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First record of *Laminaria ochroleuca* Bachelot de la Pylaie in Ireland in Béal an Mhuirthead, county Mayo

Kathryn M. Schoenrock^{1*} , Tony O'Callaghan², Rory O'Callaghan² and Stacy A. Krueger-Hadfield³

Abstract

Background: During a biodiversity survey of Béal an Mhuirthead, Co. Mayo, a small population of *Laminaria ochroleuca* Bachelot de Pylaie was discovered in a semi-protected cove on the northwest part of the headland among a mixed macroalgal assemblage including the kelps *Laminaria digitata* and *Saccharina latissima*. This is the first record of this southern European species in Irish waters.

Methods: Individuals were morphologically identified by their smooth stipes, conical, claw-like holdfasts, broad golden blades and all regions of the thallus were devoid of epibiota. Individual *L. ochroleuca* were genetically identified using the mitochondrial *atp8* gene, and all belonged to the same haplotype previously found in France and Portugal.

Results: Using 12 microsatellite loci, we found 34 alleles from 15 genotyped sporophytes. Multilocus estimates of allelic diversity and expected heterozygosity were comparable to sites sampled in the Iberian Peninsula (0.427 and 0.562 on average respectively) despite strong genetic differentiation between Scots Port and other sites throughout the known European range. There was a general trend of heterozygote excess which may indicate recent admixture following a founder event(s).

Conclusions: The appearance of this southern European kelp species raises many questions including i) how widely distributed it is in Ireland, ii) how it arrived at this northwestern point of the country if it is not widely distributed in Ireland, and iii) whether it can withstand low winter temperatures *L. ochroleuca* was previously thought not to endure. More detailed surveys in Irish kelp forests should take place to determine the distribution of this kelp and its impact on the Irish kelp forest ecosystem.

Keywords: Range expansion, Golden kelp, Ireland, Species distributions, Population genetics

Introduction

Kelp forests along European coastlines are composed of stipitate kelps in the Laminariales as well as one member of the Tilopteridales, *Saccorhiza polyschides*. Most subtidal communities from the United Kingdom (UK) and Ireland northward are dominated by the boreal kelp *Laminaria hyperborea* (Gunnerus) Foslie (Araújo et al., 2016). In the southern UK, kelp forests include a Lusitanian species, *Laminaria ochroleuca* Bachelot De la Pylaie, that is found from the lower limit of the intertidal

zone down to 18 m, in monospecific or mixed kelp populations at semi-exposed sites. The first record of *L. ochroleuca* in the UK was in the early twentieth century, either due to increased survey intensity or because the species expanded its distribution (Parke, 1948). Today, the known northern range extends from Brittany, France to its limit in Devon, UK (Araújo et al., 2016; Gayral, 1958; John, 1969), but no *L. ochroleuca* has been recorded in the Republic of Ireland during previous subtidal or intertidal surveys (Simkanin et al., 2005; Picton & Morrow, 2006).

Laminaria hyperborea and *L. ochroleuca* are easily distinguished through morphological features, especially the rugosity of *L. hyperborea* stipe and fouling

* Correspondence: kathryn.schoenrock@nuigalway.ie

¹Department of Zoology, School of Natural Sciences, Ryan Institute, National University of Ireland Galway, University Rd, Galway, Ireland H91 TK33
Full list of author information is available at the end of the article



throughout the thallus (Bunker et al., 2017). The two species also have similar growth features, such as annual rings that can be used to age individuals, but *L. ochroleuca* is host to ~86x and 12x fewer epibiota on the stipe and holdfast (respectively) than *L. hyperborea* (Smale et al., 2015; Teagle & Smale, 2018). It is thought that the distribution of *L. ochroleuca* may be restricted to southern Europe because the optimal thermal range for sporophytes is between 12 and 22 °C (Franco et al., 2018). Gametophytes have an even narrower optimal thermal range for development, fecundity and germination between 15 and 18 °C (Izquierdo et al., 2002). However, predictions for species distributions indicate both *L. ochroleuca* and *L. hyperborea* will increase in abundance in northern habitats, coupled with subsequent retraction along their southern limits (Assis et al., 2018a; Assis et al., 2018b).

