

ORIGINAL ARTICLE

Use of multiple markers demonstrates a cryptic western refugium and postglacial colonisation routes of Atlantic salmon (*Salmo salar* L.) in northwest Europe

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Glacial and postglacial processes are known to be important determinants of contemporary population structuring for many species. In Europe, refugia in the Italian, Balkan and Iberian peninsulas are believed to be the main sources of species colonising northern Europe after the glacial retreat; however, there is increasing evidence of small, cryptic refugia existing north of these for many cold-tolerant species. This study examined the glacial history of Atlantic salmon in western Europe using two independent classes of molecular markers, microsatellites (nuclear) and mitochondrial DNA variation. Alongside the well-documented refuge in the Iberian Peninsula, evidence for a cryptic refuge in northwest France is also presented. Critically, methods utilised to estimate divergence times between the refugia indicated that salmon in these two regions had diverged a long time before the last glacial maximum; coalescence analysis (as implemented in the program IMA2) estimated divergence times at around 60 000 years before present. Through the examination of haplotype frequencies, previously glaciated areas of northwest Europe, that is, Britain and Ireland, appear to have been colonised from salmon expanding out of both refugia, with the southwest of England being the primary contact zone and exhibiting the highest genetic diversity.

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INTRODUCTION

Genetic differentiation within a species is governed by both contemporary and historical processes. The Pleistocene glaciations, which lasted approximately two million years and terminated around 10 000 years ago with a period of global warming (Andersen and Borns, 1994), are deemed to be one of the most important historical events involved in shaping the large-scale population structuring observed in many species today (Bernatchez and Wilson, 1998; Taberlet *et al.*, 1998). During the major glaciations of the Pleistocene, polar ice sheets expanded considerably, extirpating many populations and compressing species' ranges to their southerly limits, thereby restricting populations to refugial locations (Hewitt, 1999). Following the onset of glacial retreat, populations of species at the northern edge of their range would have expanded into new areas of suitable habitat (Hewitt, 1999). Such rapid expansion from a few founder individuals can lead to a reduction in genetic diversity at the leading edge of recolonisation (Hewitt, 1996); however, a secondary increase in the diversity of resulting hybrid populations has also been observed as recolonisers from different refugia come into contact (Petit *et al.*, 2003). Owing to the genetic differentiation that occurred between refugial populations (due to drift and differential selection), it is possible, through phylogeographic exploration, to trace the movement of species from refugial areas into the previously glaciated

regions, which now constitute their native range (for example, Makhrov and Bolotov, 2006).

For most European species, ancestry from the Pleistocene period can be traced back to one or more of the three main refugia in the Iberian, Italian or Balkan Peninsulas (Taberlet *et al.*, 1998; Hewitt, 1999). More recently, however, several studies (Provan *et al.*, 2005; Hoarau *et al.*, 2007; Olsen *et al.*, 2010; Panova *et al.*, 2011) have identified the area comprising the Brittany peninsula in northwest France, the Channel River and Hurd Deep (Lericolais *et al.*, 2003), the undersea relic of the Channel River located just off the northwest coast of Brittany, as a glacial refuge for marine/coastal organisms within northwest continental Europe. At this time, the English Channel was largely dry land with numerous rivers, including the well-documented Channel River, running through the area (Lericolais *et al.*, 2003); modelling studies by Sarnthein (2001) suggest that sea temperatures in the region of the English Channel at this time were 1–2 °C in winter, rising to 5–6 °C in summer. In the case of Atlantic salmon, their current range extends only to the historical Iberian Peninsula refuge (MacCrimmon and Gots, 1979), which is widely accepted as a glacial refuge for Atlantic salmon during the Pleistocene glaciations (Consuegra *et al.*, 2002). However, there is no evidence for their extension into the Italian or Balkan regions at that time and, until now, no evidence of a refuge for this species in northwest France.

