

Biodiversity and conservation of “solar-powered” sea slugs from the Western Atlantic under climate change scenarios

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Abstract

Elysia is a genus of sea slugs in which some species can “steal” chloroplasts (kleptoplasty) from algae and keep them photosynthetically active inside their cells. Solar-powered animals are more susceptible to climate change as photosynthesis can increase the stress for these animals in extreme environmental conditions. Here, we used the Maxent algorithm and environmental envelopes (i.e. the multi-dimensional environmental space in which a species can occur) to model the ecological niche of 21 *Elysia* species in the Caribbean to estimate their current and future potential distribution. We then used predicted distributions to map potential taxonomical richness and to describe the representation of the genus inside the marine protected areas (MPAs). For most species, we show an expansion of the northern and southern range of distribution, but a reduction in the central part. Although changes in richness appeared in different areas, predictions emphasize four large extensions that have a potential current richness of 13 and will have no species in the future: Pamlico Sound, North Carolina; the southwest of the Gulf of Mexico; the Great Bahama Bank; and the southwest of Brazil. Out of the total area with environmental conditions adequate for at least one of the species in the genus, 24.7% is located within MPAs.

KEYWORDS

“solar-powered,” sea slugs, ecological niche, *Elysia*, gastropods, global climate change, marine protected areas

1 | INTRODUCTION

Reports have shown that climate change will affect marine species in less time than terrestrial species due to an accelerated change in oceanographic environmental conditions (Sorte et al., 2010). Nevertheless, so far, most climate change studies in marine environments have been conducted studying effects on corals and fish (Przeslawski et al., 2008). Amongst marine organisms, sessile species or those with slow displacement are the most vulnerable to environmental changes because of their difficulty in locating better conditions (Pörtner et al., 2014). Likewise, organisms in tropical zones usually have less tolerance to environmental changes than organisms in temperate zones (Compton et al., 2007; Donelson et al., 2012). In this context, mollusks in tropical areas face a

complicated future under diverse global warming scenarios (Khoo & Chin, 1983).

The genus *Elysia* (Subclass: Heterobranchia, Order: Sacoglossa) comprises 148 species of benthic gastropod that are usually known as “sea slugs.” They live in shallow waters, algae and coral reef habitats mainly along the tropical regions of the world; in the Western Atlantic Ocean, only two species occur in temperate latitudes (*E. chlorotica* and *E. patagonica*). Members of this genus present a greenish coloration and a U-shaped radula that allows them to suction cytoplasmic contents out of algae. They are simultaneous hermaphrodites with internal cross-fertilization and deposit their egg masses in host algae. When these eggs hatch, they release a veliger that may be planktotrophic or lecithotrophic, depending on the species. Some species present poecilogony (larval variation dependents

on environmental stimulus) and require a metamorphic signal for metamorphosis, such as the presence of the algae that they feed upon (Dionísio et al., 2013). Kleptoplasty—the ability to “steal” chloroplasts from the algae they feed upon and keep them active in their digestive cells—is also a peculiarity of some of the species in this group (Cruz et al., 2014; Pierce & Curtis, 2012; Rumpho et al., 2011). This physiological condition offers major advantages to the group, but it also poses a risk for individuals under environmental stress, making them more vulnerable to the effects of climate change (Dionísio et al., 2017).

Experimental laboratory research and some local-scale field studies have reported the negative impact of climate change on some species of Heterobranchia. For example, Dehnel and Kong (1979) observed the inhibition of embryonic development in *Cadlina luteomarginata* at temperatures higher than 20°C; Biermann et al. (1992) observed that the increase in solar radiation in the intertidal zone killed the embryos of *Doris montereyensis*, and a study by Moran and Woods (2007) documented that elevated temperatures resulted in low oxygen levels in *Tritonia diomedea* egg masses. Regarding the *Elysia* genus, at the time of this study, we only found a work carried out by Dionísio et al. (2017) who observed the negative effects of sea acidification and temperature increase on diverse reproductive aspects of the species *E. crispata*.

As many species in this genus are difficult to study in the wild because of their biological characteristics (e.g. low population densities, cryptic colorations), most information on the group comes from fortuitous presence records. Under these limitations, ecological niche modelling (ENM) has great potential as a tool for the study of sea slugs. With this method, the environmental requirements of the species under study are estimated by associating a set of points with geographic coordinates that represent its occurrence with the environmental conditions that correspond to each point. This information is then used to identify ecologically similar regions within the studied area and estimate the potential distribution of the species (Soberón et al., 2017). Niche models can also be projected to assess the potential effects of future climate change on species' distributions (Anderson, 2013).

Despite its potential, ENM has not been widely used to study the influence of climate change on the distribution of marine mollusk species (Dambach & Rödder, 2011; Robinson et al., 2011). Saupe et al. (2014) modelled the ecological niches of 14 species of mollusks and then projected them to future scenarios, finding a reduction in potential distribution areas and species-specific responses. Conversely, previous studies with other groups of marine organisms have identified certain general patterns regarding distribution ranges, driven by global climate change. Poloczanska et al. (2016) observed an expansion of the geographic limits of the distribution of many species towards higher latitudes and deeper zones. For some species of Heterobranchia, the poleward range expansion due to global warming has been documented (Goddard et al., 2011; Nimbs & Smith, 2016, 2017, 2018), although at present, no analysis allows for a more detailed forecast of probable changes in their distribution under future climate change scenarios.

The first objective of this investigation was to assess the potential effects of climate on the distribution of species in the *Elysia* genus through the Western Atlantic Ocean. Furthermore, we assessed present and future geographic patterns of taxonomic richness. Finally, we evaluated the representativeness of the group inside the Marine Protected Areas. To do so, we modelled the ecological niches of 21 species and projected them onto several different future scenarios. As to the possible responses of these mollusks to climate change, we worked with two hypotheses: (1) environmental suitable areas for the *Elysia* genus will be moved towards higher latitudes, and (2) there will be a general reduction in the suitable areas for the distribution of the genus.

