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Deep reefs are climatic refugia for genetic diversity of marine forests

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INTRODUCTION

As global climate conditions changed over time, so did the distribution and abundance of organisms. The glacial-interglacial cycles of the Quaternary (c. 2.6 Myr to the present) were particularly important in causing major range shifts (Hewitt, 2000, 2004). Expansion and contraction of ranges structured the genetic and evolutionary traits of many marine species (Maggs et al., 2008). In regions where climate conditions allowed populations to persist (i.e., refugia), high

ABSTRACT

Aim Past climate-driven range shifts shaped intraspecific diversities of species world-wide. Earlier studies, focused on glacial refugia, might have overlooked genetic erosion at lower latitudes associated with warmer periods. For marine species able to colonize deeper waters, depth shifts might be important for local persistence, preventing some latitudinal shifts, analogous to elevational refugia in terrestrial habitats. In this study, we asked whether past latitudinal or depth range shifts explain extant gene pools in Saccorhiza polyschides, a large habitat structuring brown alga distributed from coastal to offshore deep reefs.

Location North-east Atlantic and western Mediterranean basin.

Methods Genetic structure and diversity were inferred using seven microsatellite loci, for 27 sites throughout the entire distributional range. Ecological niche modelling (ENM) was performed with and without information about genetic structure (sub-taxon niche structure) to predict distributions for the Last Glacial Maximum (LGM), the warmer Mid-Holocene (MH) and the present.

Results Both ENM approaches predicted a wider potential distribution in deeper waters than is presently known, a post-glacial expansion to northern shores and the extirpation of southern edges during the warmer MH. Genetic data corroborated range dynamics, revealing three major genetic groups with current boundaries in the Bay of Biscay and the Lisbon coastal region, pinpointing ancient refugial origins. Despite extensive southern range contraction, the southernmost warmer regions are still the richest in genetic diversity, indicating long-term persistence of large populations. ENMs suggested that this could only have been possible due to stable refugia in deeper reefs.

Main conclusions The global distribution of gene pools of temperate marine forests is explained by past range shifts that structured both latitudinal glacial refugia and depth refugia during warmer periods. Deep rear edge populations play a fundamental role during periods of extreme climate, allowing persistence and retaining some of the largest genetic diversity pools of the species’ distribution.

Keywords climate change, depth range shifts, ecological niche modelling, genetic diversity, glacial refugia, kelp forests, marine phylogeography, north-east Atlantic, Saccorhiza polyschides, western Mediterranean

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and unique genetic diversity is expected (Provan & Bennett, 2008). Where ranges contracted or unfavourable niche conditions prevailed, diversity might be presently reduced due to bottlenecks, drift and/or reduced gene flow (Young et al., 1996; Leimu et al., 2006). Erosion of genetic diversity might have also taken place at the ‘leading edge’ of colonization during range expansions (Hewitt, 1996). These processes created an emerging pattern for several North Atlantic marine species, which now exhibit low genetic diversity and differentiation in regions formerly displaced by glaciations (such as during the Last Glacial Maximum; LGM; c. 21 ka) and high and distinct diversity where populations persisted at lower latitudes (Hewitt, 1996, 2004; Provan & Bennett, 2008; Neiva et al., 2014, 2015).

While early studies placed strong emphasis on glacial refugia (e.g., Hewitt, 2004), inferring regions of long-term persistence also requires considering the warmer extremes of climate change (e.g., Assis et al., 2014). The higher insolation during summer in the Northern Hemisphere hindcasted for the Mid-Holocene (MH; c. 6 ka) resulted in warmer seasonal temperatures when compared to the present (Wanner et al., 2008). This might have caused genetic erosion at trailing edges (e.g. Assis et al., 2014). Overlooking past warming periods may therefore miss important drivers of the current distribution of genetic diversity.