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Within Europe, Atlantic salmon appear to have differentiated into Atlantic and Baltic sublineages before the last glacial period (Verspoor *et al.*, 1999; Nilsson *et al.*, 2001); hence, it is expected that the two lineages would have differing phylogeographic histories. Extensive phylogeographic exploration in the Baltic region and around Russia to the White and Barents Seas has proved successful in elucidating likely glacial refugia for Atlantic salmon in freshwater lakes present in the Baltic region and their subsequent colonisation routes across the region (Nilsson *et al.*, 2001; Asplund *et al.*, 2004; Säisä *et al.*, 2005; Tonteri *et al.*, 2005). In contrast, the phylogeographic history of Atlantic salmon in northwest Europe (northern Spain, France, Britain and Ireland) remains speculative (Verspoor *et al.*, 1999; Nilsson *et al.*, 2001). Hence, the aim of this study was to elucidate the phylogeographic history of Atlantic salmon in this region.

With the exception of the recently published population analysis of southern European populations (Griffiths *et al.*, 2010), in most Europe-wide evolutionary studies of Atlantic salmon conducted to date, samples of wild populations from the west and northwest, that is, Spain, France, Britain and Ireland, have been largely lacking. This is particularly marked for France and England—a maximum of five samples from across the region were included in studies by Bourke *et al.* (1997) and Verspoor *et al.* (1999). In the only studies to focus directly on this region, Payne *et al.* (1971) and Child *et al.* (1976) described two lineages based on polymorphisms at the transferrin locus. The so-called ‘Boreal’ lineage radiated from a glacial lake in the southern North Sea and was proposed to occupy most of northern Europe, including the Baltic, while the ‘Celtic’ race was confined to the southwest of England (UKSouthwest). Much has been achieved in other areas of Europe since these early studies. For example, although no evidence for a Boreal–Celtic divide has since been observed (Ståhl, 1987; Bourke *et al.*, 1997; Verspoor *et al.*, 1999; Consuegra *et al.*, 2002), due to the high genetic diversity consistently reported for Britain and Ireland (Verspoor *et al.*, 1999; Nilsson *et al.*, 2001; Consuegra *et al.*, 2002), this region has been proposed as a contact zone for salmon expanding out of multiple refugia. Sound evidence of a refuge for Atlantic salmon in this region comes in the form of bone relics recovered from a cave in the Iberian Peninsula, which demonstrates the presence of Atlantic salmon in this area for at least the past 40 000 years, that is, during the last glacial period (Consuegra *et al.*, 2002). As proposed for other freshwater fish (Hanfling *et al.*, 2002), it is possible that Atlantic salmon existed north of this refuge, in northwest France or southern England (UKSouth) (Verspoor, 1986), in line with Payne *et al.*'s (1971) ‘Celtic’ hypothesis. In addition, a glacial lake present in the southern North Sea has been proposed as a potential refuge for Atlantic salmon colonising west into the Atlantic and North Sea drainages, east into the Baltic (Verspoor *et al.*, 1999; Säisä *et al.*, 2005) and north into the White and Barents Seas (Verspoor *et al.*, 1999; Asplund *et al.*, 2004; Tonteri *et al.*, 2005), in line with Payne *et al.*'s (1971) ‘Boreal’ hypothesis. However, the allozyme studies of Verspoor (1986), Ståhl (1987) and Bourke *et al.* (1997) have been brought into question by the revelation that a commonly used isoenzyme (*ME-2*, *mMEP-2**) is likely to be acting under selection pressures (Verspoor and Jordan, 1989; Bourke *et al.*, 1997) and as such is not a suitable marker for phylogeographic studies. This may also be the case for transferrin (Verspoor and Jordan, 1989) as used by Payne *et al.* (1971) and Child *et al.* (1976) in the initial investigations.

In recent years, the use of multiple classes of molecular markers has proved highly effective in elucidating phylogeographic histories of freshwater fish (Hanfling *et al.*, 2002; Koskinen *et al.*, 2002). Specifically for Atlantic salmon, the differing yet complementary

properties of microsatellite and mitochondrial DNA (mtDNA) have led to robust inferences of phylogeographic histories in the Baltic Seas and northern Europe (Säisä *et al.*, 2005; Tonteri *et al.*, 2005). Our aim, therefore, was to utilise these markers to resolve the phylogeographic history of Atlantic salmon in northwest Europe, by identifying refugial locations and determining colonisation pathways. Specifically, the null hypothesis (H_0) to be tested was that salmon colonising northwest Europe expanded out of a single refuge located in the Iberian Peninsula, with alternate hypotheses of salmon residing in additional glacial refugia located north of the Iberian peninsula (in northwest France and/or UKSouth; H_{1A}) and/or in the southern North Sea (H_{1B}). Subsequently, we aim to reconstruct the colonisation pathways of Atlantic salmon into Britain and Ireland from these potential source location(s).