2 | MATERIALS AND METHODS

2.1 | Biological data and determination of the historically accessible area

We included in our analysis all species in the genus *Elysia* that are distributed along the Western Atlantic Ocean (Krug et al., 2016; Muniain & Ortea, 1997) and that have presence records with coordinates. We obtained presence records for each species from diverse online repositories: the Ocean Biogeographic Information System (OBIS, <http://iobis.org>), the Global Biodiversity Information Facility (GBIF, <https://www.gbif.org/>), Naturalista (<https://www.naturalista.mx/>), the National Mollusk Collection of UNAM (CNMO), the Yucatan Marine Biodiversity mollusk collection (BDMY), the Academy of Natural Science (<http://clade.ansp.org/malacology/collections/>), the Florida Museum of Natural History (<http://specifyportal.flmnh.ufl.edu/iz/>), the Smithsonian National Museum of Natural History (<https://collections.nmnh.si.edu/search/iz/>), Instituto de Investigaciones Marinas y Costeras de Colombia (INVEMAR, <http://siam.invemar.org.co/>). Also, we considered occurrences collected from specialized scientific literature published from 2002 to 2017. The words that we used to search in the Google Scholar database were “*Elysia*” and the names of each species in Latin. We selected all papers that have presence records with coordinates, and which fulfil the taxonomic information presented by Krug et al. (2016) (References S1). We cleansed the final database by eliminating all duplicated records, georeferencing errors and occurrences located outside known geographic ranges for the species.

Additionally, as presence records of *Elysia crispata* were clustered in areas more intensively sampled, we performed a spatial filtering through the “Spatially Rarefy Occurrence Data” tool in the “SDMtoolbox” (Brown et al., 2017) of ArcGis 10.2 (© ESRI). We defined three buffers (10, 20 and 65 km) for the spatial filtering which result in four databases; the original plus three filtered ones. Out of these four, we chose the one with the highest evaluation metrics (described below).

The region that has been accessible to the species, according to its dispersal capacities (M area *sensu* Soberón & Peterson, 2005), was determined through the superposition of presence records with

polygons that stand for the coastal marine ecoregions of the world (Spalding et al., 2007). Specifically, the **M** of each species was defined by polygons that intersect with at least one of its presence records. We also modified the **M**'s of some species based on spatial information of the main oceanic currents, as they may influence the dispersion of many marine organisms (Gaines et al., 2003; Siegel et al., 2003).

2.2 | Environmental data

As environmental data, we used Bio-ORACLE benthic layers (Tyberghein et al., 2012) for three different temporalities: the present, the future in 2050 and the future in 2100. In turn, we used layers representing two different representative concentration pathway (RCP) emission scenarios for each future period: one with more mitigation (RCP4.5) and another with a very high level of greenhouse gas emission levels (RCP8.5). A total of 18 variables were considered for each temporality and scenario, including six factors (maximum, average, minimum, range, minimum recorded yearly average and maximum recorded yearly average) for three variables: velocity of the current, temperature and salinity. These variables were obtained in ASCII raster format with a 5-minute arc resolution (~9.2 km²) and were cropped using the **M** of each species as a mask. The inclusion of **M** prevents the model from predicting suitable environmental conditions in areas that cannot be accessed by the species, generating meaningful evaluation metrics (Barve et al., 2011). To avoid overfitting in the models, we reduced collinearity in sets of variables through a Pearson's correlation analysis with the "Remove Highly Correlated Variables" tool in the "SDMtoolbox" (Brown, 2014) of ArcGis 10.2 (© ESRI). When two variables had an $r \geq 0.8$, we only kept the variable with the most biological significance.

2.3 | Ecological niche modelling

Ecological niche models were built with MaxEnt 3.4 (Phillips et al., 2017), a machine-learning algorithm that estimates the most uniform distribution (maximum entropy) of sampling points compared with background locations given the constraints derived from the data (Phillips et al., 2006). We chose this algorithm because of its high predictive performance using only presence data and its flexibility in parameter setting (Elith et al., 2011; Pearson et al., 2007; Wisz et al., 2008). MaxEnt was only used to model the ecological niche for those species with more than six presence records because algorithms usually perform poorly with small amounts of data. Species that did not fulfil this criterion were treated with the different procedures described below. We employed the ENMeval package (Muscarella et al., 2014) in R (R Development Core Team, 2017) to identify the optimal configuration (balancing complexity and generalization) of MaxEnt parameters for each species. ENMeval provides an automated method to execute MaxEnt models with different user-specified setting combinations ("regularization multiplier" and "features"). Models were assessed through an independent set of

recorded presence data obtained through the "block" method for species with more than 20 reports and the "jackknife" method for species with less than 20 (Pearson et al., 2007; Shcheglovitova & Anderson, 2013). The parameter combination selected for each species was the one that generated a model with the lowest omission rate (OR), the largest area under the curve (AUC) and the delta Akaike's criterion corrected ($\Delta AICc$) closest to zero, in that order of priorities. The lower the omission rate, the higher the predictive capacity; AUC values higher than 0.5 indicate that the model provides more information than expected by chance, so it is a significance metric, and an $\Delta AICc < 2$ indicates models with lower complexity (Burnham & Anderson, 2002; Elith et al., 2011; Jiménez-Valverde, 2012). Once the best "features" and "regularization multipliers" were selected, we generated MaxEnt models with five replicas in the algorithm "bootstrap" functionality, 10,000 background points randomly selected within the **M** area, and a "logistic" output format, which is a raster map with continuous values that are commonly interpreted as environmental suitability (Merow et al., 2013). We used the median of replicas as the final map for each species.

Models for future scenarios were projected with two configurations for the extrapolation: clamping and truncation. In clamping, extreme values in the calibration area are used as a way to predict the transfer areas with the most extreme values, while in truncation, all the values outside the range of calibration data are not considered environmental suitable (Qiao et al., 2019). Also, we used mobility-oriented parity (MOP) (Owens et al., 2013) to identify and map the risk of extrapolation. This analysis enabled us to identify strict extrapolation areas; regions in transfer scenarios that present combinations of environmental variables outside the ranges present in the calibration area.