The size (area) and location of refugia influence the spatial patterns of genetic diversity (DeChaine & Martin, 2004; Assis et al., 2014), although this is further determined by dispersal ecology. Species with limited dispersal might experience local extinctions and bottlenecks whenever unfavourable environmental conditions arise (Parmesan, 2006; Provan & Maggs, 2012). For instance, the contraction of trailing edges predicted for many North Atlantic marine species (e.g. Jueterbock et al., 2013; Raybaud et al., 2013; Neiva et al., 2015) might not be offset by northern expansions because range shifts tend to involve local population fronts (Neiva et al., 2012a), leaving behind distinct diversity at lower latitudes (Provan & Maggs, 2012). Although species respond individually to environmental changes, making refugia species-specific, some patterns are common (Maggs et al., 2008). For example, terrestrial species found refugia in higher elevations regardless of their dispersal ability (e.g. Bush et al., 2004). Likewise, marine species able to colonize deeper colder waters might survive unfavourable sea surface changes. Such deep refugia would allow persistence of distinct gene pools during extreme climate periods, increasing diversity in the long-term. This has much biogeographical and evolutionary relevance, although there is little empirical evidence addressing this hypothesis (but see Perry et al., 2005).

Large brown algae that can form marine forests (commonly called ‘kelp’) offer an unique model to investigate the role of climate changes in shaping the global patterns of intraspecific diversity. Kelp have limited dispersal and their distributional ranges are climatically defined (e.g., Raybaud et al., 2013). These are important features to effectively track distributions as climates change. Furthermore, deep settlements of kelp may occur in specific environments (Graham et al., 2007), although their prevalence is mostly unknown and empirical evidence for their role as refugia has been missing so far.

In this paper, we use microsatellite genetic markers and ecological niche modelling (ENM) to investigate whether past climate changes might have produced major biogeographical shifts and might have shaped the extant gene pools of the large brown alga Saccharina polyschides (Lightfoot) Batters, 1902, an important ecosystem-building species that forms marine forests. We assessed in particular whether deep-water populations are predicted to persist offshore, beyond the coastal distributional limits, where waters are more transparent and colder, and whether these might function as depth refugia maintaining rich and distinct gene pools.

MATERIALS AND METHODS

Study area and focal species

The study comprised the entire distributional range of S. polyschides, from western Norway southward to Morocco. This species inhabits rocky reefs from the intertidal down to 30 m depth (e.g. in Gibraltar) along continental coastlines. Offshore, it extends deeper (maximum c. 80 m) in more transparent waters such as the Gorrinse seamount, Alboran and the Strait of Messina (Norton, 1977; Assis et al., 2009; Flores-moya, 2012).

S. polyschides is annual semelparous with a complex heteromorphic life cycle typical of most kelp species (but not Durvillaea spp., commonly called Southern Hemisphere bull kelp, nor Ascophyllum nodosum, commonly called knotted kelp), alternating between a diploid macroscopic sporophyte and a haploid microscopic gametophyte. Sporophytes recruit mainly in spring, reaching highest abundances throughout the summer. Adults mostly release spores in late summer and die during autumn. Settled spores produce gametophytes, and after fertilization sporophytes wait until spring to resume growth (Pereira et al., 2011). This typical seasonal life history fits the seasonality of upwelling processes throughout most of the distribution; however, this relationship can be weaker where nutrient levels are permanently high (Pereira et al., 2015a).

Data on species occurrence and climate

Georeferenced occurrences describing this species’ distribution were gathered from field observations and the available literature. Records were only considered from 1990 onwards, and when locations were described in detail down to shore level (132 compiled records, see Appendix S1 in Supporting Information). These were gridded to 0.1° resolution and duplicate entries were only considered once (resulting in 128 gridded records).
Seasonal environmental predictors were produced to reflect the limiting factors and essential resources acting at each stage of this species’ complex life cycle (see Norton, 1977; Pereira et al., 2011, 2015a,b). Three-dimensional profiles of ocean temperature (OTemp), ocean salinity (OSal), nutrients (Phosphates and Nitrates) and light availability at the bottom of the ocean (Light) were averaged as summer (months = JAS), winter (months = ONDJF) and spring (months = MAMJ) environmental predictors (Table 1) and gridded to match the resolution of the distributional data (for technical details on environmental data refer to Appendix S2). All environmental surfaces were clipped using the General Bathymetric Chart of the Oceans (GEBCO; BODC 2013) so models would run on coastal regions and offshore banks, where depths are down to 30 m and 80 m respectively. This restriction was performed because there is no information for light attenuation in the data used to model past distributions.

