - *nad*11	TTT TAT TGT GTG CGG TGG TG	CAC AAG AAA CTT GAG GCT TCG

*atp*9 - *orf*11	ATA CGC GAT TTT AGG TTT TGC	TGC GGG TAA AAC TGA TAC GG

Legends

Fig. 1. Phylogenetic tree obtained by ML-inference of a dataset containing six genes (partial LSU rDNA, *rbc*L, *psb*A, *cox*1, *cox*3, and *nad*1). Numbers at the nodes indicate posterior probabilities followed by ML-bootstrap.

Fig. 2. Distribution map of a global *Dictyota* data set (green) highlighting the occurrences of *D. cyanoloma* (red) and *D.* sp8 (yellow).

Fig. 3. Annual mean maximum and minimum sea surface temperatures of the distribution range of *Dictyota cyanoloma* within the native region (full lines) and within the region of introduction (dashed lines) reported on:

A. the native range

B. the region of introduction

A distinction is made between samples from this study (red), earlier published records (green), photographic evidence (blue) and herbarium samples (yellow).

Fig. 4. Haplotype network based on a ML phylogeny indicating Australian (blue), European (orange) and sequenced Split herbarium samples (asterisks). The size of the circles is proportional to the amount of individuals of that haplotype. The number specifies the haplotype. (WA: West Australia, NSW: New South Wales, VIC: Victoria, SA: South Australia, MOR: Morocco, POR: Portugal, AZ: Azores, MAD: Madeira, SP: Spain, CI: Canary Islands, CR: Croatia, UK: United Kingdom, FR: France)

Fig. 5. A. Boat hull fouled by *Dictyota cyanoloma*, photograph taken by Olivier De Clerck at Garachico Bay, Tenerife, 2014 B. *Dictyota cyanoloma* clearly showing its characteristic blue iridescent margin, photograph taken by Joana Aragay, Almeria, 2013.

Table 1. Specimen of *D. cyanoloma* employed for the network analysis, with indication of haplotype number (h), habitat, locality with coordinates, year of sampling, and accession number par phylogenetic marker.

Table 2. Primer sequence for the mitochondrial markers *nad*6 - *nad*11 and *atp*9 - *orf*11

Fig. 1S. Haplotype networks based on both best scoring MP phylogenies indicating Australian (blue), European (orange). Historical Split herbarium samples are indicated with an asterisk. The size of the circles is proportional to the amount of individuals of that haplotype. The number specifies the haplotype. Localities are indicated on the network (WA: West Australia, NSW: New South Wales, VIC: Victoria, SA: South Australia, MOR: Morocco, POR: Portugal, AZ: Azores, MAD: Madeira, SP: Spain, CI: Canary Islands, CR: Croatia, UK: United Kingdom, FR: France)

Table 1S. Specimen table employed for phylogenetic inference, indicating accession numbers par phylogenetic marker.