To represent the potential distribution of each species, we reclassified the continuous models obtained with Maxent into binary maps by applying a threshold criterion of 5% allowed omission in training data. That is, we extracted and ordered Maxent suitability scores predicted for each training occurrence from the highest to the lowest. Then, we subset the highest 95%, and for this new database, we used the least Maxent score as a threshold value. Above this value, model scores are considered to represent species potential distribution (Cooper & Soberón, 2018; Pearson et al., 2004). With this criterion, we assumed that 5% of the records with lower suitability could represent sink populations or mistakes that were not identified during the database cleansing phase. Additionally, the models were masked with a bathymetry layer with a maximum value of 40 m—the maximum depth at which the presence of the genus has been reported (Goodwin et al., 2011). The bathymetry layer was obtained from the online repository Marspec (Sbrocco & Barber, 2013).

Four maps were generated for each species (2050 RCP4.5, 2050 RCP8.5, 2100 RCP4.5 and 2100 RCP8.5). We obtained these maps by combining the present model to each of the future models allowing us to visualize potential changes in the distribution of the species (gained area, lost area and conserved area). To determine the proportion of future change, we calculated the total of suitable pixels for each future scenario out of the total number of pixels in the study's area and we compared the outcome with the present.

2.4 | Potential richness

For estimating potential richness, we included the species that were not modelled with Maxent because of the low sample size. We estimated the potential distribution of this species through a manual reclassification procedure as follows. First, ecoregions coinciding with presence records were selected and environmental layers were cropped using those ecoregion areas. For the species with only one presence record, we assigned a value of one to every pixel that coincided with the environmental value of each predictor in that record, and a value of zero to all the other pixels. In the species with two to six records, we computed the range for each predictor assigning a value of one to the pixels with values inside the range and zero to each of all the other pixels. We then summed these reclassified predictors, and a value of one was assigned to the pixels that had values in which overprediction was not observed (this value was different for each species), and zero to each of all the other pixels. This procedure was carried out for the present and future scenarios.

To represent potential taxonomic richness, we stacked all the binary maps for the present and each future scenario (the ones generated through Maxent as well as those described in this section). We also computed the expected species turnover as the difference between the present and future scenarios.

2.5 | Representation of *Elysia* in Marine Protected Areas (MPAs)

We overlaid the richness maps described in the previous section onto MPAs polygons obtained from the World Commission on Protected Areas (UNEP-WCMC & IUCN, 2019). Given that some

MPAs superpose because areas with different IUCN protection categories co-exist in the same space, these areas were conflated to avoid double counts. Finally, we calculated the number of pixels contained in the MPAs polygons for each richness value. This procedure was undertaken for the present model, as well as for every climate change scenario. We used the "Zonal Statistics as Table" tool in the "SDMtoolbox" (Brown, 2014) of ArcGis 10.2 (ESRI) to obtain the statistics on marine protected areas richness.

3 | RESULTS

We obtained 314 spatially unique presence records representing 21 out of the 29 species in this genus that occur in the Western Atlantic Ocean (Figure 1). Niche models for *E. crispata* were built using the database filtered through the 20 km buffer, as evaluation metrics showed a higher predictive power and less overfitting within this dataset (Table S1). Once collinearity had been diminished, seven out of 18 environmental predictors were used for modelling: maximum salinity, minimum salinity, maximum temperature, temperature range, the maximum velocity of currents, the minimum velocity of currents and range of the velocity of currents. Considering that the MOP only showed three strict extrapolation areas with a small surface for all scenarios (Figure S1), we chose the clamping procedure for future transfers.

In general, model assessment outcomes showed a good performance with an AUC ≥ 0.88 and omission rates for all species lower than 10%. The AICc criteria allowed us to select less complex models, with most $\Delta AICc$ values being lower than two. Nevertheless, the values for three models were greater than two, and the values for three other models could not be calculated because the number of parameters exceeded the number of presence records (Table 1).

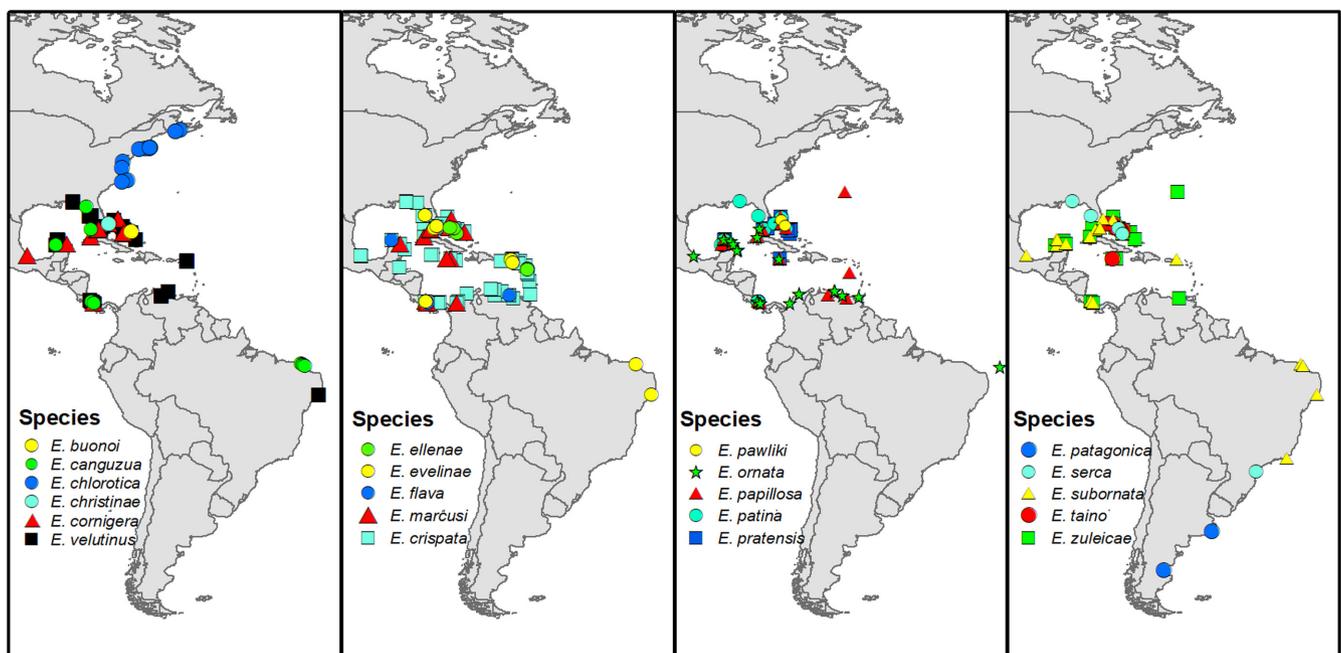


FIGURE 1 Distributional data for all 21 *Elysia* species in the West Atlantic Ocean