**Ecological niche modelling**

The ENM in our study followed the methods of Assis et al. (2014) and Neiva et al. (2014). We chose boosted regression trees for its ability to model complex, non-linear relationships (Elith et al., 2008). The framework used 100 independent cross-validation iterations to increase model generality and identify a set of environmental predictors with higher potential for transferability among numerous candidates, using true skill statistics (TSS) as measure of accuracy (for technical details on cross-validation refer to Appendix S2). Models were performed using two approaches: (1) species modelling considering the full range of *S. polyschides* and (2) sub-taxon modelling with phylogeographical structure (i.e. within-taxon niche structure; Pearman et al., 2010), using distinct models for each geographical region identified as genetically differentiated (see genetic analyses below).

**Past and present distribution of *S. polyschides***

In the cross-validation procedure, several models may be identified as equally accurate. Therefore, the final maps were produced by merging (median function) the resulting surfaces of models using the most transferable subset of predictors (i.e. ensemble modelling) along with the full or split set of distribution records, depending on the modelling approach (species or sub-taxon).

The ensembles for the LGM and MH were fed with data from two atmosphere-ocean general circulation models (AOGCMs): the Model for Interdisciplinary Research on Climate (MIROC) and the Community Climate System Model (CCSM). These were chosen as they cover the range of variability found between most AOGCMs (Ramstein et al., 2007).

<table>
<thead>
<tr>
<th>Environmental predictor</th>
<th>Units</th>
<th>TP Sp.</th>
<th>TP Sub-T.</th>
<th>Relative importance (TSS)</th>
</tr>
</thead>
<tbody>
<tr>
<td>LT Ocean Temp. of the coldest winter month</td>
<td>ºC</td>
<td>5.7</td>
<td>5.9</td>
<td>*</td>
</tr>
<tr>
<td>LT Ocean Temp. of the coldest spring month</td>
<td>ºC</td>
<td>5.2</td>
<td>5.3</td>
<td>*</td>
</tr>
<tr>
<td>LT Ocean Temp. of the hottest winter month</td>
<td>ºC</td>
<td>21.6</td>
<td>21.4</td>
<td>*</td>
</tr>
<tr>
<td>LT Ocean Temp. of the hottest summer month</td>
<td>ºC</td>
<td>23.6</td>
<td>23.3</td>
<td>*</td>
</tr>
<tr>
<td>LT Ocean Temp. of the hottest spring month</td>
<td>ºC</td>
<td>18.4</td>
<td>18.3</td>
<td>*</td>
</tr>
<tr>
<td>LT lowest Salinity of the winter months</td>
<td>PSS</td>
<td>32.7</td>
<td>33.0</td>
<td>*</td>
</tr>
<tr>
<td>LT lowest Phosphates of the summer months</td>
<td>µmol.L⁻¹</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>LT lowest Phosphates of the spring months</td>
<td>µmol.L⁻¹</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>LT lowest Nitrates of the summer months</td>
<td>µmol.L⁻¹</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>LT lowest Nitrates of the spring months</td>
<td>µmol.L⁻¹</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>LT lowest Light availability of the spring months</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
</tbody>
</table>

Table 1 Environmental predictors used in ENM of *Saccorhiza polyschides*, their units, the tipping points for the species model (TP Sp.) and sub-taxon model (TP Sub-T.), and relative importance (TSS – true skill statistics) on the response of species model (for more information refer to Appendix S2).

Deep reefs are climatic refugia for genetic diversity
Because only OTemp and OSal were available on AOGCMs, past predictions did not consider Nutrients nor Light. This was adequate for prediction because the distribution of this species was largely explained by OTemp and OSal (see Results). Additionally, an ensemble performed with OTemp and OSal data only from AOGCMs averaged for 1990–2010 showed a good description of this species’ distribution and an accuracy of 0.95 (TSS; see Fig. S2 in Appendix S2).