MATERIALS AND METHODS

Sample collection

In this study, 723 specimens of Atlantic salmon were collected from 21 rivers that drain into the east coast of the Atlantic Ocean, including the English Channel, the Irish Sea and the Bay of Biscay (Figure 1 and Table 1). The majority of sampling was carried out in 2004 and 2005 during routine juvenile salmon abundance surveys and targeted 1+ parr. The exceptions are the French specimens, which were sampled as scales from rod-caught adult salmon in 2005.

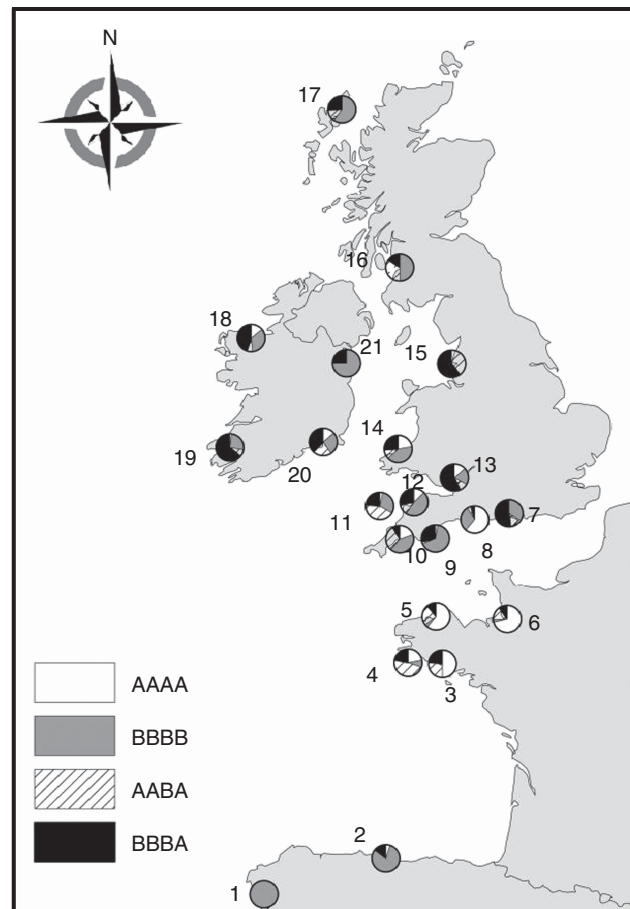


Figure 1 Sampling locations and *NDI* haplotype frequencies. Population ID follows Table 1; composite haplotypes derived from the restriction enzymes *HaeIII*, *HinfI*, *Avall* and *RsaI*.

Table 1 Genetic diversity indices for microsatellite data, mtDNA RFLP data and mtDNA RFLP haplotype frequencies