TABLE 1 Summary of ecological niche modelling inputs and evaluations

SPECIE	TO	FO	OR	AUC	$\Delta AICc$	F	RM
<i>Elysia buanoi</i>	2	2	-	-	-	-	-
<i>Elysia canguzua</i>	16	9	0.06	0.98	26.3	LQ	0.5
<i>Elysia chlorotica</i>	48	17	0.01	0.90	129.7	H	3
<i>Elysia christinae</i>	1	1	-	-	-	-	-
<i>Elysia cornigera</i>	19	14	0.02	0.96	0.0	L	1
<i>Elysia crispata</i>	262	57	0.00	0.92	0.0	L	0.5
<i>Elysia ellenae</i>	9	6	-	-	-	-	-
<i>Elysia evelinae</i>	16	14	0.02	0.96	NA	H	1
<i>Elysia flava</i>	5	4	-	-	-	-	-
<i>Elysia marcusii</i>	17	12	0.03	0.88	0.0	LQ	1.5
<i>Elysia ornata</i>	34	21	0.05	0.89	0.0	L	1
<i>Elysia papillosa</i>	19	18	0.01	0.91	0.0	L	1
<i>Elysia patagonica</i>	2	2	-	-	-	-	-
<i>Elysia patina</i>	16	16	0.01	0.92	0.0	L	1.5
<i>Elysia pawliki</i>	2	2	-	-	-	-	-
<i>Elysia pratensis</i>	19	16	0.01	0.90	0.0	LQ	1.5
<i>Elysia serca</i>	5	5	-	-	-	-	-
<i>Elysia subornata</i>	34	26	0.00	0.95	1.9	LQ	2
<i>Elysia taino</i>	11	7	0.09	0.96	NA	H	3.5
<i>Elysia velutinus</i>	63	42	0.07	0.91	0.0	LQ	3
<i>Elysia zuleicae</i>	27	23	0.03	0.91	5.9	L	3.5

Note: Only species with data for all columns were modelled in Maxent.

Abbreviations: $\Delta AICc$, delta Akaike corrected by sample size (NA: when the number of parameters is higher than the number of records); AUC, area under the curve; F, features; FO, filtered occurrences; H, hinge; L, linear; OR, omission rates; P, product; Q, quadratic; RM, regularization multiplier; TO, total occurrences.

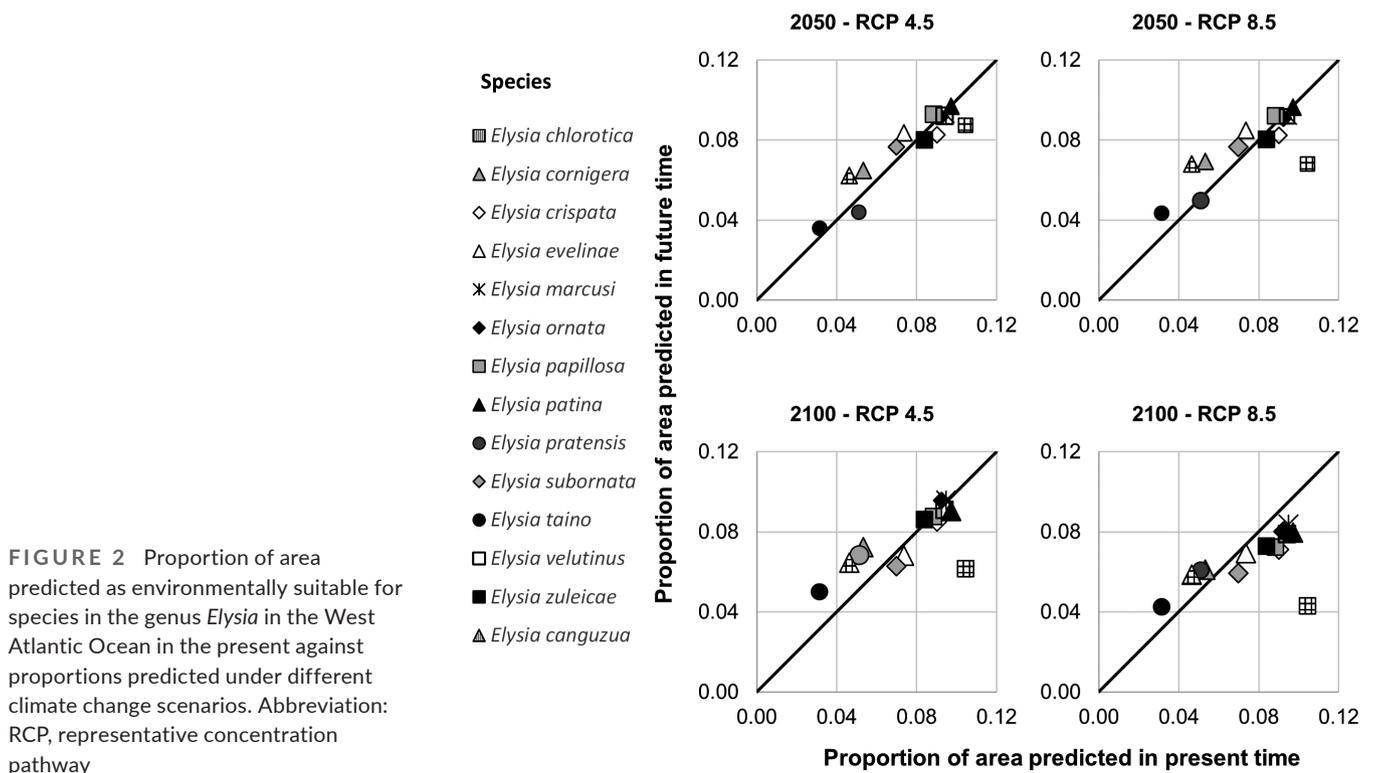


FIGURE 2 Proportion of area predicted as environmentally suitable for species in the genus *Elysia* in the West Atlantic Ocean in the present against proportions predicted under different climate change scenarios. Abbreviation: RCP, representative concentration pathway