Coastal regions and deep banks for the LGM were simulated by placing bathymetry at −120 m, below current sea level. The individual ensembles per genetic group were merged into a unique composite using a multiplicative probability function (Pearman et al., 2010). Finally, all maps were reclassified using a threshold maximizing sensitivity and specificity (the ability to detect presences and absences respectively), for the outputs (probability of occurrence) to stand for predicted presences and absences (e.g. Assis et al., 2015). Long-term refugia were inferred as those regions where the habitat was suitable during the LGM, MH and present-time (e.g. Assis et al., 2014).

Population genetic structure and diversity

Twenty-seven sites were sampled covering the whole distribution of *S. polyschides* by collecting a piece of the blade above the meristem from c. 25 haphazard individuals (Fig. 1a; Table 2). Samples were preserved in silica drying crystals. DNA extraction, polymerase chain reaction and allele scoring were performed as in Assis et al. (2013) for seven microsatellite loci developed for this species (Engel et al., 2008). Loci were tested for stuttering and null alleles using the software Micro-Cheker 2.2.3 (Van Oosterhout et al., 2004). $F_{IS}$ calculations and tests of Hardy–Weinberg equilibrium used Fstat 2.9.3 (Goudet, 1995), randomizing alleles (104 runs) among individuals within sites.

Genetic structure was inferred using Structure 2.3.4 (Pritchard et al., 2000) with admixture and without a priori population assignment. This ran the correlated allele frequency model with a burn-in time of $2 \times 10^5$ repetitions, $1 \times 10^6$ iterations and considering a range of clusters ($K$) from 1 to 10. The number of clusters was estimated using N Europe

<table>
<thead>
<tr>
<th>Region</th>
<th>Mean FST</th>
<th>Median FST</th>
<th>Jost’s D</th>
<th>HE</th>
</tr>
</thead>
<tbody>
<tr>
<td>N Europe</td>
<td>0.17±0.08</td>
<td>0.29±0.17</td>
<td>0.29±0.14</td>
<td>0.21±0.14</td>
</tr>
<tr>
<td>NW Iberia</td>
<td>0.448</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SW Iberia &amp; Morocco</td>
<td>0.46±0.18</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Figure 1 (a) List of samples and genetic subdivision of *Saccorhiza polyschides* based on Structure (individual multilocus genotypes). (b) Uppermost level of genetic structure, standardized allelic richness ($A$), standardized number of private alleles (PA) and gene diversity ($H_e$) per cluster for a common sample of 190 individuals. (c) Second hierarchical level of structure.
the DeltaK criterion of Evanno et al. (2005). Further structure was inferred by re-running Structure within clusters. Genetic structure was also inferred by factorial correspondence analysis (FCA) of population multicores using Genetix 4.05 (Bekhiri et al., 2004). Genetic differentiation was estimated between sites and within the main genetic clusters using both \( F_{ST} \) and Jost's \( D_{ST} \), using GenODive 2.0 (Meirmans & Van Tienderen, 2004). A hierarchical analysis of molecular variance (AMOVA) was performed in GenODive with \( 10^6 \) randomizations to test genetic structure (1) between individuals within sites (2), between sites within genetic clusters and (3) between genetic clusters.

Genetic diversity was estimated per site as gene diversity (expected heterozygosity, \( H_e \)), allelic richness (\( A \)) and number of private alleles (PA). These were standardized for the smallest sample sizes in terms of individuals within sites and genetic clusters, using \( 10^4 \) randomizations.