River	ID	N	Microsatellite diversity			mtDNA RFLP diversity		mtDNA RFLP haplotypes				Regional group
			A_r	H_o	H_e	Haplotype diversity	Nucleotide diversity	AAAA	AABA	BBBB	BBBA	
Ulla	1	40	8.43	0.70	0.72	0.000	0.00000	0.00	0.00	1.00	0.00	Spain/Spain
Sella	2	41	11.87	0.81	0.81	0.337	0.00883	0.05	0.00	0.80	0.15	Spain/Spain
Scorff	3	30	11.26	0.80	0.79	0.646	0.01774	0.50	0.27	0.00	0.23	France/France
Ellé	4	46	11.64	0.82	0.78	0.684	0.01949	0.22	0.48	0.09	0.22	France/France
Léguer	5	28	12.62	0.81	0.79	0.577	0.01531	0.61	0.25	0.04	0.11	France/France
Sée	6	31	11.12	0.81	0.80	0.475	0.01368	0.71	0.16	0.03	0.10	France/France
Itchen	7	29	7.79	0.74	0.75	0.616	0.01336	0.00	0.14	0.34	0.52	UKSouth/UK
Avon	8	23	7.00	0.73	0.81	0.557	0.02841	0.61	0.04	0.30	0.04	UKSouth/France
Dart	9	38	10.96	0.83	0.88	0.495	0.01016	0.03	0.03	0.66	0.29	UKSw/Spain
Fowey	10	36	11.48	0.81	0.82	0.708	0.02697	0.19	0.31	0.42	0.08	UKSw/UK
Camel	11	30	12.68	0.83	0.84	0.690	0.02170	0.03	0.43	0.30	0.23	UKSw/UK
Taw	12	32	12.57	0.84	0.87	0.692	0.02186	0.13	0.13	0.47	0.28	UKSw/UK
Usk	13	30	12.58	0.84	0.86	0.632	0.01869	0.13	0.10	0.20	0.57	UKSw/UK
Teifi	14	27	13.38	0.84	0.85	0.732	0.02600	0.22	0.11	0.41	0.26	UKSw/UK
Ribble	15	25	11.29	0.82	0.84	0.530	0.01498	0.04	0.36	0.00	0.60	UKNw/UK
Ayr	16	32	11.36	0.83	0.83	0.627	0.02054	0.00	0.34	0.50	0.16	UKNw/UK
Creed	17	35	11.90	0.83	0.83	0.570	0.01402	0.00	0.14	0.60	0.26	UKNw/UK
Moy	18	29	11.74	0.82	0.85	0.680	0.02004	0.14	0.07	0.34	0.45	UKNw/UK
Laune	19	47	12.11	0.83	0.82	0.531	0.01144	0.02	0.09	0.26	0.64	UKNw/UK
Barrow	20	37	13.33	0.86	0.86	0.739	0.02261	0.14	0.22	0.27	0.38	UKNw/UK
Boyne	21	36	11.57	0.82	0.80	0.386	0.00526	0.00	0.00	0.75	0.25	UKNw/Spain

Abbreviations: A_r , allelic richness; H_e , expected heterozygosity; H_o , observed heterozygosity; ID, population ID for Figure 1; mtDNA, mitochondrial DNA; N, number of salmon; Nw, northwest; RFLP, restriction fragment length polymorphism; Sw, south west.

mtDNA RFLP composite haplotypes were derived from restriction enzymes *Avall*, *HaeIII*, *HinfI* and *RsaI*. Two regional assignments are listed for each population: the first regional assignment classifies a population according to the microsatellite analysis, and the second is based on the mtDNA analysis.

DNA analysis: microsatellites

Genomic DNA was extracted from scales or fin clips of Atlantic salmon according to a Chelex resin protocol (Estoup *et al.*, 1996). Genotypes were determined at 12 microsatellite loci: *Ssa157a*, *SsaD144b* (King *et al.*, 2005), *Ssa197*, *Ssa202*, *Ssa171* (O'Reilly *et al.*, 1996), *SSsp2210*, *SSsp1605*, *SSsp2201*, *SSspG7* (Paterson *et al.*, 2004), *Ssa289* (McConnell *et al.*, 1995) and *SSOSL417*, *SSOSL85* (Slettan *et al.*, 1996).

Microsatellite analysis followed the protocol of Griffiths *et al.* (2010). Polymerase chain reactions (PCRs) were carried out in 10 μ l reaction volumes and standard PCR reagents were used in a mixture containing 50–100 ng DNA, 0.5 μ M of each primer, 1.5 mM MgCl₂, 200 μ M of each dNTP, 1 \times reaction buffer and 0.5 U of *Taq* DNA polymerase (Biolone, London, UK). The PCR amplification profile consisted of a single denaturing step lasting 3 min at 94 °C, followed by 30 iterations of: 94 °C for 30 s, an annealing step of 30 s at 53–58 °C, depending on the locus being amplified (see Supplementary Information and Supplementary Table 1), and 72 °C for 30 s, with a single final elongation step of 72 °C for 10 min. Primer annealing temperatures for each locus are given in the Supplementary Information and Supplementary Table 1; see Finnegan and Stevens (2008) for additional details.

Size determination of the labelled PCR products was performed using a Beckman-Coulter CEQ 8000 automated DNA sequencer with an internal size standard, according to the manufacturer's instructions. The raw data were analysed with the platform's associated fragment analysis software (Beckman-Coulter, High Wycombe, UK).