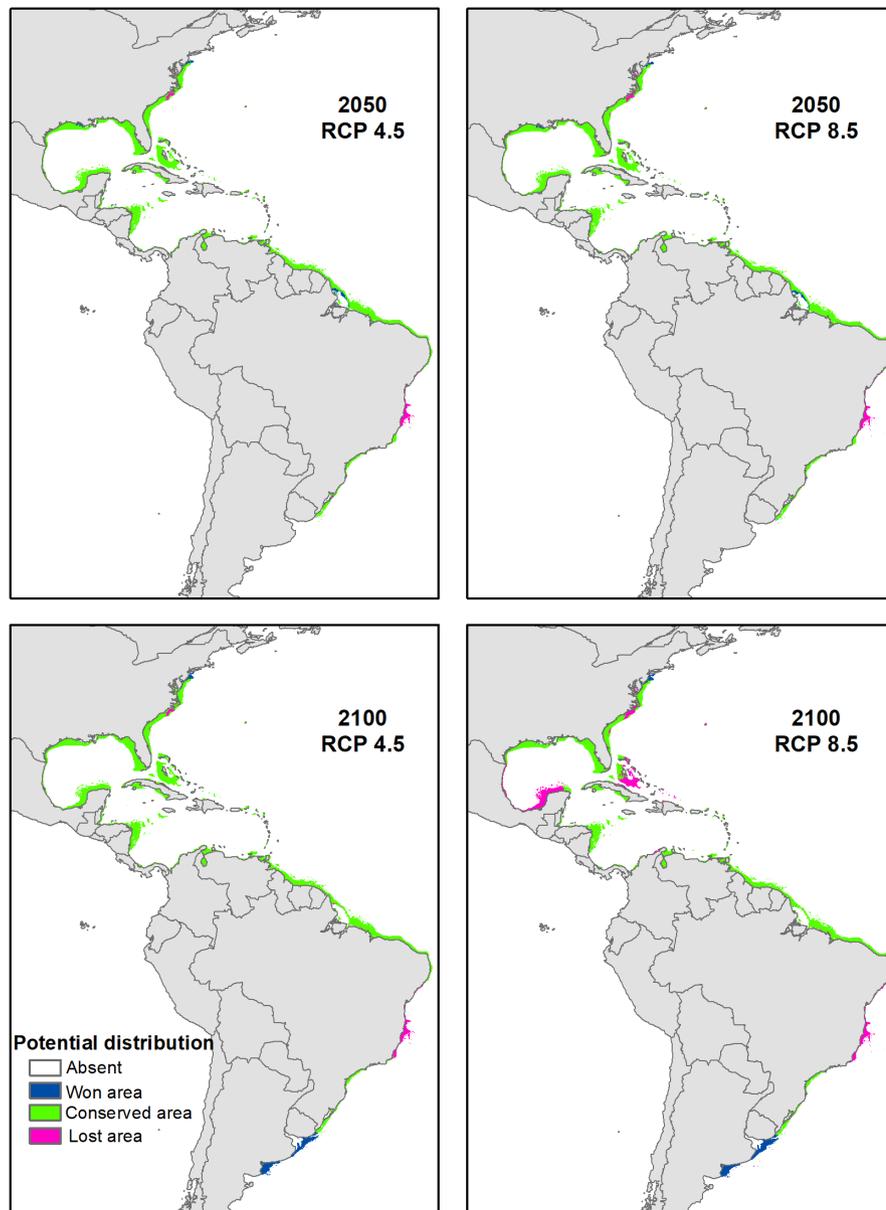


FIGURE 3 Potential shifts in the area environmentally suitable for *Elysia ornata* under different climate change scenarios. Abbreviation: RCP, representative concentration pathway

Future projections show that environmentally suitable areas will be reduced for eight species by 2050 and 10 species by 2100 RCP8.5. The most drastic reduction in the suitable area will amount to 59.1% for *E. chlorotica* in 2100 RCP8.5. However, an increase in the suitable area for *E. canguzua*, *E. cornigera* and *E. taino* is predicted for every scenario. Also, the general pattern is that suitable areas will likely expand at the extremes and contract in the tropics for most species. Displacements towards the northern extremes were predicted for 10 species in 2050 for both RCPs, while in 2100 RCP8.5, 12 species will present displacements in that direction. Predictions show that seven species will be displaced to the southern extreme by 2050 for both RCPs and 11 species by 2100 RCP8.5. Species that did not present a 2100 southward displacement were *E. chlorotica*, *E. evelinae* and *E. subornata* (Figure 2) (Figures S2–S14).

Although reduction percentages and potentially affected regions were different for each species, we identified four large common contraction areas shared by most taxa: the first one is located in

Brazil, from Alagoas up to the border of Bahia with Espírito Santo; the second is in Pamlico Sound, North Carolina, USA; the third is located in the Gulf of Mexico, from Cape Catoche in the Yucatan Peninsula to the border of Mexico with USA; and the fourth one is in the Great Bahama Bank. We selected *E. ornata* as an example for the visualization of future potential changes in geographical distributions (Figure 3) and the individual models for all other species are included in the Supplementary Material S2–S14.