**RESULTS**

**Distribution of Saccorhiza polyschides through time**

The distribution of *S. polyschides* at this scale is mainly explained by ocean temperatures and salinity, particularly during winter and spring when generally only gametophytes and young sporophytes are present (\( O\text{Temp} \) ranging from 5.2°C to 21.6°C, and \( O\text{Sal} \) from 32.7 Practical Salinity Scale; Table 1; see Table S2 in Appendix S2). When modelled alone, these predictors obtained good accuracy scores (\( TSS > 0.60 \)) and when combined with others they produced gains in \( TSS \) from 0.11 ± 0.02 to 0.15 ± 0.03 (Table 1). Nitrates and Light produced poor to fair models when used alone (0.2 < \( TSS < 0.6 \)), while Phosphates had no ability to predict distributions (\( TSS < 0.2 \)). In general, Nitrates, Phosphates and Light had little contribution to model transferability, adding marginal gains to \( TSS \) when combined with other variables (gains in \( TSS < 0.05 \)).

The species and sub-taxon models produced for present times showed high resemblance to the known species' distribution (Fig. 2c) and retrieved accuracy scores (\( TSS \)) of 0.99 and 0.98 respectively. Both agreed that the niche of *S. polyschides* is currently available in depth throughout many north-eastern Atlantic and western Mediterranean seamounts, such as those adjacent to the Gulf of Cadiz, the Alboran Basin and in northern Lanzarote (Conception Bank). Despite similarities, the sub-taxon model predicted less suitable habitat throughout eastern Scottish shores, the seamounts of Celtic Sea, southern Bay of Biscay and southern Morocco. Hindcasting to the LGM

**Table 2** List of samples of *Saccorhiza polyschides*. Site number (\#) and name, country, longitude (Lon) and latitude (Lat) in decimal degrees, depth range (m), sample size (\( N \)), standardized allelic richness (\( A \)) and standardized number of private alleles (\( PA \)) for a common sample size of 18 individuals (\( \dagger \) indicates no standardized estimates due to sample size < 18), expected heterozygosity (\( H_e \)) and \( F_{IS} \) multilocus estimates (\( * \) indicates significant deviations from Hardy–Weinberg expectations, with Bonferroni correction for \( \alpha = 0.05 \)).
indicated that *S. polyschides* might have been distributed from Brittany to the south-west of France (Bay of Biscay), and continuously from north-west Iberia to Cape Bojador in Western Sahara (Fig. 2a). This analysis also supported its past occurrence in Canary and Madeira islands, in the Atlantic seamounts adjacent to the Gulf of Cadiz, and throughout the western Mediterranean Basin. Hindcasting to the MH set ranges similar to present times (Fig. 2b), but with the main difference that no suitable habitat was predicted for south-west Iberian and Norwegian shores (Fig. 2b,c). Additionally, the MH sub-taxon model predicted more suitable habitat in the English Channel and Balearic Islands, and less in NW Iberia and the Alboran Basin.

Predicting distributions through time pinpointed 4 main regions of long-term persistence (Fig. 2c), although with few differences depending on the modelling approach: (1) Brittany to Charentes (49.0°N to 45.5°N) and adjacent seamounts, (2) Northwest Iberia (44.0°N to 39.0°N or to 38.5°N in species model), (3) Gibraltar and Alboran Basin (36.5°N to 35.5°N), the (4) Atlantic seamounts adjacent to the Gulf of Cadiz (37.0°N to 33.3°N) plus Conception bank in Lanzarote (29.5°N) and Dagia seamount (31.0°N; species model only).

**Population genetic structure and diversity**

A total of 162 alleles resulted from 714 unique multilocus genotypes (23.14 ± 9.71 alleles per locus, ranging from 10 to 38) sampled throughout 27 sites (Fig. 1a; Table 2). Microchecker showed no signs of stuttering error while null alleles were rare to uncommon (proportion per locus < 0.2) and with no consistency among regions or sites. Significant $F_{IS}$ values were obtained in 12 out of 27 sites (Table 2).

The Structure analysis performed with the Evanno criterion revealed three main clusters: (1) northern Europe, (2) north-west Iberia and (3) south-west Iberia & Morocco (Fig. 1b; see Appendix S3). The subsequent hierarchical level of genetic Structure divided N Europe and NW Iberia in two sub-clusters, whereas SW Iberia & Morocco was divided into three sub-clusters (Fig. 1c; see Appendix S3). The FCA retrieved similar results (Fig. 3), supporting the aforementioned clusters of N Europe, NW Iberia (including Arrábida and Lagos; sites 20 and 23) and SW Iberia & Morocco.