DNA analysis: mtDNA RFLPs

The NADH dehydrogenase subunit I (*ND1*) region of mtDNA was amplified using the primers of Hall and Nawrocki (1995), as modified by Nilsson *et al.* (2001). The 30 μ l reaction volume contained 0.25 U of *Taq* DNA polymerase (Biolone), 1 \times reaction buffer, 0.2 mM dNTP, 2 mM MgCl₂ and 0.5 μ M of each primer and approximately 50 ng of purified template DNA. PCR amplification consisted of an initial denaturation step of 95 °C for 3 min, followed by

35 cycles of 95 °C for 30 s, 58 °C for 45 s and 72 °C for 60 s, concluding with a final extension phase of 5 min at 72 °C.

Amplified DNA was digested with the restriction enzymes *HaeIII*, *HinfI*, *Avall* and *RsaI* in individual 10 μ l reactions; all enzymes were supplied by Promega at a concentration of 10 U μ l⁻¹. Individual reactions comprised 0.3 μ l enzyme, 0.5 μ l corresponding buffer mix, 3.2 μ l dH₂O and 6 μ l of amplified DNA, and were incubated at 37 °C overnight. Fragments were separated by electrophoresis and variant fragment patterns, that is, composite haplotypes, were determined following the original *ND1* haplotype designation system of Nielsen *et al.* (1996), and see also Nilsson *et al.* (2001).

DNA analysis: mtDNA *ND1* sequencing

On the basis of the haplotypes identified by mtDNA restriction fragment length polymorphism (RFLP) analysis (see above), a subset of samples that included representatives of all haplotypes identified was subjected to additional *ND1* sequencing. This analysis identified additional within-haplotype variation, visualised using a haplotype median-joining network constructed using the program NETWORK v.4.6.1.1 (available at: www.fluxus-engineering.com/sharenet.htm; Bandelt *et al.*, 1999); in turn, this allowed us to use the software IMA2 (Hey, 2010) to investigate divergence times between haplotype groups.

Primers *ND1-F* and *ND1-R* (Nilsson *et al.*, 2001) were used to amplify a 1410 bp region of the mtDNA that includes the *ND1* gene. PCR reactions were carried out in a total volume of 25 μ l consisting of 1 \times HotStar Taq Plus Master Mix (Qiagen, Manchester, UK), 0.2 μ M of each forward and reverse primer and approximately 50 ng of purified template DNA. After an initial denaturing step at 94 °C for 2 min 30 s, amplification proceeded for 35 cycles at 94 °C for 30 s, 58 °C for 30 s, 72 °C for 60 s and a final extension at 72 °C for 10 min.

PCR products (10 μ l) were purified using 0.25 U each of Exonuclease I (New England Biolabs, Hitchin, UK) and Antarctic Phosphatase (USB) incubated at 37 °C for 45 min and 80 °C for 15 min. Sequencing was carried out on a 3130xl Genetic Analyzer (Applied Biosystems, Paisley, UK) using Big Dye (v.1.1) sequencing chemistry.

Microsatellite data analyses

Allele number and allelic richness (A_r) (allele number corrected for sample size) were calculated for all loci within populations using FSTAT v.2.9.3 (Goudet, 1995). Deviations from Hardy–Weinberg expectations and the occurrence of linkage disequilibrium between loci was tested for using the default parameters in GENEPOP v.3.4 (Raymond and Rousset, 1995) with sequential Bonferroni corrections applied for multiple tests across populations (Rice, 1989). To identify null alleles and mis-scoring, all data were run through the program MICRO-CHECKER (Van Oosterhout *et al.*, 2004).

FSTAT v.2.9.3 was used to calculate F_{ST} values between populations and their significance. Genetic distances between populations were estimated according to Nei's (1987) D_A distance, from which a phylogenetic tree was constructed using the neighbour-joining method as implemented in POWER-MARKER v.3.25 (Liu and Muse, 2005). Strength of support for each node was assessed with 1000 bootstrap replicates and a consensus tree was obtained using the CONSENSE program in PHYLIP v.3.67 (Felsenstein, 1993).

The optimal number of regional groups was explored using STRUCTURE v.2.3.3 (Pritchard *et al.*, 2000). A burn-in period of 30 000 steps was set, followed by 1 000 000 Markov chain Monte Carlo replicates; allele frequencies were set as 'weakly correlated' as recommended by Pritchard *et al.* (2000). The number of groups to be simulated (K) was set as 1 to 10, with 10 replicates for each group. The optimal number of groups was estimated using the method of Evanno *et al.* (2005).