In the present, our models predict three coastal areas with high potential richness (the Caribbean, the Gulf of Mexico and the central part of Brazil). The highest richness is observed between the Bahamas and the Dominican Republic. Nevertheless, richness in this region will be probably reduced in different climate change scenarios (Figure 4). The lowest richness is predicted for the northern and southern extremes of the study area in all time periods (Figure 4). However, in climate change scenarios, there is an increase in richness towards temperate zones (Figure 5). In contrast, a reduction

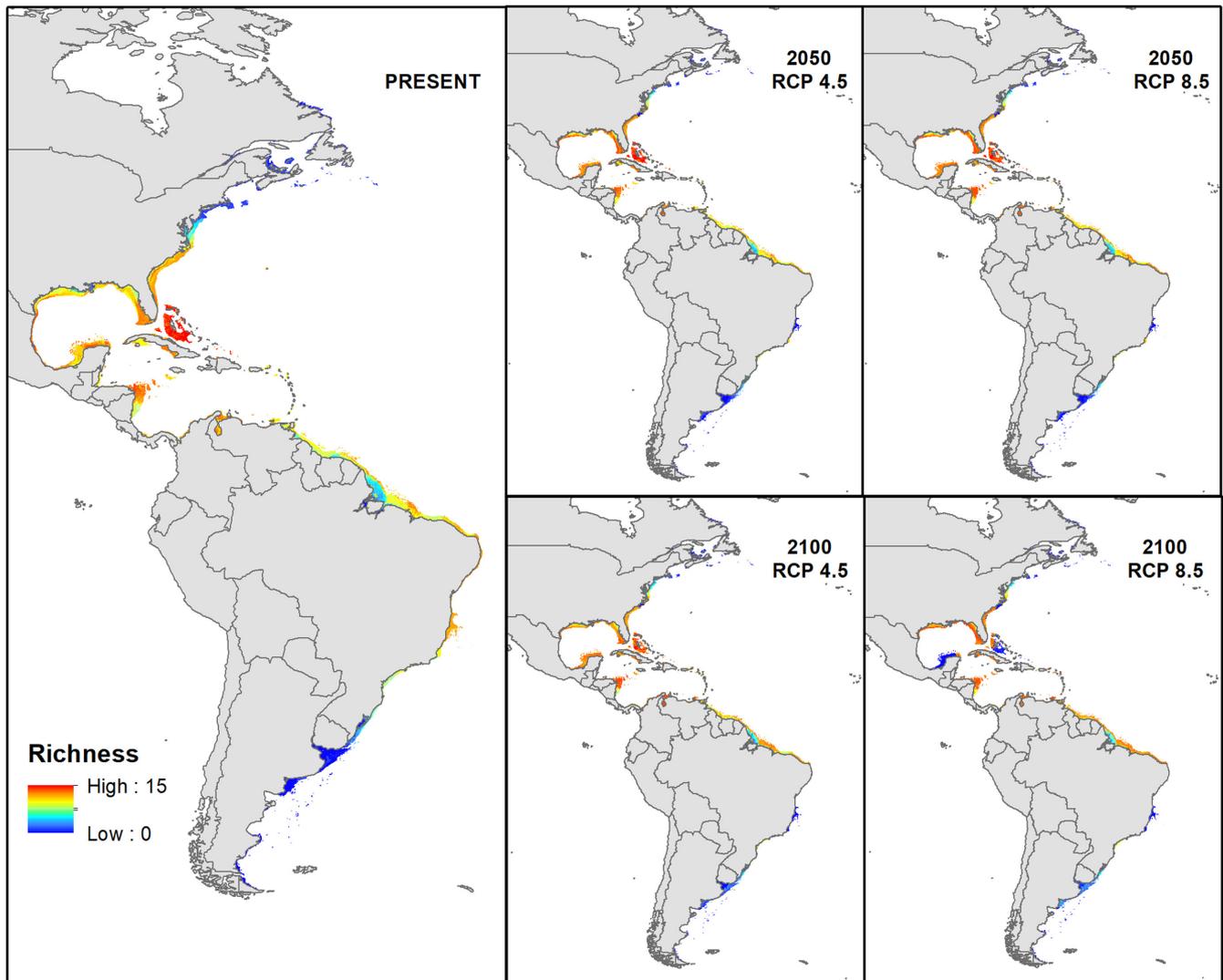


FIGURE 4 Potential taxonomic richness of the genus *Elysia* in the West Atlantic Ocean. Abbreviation: RCP, representative concentration pathway

in richness to zero was estimated for North Carolina, USA, and the area between Alagoas and the borders of Bahia with Espírito Santo, Brazil, in every future scenario. In 2100 RCP8.5, richness was reduced to zero between Cape Catoche in the Yucatan Peninsula and the border of Mexico with the USA, and in the Great Bahama Bank (Figure 5).

Out of the total area with suitable environmental conditions for at least one of the species in the genus, 24.7% is represented inside MPAs. This area is reduced in the different climate change scenarios, even if only slightly. Regarding the greatest potential richness (15 species), 7.5% is contained in MPA systems. Specifically in the Bahamas, the Turks and Caicos Islands and the Dominican Republic, this percentage increased up to 100% for 2100 RCP8.5 as, in this scenario, only one small area remains with a richness of 15 and it is wholly contained in the Silver and Navidad Bank Sanctuary in the Dominican Republic. On the contrary, some areas maintain a high potential richness in all scenarios, five of them stand out for having a

richness higher than 13 and a larger extension, and they are not contained in MPAs: the north of the Bahamas, the southwest of Florida, the southwest of Cuba, the limit of Honduras and Nicaragua and the middle part of Brazil (Figure 6).