Kelp ecosystems are fluctuating in abundance and distribution, and undermanaged worldwide in terms of restoration and basic understanding of ecosystem function (Wernberg et al., 2019). The loss of these foundation species could lead to ecosystem collapse (Castorani et al., 2018) and changeover of dominance to alien primary producers, whether as biological invasions or 'natural' range expansions, can result in a significant reduction of alpha-diversity (Bernard-Verdier & Hulme, 2015), which has been shown in the epibiotic communities that certain members of European kelp forests can support (Smale et al., 2015; Teagle & Smale, 2018). Understanding the population dynamics and genetic variation of species is important for habitat monitoring and monitoring ecosystem function (Epstein & Smale, 2017; Krueger-Hadfield et al., 2017). Here, we report the first record of *Laminaria ochroleuca* in the Republic of Ireland, discovered during a citizen science marine habitat survey effort (inter- and subtidal) between National University of Ireland (NUI) Galway, Porcupine Marine Natural History Society (PMNHS), and Seasearch Ireland in Béal an Mhuirthead, Co. Mayo. We also report and compare the genetic diversity differentiation of the *L. ochroleuca* Scots Port population, the only known Irish population, to other sites in Europe (Assis et al. 2018b).

Methods

Surveys

Marine habitat surveys took place as a joint-effort between PMNHS and Seasearch Ireland during September 2018. SCUBA surveys in kelp habitats took place around the coastline of Béal an Mhuirthead from 0 to 11 m depth (Table 1), and species presence and abundance were noted using standard SeaSearch methodologies (SACFORN method; <https://bd.eionet.europa.eu/>). A small population of *L. ochroleuca* (~100 individuals

Table 1 Coordinates of dives sites where kelp populations were found in Béal an Mhuirthead, county Mayo, Republic of Ireland. Site names and dominant kelps within communities are noted (*Laminaria hyperborea*: Lh, *Laminaria ochroleuca*: Lo)

Site	Kelp	Latitude	Longitude
Muing Creena	Lh	54.27270556	-9.95722
Blacksod Pier	Lh	54.09106944	-10.055
Blacksod Harbor	Lh	54.10380278	-10.0625
Danish Cellar	Lh	54.289875	-9.9875
Scots Port	Lo	54.256775	-10.0775

counted) was discovered in a sheltered cove called Scots Port (Table 1) on the northwest facing coastline of Béal an Mhuirthead, September 10th, 2018. Divers returned to Scots Port on September 13th, 2018 and collected small portions of the *L. ochroleuca* blades near the apical meristem. Samples from 15 individuals were wiped clean of epiphytic diatoms and filamentous algae, preserved in silica gel, and shipped to the Krueger-Hadfield Lab at the University of Alabama at Birmingham (UAB) for genetic identification and diversity analyses.

DNA extraction

Approximately 12 mg of silica-dried tissue from each specimen was placed in 1.5 mL microcentrifuge tubes and were, then, ground with 2.8 mm ceramic beads using a bead mill (BeadMill24, Fisher Scientific, Waltham, MA, USA). Total genomic DNA was extracted using the Nucleospin® 96 Plant Kit (Macherey-Nagel, Düren, Germany) according to manufacturer's instructions except for the lysis step in which samples were incubated for 1 h at room temperature. DNA was eluted in 100 µL of molecular grade deionized water.

Genetic species identification

In order to genetically confirm specimens were *Laminaria ochroleuca*, we sequenced the mitochondrial intergenic spacer region between *atp8* and t-RNA serine genes using the primers developed by Voisin et al. (2005). Polymerase Chain Reaction (PCR) amplification was performed on a total volume of 25 µL, containing 1 U of *taq* DNA polymerase, 2.5 mM of each dNTP, 2 mM MgCl₂, 1 x reaction buffer, 250 nM of each primer and 5 µL of template DNA (diluted 1:100). The PCR program included 1 min at 95 °C, 32 cycles of 30 s at 95 °C, 30 s at 50 °C, and 30 s at 72 °C, followed by a final elongation at 72 °C for 5 min. Approximately, 5 µL of PCR product using 1 µL of Orange G loading dye were visualized on 1.5% agarose gels stained with GelRed (Biotium, Fremont, CA, USA).

One µL of ExoSAP-It (Affymetrix, Santa Clara, CA, USA) was added to 7 µL of PCR product and incubated for 15 min at 37 °C followed by 15 min at 80 °C. Four µL

of 2 μ M primer were added to each product and sequenced in the forward direction commercially by Eurofins Genomics (Louisville, KY, USA). Sequences were edited using *4Peaks* (Nucleobytes, The Netherlands), aligned with the haplotypes listed in Table 1 from Rothman et al. (Rothman et al., 2017): DQ841612 (France), KY911984 (Portugal), and DQ841611 (Portugal) using *Muscle* (Edgar, 2004) in *Seaview* ver. 4.6 (Gouy et al., 2010) with default parameters.