An analysis of molecular variance, as implemented in ARLEQUIN v.3.5 (Excoffier and Lischer, 2010), was used to examine how genetic variation was partitioned among different hierarchical levels in Atlantic salmon in northwest Europe. Three hierarchical levels were defined: (i) between regional groups; (ii) between populations within regional groups; and (iii) between individuals within populations. Regional groups were defined based on the outcome of the STRUCTURE analysis and the phylogenetic tree (Figure 2), which resolved five broad regions (Spain, France, UKSouth, UKSouthwest, northwest of England (UKNorthwest)/Ireland; see Results). Differences in the average values of A_r , observed heterozygosity (H_o) and expected heterozygosity (H_e) among these regions were also assessed statistically using FSTAT v.2.9.3.

It has previously been suggested that, taking into account the mutation rate of microsatellite loci and the generation time of salmon, stepwise mutations

will only have had a significant effect on differentiation between populations if they diverged before the last glacial maximum (for full details see Tonteri *et al.*, 2005). Therefore, an allele size permutation test (Hardy *et al.*, 2003) implemented in SPAGeDi v.2.1 (Hardy and Vekemans, 2002) was used to assess if $R_{ST} > F_{ST}$ for populations within and between the five regions identified using STRUCTURE. A significant result ($R_{ST} > F_{ST}$) would be indicative of colonisation from multiple sources (Hardy *et al.*, 2003), in this study the French and Spanish refugia. Confidence intervals were calculated with 10 000 permutations of allele sizes among alleles within each locus. The locus *Ssa171* was excluded from this analysis as both di- and tetranucleotide repeats are observed at this locus; therefore, it could not have mutated through a stepwise process alone.

PCR–RFLP mtDNA data analyses

The sizes of restriction fragments (cross-referenced with the RFLP scoring system of Nielsen *et al.*, 1996) were used to generate a restriction site binary matrix of presence/absence of fragment bands for each enzyme, and a binary representation of the composite haplotypes of each individual using REAP v.4.0 (McElroy *et al.*, 1992). These were used in subsequent programs in the REAP v.4.0 package to calculate haplotype and nucleotide diversity within populations and a matrix of pairwise distances between populations (Nei, 1987) based on population haplotype frequencies. Subsequently, an unweighted pair-group method using arithmetic averages phylogenetic tree was constructed in PHYLIP v.3.67. Mann–Whitney U -tests were used to statistically investigate the difference of haplotype and nucleotide diversity between the three broad geographic regions depicted in the phylogenetic tree (Spain, France and United Kingdom/Ireland; see Results). Hierarchical diversity was assessed with an analysis of molecular variance implemented in ARLEQUIN v.3.5 as for the microsatellite analysis (see above), except with the regions defined as Spain, France and Britain/Ireland (see above).

ND1 sequence analysis

Sequences were edited in the ABI program AutoAssembler v.2.0 and aligned in Clustal X (Thompson *et al.*, 1997). A principal coordinates analysis, based on the population pairwise matrix of F_{ST} values, was constructed using GenALEX v.6 (Peakall and Smouse, 2006) to identify population groupings for subsequent estimation of divergence times. In addition, F_S (Fu, 1997) was used to test if populations were at drift-migration equilibrium using ARLEQUIN v.3.5.

Timing of divergence between groups of populations was estimated using the isolation with migration (IM) model of population divergence using the program IMA2 (Hey, 2010), with the HKY model of sequence evolution. Analyses were run three times using 40 Markov chain Monte Carlo chains with geometric heating. Following a burn-in of 1×10^6 generations, posterior probabilities of parameters were calculated from 25×10^6 generations of data, sampling every 100 generations. Parameter estimates were adjusted to demographic scales assuming an average salmon generation time of 4 years and a mutation rate of 5.7×10^{-9} substitutions per site per year (Doiron *et al.*, 2002), with upper and lower limits around this rate set at 1×10^{-8} and 1×10^{-9} . This mutation rate represented the average of the two mutation rates estimated by Doiron *et al.* (2002) for *ND1* between two charr species and rainbow trout (*Oncorhynchus mykiss*). Critically for this study, Doiron *et al.* (2002) looked at mutation rates across 13 mtDNA genes in a range of other salmonid species, including Atlantic salmon, and concluded that the relatively constant mutational differences observed suggested that comparable estimates of divergence would be obtained among salmonid species, regardless of the mitochondrial genes studied.