4 | DISCUSSION

The results of this study allowed us to prove our two hypotheses. Regarding the first, most of the species presented an expansion towards higher latitudes in all scenarios. This displacement could be caused by the limitation of oxygen distribution mechanisms and alterations in the functions of organisms because of a decrease in cellular energy due to an increase in temperature in the present distribution area (Pörtner & Knust, 2007). Furthermore, marine ectotherms, in general, occupy all latitudes within their thermal tolerance limits, so an increase in sea temperature would also cause

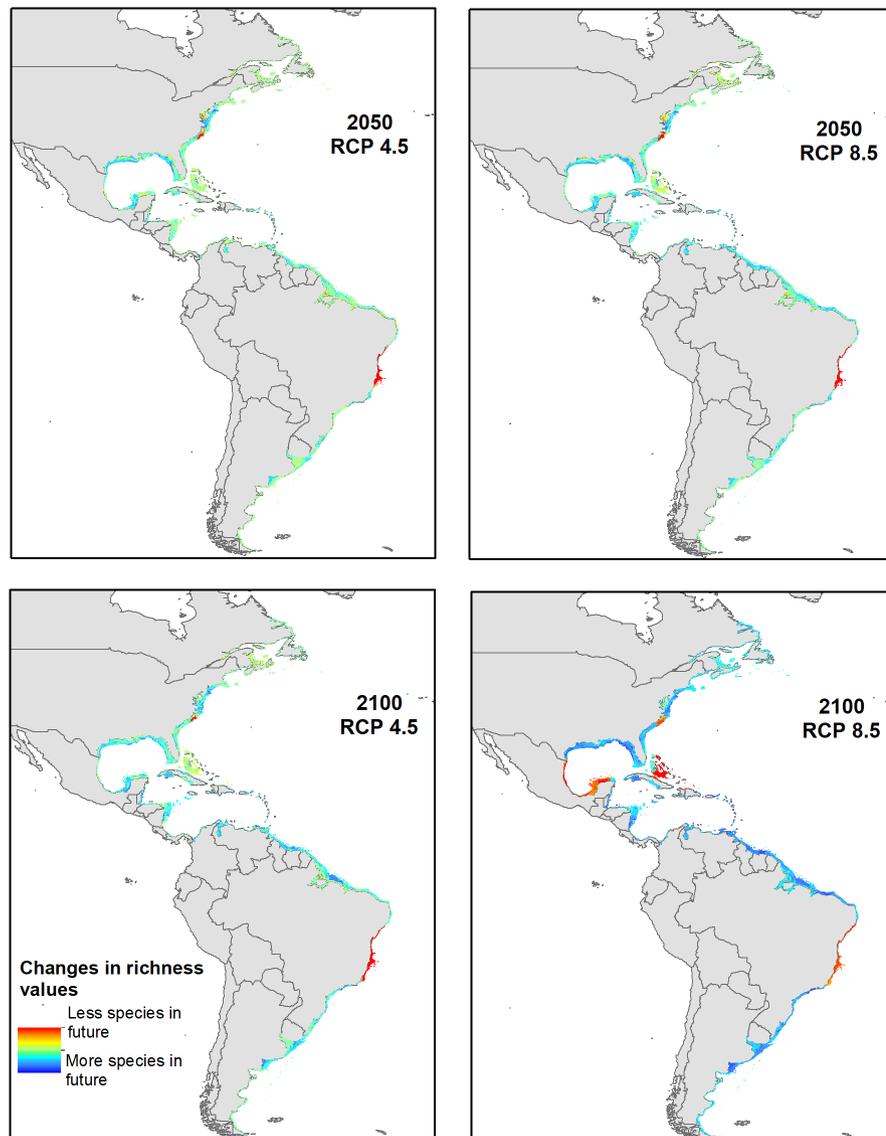


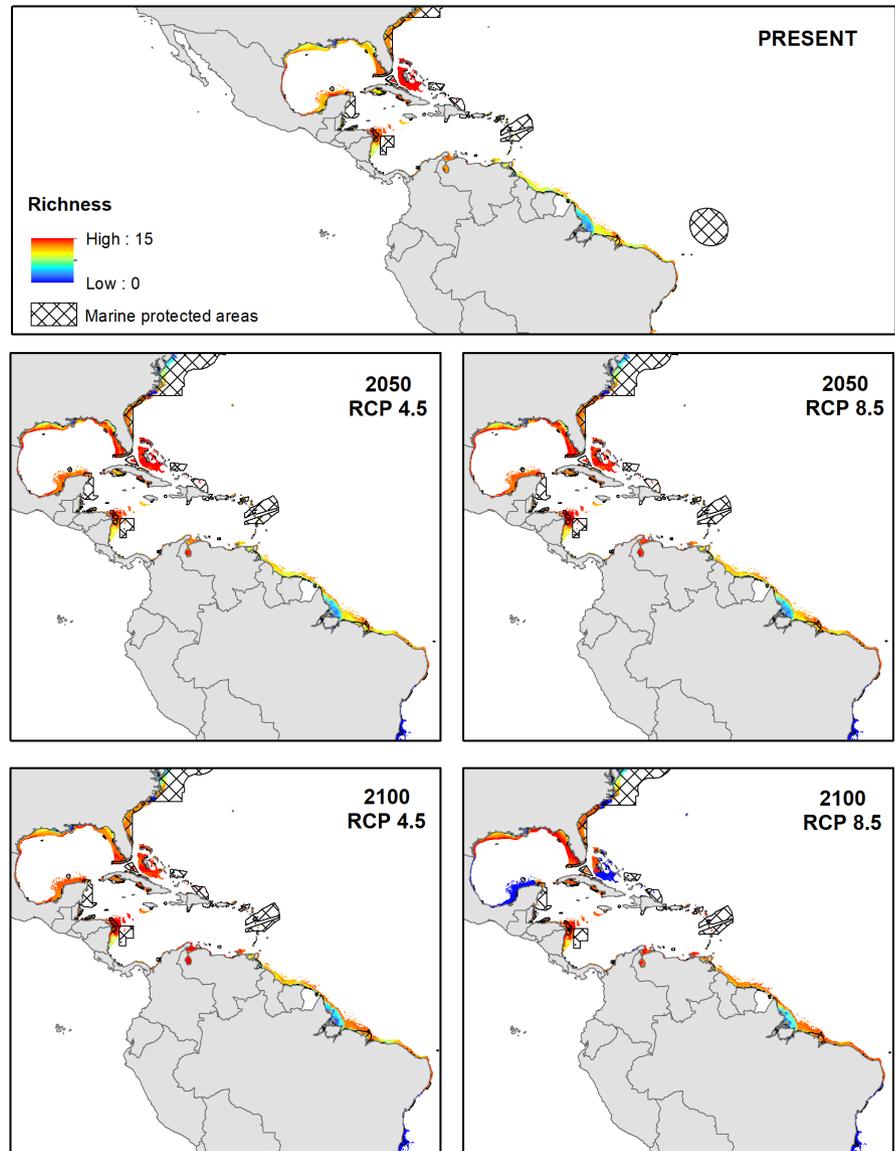
FIGURE 5 Potential shifts in estimated richness of the genus *Elysia* in the West Atlantic Ocean under different climate change scenarios as compared to the present. Abbreviation: RCP, representative concentration pathway