Fragment analysis and allele calling

Twelve microsatellites previously developed for *L. ochroleuca* (LoIVVIV-23, LoIVVIV-26, LoIVVIV-17, LoIVVIV-7, Lo5–8, LoIVVIV-13, LoIVVIV-16, LoIVVIV-27, LoIVVIV-10, LoIVVIV-15, LoIVVIV-28, LoIVVIV-24; Coelho et al., 2014) were used to genotype 15 *L. ochroleuca* specimens. All microsatellite loci were amplified in simplex PCRs using either SimpliAmp or ProFlex thermocyclers (Applied Biosystems, Foster City, CA, USA). We used a 15 μ L final volume containing 1X GoTaq[®] Flexi colorless reaction buffer (Promega Corp., Madison, WI, USA), 1.5 mM MgCl₂, 250 μ M of each dNTP, 0.5 units of GoTaq[®] DNA polymerase (Promega Corp.) 150 nM labeled forward primer, 150 nM unlabeled forward primer, 250 nM unlabeled reverse primer, and 2 μ L of template DNA (diluted to 1:100).

PCR products from each locus were combined into three poolplexes for fragment analysis: M1 (LoIVVIV-23 VIC, LoIVVIV-26 PET, LoIVVIV-17 NED, LoIVVIV-7 6-FAM), M2 (LoIVVIV-58 VIC, LoIVVIV-13 PET, LoIVVIV-16 NED, LoIVVIV-27 6-FAM), and M3 (LoIVVIV-10 VIC, LoIVVIV-15 PET, LoIVVIV-28 NED, LoIVVIV-24 6-FAM). One μ L of each PCR product was added to a poolplex containing 10 μ L of loading buffer including 9.7 μ L of HiDi Formamide (Applied Biosystems, Foster City, CA, USA) and 0.35 μ L of size standard (GeneScan500 Liz; Applied Biosystems). Samples were electrophoresed on an ABI 3730xL genetic analyzer equipped with a 96-capillary array (Applied Biosystems). Alleles were scored manually using GENEIOUS PRIME 2019.0.3 (<https://www.geneious.com>). We attempted to re-PCR individuals missing genetic information at a locus at least twice. Allele sizes were binned with TANDEM software (Matschiner & Saltzburger, 2009). Microsatellite loci whose average rounding error was below 10% of the repeat size, as assessed by TANDEM (Matschiner & Saltzburger, 2009), are useful for subsequent analyses. In order to compare our data to that recently published by Assis et al. (2018a), we merged our allele calls by comparing the most frequent allele in the closest populations (located in Plymouth, United Kingdom, and sites in Brittany, France). Differences in allele sizes are constant through the range of a locus and differences between studies can be due to different PCRs

or allele calling methods. After converting our alleles, the frequency of null alleles was estimated using ML-NullFreq (Kalinowski & Taper, 2006) with 1000 randomizations.