The FCA analysis also showed that genetic differentiation within each of the three main clusters increases from north–south. Sites are less differentiated within the N European cluster, followed by NW Iberia and SW Iberia & Morocco. This trend was supported by pairwise Jost’s $D$ but not by pairwise $F_{ST}$ (Fig. 1b; see Appendix S3).

Allelic richness per site was highest in the southern sites Tarifa, Arrifana and Ormonde, followed by the northern Iberian sites from Cabo Vidio to Caion and by Arrábida and Odeceixe in SW Iberia (Table 2). These sites had approximately 1.5–2-fold higher diversity than most of the others.
Kamykowski & Zentara, 1986), temperature responses could come from high temperature waters are generally nutrient depleted than the adults (Norton, 1997; Fernandes et al., 1996). The minor contribution of Light in the models is likely the result of our modelling space structure, which reflected a prior step segregating coastal cells (down to 30 m depth) from offshore banks, and missing enough spatial resolution to distinguish areas above and below depth limits where light effectively restricts coastal distributions (e.g. Graham et al., 2007).

Both the species and the sub-taxon models retrieved very similar predictions, physiological tipping points and accuracy scores. These results do not support a previous study showing that sub-taxon models predict wider suitable habitats and improve accuracies, when compared to entire range models (Pearman et al., 2010). The non-overlapping character of phylogroups, together with the conservative nature of our pseudo-absences (high thresholds), may be the cause for the more truncated niche distributions of sub-taxon models. Either way, because this class of models relies on combining distinct niche responses throughout ranges, the general agreement found between modelling approaches points to niche conservatism across distinct genetic groups in S. polyschides; a hypothesis already verified for populations belonging to different genetic groups (N Europe versus NW Iberia), which showed identical physiological responses to extreme environmental stress (Pereira et al., 2015b). The lack of niche differentiation provides better support for our modelling results, which are particularly relevant for some regions like deep offshore reefs, where this kelp may currently find favourable habitat conditions. While we were able to validate this for Ormonde (c. 35 m depth), many other Atlantic and Mediterranean seamounts, unsurveilled to date, seem plausible candidates. For instance, loose fronds of S. polyschides were found c. 30 km from Conception Bank (northern Lanzarote; Ballesteros et al., 1992), where our models predicted it at depth (c. 70 m depth, as inferred from GEBCO).

Hindcasting to the LGM showed that the distribution in northern Europe might have been restricted to a single population distributed from Brittany to the Bay of Biscay, whereas a wider distribution was likely throughout northern Africa, the Atlantic islands and the Mediterranean, as predicted for other brown algae (e.g. Neiva et al., 2014). Hindcasting to the MH suggested a contrasting trend, with extensive range expansion to northern regions and southern contraction, as in other marine taxa displaying similar distribution (Assis et al., 2014). By combining the ENM outcomes, we were able to identify four regions where this species may have found refugia. Other studies partially agree with our findings, also suggesting a broad region from...
Brittany to Charentes and NW Iberia as putative refugia for cold-temperate species (e.g., Maggs et al., 2008; Neiva et al., 2014). In contrast, neither the deep Gibraltar and Alboran regions, nor Atlantic seamounts had been previously highlighted for their refugial roles. While the former two fall within the NW Africa refugium where intertidal species may have persisted (Assis et al., 2014), their deep refugial role and that of seamounts are novel and bring forward new hypotheses for the role of deep reefs in harbouring persistent populations of subtidal species during warmer periods like the MH or the near future (e.g. Raybaud et al., 2013).

