

Marine protected areas are insufficient to conserve global marine plant diversity

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Abstract

Aim Marine plants are only incidentally included in conservation efforts for marine biodiversity. Here, we apply phylogenetic methods for the first time to marine macrophytes (mangroves and seagrass species) to test for gaps in the current conservation network by identifying global diversity hotspots for these plant groups, and assessing the degree to which hotspots are represented within the current network of Marine Protected Areas (MPAs).

Location Global.

Methods We calculated five metrics of marine plant diversity: phylogenetic diversity, species richness, species endemism, phylogenetic endemism, and ‘evolutionary distinctiveness and global endangerment’ (EDGE).

Results Overall, the diversity of marine plants was poorly represented by current MPAs. Different measures of diversity showed spatial mismatch, demonstrating how strategies maximizing one diversity measure may be inefficient at protecting other facets of marine plant biodiversity. However, complementarity analyses revealed that complete representation can be achieved very efficiently with few additional locations.

Main conclusion Our study highlights the need for an integrative approach to conserve both the species and phylogenetic diversity of marine plants. While MPAs are a valuable instrument for conserving marine biodiversity, we now face the challenge of increasing coverage to protect other branches of the marine tree of life.

Keywords: biodiversity hotspots, complementarity analyses, mangroves, marine plants, phylogenetic diversity, protected areas, seagrasses

INTRODUCTION

Although the marine protected area system (MPA) remains the most significant instrument for managing and protecting the oceans' biological resources, MPAs were initially designed for preserving fish stocks, coral reefs and other animal resources

(Gaines *et al.*, 2010). This suggests that non-target taxa and their associated habitats are often only incidentally included in current biodiversity protection efforts in the marine realm. Moreover, the major groups of conservation focus in the marine world, mainly marine mammals, coral reefs, and fish, may not fully represent the diversity of other taxa due to their different evolutionary histories (see e.g. Rodrigues & Brooks, 2007; Mellin *et al.*, 2011). Indeed, there is inconsistent support for the use of cross-taxon surrogates (where well-studied taxonomic groups can effectively serve as surrogates in representing patterns of diversity of more poorly known taxa; Rodrigues & Brooks, 2007) in conservation planning. For example, some studies have suggested that environmental factors may be a more efficient proxy for biodiversity (e.g. Tittensor *et al.*, 2010; Beier & de Albuquerque, 2015), while others have found spatial mismatches between various taxonomic groups (e.g. Zupan *et al.*, 2014), suggesting that usefulness of cross-taxon surrogates may depend on the scale or context of the study (e.g., Ferrier & Watson, 1997; Rodrigues & Brooks, 2007). As a result, explicit examination of non-target species representation within MPAs is necessary to assess their protection status. Moreover, given that marine species are more prone to extinction than previously thought (McKinney, 1998) due to human pressures (Roberts *et al.*, 2002; McCauley *et al.*, 2015), it is critical to determine the extent to which MPAs conserve species of other distinct evolutionary branches of the marine tree of life (Murdoch *et al.*, 2007).

A common approach for designating areas of conservation priority is via hotspots i.e. geographic clusters of biodiversity (Myers *et al.*, 2000; see also Orme *et al.*, 2005). In the marine realm, biodiversity hotspots have been defined using taxonomic metrics such as species richness, endemism, or risk of extinction (Roberts *et al.*, 2002; Davidson *et al.*, 2012), thereby missing out on the full richness of biodiversity captured by phylogenetic information (Faith, 1994; Williams *et al.*, 1994). Even with simple taxonomic metrics of diversity, spatial mismatches between individual taxonomic metrics have often been reported (Roberts *et al.*, 2002), suggesting that current marine hotspots are insufficient to capture even species-level diversity.

Some lineages differ markedly in the amount of evolutionary history they embody (Vane-Wright *et al.*, 1991; Faith, 1992). As a result, integrating phylogenetic information is an important advance in conservation (Bininda-Emonds *et al.*, 2000), allowing reserve networks to be planned that maximize the amount of unique evolutionary history captured (Sechrest *et al.*, 2002; Jetz *et al.*, 2014). For instance, considering phylogenetic metrics in conservation prioritization allows identification of areas harbouring evolutionarily distinct lineages, i.e. once-diverse lineages that are now reduced due to historical extinctions, or identify regions with recently diversified clades that may represent centres of speciation (e.g. Forest *et al.*, 2007). Phylogenetic metrics, including phylogenetic diversity, phylogenetic endemism, and evolutionary distinctiveness and global endangerment, all measure different facets of evolutionary diversity (Isaac *et al.*, 2007; Cadotte *et al.*, 2010) and have been used to delineate biodiversity hotspots but only in the terrestrial realm (Faith, 1992; Rosauer *et al.*, 2009; Safi *et al.*, 2013; Jetz *et al.*, 2014; Zupan *et al.*, 2014; Daru *et al.*, 2015; Guilhaumon *et al.*, 2015). Despite the

growing interest in integrating taxonomic and phylogenetic methods to assess biodiversity (Devictor *et al.*, 2010; Mishler *et al.*, 2014; Zupan *et al.*, 2014; Daru *et al.*, 2015), phylogenetic metrics have not been implemented in conservation planning for marine species. While the selection of hotspots based solely on the top grid cells for each metric could ensure protection of certain habitats, this approach may be inefficient (and even ineffective) for maximizing biodiversity protection (Daru *et al.*, 2015).

Complementarity methods, which aim to include the maximum number of unrepresented species or phylogenetic branch lengths with each new location conserved, offer a more powerful and efficient approach to identifying a minimum conservation network that includes all species or phylogenetic branches of interest. Therefore, considerable opportunity exists for improving the representation and efficiency of marine conservation networks, as previously already advocated (e.g. Justus & Sarkar, 2002; Faith *et al.*, 2004), through the incorporation of phylogenetic information and the application of complementarity methods.

To this aim, we develop an integrative approach to assess current marine protection efforts by combining spatial analyses with taxonomic and phylogenetic techniques to identify hotspots for two important aquatic and semi-aquatic plant groups, seagrasses and mangroves. These two groups are the only vascular plants inhabiting coastal environments and estuaries throughout the world that can live exclusively in marine environment without any freshwater input, and present an excellent opportunity to explore the degree of protection of an often non-target group in the current marine conservation network. Both seagrasses and mangroves are keystone species, having a disproportionately strong influence on co-occurring species, largely via ecosystem

engineering effects. Seagrasses, 72 species (Hemminga & Duarte, 2000) and mangroves, 70 species (Spalding *et al.*, 1997) play critical roles in sediment accumulation, carbon sequestration and nutrient cycling, and act as nursery for many fish and invertebrates and anchor several foodwebs (Beck *et al.*, 2001; Green & Short, 2003). Cumulatively, their ecosystem services are valued at c. USD 2 trillion annually (Costanza *et al.*, 1997; Field *et al.*, 1998; Waycott *et al.*, 2009). We refer to these two ecological groups collectively as ‘macrophytes’.

Here, we apply phylogenetic methods for the first time to marine macrophytes to test for gaps in the current conservation network. Specifically, we address three objectives. First, we map patterns and hotspots (defined as the top 2.5% cells) of species richness (SR), phylogenetic diversity (PD), corrected weighted endemism (CWE), phylogenetic endemism (PE), and evolutionary distinctiveness and global endangerment (EDGE) for each taxonomic group. Second, we explore the complementarity of macrophyte species richness and phylogenetic diversity in representing all species/branch lengths in as small an area as possible. Lastly, we evaluate the degree to which the current global network of Marine Protected Areas (MPAs) covers macrophyte hotspots.

METHODS

Distribution data and phylogenetic reconstruction

We compiled data on the global distribution of all 72 seagrass species and 55 (of 70) mangrove species from IUCN Red List database’s extent of occurrence maps (EOO) (<http://www.iucnredlist.org/technical-documents/spatial-data>). These maps have been extensively assessed and updated, providing accurate presence/absence data at the scale

of $1^{\circ} \times 1^{\circ}$ degree grids (ca. 110×110 km), a resolution commonly used in global scale macroecological studies (e.g. Storch *et al.*, 2012).

Phylogenetic reconstruction and divergence time estimation for seagrass species

DNA sequences (*rbcL*, ITS and 18S) for 55 (of 72) seagrass species were obtained from GenBank/EBI. The sequences were aligned using SEAVIEW v.4 (Gouy *et al.*, 2010) and manually adjusted using MESQUITE v.2.5 (Maddison & Maddison, 2008). The combined data set comprised 1137, 930, and 1671 base pairs for *rbcL*, ITS and 18S, respectively. Information on DNA sequences retrieved from GenBank/EBI are presented in Table S1 in Appendix S1 in Supporting Information.

Phylogenetic relationships were reconstructed on the combined dataset using maximum likelihood (ML; Stamatakis *et al.*, 2008) on the CIPRES cluster (Miller *et al.*, 2009), transforming branch lengths to millions of years by enforcing topological constraints assuming the APG III backbone from Phylomatic v.3 (Webb & Donoghue, 2005). An XML file generated in the software BEAUti v.1.7.5 (Drummond & Rambaut, 2007) was used for the reconstruction of the dated phylogenetic tree using a Bayesian Markov chain Monte Carlo (hereafter MCMC) approach implemented in the software BEAST v.1.7.5 (Drummond & Rambaut, 2007). Branch lengths were then calibrated in millions of years using a Bayesian MCMC approach in BEAST v.1.7.5 (Drummond & Rambaut, 2007). A RAxML tree was used as a starting tree, but branch lengths were adjusted to match secondary fossil calibrations using PATHd8 v.1.0 to ensure topological constraints were satisfied (Britton *et al.*, 2007). It is possible that differences in tree reconstruction approaches (e.g. r8s versus PATHd8) might provide additional

information on diversity patterns and may merit further investigation. We then used the GTR +G+I model, corresponding to general time reversible model with rate variation among sites and proportion of invariant sites, as the best model of sequence evolution based on the result of Akaike information criterion evaluated using Modeltest v.2.3

(Nylander, 2004). In addition, a Yule process was selected as the tree prior, along with an uncorrelated lognormal relaxed molecular clock model selected in BEAST v.1.7.5

(Drummond & Rambaut, 2007) for rate variation among branches. Next, we applied a normal prior distribution and a total of six calibration points, representing lineages at various

phylogenetic depths: Alismatales crown node 128 Ma; Cymodoceae crown node 61 Ma, Zosteraceae crown node 17 Ma, Hydrocharitaceae crown node 75 Ma, and Tofieldiaceae crown node 100 Ma (Janssen & Bremer, 2004); and *Alocasia* crown node 19.28 Ma

(Nauheimer *et al.*, 2012). We then ran two independent runs of MCMC analyses in BEAST, each for 100 million generations, sampling every 1000th iteration. The adequacy of sampling and run convergence was assessed using the effective sample size (ESS) diagnostic in TRACER (Rambaut & Drummond, 2007). The ESS values ranged from 296-29217 for the age estimates (Table S2 in Appendix S1 in Supporting Information), confirming stationarity.

The posterior tree distributions from the different chains were then summarized into a maximum clade credibility (MCC) tree using TreeAnnotator v.1.7.5 (Drummond & Rambaut, 2007) after removal of 25% trees as burn-in. The following species were used as outgroups:

Alocasia cucullata, *A. macrorrhizos*, *A. odora*, *A. sandariana*, *Harperocallis flava*, and *Tofieldia furusei* (Table S1 in Appendix S1).

Seventeen species did not have DNA sequences available and were placed on the MCC phylogeny by grafting them in a multichotomy to the node from which their closest relatives descended based on their taxonomic classification using the R library PASTIS (Thomas *et al.*, 2013). This approach has recently been used, for example, to assemble a complete phylogeny for birds (Jetz *et al.*, 2012) or fruitflies (Yassin *et al.*, 2008). The reconstructed phylogeny is available in Fig. S1 in Appendix S1 in Supporting Information.