Genetic diversity and differentiation analyses

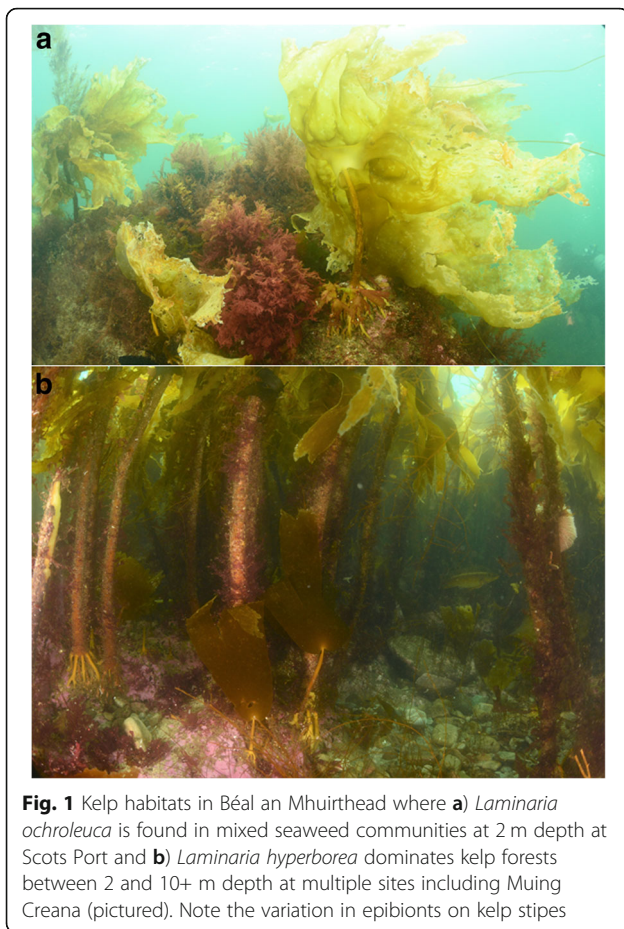
Using the 12 loci described above, we first evaluated gametic disequilibrium using the single multilocus estimate \bar{r}_d (Agapow & Burt, 2001) and implemented in the *R* package *poppr* ver. 2.0.2 (Kamvar et al., 2014). In order to test for departure from random associations between loci, the observed data set was compared to 1000 simulated datasets in which sex and recombination was imposed by randomly reshuffling the alleles among individuals for each locus (Agapow & Burt, 2001) followed by Bonferroni correction (Sokal & Rohlf, 1995). The two alleles of the same locus were shuffled together to maintain associations between alleles within loci in the randomized dataset. In addition to physical linkage on a chromosome, disequilibria may be due to a lack of recombination caused by selfing (mating system) or to differences in allele frequencies among populations (spatial genetic structure). Second, the average expected heterozygosity (H_E) and observed heterozygosity (H_O) were calculated using GenAlEx ver. 6.5 (Peakall & Smouse, 2006; Peakall & Smouse, 2012). Third, tests for Hardy-Weinberg proportions were performed using FSTAT, ver. 2.9.3.2 (Goudet, 1995). F_{is} was calculated for each locus and over all loci according to (Weir & Cockerham, 1984) and significance was tested by running 1000 permutations of alleles among individuals within samples.

Next, we compared our data from Scots Port to the data set from Assis et al. (Assis et al., 2018a). We combined our data sets and used the following 10 loci in which we had both genotyped our specimens: LoIVVIV-23, LoIVVIV-26, LoIVVIV-17, LoIVVIV-7, LoIVVIV-16, LoIVVIV-27, LoIVVIV-10, LoIVVIV-15, LoIVVIV-28, LoIVVIV-24. We re-estimated the mean expected number of alleles (A_E) and the private allelic richness (P_E) on the smallest sample size of 11 sporophytes (i.e., 22 alleles) as previously analyzed by Assis et al. (2018a) using the program HP-Rare ver. 1.0 (Kalinowski, 2005). Finally, we calculated pairwise genetic differentiation for each pair of sites as *Jost's D* in *Genodive* ver. 2.0b23 (Meirmans & Van Tienderen, 2004).

Results

Surveys and species identification

Scots Port has a mixed bottom, with bedrock and boulders on the north side of the cove where *L. ochroleuca* (Fig. 1a) and the kelp *L. digitata* were found, and a cobble bottom modified by waves throughout the mid-south part of the cove where the kelp *Saccharina latisima* and many mixed seaweeds were found. *Laminaria*



ochroleuca is identified by its smooth, stiff stipe, golden broad blade, and relatively uncolonized claw-like holdfast (Fig. 1a; Bunker et al., 2017). Interestingly, *L. ochroleuca* was not found at other kelp forest sites along the coastline of Béal an Mhuirthead (Table 1) which are dominated by *L. hyperborea* (Fig. 1b), and include *Alaria esculenta*, *Saccorhiza polyschides*, *S. latissima* and *L. digitata*. Potential vectors for *L. ochroleuca* are few in the area, as Black Sod Pier is only open to small fishing vessels and recreational craft, but there is potential that the bay may offer refuge to larger vessels in bad weather conditions.

All thalli sequenced with the *atp8* mitochondrial marker belonged to the same haplotype (GenBank Acc. No. TBD) that matched the haplotype found in France and Portugal and reported in Rothman et al. (2017).