Phylogeography of *S. polyschides*

Our results revealed three main genetic clusters, followed by a second and more complex level of structure comprising seven clusters. All showed significant differentiation and private alleles, suggesting large effects of drift, not offset by regular gene flow. The isolation of phylogroups was in general agreement with our models, which predicted disjunct distributions between N Europe and NW Iberia. Most of SW Iberia & Morocco was further predicted far apart (Atlantic seamounts, Gibraltar and Morocco). However, differentiation between Arrabida and its northern neighbouring sites was higher than expected given their proximity. This region displays identical genetic breaks for other marine species, a pattern previously explained by nearshore discontinuities in ocean currents (Diekmann et al., 2005). Sharp genetic structure at such short distances may also result from the higher densities found north of Arrabida (Assis et al., 2013), which could halt the expansion of immigrant genes by density barrier effects (Neiva et al., 2012b). Likewise, the absence of strong oceanographic barriers between the west and north shores of Iberia (Ruiz-Villarreal et al., 2006), where structure was found at short distances (sites 13–14, Fig. 1c), further suggests that density may influence gene flow in *S. polyschides*.

The current northern European distribution may stem from a single refugium, from which complex colonization routes are suggested by the patterns of genetic structure and differentiation. During expansion, northern territories might have been colonized using both the alongshore current (Charria et al., 2013) across the English Channel and into the Irish Sea, and the deeper offshore current (Pingree & Le Cann, 1989), from Charentes polewards to western Ireland, Scotland and Norway. In any case, founder effects may have contributed markedly to the current genetic structure in northern Europe.

The lower diversity and fewer private alleles in sites colonized after the LGM is expected from founder effects at leading edges (Hewitt, 1996; Excoffier et al., 2009). However, the decreasing gradient in diversity found from Plymouth towards Charentes was unexpected, because our models predicted some degree of persistence in that region. Hence, erosion of genetic diversity might have occurred there, possibly due to low effective population size when currently found at a distributional edge (near a range gap), off their climatic optima (Eckert et al., 2008; Assis et al., 2014). Indeed, our models predicted marginal, although persistent, populations in Charentes during the MH and the present.

The diversity and private alleles found in Tarifa and Ormonde agree with our models, which placed these sites within refugia. Unexpectedly, Tarifa is the hotspot of genetic diversity for this species, despite being very isolated and located at the warm range edge. This might be related to the persistent upwelling system occurring there, which provides nutrients to sub-surface waters (Sarhan et al., 2000). The also remarkable private diversity found in Arrabida likewise supports long-term persistence, as predicted by the species modelling approach. These sites could be the remnants of a much wider southern population that may have (re)colonized SW Iberia (Arrifana and Odeceixe) and Morocco (El Jadida and Essaouira) after the predicted range contraction during the MH; thereby preserving the high regional diversity of these lower latitudes. However, the large number of private alleles in some SW Iberian sites (e.g. Arrifana), suggests population reestablishment from other unknown sources of diversity, or persistence there, in contrast to our predictions. The genetic bottlenecks inferred there could result either from the recent documented local extinctions (Assis et al., 2013) or from the MH contraction per se, because populations could have persisted, although with lower effective sizes. The low diversity throughout Morocco, where populations are currently restricted to small (area) and isolated upwelling pockets (Pastor et al., 2008), could have resulted from random drift. However, the few private alleles there do not support persistence but rather a post-MH (re)colonization.

The present diversity in NW Iberia, although lower relative to southern sites, also coincides with an inferred climatic refugium. The lower diversities may result from the smaller population sizes, as this region only comprises c. 200 km of coastline (as for Morocco). Additionally, recent bottlenecks due to poorer niche conditions may also have occurred, as populations now have shorter generations and a smaller fraction becomes reproductive (Fernández, 2011). Peripheral niche conditions may further explain the even lower diversity found from that region southwards (from Porto Novo to Ericeira), as it might have been the rear edge of the Iberian distribution during the MH. Because these sites are mostly restricted to shallow waters (Assis et al., 2009), deeper colonizations might not have been possible during warming periods. Later, as climate conditions ameliorated, dispersal barriers acting there (e.g. oceanographic and/or density, as previously discussed) might have blocked admixture with richer populations, maintaining the lower levels of diversity.