Phylogenetic reconstruction and divergence time estimation for mangrove species

The mangrove phylogeny is a fully dated molecular phylogenetic tree for 55 (of 70) mangrove species based on *rbcL*, ITS and 18S from Daru *et al.* (2013), reconstructed using Bayesian inference and five independent fossil calibrations with normal prior distributions as follows: Vitaceae crown node (43 Ma, SD 9 Ma), Moraceae crown node (31 Ma, SD 4 Ma), Oleaceae crown node (41 Ma, SD 6 Ma), Malvaceae crown node (39 Ma, SD 4 Ma), and angiosperm crown (Amborellaceae; 149 Ma, SD 3 Ma) (see Daru *et al.*, 2013 for full description of tree reconstruction, Table S3 in Appendix S1 for GenBank accession numbers, and Fig. S2 in Appendix S1 for the mangrove phylogenetic tree). We recognize that our phylogenetic reconstruction may introduce some error into the data, but given that all 15 missing mangrove species are represented by sister relatives, it is unlikely that the incomplete sampling of the macrophytes will alter any results here.

Diversity metrics

We calculated five metrics commonly used in quantifying biodiversity at various organizational scales: SR, PD, CWE, PE, and EDGE (Safi *et al.*, 2013; Jetz *et al.*, 2014; Daru *et al.*, 2015).

PD estimates the amount of evolutionary history captured by a set of taxa by summing the branch lengths that connect species from the tip to the root of a dated phylogenetic tree (Faith, 1992). It has gained recognition from its use in prioritising terrestrial conservation areas (e.g. Forest *et al.*, 2007; Jetz *et al.*, 2014). The range-weighted variant of PD, phylogenetic endemism (PE) identifies geographic concentrations of phylogenetically and geographically restricted species (Rosauer *et al.*, 2009). PE not only estimates the degree to which phylogenetic diversity is captured by a clade, but also how much of the clade is restricted in a geographical location. PE was measured by multiplying each branch length by the fraction of its range found within a given area (Rosauer *et al.*, 2009). Species endemism was calculated using Crisp's *et al.* (2001) corrected weighted endemism (CWE) which represents endemism as counts of species in a grid cell by the inverse of their range size, weighted over total richness.

The evolutionary distinctiveness and global endangerment (EDGE) metric was measured by calculating the evolutionary distinctiveness (ED) score of each species, i.e. the degree of phylogenetic isolation, and combining it with global endangerment (GE) from IUCN conservation threat categories (Isaac *et al.*, 2007). The EDGE metric is expressed as:

$$\text{EDGE} = \ln(1 + \text{ED}) + \text{GE} * \ln(2)$$

where GE is the probability of extinction based on the following IUCN threat categories: Least Concern = 0, Near Threatened and Conservation Dependent = 1, Vulnerable = 2, Endangered = 3, and Critically Endangered = 4 (Purvis *et al.*, 2005).

As phylogenetic metrics are often expressed in units of time, and species richness and endemism in space, we standardized all metrics by representing their attributes across grid cells where they occur to identify hotspots. CWE, PD, PE and SR were calculated using BIODIVERSE (Laffan *et al.*, 2010). All other analyses were performed using R (R Core Team, 2013).

Statistical analysis

For each metric, we defined hotspots as the top 2.5% of grid cells, following a commonly used method in the geographical assessment of biodiversity (Orme *et al.*, 2005; Ceballos & Ehrlich, 2006; Daru *et al.*, 2015). Relationships among the diversity measures were tested by applying spatial autoregressive models using Moran's I statistic to correct for geographic dependence of the variables, computed using SAM v.4.0 software (Rangel *et al.*, 2010).

Complementary sites for species richness were selected by choosing the richest cell, and subsequently adding cells based on richness of the unrepresented cells until all species are captured at least once (Vane-Wright *et al.*, 1991). Complementary PD sites were chosen in a similar manner, capturing all branch lengths at least once in as small a subset of sites as possible (Faith *et al.*, 2004).

The performance of the current MPA network was assessed by overlaying hotspots and complementary areas onto GIS base maps of MPAs from the World

Database on Protected Areas (IUCN & UNEP-WCMC, 2015); all grid cells included within MPAs were identified. A cell was considered protected when at least 50% of its area was within an MPA.

RESULTS

Species richness for both groups of coastal macrophytes is unevenly distributed across the globe, revealing the classic latitudinal gradient with higher richness in the tropics than temperate regions (Fig. S3 in Appendix S1 in Supporting Information). The Central Indo-Pacific region is particularly species rich with a maximum richness of 22 seagrass and 37 mangrove species per $1^{\circ} \times 1^{\circ}$ grid cell (Fig. S3 in Appendix S1).

The five types of hotspots for each aquatic macrophyte showed varying degrees of spatial congruence (Figs. S4 and S5 in Appendix S1). Seagrasses shared only 6% (26 out of 430) of hotspot cells among all five metrics (Fig. 1a), and no grid cells were identified by all five diversity metrics as hotspots for mangroves. All diversity measures were positively correlated, but with variation in the strength of the positive relationship ranging from $r = 0.44$ (for CWE vs SR) to 0.99 (PD vs EDGE) in the spatial autoregressive models for seagrasses (Table 1), and from 0.61 for EDGE vs SR, to 0.99 for EDGE vs PD in mangroves (Table 2). Cumulatively, marine macrophytes occurred in 16 hotspots covering 606 grid cells ($\approx 7,500,000 \text{ km}^2$, Fig. 2 and Table S4 in Appendix S1) for all five metrics combined together. Separately, seagrass hotspots occupied $5,329,000 \text{ km}^2$ (6.5% of the global distribution of seagrass species; Fig. 3a), while mangrove hotspots covered $2,379,000 \text{ km}^2$ (6% of the total mangrove area; Fig. 3b).

The effectiveness of the current MPA network at representing the hotspots differs between diversity metrics and the two macrophyte groups (Fig. 4). In general, seagrass hotspots and complementary areas are better protected than those of mangroves. For example, whereas hotspots and complementary areas of seagrass diversity measures have protection exceeding 60%, mangrove hotspots of SR, PD, and SR-complementarity do not have any protection in the current network of MPAs (Fig. 4).

Complementarity analysis of PD and SR showed that all seagrass species could be represented at least once in a selection of 19 grid cells (235,000 km²; Fig. 5a), and complementary PD in 13 cells (161,000 km²; Fig. 5b). Complementary SR cells of mangrove species could be represented in five cells (61,000 km²; Fig. 5c), and all their complementary phylogenetic branch lengths captured in only three cells (37,000 km²; Fig. 5d). Several locations are identified repeatedly by these analyses, suggesting their greater conservation priority; for example SW Australia, NW America and southern Japan. In all cases, complementary selection of cells performed significantly more efficiently than random selection of sites (Fig. S6 in Appendix S1).

DISCUSSION

Marine plant species richness and phylogenetic diversity are inadequately protected by current MPAs, a conservation challenge that is aggravated by the different diversity metrics showing little spatial congruence. As a result, conserving additional sites might, for example, improve the representation of species within the MPA network but have little benefit for the conservation of evolutionary distinctiveness or phylogenetic diversity. However, by incorporating phylogenetic information in hotspot analyses and

using complementarity techniques, gaps at the species- and phylogenetic-level in the conservation network can be identified and efficiently addressed. Improved conservation of these marine plants must be a priority given their keystone roles in the marine realm (Costanza *et al.*, 1997), along with their impacts extending far beyond their spatial extent (e.g. acting as nursery grounds for fish populations, supporting fisheries beyond their geographical boundaries; Beck *et al.*, 2001; Green & Short, 2003).

While phylogenetic diversity has been incorporated into terrestrial biodiversity conservation planning (e.g. Jetz *et al.*, 2014; Zupan *et al.*, 2014), this study represents the first integrative application of recently developed diversity metrics in the marine realm. The five diversity measures examined here showed a high degree of spatial incongruence for seagrasses and mangroves, with very few hotspots shared among all (or even most) diversity metrics, reflecting similar patterns as observed for terrestrial species (e.g. Devictor *et al.*, 2010; Zupan *et al.*, 2014), particularly terrestrial plants (e.g. Daru *et al.*, 2015). Thus, if the conservation goal is the protection of centres of seagrass species endemism, efforts should be focused in Hawaii, Central Chile and Temperate Australasia. However, these efforts would do little to improve the protection of mangroves species endemism (highest in Mesoamerica) or phylogenetic endemism (focused in the Central Indo-Pacific for mangroves and Temperate Australasia for seagrasses). Therefore, conservation planning cannot assume that one diversity metric can act as a surrogate for the others, necessitating an integrative approach to maximize protection of both phylogenetic diversity and species diversity.

Complementarity methods for PD and SR are efficient in capturing diversity, ensuring maximum representation of all species or branch lengths within the smallest

possible area. For instance, mangroves species are completely captured in only five complementary cells (<1% of mangrove area), and PD in three complementary cells, matching findings from terrestrial systems that careful selection of additional conservation areas can greatly improve conservation network representativeness (e.g. Pollock *et al.*, 2015). Although complementary methods have drawbacks – e.g. that sites are often distant from existing protected areas, potentially reducing connectivity among reserve networks – representing all species and/or branch lengths in a small area is a pragmatic conservation priority given high rates of coastal marine habitat loss (Waycott *et al.*, 2009). We therefore propose a two-pronged strategy when selecting protected areas, using complementarity analyses to ensure complete representation, in tandem with the identification of hotspot cells that improve the connectivity of conservation areas.

We show that analysing evolutionary diversity (including PD, PE and EDGE) provides additional information about the evolutionary history of taxa and the feature diversity (traits) they comprise. This information is not adequately captured by species-level metrics (although see Li *et al.*, 2015) and is relevant to policy makers (Laity *et al.*, 2015). Indeed, the conservation of the marine macrophytes phylogenetic diversity maximizes future options (*sensu* Forest *et al.*, 2007), contributing to ensuring the long-term provisioning of ecosystem services (e.g. medicinal compounds for humans and nursery grounds for fisheries). In addition, identifying areas with higher or lower phylogenetic diversity than expected could reveal theatres of unusual evolutionary events, highlighting regions of particular conservation value with evolutionarily old or young lineages or centres of speciation (Winter *et al.*, 2013; Laity *et al.*, 2015). Thus, the spatial incongruence observed among the macrophytes evolutionary metrics and species-

level metrics illustrates the opportunities available to conservation planners and policy makers in protecting both species diversity and phylogenetic diversity. While the addition of phylogenetic information into conservation planning may complicate some prioritization decisions (e.g. how to weight PD relative to SR), we believe that the explicit consideration of the evolutionary history (and adaptive potential) of lineages allows for more informed and, potentially, more comprehensive planning.

Our approach identified global conservation priorities for macrophytes, a group that is only incidentally included within MPAs, and highlights the need to incorporate other phylogenetic branches of the marine tree of life when designating future MPAs. Specifically, taxa occurring abundantly and richly in cold waters (as opposed to macrophytes and coral reef species) and with functional traits different from taxa already considered (e.g., benthic and/or decomposer taxa) are likely to provide the most unique data, and should therefore be targeted as a priority for inclusion in subsequent analyses. Because the marine macrophytes examined in this study occur in the coastal regions of the world, our results indicate near-shore conservation priorities. Off-shore conservation planning would also benefit from the consideration of widely distributed taxa, including marine mammals (Pompa *et al.*, 2011) and lobsters (Williams, 1986), using these integrative methods.

Our approach incorporates traditional taxonomic metrics such as CWE and SR, along with evolutionary metrics such as PD, PE and EDGE, and offers a powerful means of identifying conservation areas in need of protection, which lie outside the existing MPA network. Conservation decision-making can be guided by such integrative

approach when designing marine reserves to ensure maximum protection of areas of high diversity and unique evolutionary history.

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SUPPORTING INFORMATION

Additional supporting information may be found in the online version of this article at the publisher's web-site.