Genetic diversity and differentiation

All loci exhibited rounding errors below 10% of the repeat size (Additional file 1: Table S1). Only loci LoIVVIV-58 and LoIVVIV-13 showed evidence of null alleles (Additional file 1: Table S1). For LoIVVIV-58, the frequency was 0.05, whereas, for LoIVVIV-13, the

frequency was 0.31. Therefore, we performed some of the subsequent analyses for Scots Port specifically on a dataset with and without LoIVVIV-13. Maximum likelihood estimators, such as ML-NullFreq, assume random mating in order to estimate null allele frequency (Kalinowski & Taper, 2006), but have been shown to be biased in other seaweeds in populations in which random mating does not occur (Krueger-Hadfield et al., 2013; Krueger-Hadfield et al., 2016). Thus, simply removing the locus may obscure important biological information (see, for example, Hansen & Taylor 2008).

The number of alleles per locus ranged from 1 to 4 (Additional file 1: Table S1), for a total of 34 alleles detected across the 15 individuals at 12 loci (Additional file 1: Table S2).

There was no evidence of gametic disequilibrium based on the multilocus estimate \bar{r}_d (including LoIVVIV-13: $\bar{r}_d = 0.017$, p -value > 0.3; excluding LoIVVIV-13: $\bar{r}_d = 0.044$, p -value > 0.1).

Expected heterozygosity varied from 0 to 0.696, with multilocus estimate of 0.427, and observed heterozygosity varied from 0 to 0.933, with a multilocus estimate of 0.562. Locus LoIVVIV-13 was the only locus with a positive F_{is} , though it was not significantly different from 0 (Table 2). The other loci were all generally negative and the overall F_{is} value was significantly negative after Bonferroni correction when LoIVVIV-13 was removed, and when only 10 loci used by this study and by Assis et al. (2018a) were used.

The *L. ochroleuca* population at Scots Port exhibited allelic and private allelic richness, expected heterozygosity, and observed heterozygosity levels that were greater than nearby sites grouped in the Western English Channel by Assis et al. (2018a) (see Table 3 this study). Indeed, estimates were more similar to sites sampled in the southern Iberian Peninsula, the Azores, and north western Africa despite strong differentiation from these populations (Table 4). While the level of genetic differentiation was lower when compared to the sites in the Western English Channel, the average differentiation was 0.331, suggesting strong variation between this Irish site and sites in England and France (Table 4).

Discussion

We confirm the presence of *Laminaria ochroleuca* in the Republic of Ireland. Scots Port is located ~ 1040 km away from the nearest population of *L. ochroleuca* in the UK and ~ 1630 km away from the nearest population in France. The knowledge of Irish kelp forest ecosystem is woefully inadequate, including simple natural history information, such as species distributions. Thus, the presence of *L. ochroleuca*, which is known to harbor much less biodiversity than *L. hyperborea*, its congeneric

Table 2 Multilocus genetic and genotypic diversity estimates for *Laminaria ochroleuca* based on 12 microsatellite loci including LoIWIV-23, 11 loci excluding LoIWIV-13, and 10 loci excluding Lo5–8 and LoIWIV-13 (Lo5–8 was not used in Assis et al. 2018b)

Locus	H_E	H_O	F_{IS}
LoIWIV-23	0.067	0.067	0.000
LoIWIV-26	0.000	0.000	NA
LoIWIV-17	0.557	0.769	-0.404
LoIWIV-7	0.625	0.933	-0.519
Lo5–8	0.591	0.615	-0.043
LoIWIV-13 *	0.696	0.286	0.598
LoIWIV-16	0.516	0.643	-0.258
LoIWIV-27	0.395	0.467	-0.188
LoIWIV-10	0.538	0.769	-0.455
LoIWIV-15	0.611	0.714	-0.176
LoIWIV-28	0.460	0.667	-0.474
LoIWIV-24	0.568	0.600	-0.059
Multilocus including LoIWIV-13 (12 loci)	0.469 ± 0.063	0.544 ± 0.083	-0.168
Multilocus excluding LoIWIV-13 (11 loci)	0.448 ± 0.065	0.568 ± 0.087	-0.280
Multilocus excluding LoIWIV-13 and Lo5–8 (10 loci)	0.429 ± 0.071	0.556 ± 0.097	-0.313

H_E , Nei's unbiased expected heterozygosity; H_O , observed heterozygosity; F_{IS} , inbreeding coefficient (adjusted p -value = 0.0045). Significant values are shown in bold. * Locus LoIWIV-13 had null alleles (see Additional file 1: Table S1)

and current dominant species in Boreal kelp forests, necessitates further studies beginning with obtaining distributional data.