a displacement towards latitudes with suitable conditions (Sunday et al., 2012). This coincides with other global research on marine organisms (Cheung et al., 2009; Poloczanska et al., 2016; Sunday et al., 2012), including Heterobranchia (Goddard et al., 2011, 2016; Nimbs & Smith, 2016). Specifically, in the West Atlantic Ocean, distributional poleward shifts have been documented for fiddler crabs (De Grande et al., 2021), common snook (Purtlebaugh et al., 2020), dinoflagellates (Kibler et al., 2015) and another species of sea slug, *Bulla occidentalis* (Saupe et al., 2014). In contrast, another climate change research forecasted that some gastropod in this region will not shift their distribution poleward as temperatures warm (Saupe et al., 2014), and that difference could be due to the complexity of each species' niche. Nevertheless, we should keep in mind that sea slugs disperse during their larval stage and that larval displacement and duration are closely linked to sea temperatures (O'Connor et al., 2007). As spawning is also regulated by temperature, species with planktotrophic larvae may be unable to find the phytoplankton required for feeding because of changes in sea thermal conditions

(Edwards & Richardson, 2004; Hay et al., 2005). Certain species, including some in the *Elysia* genus, that need a substrate as a metamorphic signal may be affected if changes in spawning periods prevent them from coinciding with the required substrate (Przeslawski et al., 2008). Therefore, even if our predictions show a potential expansion of favourable environments towards higher latitudes, the effects of temperature during the larval stage could limit the dispersion of these organisms.

Concerning the second hypothesis, we observed a reduction in the favourable area for most species. Even if suitable conditions were displaced towards the extremes of the distribution, this expansion did not compensate for the loss caused by climate change. According to the climatic variability hypothesis, unlike species that originated in temperate areas, species in tropical areas present less adaptation to temperature changes for having evolved in more stable thermal environments and because the maximum temperatures of the environments they inhabit are closer to their lethal limits (Stuart-Smith et al., 2017; Sunday et al., 2012; Tewksbury et al., 2008). This

FIGURE 6 Potential taxonomic richness of the genus *Elysia* in marine protected areas. The enlargement shows areas with high richness values that remain in every scenario and are not contained in MPAs. Abbreviations: MPA, marine protected area; RCP, representative concentration pathway



coincides with the loss of area predicted in our analysis for most species. Nevertheless, our predictions showed that favourable areas for the species *E. chlorotica* (which inhabits temperate zones) will be most affected by climate change, whereas those for three tropical species (*E. canguzua*, *E. cornigera* and *E. taino*) will increase in all scenarios. As the geographic range of *E. chlorotica* is limited to the south by more tropical environments, its distribution in that direction would be further limited by an increase in sea temperatures. On the contrary, although we expected a northward displacement in the potential distribution of this species as a result of climate change, our results indicate that this expansion would not compensate for the reduction predicted for the southern part. Although there are no population studies of *E. chlorotica* that confirm the diminution of its distribution area, some studies report a reduction in the number of individuals and locations where they have been observed (Main, 2018). No common morphological or physiological characteristic was found that could explain the future increase in favourable conditions for *E. canguzua*, *E. cornigera* and *E. taino*.

Regarding potential richness patterns, in the regions where a greater loss is predicted, there is empirical evidence of the vulnerabilities and negative effects caused by climate change. For instance, an important increase in sea surface temperature has already been reported for the south of the Gulf of Mexico. It has also been described an increase in the speed of sea-level rise, changes in the rainfall regime affecting freshwater discharge patterns, and alterations in the frequency and intensity of tropical storms (Yáñez-Arancibia et al., 2014). There are reports of coral mortality in the Great Bahama Bank as an outcome of the warming generated during ENSO and the extreme cooling events associated with cold fronts due to the proximity to North America (Riegl, 2007). An increase in coral bleaching because of increasing temperatures was recorded in the coastal reefs in the southwest part of Brazil between 1998 and 2005 (Leão et al., 2010). The region of Pamlico Sound, USA, has also been considered highly vulnerable to climate change. A larger increase in temperature salinity and sea levels is predicted for this region because it is a semi-closed ecosystem separated from the ocean by an island barrier

(Kennish & Paerl, 2010). Even if MPAs represent an important conservation strategy, they may not play a very effective role when facing a threat such as climate change (Hughes et al., 2017; Jones et al., 2004). Therefore, identifying geographical regions where the suitability for organisms remains stable in time may be an effective strategy for the conservation of species in a changing environment. In the case of the *Elysia* genus, conservation of areas with high richness inside areas that fulfil these conditions is recommended. For instance: the north of the Bahamas, southwest Florida, southwest Cuba, the border of Honduras with Nicaragua, and the central part of Brazil.

The procedure implemented in this work allowed us to estimate the potential distribution of species with few presence records, thus making a contribution to the knowledge of the geographic patterns of taxonomic richness and providing information that may be used for the conservation of these organisms. The preservation of this genus implies that a rare process in the animal kingdom will also be conserved: kleptoplasty. Finally, our maps also could be used as inputs to model and describe other dimensions of biodiversity (e.g. phylogenetic and functional), as well as to test biogeographical and macroecological hypothesis.

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DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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