Appendix S1 Supporting tables (Table S1–S4) and figures (Figs S1–S6).

Barnabas H. Daru is a Lecturer in the Department of Plant Science at University of Pretoria, South Africa. His research integrates ecology, biogeography and conservation biology, mostly using phylogenetic comparative methods and spatial statistical modeling.

Peter C. le Roux is interested in the determinants of species ranges and the influence of biotic interactions on the ecological consequences of climate change.

Table 1: Pairwise correlation of seagrass diversity metrics after accounting for spatial autocorrelation using spatial autoregressive models. The correlation coefficients (r) are indicated. ** P < 0.001, * P < 0.01, NS P > 0.05. SR species richness, PD phylogenetic diversity, CWE corrected weighted endemism, PE phylogenetic endemism, EDGE evolutionary distinctiveness and global endangerment.

	PD	CWE	PE	EDGE
SR	0.93**	0.44*	0.65**	0.99**
PD		0.41 ^{NS}	0.71**	0.99**
CWE			0.73**	0.42 ^S
PE				0.61**

Table 2: Pairwise correlation of mangrove diversity metrics after accounting for spatial autocorrelation using spatial autoregressive models. The correlation coefficients (r) are indicated. ** P < 0.001, * P < 0.01, NS P > 0.05. SR species richness, PD phylogenetic diversity, CWE corrected weighted endemism, PE phylogenetic endemism, EDGE evolutionary distinctiveness and global endangerment.

	PD	CWE	PE	EDGE
SR	0.95*	0.89 ^{NS}	0.95**	0.61**
PD		0.89 ^{NS}	0.95**	0.99**
CWE			0.67**	0.41 ^{NS}
PE				0.86**

Figure legends

Fig. 1. Venn diagram of spatial overlap among five types of hotspots, indicating the proportion of hotspot cells shared by all five metrics and the proportion of hotspot cells unique to each metric. (a) seagrasses, (b) mangroves. SR = species richness, PD = phylogenetic diversity, CWE = corrected weighted endemism, PE = phylogenetic endemism, EDGE = evolutionary distinctiveness and global endangerment. The phylogenetic trees used for computing the evolutionary metrics are derived from BEAST analysis and represent the 50% majority rule consensus tree for mangroves, and maximum clade credibility tree for seagrasses.

Fig. 2. Global marine plant diversity hotspots. The hotspots are the top 2.5% grid cells (shown in red) derived from a combination of five measures of diversity; species richness, phylogenetic diversity, species endemism, phylogenetic endemism, and evolutionary distinctiveness and global endangerment, for seagrass and mangrove species combined. The map was generated using Equal Behrmann Projection. The phylogenetic trees used for computing the evolutionary metrics are derived from BEAST analysis and represent the 50% majority rule consensus tree for mangroves, and maximum clade credibility tree for seagrasses.

Fig. 3. Union map of hotspots derived from the combination of species richness, phylogenetic endemism, species endemism, phylogenetic endemism, and evolutionary distinctiveness and global endangerment. (a) seagrass species (b) mangrove species. The richest 2.5% hotspots cells are shown in red, and the 5.0% hotspots in yellow.

Fig. 4. Degree of *in situ* protection of marine plants diversity measures within existing Marine Protected areas (black = proportion of hotspot cells represented within marine protected areas).

Fig. 5. Distribution of complementarity grid cells using a greedy algorithm that maximally represents species richness (red cells) and phylogenetic diversity (blue cells) in as few grid cells as possible; (a and b) seagrasses, (c and d) mangroves. The phylogenetic trees used for computing the evolutionary metrics are derived from BEAST analysis and represent the 50% majority rule consensus tree for mangroves, and maximum clade credibility tree for seagrasses.