Assis et al. (2018a) suggested that the dispersal capability of *L. ochroleuca* can be as far as thousands of kilometres, but fewer than 5% of dispersal events would extend beyond 3.63 km. All estimates are greater than dispersal distances of conspecific *L. hyperborea*, which is estimated to be 300 m for zoospores (Fredriksen et al., 1995). Thus, greater predicted dispersal distances in *L. ochroleuca* may explain its arrival, via rafting or another mechanism, in this remote cove in Co. Mayo. Alternatively, *L. ochroleuca* may be far more widespread than originally thought, extending in linear series along Ireland's coastline. Other kelps, such as *L. digitata* and *L. hyperborea*, exhibit strong patterns of isolation by distance (e.g., Robuchon et al. 2014). If there are more *L. ochroleuca* populations in Ireland, we may expect a similar pattern to the stepping-stone connectivity suggested by Assis et al. (2018a), in which case we would expect strong differentiation between English and French sites with Scots Port. In addition to genetic patterns, tolerance to the average winter temperature (8 ± 1 °C; www.met.ie) and low irradiance in this area of Ireland is not expected for *L. ochroleuca* and suggests physiological plasticity in this species that warrants further investigation.

We found allelic diversity and expected heterozygosity to be more like populations in the Iberian Peninsula than France and the UK (Table 3) when adjusting for the

same sample size and the same set of markers from a previous study of *L. ochroleuca* (Assis et al., 2018a). While this Irish population appears to be reproducing sexually, the overall F_{IS} value was negative, indicating heterozygote excess. The breeding population at Scots Port could be small, in which only a few individuals contribute to the next generation such that there are allele frequency differences between female and male gametophytes by chance alone (Rassmussen, 1979). In small, sexual populations, if individuals cannot undergo selfing, then the chances of producing homozygous offspring are less (Balloux, 2004). Though *L. ochroleuca* could, in theory, undergo intergametophytic selfing (Klekowski, 1969), in which gametophytes mate that share the same diploid sporophytic parent, there is no evidence of which we are aware to suggest this type of mating system as F_{IS} values were zero or generally negative (Table 2; see Assis et al. 2018a). We only genotyped adult sporophytes and would need to genotype young sporophytes to determine if there were departures from Hardy-Weinberg in germ-lings as well (Stoeckel et al., 2006). Alternatively, some species may be more prone to heterosis (Hansson & Westerberg, 2002) in which the most homozygous individuals are lost over time. To determine whether this might be true in the Scots Port population of *L. ochroleuca*, we would also need to genotype young sporophytes to determine if there is a general trend of increasing heterozygosity in older sporophytes. This is especially interesting because site conditions are outside the thermal niche of *L. ochroleuca* (Franco et al., 2018;

Table 3 A_E , allelic richness, and P_E , private allelic richness, calculated using rarefaction based on a sample size of 11 diploids or 22 alleles based on the smallest sample size included in analyses by Assis et al. (2018b)

Site	A_E	P_E	H_E	H_O
Scots Port, Ireland	2.49	0.29	0.429	0.556
Plymouth	1.81	0.03	0.177	0.185
Port Blanc	1.68	0.06	0.185	0.197
Lorient	2.16	0.13	0.223	0.187
A Coruña	2.87	0.13	0.342	0.340
Laxe	2.80	0.17	0.363	0.364
Camariñas	3.04	0.04	0.372	0.363
Viana do Castelo	2.51	0.05	0.298	0.275
Amorosa	3.75	0.17	0.446	0.437
S. Bartolomeu do Mar	1.89	0.08	0.266	0.215
Peniche	3.94	0.21	0.503	0.498
Espichel	2.10	0.17	0.321	0.339
Sesimbra	3.33	0.13	0.386	0.341
Ormonda seamount	2.80	0.07	0.320	0.398
Gorringe seamount	2.78	0.23	0.319	0.279
Gettysburg seamount	2.89	0.14	0.316	0.307
Tarifa	4.82	0.44	0.459	0.450
El Jadida	3.97	0.56	0.443	0.396
Essaouira	2.65	0.23	0.321	0.309
Formigas Bank	3.11	0.50	0.335	0.306
<i>Regions</i>				
W English Channel	1.88 ± 0.14	0.07 ± 0.03	0.195 ± 0.014	0.190 ± 0.004
W Iberia	2.91 ± 0.23	0.13 ± 0.02	0.366 ± 0.024	0.352 ± 0.027
Iberian Seamounts	2.82 ± 0.03	0.15 ± 0.05	0.318 ± 0.001	0.328 ± 0.036