As demonstrated by Ho and Larson (2006), however, extrapolating mutation rates between species and across evolutionary timescales is seldom straightforward and recent rates of molecular evolution for intraspecific comparisons or newly emerging species may be far more rapid than those estimated from more ancient divergence events. In light of this, additional runs of IMA2 were undertaken with rate parameters derived from divergences between other groups of salmonid fish, including one based on a considerably more recent divergence event (Jacobsen *et al.*, 2012). The additional rates explored comprised one based on divergence of the *ND4* gene between

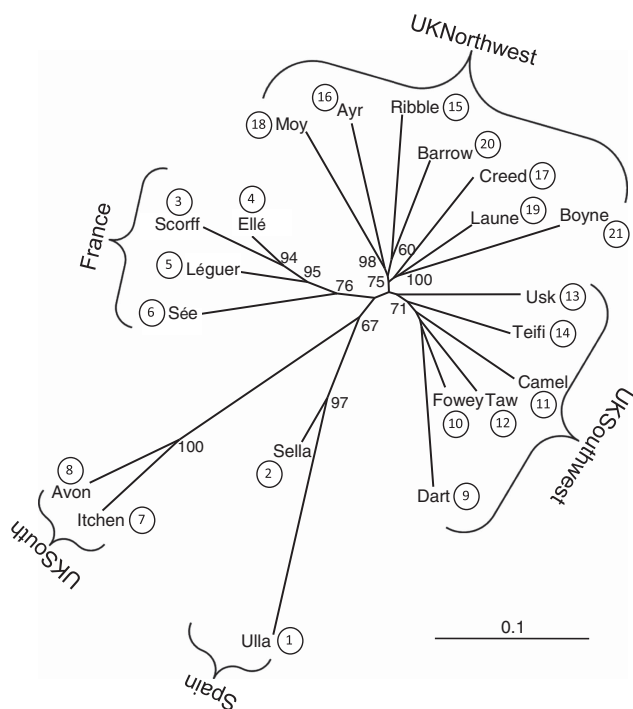


Figure 2 Neighbour-joining phylogenetic tree generated from microsatellite data. Bootstrap values $> 50\%$ are shown.

Oncorhynchus species (9.7×10^{-9} ; Wilson and Turner, 2009) and the other a whole mtDNA genome-derived rate based on recent divergences between whitefish species (*Coregonus* spp.; 1.537×10^{-8} ; Jacobsen *et al.*, 2012). A recent, comprehensive study of salmonid evolution and interspecific divergence times (Crête-Lafrenière *et al.*, 2012) estimated the rate of mitochondrial molecular divergence within Salmonidae at 0.31% per million years (that is, 3.1×10^{-9} ; confidence interval (CI): 0.27–0.36% per MY), reaffirming the suitability of the rate parameters used in this study. Until such time as we are reliably able to estimate differential intraspecific rates of mtDNA evolution in salmonids, we have employed rates for which we have reliable supporting information.

RESULTS

Microsatellite analyses

Genetic diversity indices are summarised in Table 1 (see also Supplementary Information and Supplementary Table 2). After sequential Bonferroni corrections were applied, significant deviations from Hardy–Weinberg expectations were observed on 11 occasions; these involved nine populations and six loci (Supplementary Information and Supplementary Table 2). No locus was consistently implicated in departure from Hardy–Weinberg expectations across different samples; thus, data from all 12 loci were retained for subsequent analysis. Of the 1386 tests of linkage disequilibrium between loci, only 26 (that is, <2%) were found to be significant after correction. The majority were single observations, which only occurred in one population. Hence, linkage disequilibrium of loci was deemed to be negligible. The results from MICRO-CHECKER indicated that no locus consistently showed evidence for null alleles nor error due to stuttering across samples.

Global F_{ST} was estimated at 0.0436, with pairwise estimates ranging from 0.001 (Ellé–Léguer; Ellé–Scorff) to 0.156 (Ulla–Itchen). All were significant at $P < 0.05$, except the two lowest values; these involved populations from northwest France that shared the same river mouth and comprised samples of adults ascending the rivers (Supplementary Information and Supplementary Table 3). The neighbour-joining population tree depicted five broad groups of populations reflecting geographical regions (Figure 2). Bootstrap analysis indicated very strong support for the group of Spanish populations (96.2%) and reasonably strong support for the group of French populations (75.2%). Within the United Kingdom and Ireland, the clustering of populations into three geographic regions was clearly depicted: UKSouth, UKSouthwest and UKNorthwest/Ireland. Bootstrap support was very strong for the two UKSouth populations branching together (100%), but less so for the grouping of the UKSouthwest (39.4%) and UKNorthwest/Ireland (26.5%) populations, although within these groups there was stronger support at some branches (Figure 2).