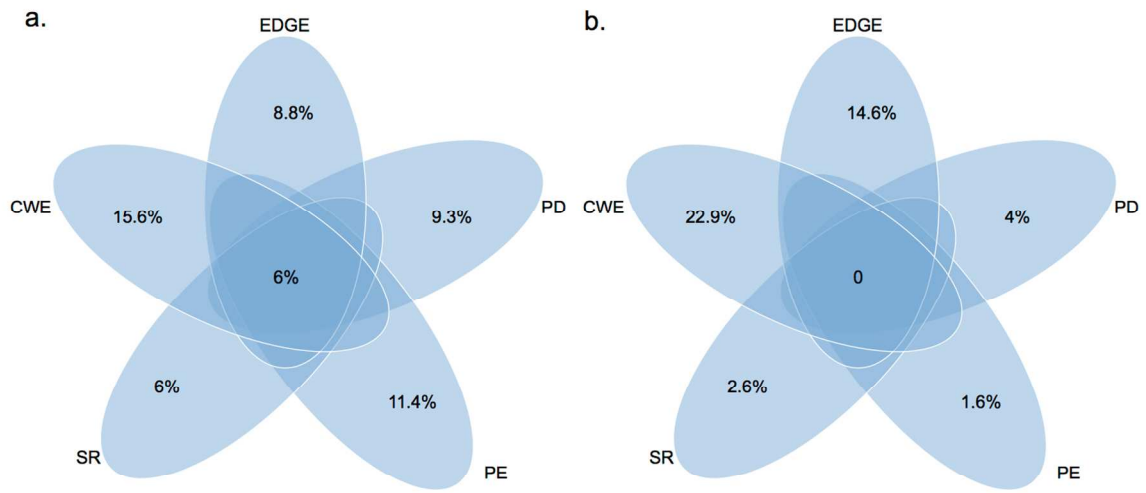


Fig. 1

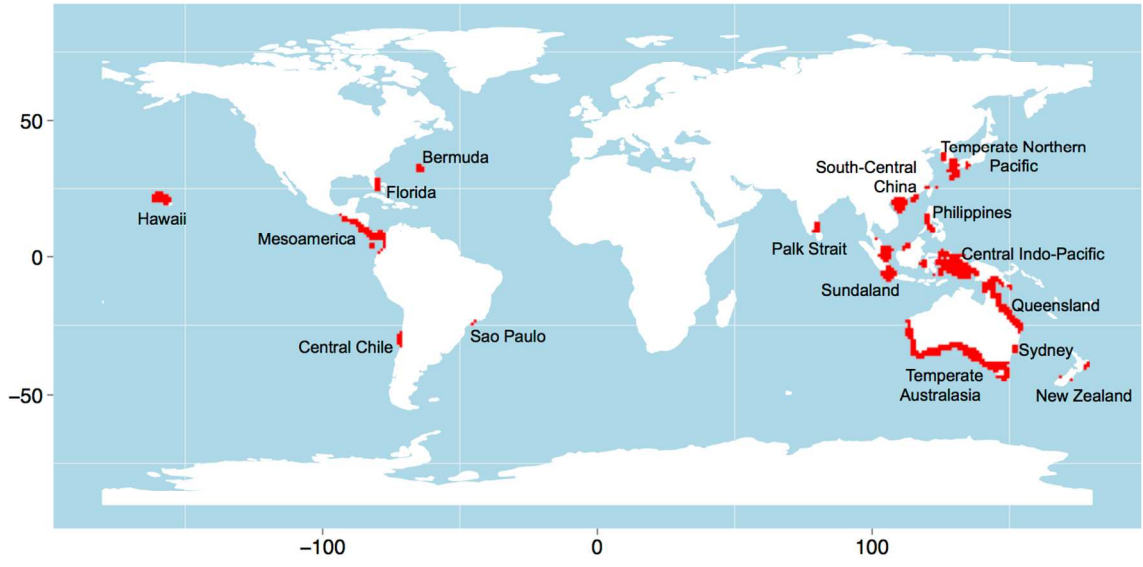


Fig. 2

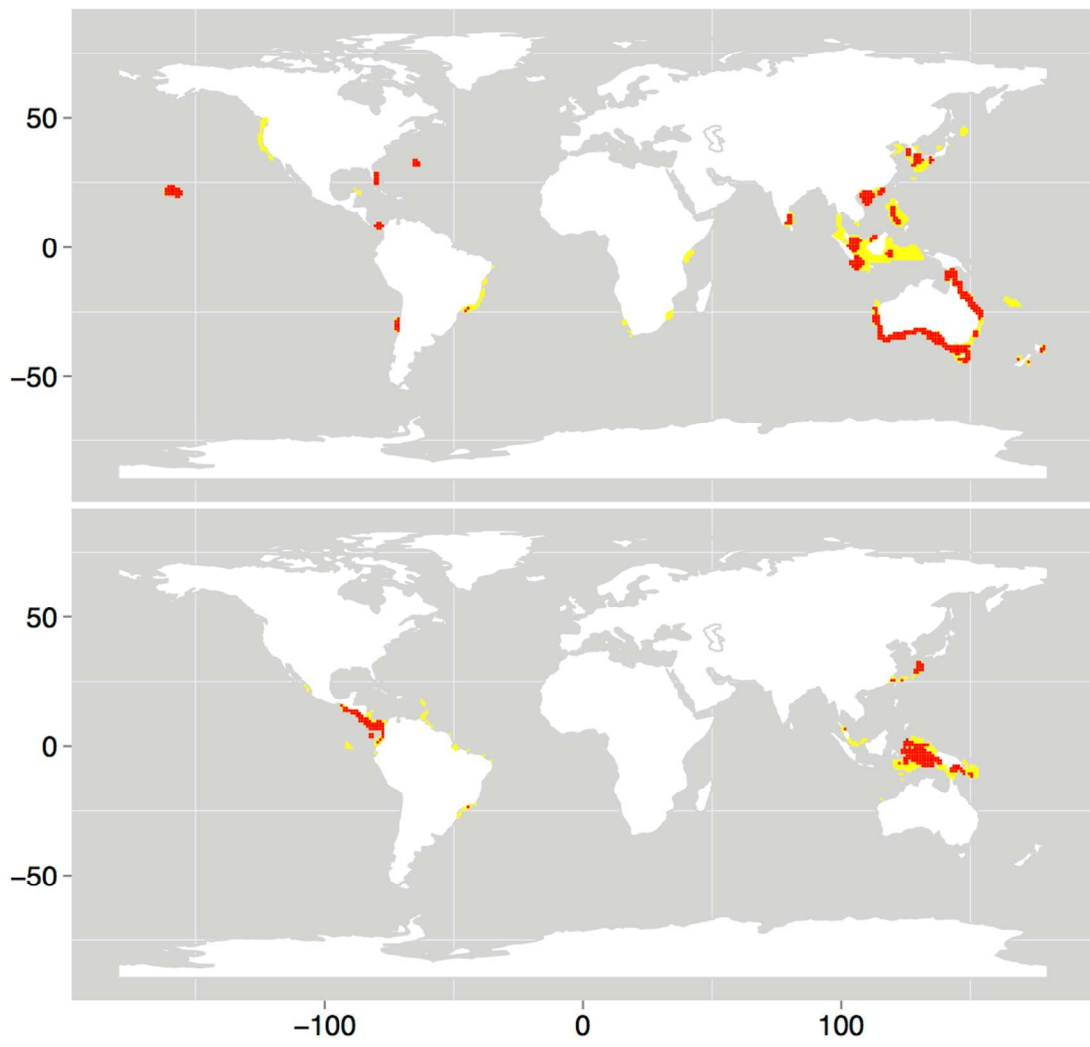


Fig. 3

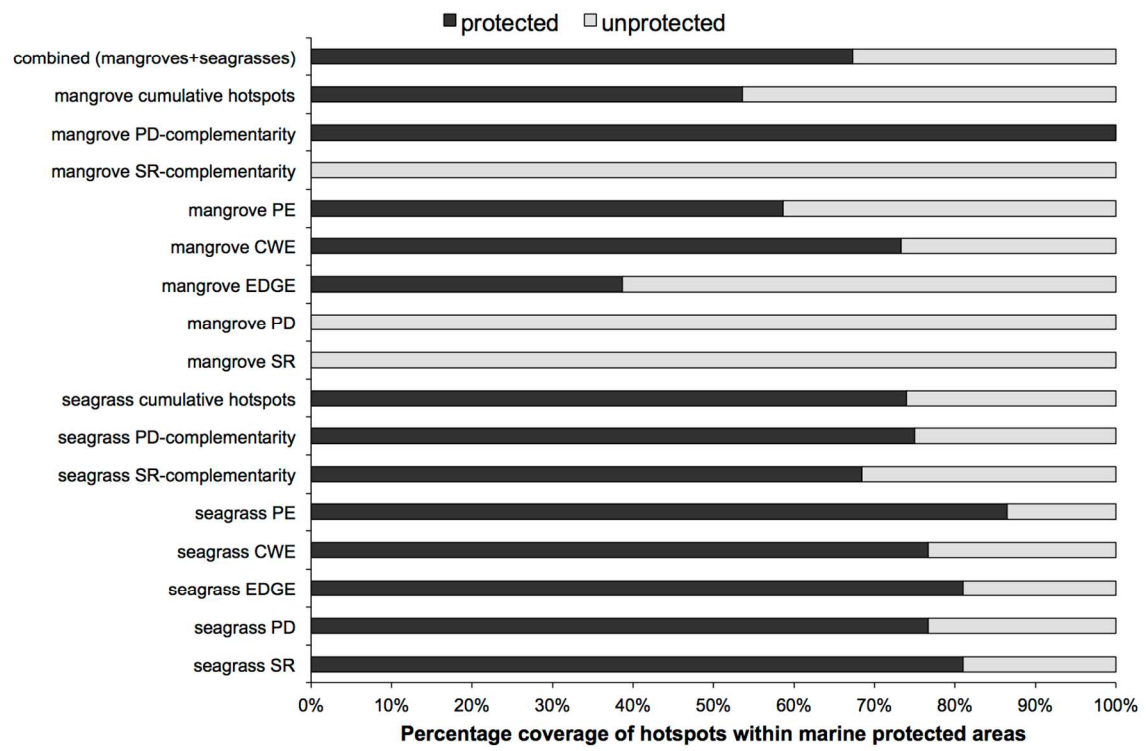


Fig. 4

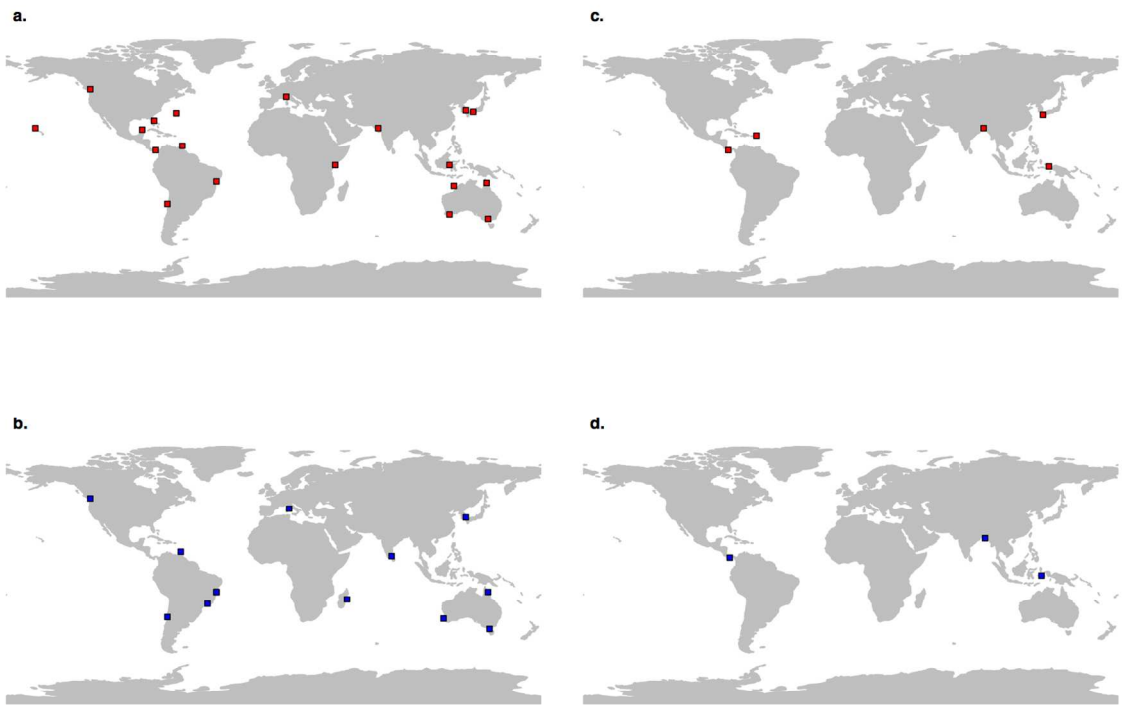


Fig. 5

Global Ecology and Biogeography
SUPPORTING INFORMATION

Marine protected areas are insufficient to conserve global marine plant diversity

Barnabas H. Daru and Peter C. le Roux

Appendix S1 Supporting tables (Table S1–S4) and figures (Figs S1–S6).

Table S1. List of seagrass taxa included in phylogeny with GenBank accession numbers. Missing sequences are indicated with a dash in the relevant position.

Taxon Author	Family APG	GenBank ITS	GenBank 18S	GenBank <i>rbcL</i>
<i>Amphibolis antarctica</i> (Labill.) Asch.	Cymodoceaceae	–	–	U80686
<i>Amphibolis griffithii</i> (J.M.Black) Hartog	Cymodoceaceae	–	–	HQ901574
<i>Cymodocea nodosa</i> (Ucria) Asch.	Cymodoceaceae	AF102272	–	U80688
<i>Cymodocea rotundata</i> Asch. & Schweinf.	Cymodoceaceae	–	JN034102	JQ031763
<i>Cymodocea serrulata</i> (R.Br.) Asch. & Magnus	Cymodoceaceae	–	–	U80687
<i>Enhalus acoroides</i> (L.f.) Royle	Hydrocharitaceae	AY870347	AY952403	AB004889
<i>Halodule beaudettei</i> (Hartog) Hartog	Cymodoceaceae	–	–	U80689
<i>Halodule pinifolia</i> (Miki) Hartog	Cymodoceaceae	–	–	U80690
<i>Halodule uninervis</i> (Forssk.) Boiss.	Cymodoceaceae	–	AY952401	AB571210
<i>Halodule wrightii</i> Asch.	Cymodoceaceae	–	–	HQ901575
<i>Halophila australis</i> Doty & B.C.Stone	Hydrocharitaceae	AF366414	–	–
<i>Halophila beccarii</i> Asch.	Hydrocharitaceae	AF366441	–	JN225339
<i>Halophila decipiens</i> Ostenf.	Hydrocharitaceae	AF395673	–	U80698
<i>Halophila euphlebia</i> Makino	Hydrocharitaceae	AB243968	–	–
<i>Halophila hawaiiiana</i> Doty & B.C.Stone	Hydrocharitaceae	AF366426	–	–
<i>Halophila johnsonii</i> Eiseman	Hydrocharitaceae	AF366425	–	–
<i>Halophila minor</i> (Zoll.) Hartog	Hydrocharitaceae	AF366406	–	JN225347

<i>Halophila nipponica</i> J.Kuo	Hydrocharitaceae	HQ687164	–	–
<i>Halophila ovalis</i> (R.Br.) Hook.f.	Hydrocharitaceae	AF366434	AY952400	AB004890
<i>Halophila spinulosa</i> (R.Br.) Asch.	Hydrocharitaceae	AF366440	–	–
<i>Halophila stipulacea</i> (Forssk.) Asch.	Hydrocharitaceae	AY352637	–	JN225356
<i>Halophila tricostata</i> M.Greenway	Hydrocharitaceae	AF366438	–	–
<i>Lepilaena australis</i> J.Drumm. ex Harv.	Potamogetonaceae	–	–	U80729
<i>Phyllospadix iwatensis</i> Makino	Zosteraceae	JQ766110	HQ660595	–
<i>Phyllospadix scouleri</i> Hook.	Zosteraceae	–	–	DQ859172
<i>Phyllospadix torreyi</i> S.Watson	Zosteraceae	AY077985	–	U80731
<i>Posidonia angustifolia</i> Cambridge & J.Kuo	Posidoniaceae	GQ927719	–	–
<i>Posidonia australis</i> Hook.f.	Posidoniaceae	GQ927720	–	HQ901573
<i>Posidonia coriacea</i> Cambridge & J.Kuo	Posidoniaceae	GQ927721	–	–
<i>Posidonia denhartogii</i> J.Kuo & Cambridge	Posidoniaceae	GQ927722	–	–
<i>Posidonia kirkmanii</i> J.Kuo & Cambridge	Posidoniaceae	GQ927724	–	–
<i>Posidonia oceanica</i> (L.) Delile	Posidoniaceae	GQ927725	AY491942	U80719
<i>Posidonia ostenfeldii</i> Hartog	Posidoniaceae	GQ927726	–	–
<i>Posidonia sinuosa</i> Cambridge & J.Kuo	Posidoniaceae	GQ927727	–	–
<i>Ruppia cirrhosa</i> (Petagna) Grande	Ruppiaceae	JQ034335	–	JN113277
<i>Ruppia maritima</i> L.	Ruppiaceae	JN034094	JN034103	HQ901576
<i>Ruppia megacarpa</i> R.Mason	Ruppiaceae	JQ034337	–	JQ034324

<i>Ruppia polycarpa</i> R.Mason	Ruppiaceae	–	–	AB507898
<i>Ruppia tuberosa</i> J.S.Davis & Toml.	Ruppiaceae	–	–	AB507899
<i>Syringodium filiforme</i> Kütz.	Cymodoceaceae	–	AF168876	U03727
<i>Syringodium isoetifolium</i> (Asch.) Dandy	Cymodoceaceae	–	–	U80691
<i>Thalassia hemprichii</i> (Ehrenb. ex Solms) Asch.	Hydrocharitaceae	–	AY952386	AB004897
<i>Thalassia testudinum</i> Banks & Sol. ex K.D.Koenig	Hydrocharitaceae	AY870348	AF168878	HQ901568
<i>Thalassodendron ciliatum</i> (Forssk.) Hartog	Cymodoceaceae	–	–	U80692
<i>Thalassodendron pachyrhizum</i>	Cymodoceaceae	–	–	U80692
<i>Zostera asiatica</i> Hartog	Zosteraceae	EF198347	–	AB125352
<i>Zostera caespitosa</i> Miki	Zosteraceae	JQ937100	–	AB125351
<i>Zostera capensis</i> Setch.	Zosteraceae	JQ937097	–	AM235166
<i>Zostera caulescens</i> Miki	Zosteraceae	JQ937099	–	AB125350
<i>Zostera japonica</i> Asch. & Graebn.	Zosteraceae	JQ766111	–	AB125353
<i>Zostera marina</i> L.	Zosteraceae	JN034095	HQ445940	AB125349
<i>Zostera muelleri</i> Irmisch ex Asch.	Zosteraceae	AY078004	–	AY077962
<i>Zostera noltii</i> Hornem.	Zosteraceae	AY077992	AF207058	U80733
<i>Zostera pacifica</i> S.Watson	Zosteraceae	EF198348	–	–
<i>Zostera tasmanica</i> M.Martens ex Asch.	Zosteraceae	AY077990	–	U80730
Outgroups				
<i>Alocasia cucullata</i> (Lour.) G.Don	Araceae	AB429340	–	JQ237188

<i>Alocasia macrorrhizos</i> (L.) G.Don	Araceae	–	–	JF828103
<i>Alocasia odora</i> (Lindl.) K.Koch	Araceae	AF469030	–	JQ933213
<i>Alocasia sandariana</i> W.Bull	Araceae	–	–	EU193192
<i>Harperocallis flava</i> McDaniel	Tofieldiaceae	AB541108	–	HQ901586
<i>Tofieldia furusei</i> (Hiyama) M.N.Tamura & Fuse	Tofieldiaceae	AB561187	–	–

Table S2. Summary of priors and uncorrelated lognormal relaxed molecular clock BEAST analysis of seagrass species.