H_E , Nei's unbiased expected heterozygosity; H_O , observed heterozygosity using the following 10 loci that were used in this study and Assis et al. (2018b)

Izquierdo et al., 2002), potentially exerting a selective pressure on genotypes. A third explanation could be negative assortative mating in which individuals avoid mating with close relatives (Hartl & Clark, 1999). Alternatively, fourth, if long distance dispersal is possible (see discussion in Assis et al. (2018a), there may have been multiple sources of the Scots Port population, generating

Table 4 Estimates of Jost's D between Scots Port and other regions or sites throughout Europe based on genotypes from Assis et al. (2018b)

Site or Region	Scots Port
Western English Channel (4 sites)	0.331 ± 0.057
Western Iberia (12 sites)	0.496 ± 0.016
Iberian seamounts (4 sites)	0.549 ± 0.010
Tarifa	0.598
El Jadida	0.854
Essaouira	0.762
Formigas	0.792

an excess of heterozygotes through admixture (reviewed in Rius and Darling, 2014). Future studies or surveys of the Irish coastline should include collection and genotyping of *L. ochroleuca* gametophytes and sporophytes to tease these hypotheses apart.

The present range expansion of *L. ochroleuca* highlights a critical need to monitor Irish kelp forests. Citizen science organizations like Seasearch Ireland can be an excellent way to involve local communities that have a vested interest in the health of these ecosystems, but resources should be made available for long term ecological research (LTER) as well. The lack of any subtidal LTER in Ireland and the UK until recently (Smale et al., 2013) prevents us from monitoring ecosystem shifts driven by climate changes, species range expansions, and other man-made disturbances including wild-harvest. This new record of *L. ochroleuca* in Ireland is a sign that subtidal kelp forests are changing in Ireland and there will be associated impacts to ecosystems services that are not thoroughly understood.

Conclusion

This is the first record of an *L. ochroleuca* population in the Republic of Ireland. Its remote location indicates there are likely more populations along the coastline, however the allelic richness and heterozygosity reflect that of Iberian populations within its distribution center. Future investigations of dispersal vectors and population connectivity are warranted and this discovery highlights the importance of citizen science and need for monitoring systems in the changing marine environment.

Additional file

Additional file 1: Table S1. The number of alleles, allele range, null allele frequency, and *TANDEM* ver. 1.09 output (Matschiner & Saltzburger 2009), including the specified repeat size, rounding method, average rounding error and error threshold for each microsatellite locus used to genotype *L. hyperborea* populations. The only locus with a higher rounding error than 10% of the repeat size was locus Gver_6311, shown in red and bold. All individuals flagged as errors were manually checked to make sure they were manually binned (Krueger-Hadfield et al. 2013). **Table S2.** Microsatellite genotypes of 15 *Laminaria ochroleuca* sporophytes from Béal an Mhuirthead. Lo is the same as LolWIV. (DOCX 36 kb)

Abbreviations

DNA: Deoxyribonucleic acid; dNTP: Nucleoside triphosphate; LTER: Long term ecological research; NUI Galway: National University of Ireland Galway; PCR: Polymerase chain reaction; PMNHS: Porcupine Marine Natural History Society; RNA: Ribonucleic acid; SCUBA: self contained underwater breathing apparatus; UAB: University of Alabama at Birmingham; UK: United Kingdom

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Availability of data and materials

Mitochondrial sequences are provided with Genbank Acc. TBD. Microsatellite genotypes are provided in Additional file 1: Table S2.

Authors' contributions

KMS participated in PMNHS and Seasearch surveys, collected the kelp samples, and wrote the manuscript. TO and RO participated and ran PMNHS and Seasearch surveys and edited the manuscript. SAKH did the laboratory work, processed the data, and wrote the manuscript. All authors read and approved the final manuscript.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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Author details

¹Department of Zoology, School of Natural Sciences, Ryan Institute, National University of Ireland Galway, University Rd, Galway, Ireland H91 TK33.

²Seasearch Ireland, Galway, Ireland. ³Department of Biology, University of Alabama at Birmingham, Campbell Hall 464, 1300 University Blvd, Birmingham, AL 35294, USA.

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