Higher genetic differentiation towards southern latitudes was revealed both by FCA and Jost’s D, which is more appropriate than $F_{ST}$ to compare populations with contrasting levels of diversity (Whitlock, 2011), as in our case. This differentiation is consistent with the isolated nature of south-
ern sites, mostly found at deeper reefs or particular regions of upwelling. The exceptionally high differentiation between Lagos and its neighbouring sites while being very similar to sites further north, is likely the result of a recent colonization taking place after 1970 (absent before, Ardré, 1970), probably from Arrábida or Ericeira (Fig. 3; see Appendix S3). The low diversity and complete absence of private alleles in Lagos further supports this and points to the effectiveness of rare dispersal events driven by floating rafts.

We also found a southward trend in increasing homozygosity, despite the increasing diversity. One hypothesis for this pattern is related to subpopulation structure. If arrested, development of microscopic stages (Carney et al., 2013) is more common towards the warmer and nutrient-poorer south (one of the hypotheses in Assis et al., 2013), it could generate co-existence of multiple subpopulations thereby promoting departures from random mating (temporal Wahlund effect; Morand et al., 2002). A second and non-exclusive hypothesis is supported by the lower sporophyte densities at most southern sites (Assis et al., 2013). The higher spatial distance between sporophytes in the south implies that spores settle surrounded by siblings, resulting in gametophytes that are less intermingled with those from more genetically distant individuals, thereby increasing selfing and biparental inbreeding. The presence of null alleles could also explain such pattern, although this is poorly supported given their low prevalence in our data and the absence of a particular geographical trend.

Taken together, our results show evidence of how diverse factors shape the genetic traits of species at multiple scales. At larger scales, the trajectory of climate changes defines source and sink ranges, while at finer scales, nearshore currents and density barrier effects result on a mismatch of gene flow and the dispersal capacity of S. poly-schides. Most of this species’ phylogeography was also unravelled, particularly from the LGM to present times. Great part of the present species range comprises the post-glacial expansion zone, which may stem from an unique source from the Brittany to Charentes region, whereas there is no evidence for range expansion derived from the NW Iberian refugium. The deep populations in Gibraltar, Alboran and the Atlantic seamounts are supported as important safekeepers of divergent lineages in a marine brown alga.

The implementation of the MH in our models showed that the erosion of genetic diversity driven by climate changes may not be unique to the lower latitude trailing edges. These processes may mask regions of persistence with lower diversity, despite formerly richer states. Furthermore, the predicted consequences of the warmer MH may serve as a reasonable proxy for those happening in the near future. While local extinctions reduce the overall genetic diversity and therefore the evolvability of species as a whole (Hampe & Petit, 2005), our study suggests that species like kelp may find refugia at depth, away from the overall warming trend of surface waters. Depth range shifts have been reported for other kelp species in response to warming trends (e.g., Ladah & Zertuche-Gonzalez, 2004; Pehlke & Bartsch, 2008). Like terrestrial elevational range shifts in the face of climate change (Epps et al., 2006), going deep may allow unique genetic lineages to persist in small pockets of cryptic refugia that might otherwise become extinct, in contrast with vanishing intertidal populations likely unable to shift in depth (e.g., Assis et al., 2014; Neiva et al., 2015).

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Assis, J., Tavares, D., Tavares, J., Cunha, A., Alberto, F. & Serrão, E.A. (2013) Genetic diversity and complete absence of private alleles in Lagos and its neighbouring sites while being very similar to sites further north, is likely the result of a recent colonization taking place after 1970 (absent before, Ardré, 1970), probably from Arrábida or Ericeira (Fig. 3; see Appendix S3). The low diversity and complete absence of private alleles in Lagos further supports this and points to the effectiveness of rare dispersal events driven by floating rafts.

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**SUPPORTING INFORMATION**

Additional Supporting Information may be found in the online version of this article:

**Appendix S1** Records of occurrence for ENM.

**Appendix S2** Supplementary methods and results regarding climate data and ENMs.

**Appendix S3** Supplementary results regarding genetic structure, diversity and differentiation.

**DATA ACCESSIBILITY**

Microsatellite data used for genetic analyses are available in the Figshare repository at http://dx.doi.org/10.6084/m9.figshare.1510947.
BIOSKETCH

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