Summary Statistic	mean	stderr of		variance	median	95% HPD Interval	auto-	effective
		mean	stdev				correlation	sample size
							time (ACT)	(ESS)
posterior	-48441.2051	0.2866	13.7369	188.7034	-48440.8984	[-48468.1813, -48414.3191]	78374.5785	2296.6886
prior	-888.0255	0.2446	5.6093	31.4642	-887.8744	[-898.8736, -876.9262]	3.42E+05	525.8441
likelihood	-47553.1796	0.1813	12.4859	155.8967	-47552.8452	[-47577.7934, -47529.0036]	37936.0129	4744.8845
treeModel.rootHeight	367.1544	0.5018	12.6266	159.432	364.4882	[361.1534, 383.2016]	2.84E+05	633.2052
tmrca(Alismatales)	128.0338	6.24E-03	0.9889	0.9778	128.0333	[126.1092, 129.991]	7162.0606	25132.711
tmrca(Alocasia)	19.1236	6.00E-03	0.8092	0.6548	19.1296	[17.5599, 20.7165]	9908.947	18165.6032
tmrca(Cymodoceae)	60.7706	6.80E-03	1.0014	1.0029	60.77	[58.8043, 62.7381]	8296.7159	21695.5725
tmrca(Hydrocharitaceae)	74.9883	6.68E-03	0.9998	0.9996	74.987	[73.0153, 76.9355]	8026.6067	22425.666
tmrca(Tofieldiaceae)	99.9251	5.84E-03	0.999	0.9981	99.924	[97.995, 101.9071]	6160.8399	29217.1201
tmrca(Zosteraceae)	17.6572	0.0101	0.96	0.9216	17.6565	[15.8041, 19.5486]	20007.8571	8996.5657
yule.birthRate	0.0239	4.36E-05	2.25E-03	5.07E-06	0.0238	[0.0195, 0.0283]	67467.6505	2667.9749
ac	0.2964	2.68E-04	0.0179	3.21E-04	0.296	[0.2608, 0.3308]	40402.8656	4455.179
ag	0.6749	6.48E-04	0.038	1.45E-03	0.6741	[0.6032, 0.7513]	52317.5909	3440.5636
at	0.2694	1.89E-04	0.0168	2.84E-04	0.269	[0.2368, 0.3027]	22595.9198	7966.1285
cg	0.3409	7.29E-04	0.0197	3.90E-04	0.3403	[0.3035, 0.3807]	2.45E+05	734.08
gt	0.3438	1.64E-04	0.0174	3.04E-04	0.3433	[0.3095, 0.3781]	15942.9765	11290.3635
frequencies1	0.2314	7.95E-05	4.96E-03	2.46E-05	0.2315	[0.2215, 0.2409]	46227.6255	3893.8189
frequencies2	0.2674	8.26E-05	4.59E-03	2.11E-05	0.2674	[0.2585, 0.2765]	58184.9403	3093.6184
frequencies3	0.2583	6.76E-05	4.69E-03	2.20E-05	0.2583	[0.2492, 0.2674]	37405.9071	4812.1277
frequencies4	0.2428	1.39E-04	4.78E-03	2.28E-05	0.2428	[0.2338, 0.2523]	1.53E+05	1180.1965

alpha	0.2024	2.13E-04	4.26E-03	1.82E-05	0.2024	[0.194, 0.2107]	4.49E+05	401.1294
uclid.mean	2.64E-03	1.25E-05	2.15E-04	4.62E-08	2.63E-03	[2.2465E-3, 3.0805E-3]	6.07E+05	296.7538
uclid.stdev	0.7542	2.67E-03	0.0606	3.67E-03	0.7511	[0.639, 0.875]	3.48E+05	516.5355
meanRate	2.43E-03	4.68E-06	1.10E-04	1.21E-08	2.43E-03	[2.219E-3, 2.649E-3]	3.25E+05	553.5653
coefficientOfVariation	0.8523	2.78E-03	0.0826	6.82E-03	0.8446	[0.6998, 1.0185]	2.04E+05	880.9841
covariance	0.0533	1.74E-03	0.063	3.97E-03	0.0507	[-0.0668, 0.1769]	1.38E+05	1306.2967
treeLikelihood	-47553.1796	0.1813	12.4859	155.8967	-47552.8452	[-47577.7934, -47529.0036]	37936.0129	4744.8845
speciation	-626.7371	0.2454	4.9681	24.6823	-626.6838	[-636.6009, -617.1658]	4.39E+05	409.8593

Table S3. List of mangrove taxa included in phylogeny with GenBank accession numbers. Missing sequences are indicated with a dash in the relevant position.

Taxon Author	Family APG	GenBank 18S	GenBank <i>rbcL</i>	GenBank ITS
<i>Abroma augustum</i> (L.) L. f	Lythraceae	–	AJ012208	AJ277462
<i>Acanthus ebracteatus</i> Vahl	Acanthaceae	AY289642	AY289682	–
<i>Acanthus ilicifolius</i> L.	Acanthaceae	–	–	GQ141552
<i>Acrostichum aureum</i> L.	Pteridaceae	–	AB574794	–
<i>Acrostichum danaeifolium</i> (Fée) C. Presl	Pteridaceae	–	EF452129	–
<i>Acrostichum speciosum</i> (Fée) C. Presl	Pteridaceae	–	AB246707	–
<i>Aegialitis annulata</i> R.Br.	Plumbaginaceae	AY289640	AJ312252	–
<i>Aegiceras corniculatum</i> (L.) Blanco	Myrsinaceae	AY671951	U96653	FJ976669
<i>Aglaia cucullata</i> (Roxb.) Pellegr.	Meliaceae	–	JF738768	AY695572
<i>Avicennia alba</i> Blume	Avicenniaceae	–	AY008831	EF540977
<i>Avicennia bicolor</i> Standl.	Avicenniaceae	–	AY008829	EF540989
<i>Avicennia germinans</i> (L.) L.	Avicenniaceae	–	AY008830	DQ469860
<i>Avicennia marina</i> (Forssk.) Vierh.	Avicenniaceae	AY289641	AY289681	EF540978
<i>Avicennia schaueriana</i> Stapf & Leechm. ex Moldenke	Avicenniaceae	–	–	EF540986
<i>Brownlowia tersa</i> (L.) Kosterm.	Lythraceae	–	AJ233147	–

<i>Bruguiera cylindrica</i> (L.) Blume	Rhizophoraceae	–	AF127694	HM366080
<i>Bruguiera exaristata</i> Ding Hou	Rhizophoraceae	–	AF127695	AF130335
<i>Bruguiera gymnorhiza</i> (L.) Lam.	Rhizophoraceae	AF206875	DQ659092	HM366108
<i>Bruguiera hainesii</i> C.G.Rogers	Rhizophoraceae	–	–	EU000399
<i>Bruguiera parviflora</i> (Roxb.) Wight & Arn. ex Griff.	Rhizophoraceae	–	AF127692	HM366110
<i>Bruguiera sexangula</i> (Lour.) Poir.	Rhizophoraceae	AY289626	AF127691	HM366136
<i>Camptostemon schultzei</i> Mast.	Lythraceae	–	AF022120	HQ658360
<i>Ceriops australis</i> (C.T.White) Ballment, T.J.Sm. & J.A.Stoddart	Rhizophoraceae	–	AF127683	EF118998
<i>Ceriops decandra</i> (Griff.) W.Theob.	Rhizophoraceae	–	–	EF119014
<i>Ceriops tagal</i> (Perr.) C.B.Rob.	Rhizophoraceae	AY289624	AF127684	AF105083
<i>Ceriops zippeliana</i> Blume	Rhizophoraceae	–	–	EF119070
<i>Conocarpus erectus</i> L.	Combretaceae	AY289636	AF281477	AY050562
<i>Cynometra iripa</i> Kostel.	Fabaceae	AY289630	AY289677	–
<i>Diospyros littorea</i> (R.Br.) Kosterm.	Ebenaceae	–	EU980774	DQ499076
<i>Dolichandrone spathacea</i> (L.f.) Seem.	Bignoniaceae	AY289643	AY289683	–
<i>Excoecaria agallocha</i> L.	Euphorbiaceae	AY289628	AY794839	–
<i>Excoecaria indica</i> (Willd.) Müll.Arg.	Euphorbiaceae	AB233573	AB233885	GU441816
<i>Heritiera littoralis</i> Aiton	Lythraceae	AY289633	AY082358	AY083659

<i>Kandelia candel</i> (L.) Druce	Rhizophoraceae	AY289625	AF127682	AF105081
<i>Kandelia obovata</i> Sheue, H.Y. Liu & J. Yong	Rhizophoraceae	–	–	EU000402
<i>Laguncularia racemosa</i> (L.) C.F.Gaertn.	Combretaceae	AY289635	FJ381826	AF425685
<i>Lumnitzera littorea</i> (Jack) Voigt	Combretaceae	AY289637	AF425718	AF160468
<i>Lumnitzera racemosa</i> Willd.	Combretaceae	–	FJ381827	AF160467
<i>Nypa fruticans</i> Wurmb	Arecaceae	AY289649	M81813	–
<i>Osbornia octodonta</i> F.Muell.	Myrtaceae	–	–	EF041844
<i>Pelliciera rhizophorae</i> Planch. & Triana	Tetrameristaceae	AF206983	AF421099	AY452670
<i>Pemphis acidula</i> J.R. Forst.	Lythraceae	AY289639	AY036138	AY035762
<i>Rhizophora apiculata</i> Blume	Rhizophoraceae	–	AF127685	HQ337923
<i>Rhizophora mangle</i> L.	Rhizophoraceae	–	JX664070	HQ337957
<i>Rhizophora mucronata</i> Lam.	Rhizophoraceae	–	AF127687	HQ337953
<i>Rhizophora racemosa</i> G.Mey.	Rhizophoraceae	–	AF127690	HQ337960
<i>Rhizophora samoensis</i> (Hochr.) Salvoza	Rhizophoraceae	–	–	HQ337959
<i>Rhizophora stylosa</i> Griff.	Rhizophoraceae	AY289627	AF127686	HQ337941
<i>Sonneratia alba</i> Sm.	Lythraceae	–	GQ122038	AY680875
<i>Sonneratia apetala</i> Buch.-Ham.	Lythraceae	–	–	AF163697
<i>Sonneratia caseolaris</i> (L.) Engl.	Lythraceae	–	AY036143	AF420219
<i>Sonneratia ovata</i> Backer	Lythraceae	AY289638	AY036143	AF163702
<i>Tabebuia palustris</i> Hemsl.	Bignoniaceae	–	JQ590857	–

<i>Xylocarpus granatum</i> J. Koenig	Meliaceae	AY289634	AY289680	–
<i>Xylocarpus moluccensis</i> (Lam.) M. Roem.	Meliaceae	–	DQ238071	FJ518907
Outgroups				
<i>Amborella trichopoda</i> Baill.	Amborellaceae	U42497	L12628	–
<i>Ampelocissus thyrsoiflora</i> (Blume) Planch.	Vitaceae	–	AJ402919	–
<i>Ampelopsis megalophylla</i> Diels & Gilg	Vitaceae	–	AJ402920	–
<i>Bagassa guianensis</i> Aubl.	Moraceae	–	JQ625997	FJ917001
<i>Brosimum alicastrum</i> Sw.	Moraceae	–	AF500346	–
<i>Castilla elastica</i> Cerv.	Moraceae	–	AF500348	FJ916997
<i>Fontanesia phillyreoides</i> Labill.	Oleaceae	–	DQ673293	AF534816
<i>Jasminum simplicifolium</i> subsp. <i>suavissimum</i> (Lindl.) P.S.Green	Oleaceae	AJ236035	L01929	–
<i>Ligustrum vulgare</i> L.	Oleaceae	–	HQ384901	EU314901
<i>Naucleopsis guianensis</i> (Mildbr.) C.C. Berg	Moraceae	–	JQ626013	FJ037848
<i>Osmanthus americanus</i> (L.) A.Gray	Oleaceae	–	DQ673311	EF362761
<i>Picconia azorica</i> (Tutin) Knobl.	Oleaceae	–	HM850258	–
<i>Vitis rotundifolia</i> Michx.	Vitaceae	–	AF119174	–

Table S4: Characteristics of global diversity hotspots of marine plants.