Table 2S. Links to photographical evidence of *D. cyanoloma* occurrences
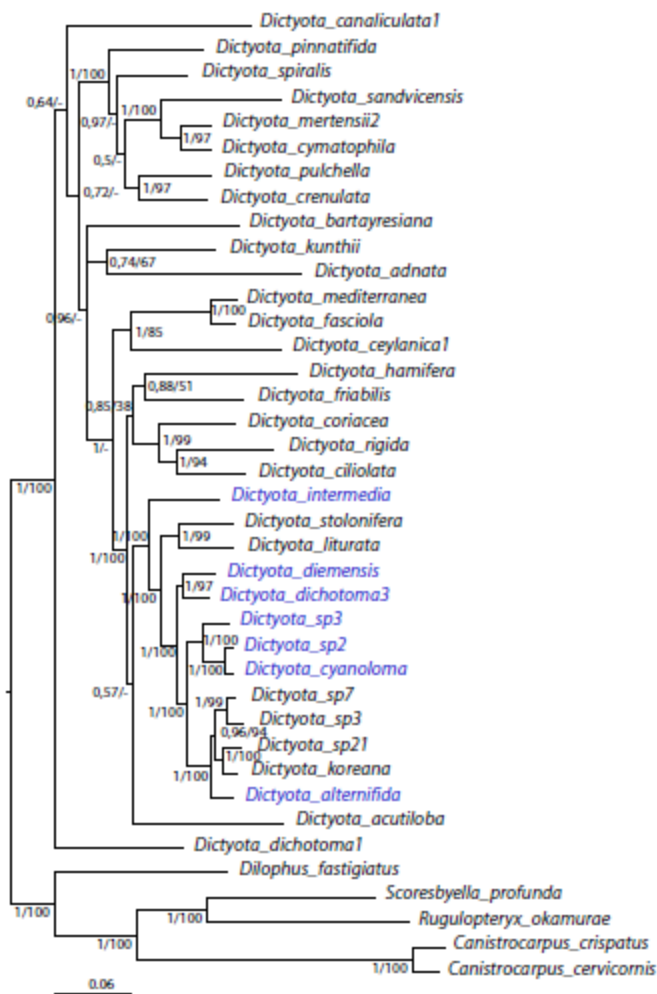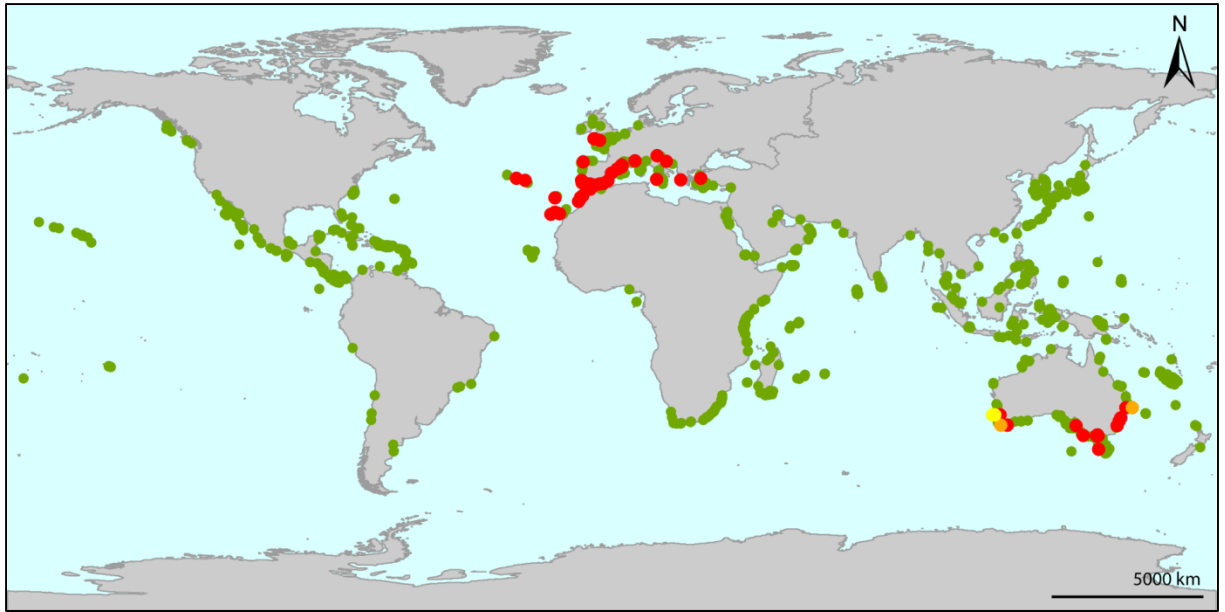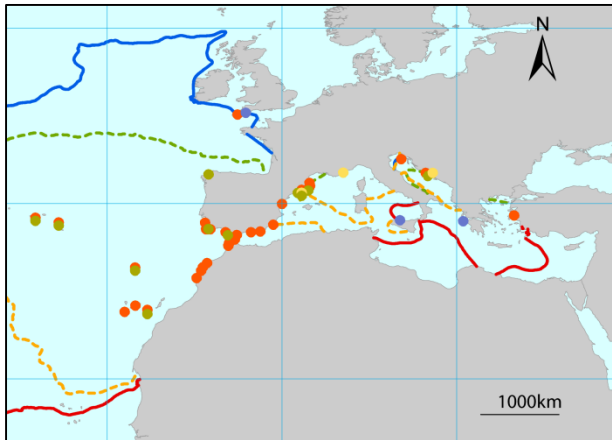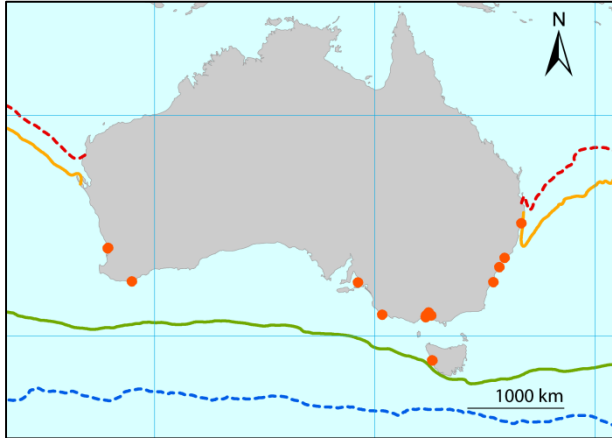
Fig. 1

Fig. 2

Fig. 3

Fig.4

Fig. 5

A

B

Fig. 1 S