Hotspot	Size of hotspot (km ²)	Species composition
Bermuda	8 (99,100)	<i>Avicennia germinans</i> , <i>Halodule bermudensis</i> , <i>Halodule wrightii</i> , <i>Halophila decipiens</i> , <i>Rhizophora mangle</i> , <i>Syringodium filiforme</i> , <i>Thalassia testudinum</i>
Central Chile	10 (123,900)	<i>Ruppia filifolia</i> , <i>Zostera chilensis</i>
Central Indo-Pacific	112 (1,387,900)	<i>Acanthus ebracteatus</i> , <i>Acanthus ilicifolius</i> , <i>Acrostichum aureum</i> , <i>Acrostichum speciosum</i> , <i>Aegialitis annulata</i> , <i>Aegiceras corniculatum</i> , <i>Aglaia cucullata</i> , <i>Avicennia alba</i> , <i>Avicennia marina</i> , <i>Brownlowia elata</i> , <i>Bruguiera cylindrica</i> , <i>Bruguiera exaristata</i> , <i>Bruguiera gymnorhiza</i> , <i>Bruguiera hainesii</i> , <i>Bruguiera parviflora</i> , <i>Bruguiera sexangula</i> , <i>Camptostemon schultzei</i> , <i>Ceriops australis</i> , <i>Ceriops tagal</i> , <i>Ceriops zippeliana</i> , <i>Cymodocea rotundata</i> , <i>Cymodocea serrulata</i> , <i>Cynometra iripa</i> , <i>Dolichandrone spathacea</i> , <i>Enhalus acoroides</i> , <i>Excoecaria agallocha</i> , <i>Halodule pinifolia</i> , <i>Halodule uninervis</i> , <i>Halophila beccarii</i> , <i>Halophila decipiens</i> , <i>Halophila minor</i> , <i>Halophila ovalis</i> , <i>Halophila ovata</i> , <i>Halophila spinulosa</i> , <i>Halophila sulawesii</i> , <i>Heritiera littoralis</i> , <i>Kandelia candel</i> , <i>Lumnitzera littorea</i> , <i>Lumnitzera racemosa</i> , <i>Nypa fruticans</i> , <i>Osbornia octodonta</i> , <i>Pemphis acidula</i> , <i>Rhizophora apiculata</i> , <i>Rhizophora mucronata</i> , <i>Rhizophora stylosa</i> , <i>Sonneratia alba</i> , <i>Sonneratia caseolaris</i> , <i>Sonneratia ovata</i> , <i>Syringodium isoetifolium</i> , <i>Thalassia hemprichii</i> , <i>Thalassodendron ciliatum</i> , <i>Xylocarpus</i>

		<i>granatum, Xylocarpus moluccensis</i>
Florida	10 (123,900)	<i>Acrostichum aureum, Acrostichum danaeifolium, Avicennia germinans, Conocarpus erectus, Halodule wrightii, Halophila decipiens, Halophila engelmanni, Halophila johnsonii, Laguncularia racemosa, Rhizophora mangle, Ruppia maritima, Syringodium filiforme, Thalassia testudinum.</i>
Hawaii	25 (309800)	<i>Halophila decipiens, Halophila hawaiiiana, Ruppia maritima,</i>
Mesoamerica	57 (706,400)	<i>Acrostichum aureum, Acrostichum danaeifolium, Avicennia bicolor, Avicennia germinans, Conocarpus erectus, Halodule ciliata, Halodule wrightii, Halophila decipiens, Laguncularia racemosa, Pelliciera rhizophorae, Rhizophora mangle, Rhizophora racemosa, Rhizophora samoensis, Ruppia maritima, Syringodium filiforme, Tabebuia palustris, Thalassia testudinum</i>
New Zealand	6 (74,400)	<i>Ruppia megacarpa, Ruppia tuberosa, Zostera muelleri</i>
Palk Strait	9 (111,500)	<i>Acanthus ilicifolius, Acrostichum aureum, Aegiceras corniculatum, Avicennia alba, Avicennia marina, Bruguiera cylindrica, Bruguiera gymnorrhiza, Bruguiera parviflora, Ceriops decandra, Ceriops tagal, Cymodocea rotundata, Cymodocea serrulata, Dolichandrone spathacea, Enhalus acoroides, Excoecaria agallocha, Halodule pinifolia, Halodule uninervis, Halodule wrightii, Halophila beccarii, Halophila decipiens, Halophila ovalis, Halophila ovata, Halophila stipulacea, Heritiera littoralis, Lumnitzera littorea, Lumnitzera racemosa, Nypa fruticans, Pemphis acidula, Rhizophora apiculata, Rhizophora mucronata, Sonneratia alba, Sonneratia apetala, Sonneratia caseolaris, Syringodium isoetifolium, Thalassia</i>

		<i>hemprichii</i> , <i>Thalassodendron ciliatum</i> , <i>Xylocarpus granatum</i>
Philippines	15 (185,900)	<i>Acanthus ebracteatus</i> , <i>Acanthus ilicifolius</i> , <i>Acrostichum aureum</i> , <i>Aegiceras corniculatum</i> , <i>Aglaia cucullata</i> , <i>Avicennia alba</i> , <i>Avicennia marina</i> , <i>Brownlowia elata</i> , <i>Bruguiera cylindrica</i> , <i>Bruguiera gymnorhiza</i> , <i>Bruguiera parviflora</i> , <i>Bruguiera sexangula</i> , <i>Ceriops tagal</i> , <i>Ceriops zippeliana</i> , <i>Cymodocea rotundata</i> , <i>Cymodocea serrulata</i> , <i>Cynometra iripa</i> , <i>Dolichandrone spathacea</i> , <i>Enhalus acoroides</i> , <i>Excoecaria agallocha</i> , <i>Halodule pinifolia</i> , <i>Halodule uninervis</i> , <i>Halophila beccarii</i> , <i>Halophila decipiens</i> , <i>Halophila minor</i> , <i>Halophila ovalis</i> , <i>Halophila spinulosa</i> , <i>Heritiera littoralis</i> , <i>Lumnitzera littorea</i> , <i>Lumnitzera racemosa</i> , <i>Nypa fruticans</i> , <i>Osbornia octodonta</i> , <i>Pemphis acidula</i> , <i>Rhizophora apiculata</i> , <i>Rhizophora mucronata</i> , <i>Rhizophora stylosa</i> , <i>Ruppia maritima</i> , <i>Sonneratia alba</i> , <i>Sonneratia caseolaris</i> , <i>Sonneratia ovata</i> , <i>Syringodium isoetifolium</i> , <i>Thalassia hemprichii</i> , <i>Thalassodendron ciliatum</i> , <i>Xylocarpus granatum</i> , <i>Xylocarpus moluccensis</i>
Queensland	82 (1,016,200)	<i>Acanthus ebracteatus</i> , <i>Acanthus ilicifolius</i> , <i>Acrostichum aureum</i> , <i>Acrostichum speciosum</i> , <i>Aegialitis annulata</i> , <i>Aegiceras corniculatum</i> , <i>Avicennia alba</i> , <i>Avicennia marina</i> , <i>Brownlowia elata</i> , <i>Bruguiera cylindrica</i> , <i>Bruguiera exaristata</i> , <i>Bruguiera gymnorhiza</i> , <i>Bruguiera hainesii</i> , <i>Bruguiera parviflora</i> , <i>Bruguiera sexangula</i> , <i>Camptostemon schultzei</i> , <i>Ceriops australis</i> , <i>Ceriops tagal</i> , <i>Ceriops zippeliana</i> , <i>Cymodocea rotundata</i> , <i>Cymodocea serrulata</i> , <i>Cynometra iripa</i> , <i>Dolichandrone spathacea</i> , <i>Enhalus acoroides</i> , <i>Excoecaria agallocha</i> , <i>Halodule pinifolia</i> , <i>Halodule uninervis</i> , <i>Halophila capricorni</i> , <i>Halophila decipiens</i> , <i>Halophila minor</i> , <i>Halophila ovalis</i> , <i>Halophila ovata</i> , <i>Halophila spinulosa</i> , <i>Halophila tricostata</i> , <i>Heritiera</i>

		<i>littoralis</i> , <i>Lepilaena australis</i> , <i>Lumnitzera littorea</i> , <i>Lumnitzera racemosa</i> , <i>Nypa fruticans</i> , <i>Osbornia octodonta</i> , <i>Pemphis acidula</i> , <i>Rhizophora apiculata</i> , <i>Rhizophora mucronata</i> , <i>Rhizophora stylosa</i> , <i>Ruppia maritima</i> , <i>Sonneratia alba</i> , <i>Sonneratia caseolaris</i> , <i>Sonneratia ovata</i> , <i>Syringodium isoetifolium</i> , <i>Thalassia hemprichii</i> , <i>Thalassodendron ciliatum</i> , <i>Xylocarpus granatum</i> , <i>Xylocarpus moluccensis</i> , <i>Zostera muelleri</i>
Sao Paulo	2 (24,800)	<i>Avicennia schaueriana</i> , <i>Halodule emarginata</i> , <i>Halodule wrightii</i> , <i>Laguncularia racemosa</i> , <i>Rhizophora mangle</i> , <i>Ruppia maritima</i>
South-Central China	36 (446,100)	<i>Acanthus ebracteatus</i> , <i>Acanthus ilicifolius</i> , <i>Acrostichum speciosum</i> , <i>Aegiceras corniculatum</i> , <i>Avicennia marina</i> , <i>Bruguiera cylindrica</i> , <i>Bruguiera gymnorrhiza</i> , <i>Bruguiera sexangula</i> , <i>Ceriops tagal</i> , <i>Ceriops zippeliana</i> , <i>Cymodocea rotundata</i> , <i>Cymodocea serrulata</i> , <i>Enhalus acoroides</i> , <i>Excoecaria agallocha</i> , <i>Halodule pinifolia</i> , <i>Halodule uninervis</i> , <i>Halophila beccarii</i> , <i>Halophila decipiens</i> , <i>Halophila minor</i> , <i>Halophila ovalis</i> , <i>Halophila ovata</i> , <i>Heritiera littoralis</i> , <i>Kandelia obovata</i> , <i>Lumnitzera littorea</i> , <i>Lumnitzera racemosa</i> , <i>Nypa fruticans</i> , <i>Pemphis acidula</i> , <i>Rhizophora apiculata</i> , <i>Rhizophora mucronata</i> , <i>Rhizophora stylosa</i> , <i>Ruppia maritima</i> , <i>Sonneratia alba</i> , <i>Sonneratia caseolaris</i> , <i>Sonneratia ovata</i> , <i>Syringodium isoetifolium</i> , <i>Thalassia hemprichii</i> , <i>Xylocarpus granatum</i> , <i>Zostera japonica</i>
Sundaland	48 (594,800)	<i>Acanthus ebracteatus</i> , <i>Acanthus ilicifolius</i> , <i>Acrostichum aureum</i> , <i>Acrostichum speciosum</i> , <i>Aegiceras corniculatum</i> , <i>Aglaiia cucullata</i> , <i>Avicennia alba</i> , <i>Avicennia marina</i> , <i>Brownlowia elata</i> , <i>Bruguiera cylindrica</i> , <i>Bruguiera exaristata</i> , <i>Bruguiera gymnorrhiza</i> , <i>Bruguiera hainesii</i> , <i>Bruguiera parviflora</i> , <i>Bruguiera sexangula</i> , <i>Ceriops tagal</i> , <i>Ceriops zippeliana</i> , <i>Cymodocea</i>

		<p><i>rotundata, Cymodocea serrulata, Cynometra iripa, Dolichandrone spathacea, Enhalus acoroides, Excoecaria agallocha, Halodule pinifolia, Halodule uninervis, Halophila beccarii, Halophila decipiens, Halophila minor, Halophila ovalis, Halophila ovata, Halophila spinulosa, Heritiera littoralis, Kandelia candel, Kandelia obovata, Lumnitzera littorea, Lumnitzera racemosa, Nypa fruticans, Osbornia octodonta, Pemphis acidula, Rhizophora apiculata, Rhizophora mucronata, Rhizophora stylosa, Ruppia maritima, Sonneratia alba, Sonneratia caseolaris, Sonneratia ovata, Syringodium isoetifolium, Thalassia hemprichii, Thalassodendron ciliatum, Xylocarpus granatum, Xylocarpus moluccensis</i></p>
Sydney	6 (74,400)	<p><i>Aegiceras corniculatum, Avicennia marina, Excoecaria agallocha, Halophila ovalis, Lepilaena australis, Posidonia australis, Ruppia megacarpa, Zostera muelleri, Zostera nigricaulis</i></p>
Temperate Australasia	143 (1,772,100)	<p><i>Amphibolis antarctica, Amphibolis griffithii, Avicennia marina, Cymodocea angustata, Cymodocea serrulata, Halodule pinifolia, Halodule uninervis, Halophila australis, Halophila decipiens, Halophila ovalis, Halophila ovata, Halophila spinulosa, Lepilaena australis, Lepilaena marina, Posidonia angustifolia, Posidonia australis, Posidonia coriacea, Posidonia denhartogii, Posidonia kirkmanii, Posidonia ostenfeldii, Posidonia sinuosa, Rhizophora stylosa, Ruppia maritima, Ruppia megacarpa, Ruppia polycarpa, Ruppia tuberosa, Syringodium isoetifolium, Thalassodendron ciliatum, Thalassodendron pachyrhizum, Zostera muelleri, Zostera nigricaulis, Zostera polycllamys, Zostera tasmanica,</i></p>

Temperate Northern Pacific	37 (458,500)	<i>Bruguiera gymnorhiza, Cymodocea rotundata, Cymodocea serrulata, Enhalus acoroides, Halodule pinifolia, Halodule uninervis, Halophila decipiens, Halophila euphlebia, Halophila minor, Halophila nipponica, Halophila ovalis, Kandelia obovata, Phyllospadix iwatensis, Phyllospadix japonicus, Rhizophora mucronata, Syringodium isoetifolium, Thalassia hemprichii, Zostera asiatica, Zostera caespitosa, Zostera caulescens, Zostera geojeensis, Zostera japonica, Zostera marina</i>
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Hotspots are based on five measures of diversity; species richness, phylogenetic diversity, species endemism, phylogenetic endemism, and evolutionary distinctiveness and global endangerment.

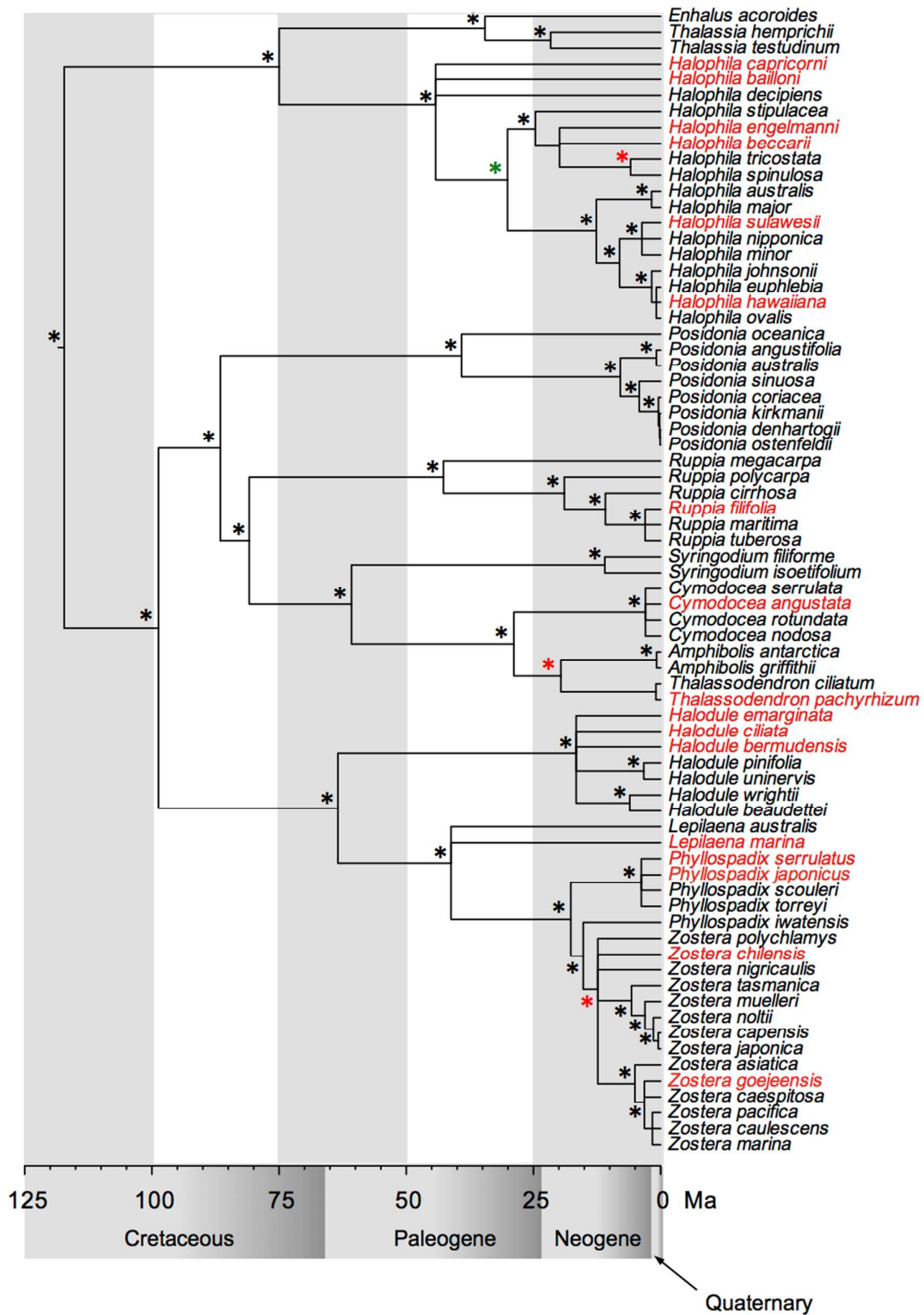


Figure S1. Results from divergence dating with BEAST for seagrass species obtained from a combined plastid and nuclear dataset. Stars at nodes indicate levels of support;

black: $PP > 0.99$, green $PP > 0.95$, red: $PP < 0.9$. Tip labels indicated in red are those with missing DNA sequences.

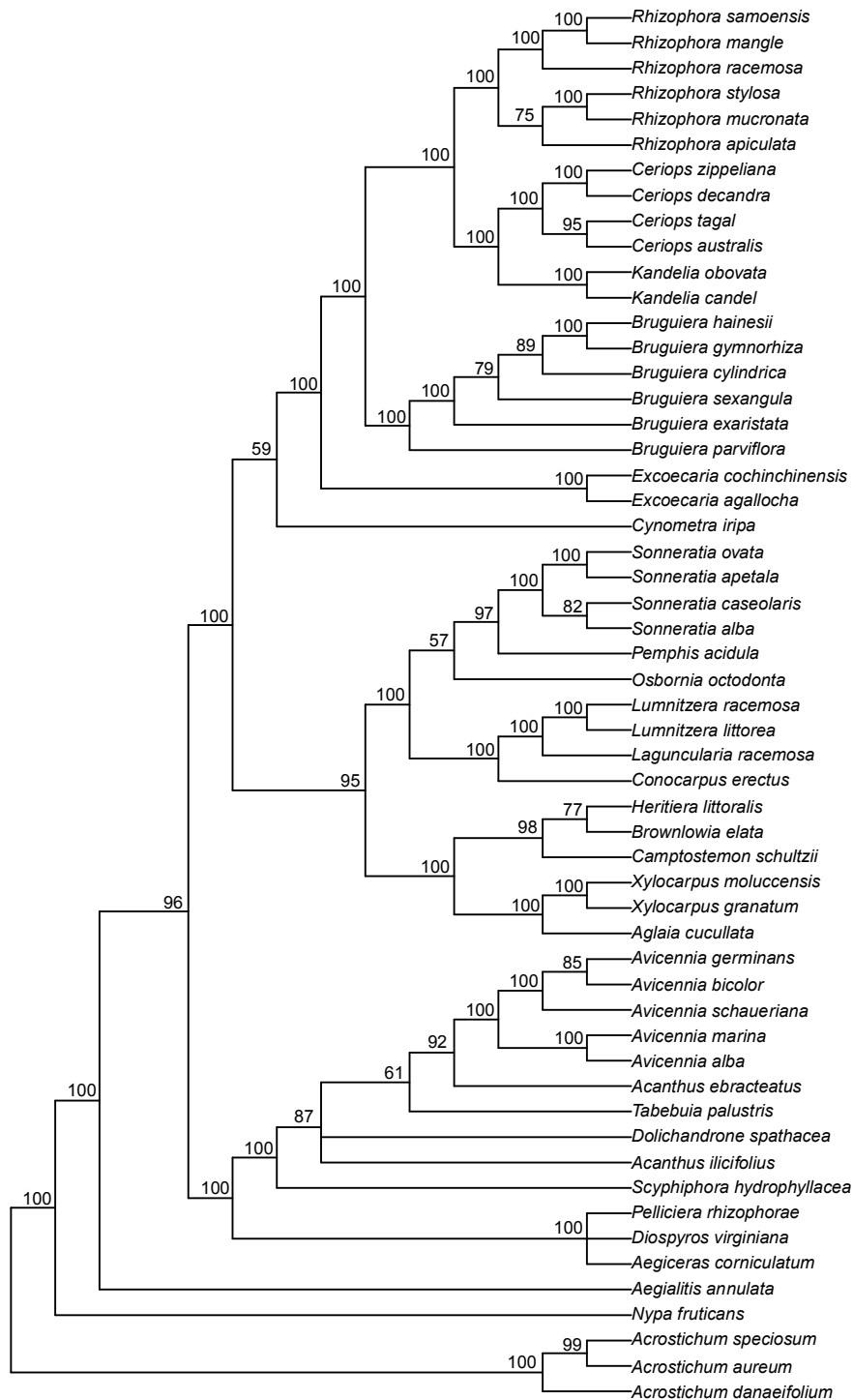


Figure S2. The 50% majority rule consensus tree of mangrove species obtained from a Bayesian analysis of the combined dataset (*rbcL*+ITS +18S). Numbers above branches are posterior probability above 50%. Outgroups and taxa used for calibration were pruned from the tree prior to further analyses.

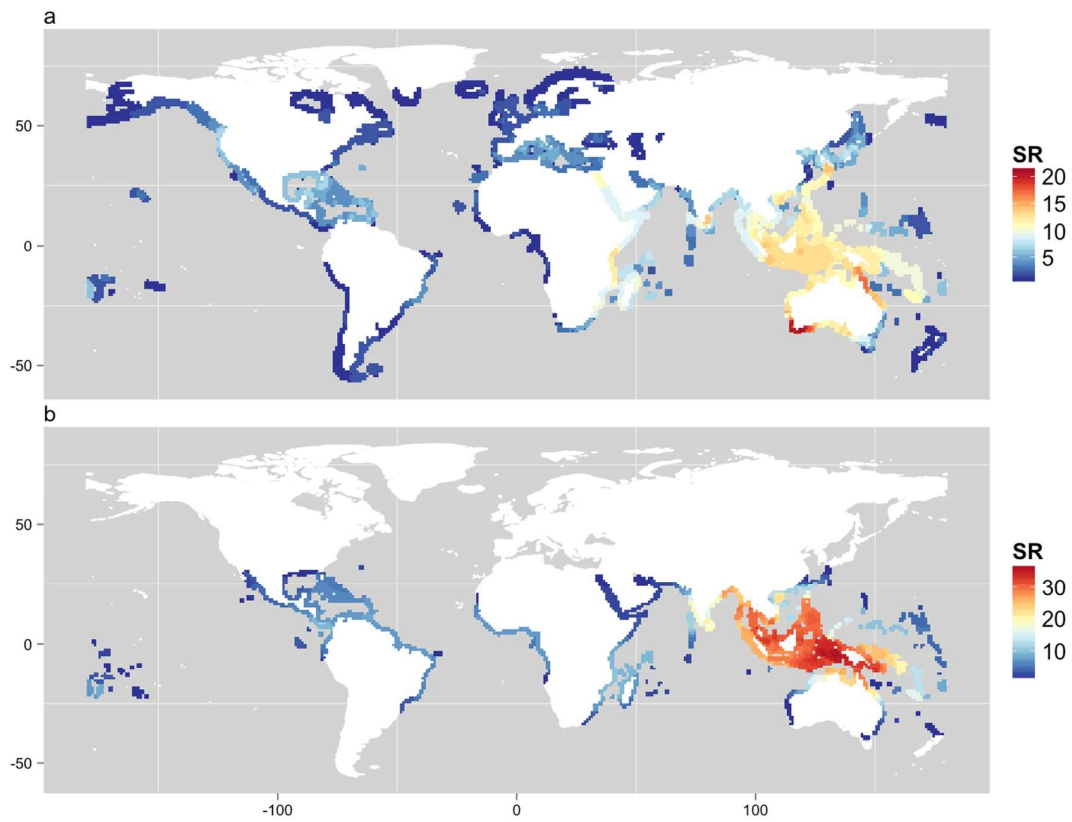


Figure S3 Maps of global distribution of species richness for aquatic macrophytes. (a) seagrass, and (b) mangrove species, within 1.0×1.0 degree grids (Behrmann equal area projection).

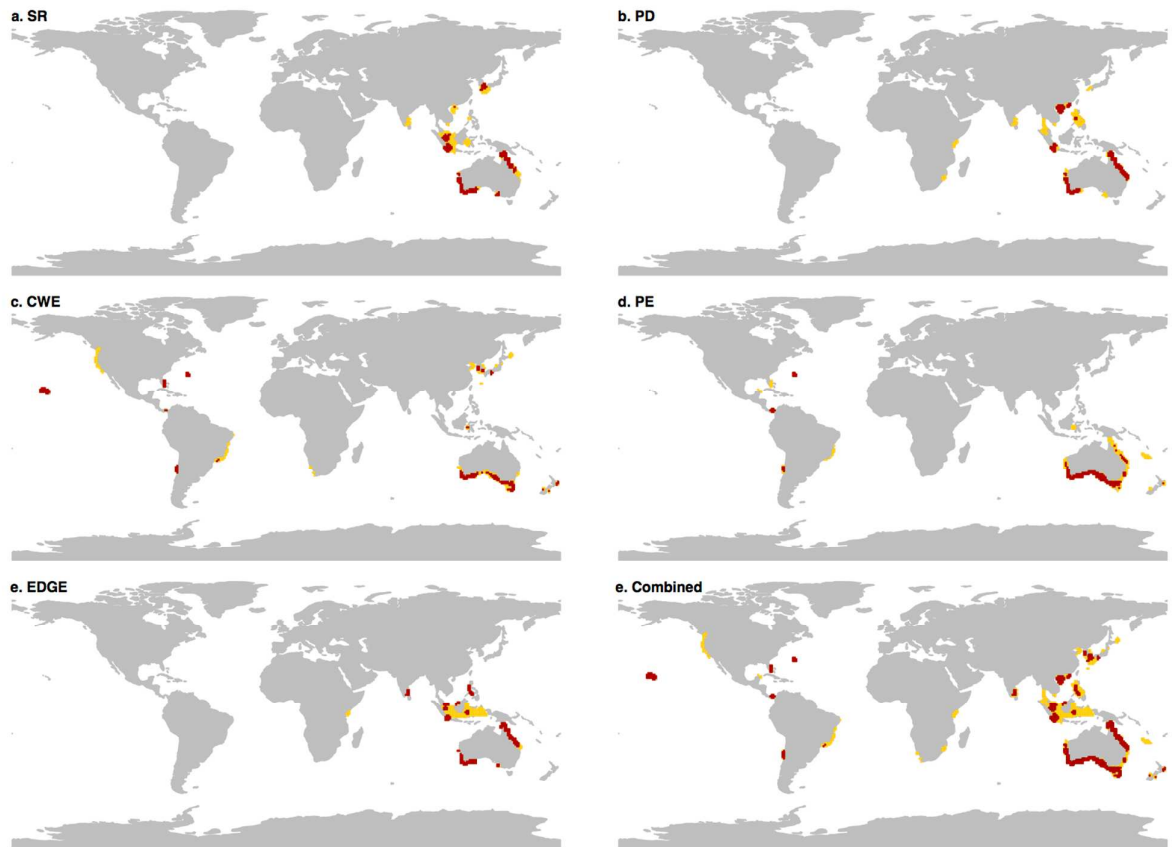


Figure S4 Diversity hotspots for five measures of seagrasses diversity. The top 2.5% hotspots cells are shown in red, and the 5.0% hotspots in yellow. SR species richness, PD phylogenetic diversity, CWE corrected weighted endemism, PE phylogenetic endemism, EDGE evolutionary distinctiveness and global endangerment.

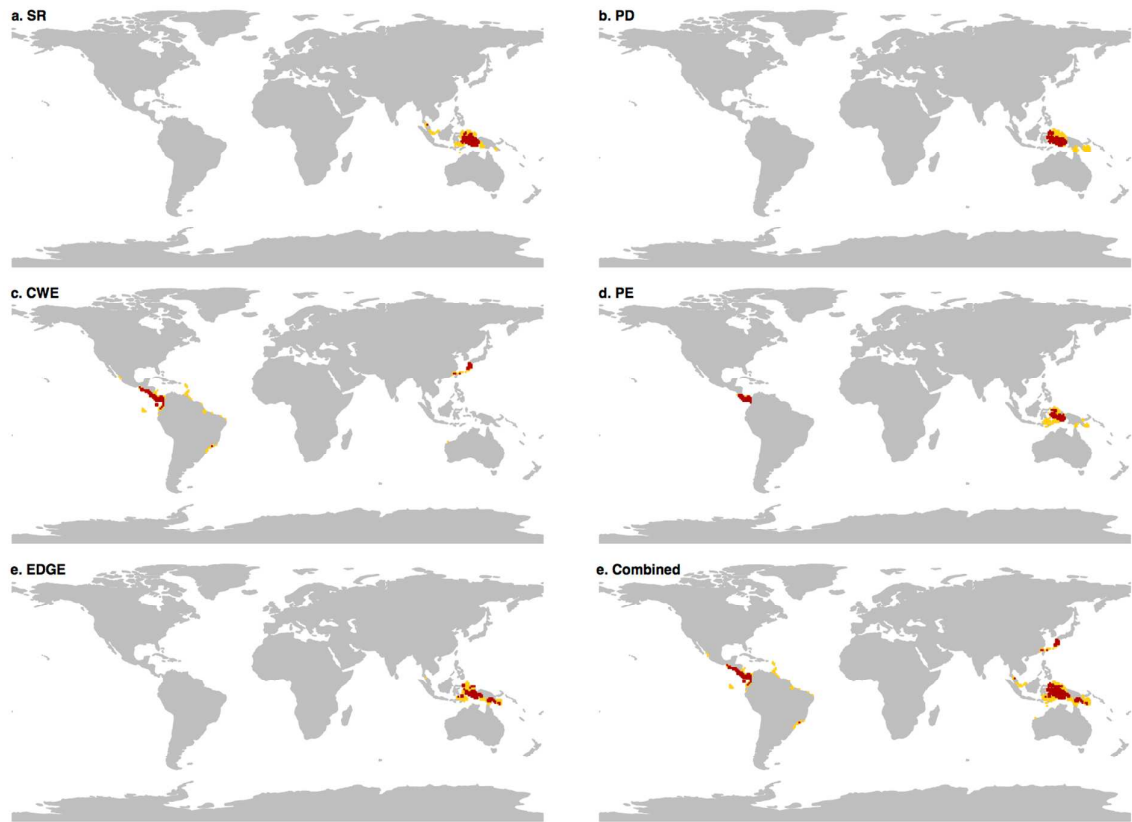


Figure S5 Diversity hotspots for five measures of mangroves diversity. The top 2.5% hotspots cells are shown in red, and the 5.0% hotspots in yellow. SR species richness, PD phylogenetic diversity, CWE corrected weighted endemism, PE phylogenetic endemism, EDGE evolutionary distinctiveness and global endangerment.

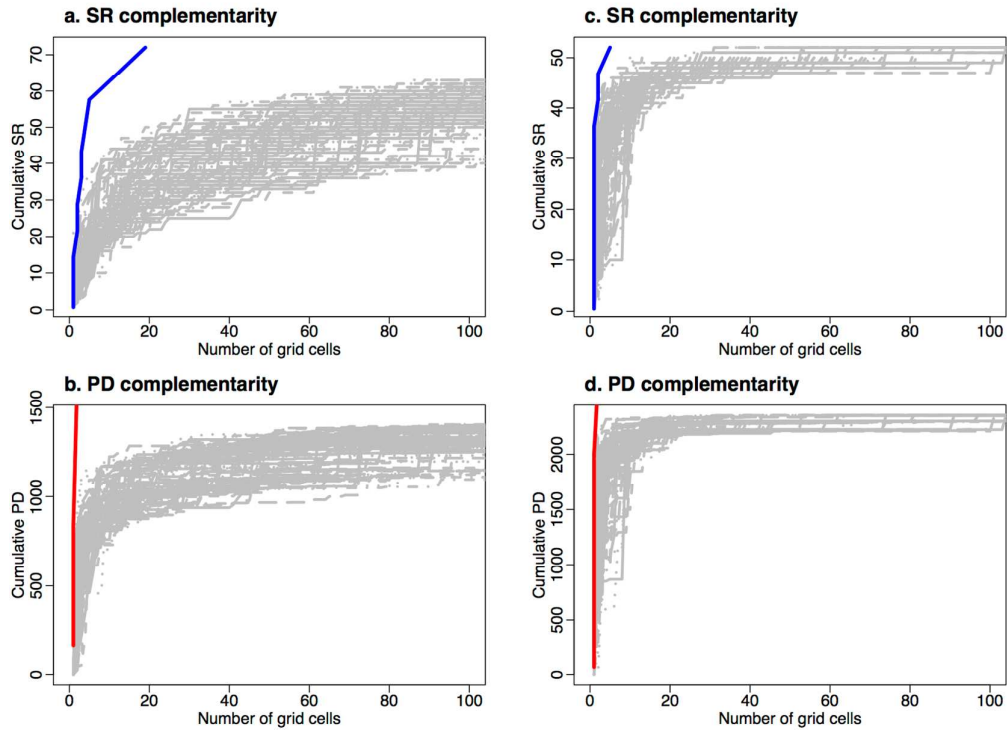


Figure S6 Gains in PD and species richness complementarity. (a and b) seagrasses, (c and d) mangroves. Red (SR) and blue (PD) lines indicate cell selection to maximize protection of species richness and phylogenetic diversity respectively. Grey lines denote 1000 cells selected randomly. PD phylogenetic diversity, SR species richness.