The clustering analysis, as implemented in STRUCTURE, defined an optimum of five regions (that is, $k = 5$), corresponding well with geographic origins (Figure 3). Complementing the neighbour-joining population tree, individuals clustered into the five regions of Spain, France, UKSouth, UKSouthwest and UKNorthwest/Ireland. Similarly, Spain, France and UKSouth all formed very distinct clusters, while the UKSouthwest and UKNorthwest clusters were less distinct and showed considerable overlap.

Hierarchical analysis demonstrated that 3% of variation lay among these five regional groups, 2.2% lay among populations within these regions and the remaining 94.8% lay within populations. Genetic diversity, expressed as average allelic richness and heterozygosity, was lowest in the UKSouth regional group; this was significantly lower ($P < 0.05$) compared with all other regional groups, except Spain (which was close to being significant; A_r : $P = 0.057$; H_e : $P = 0.038$) (Table 2).

The allele size permutation test revealed that, on a global scale, multilocus R_{ST} values were significantly higher than F_{ST} values ($F_{ST} = 0.0436$, $R_{ST} = 0.0635$, $P < 0.01$; Supplementary Information and Supplementary Figure 1). This suggests that stepwise mutations of microsatellite repeat regions have contributed to the genetic differentiation of the five broad regions and is consistent with the hypothesis that northwest Europe was colonised by Atlantic salmon from different refugia. A significant result was also produced in the comparison of Spain and northwest France ($F_{ST} = 0.0511$, $R_{ST} = 0.0985$, $P < 0.05$), indicating that these two regions were colonised from, or acted as, different refugia. To test the competing hypotheses of colonisation of the United Kingdom and Ireland, populations from the three clusters comprising this region (UKSouth, UKSouthwest and UKNorthwest/Ireland) were compared. No significant contribution of stepwise mutations to genetic differentiation was observed, suggesting that the three regions were colonised from the same refugial population(s). However, when the UK and Ireland

Table 2 Regional genetic diversity indices

	Microsatellite diversity		mtDNA RFLP diversity	
	A_r	H_e	Haplotype diversity	Nucleotide diversity
Spain	10.151	0.771	0.166	0.0044
France	11.661	0.834	0.586	0.0166
UKSouth	7.396	0.767	0.575	0.0209
UKSouthwest	12.276	0.86	0.647	0.0209
UKNorthwest	11.9	0.856	0.571	0.0156

Abbreviations: A_r , allelic richness; H_e , observed heterozygosity; H_e , expected heterozygosity.

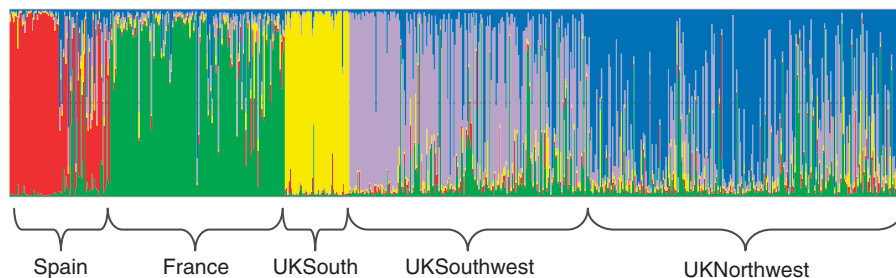


Figure 3 Output from STRUCTURE analysis indicating admixture of individuals in each cluster, defined as $k = 5$. Estimation of the membership fraction to each of five inferred clusters (red, yellow, blue, green and purple) based on microsatellite data; each vertical bar represents one individual and horizontal brackets indicate the geographical regions from which individual fish were sampled.

populations were then compared with the potential source/refugial populations of Spain and France, both comparisons were found to be significant (France vs United Kingdom: $F_{ST}=0.0352$, $R_{ST}=0.0457$, $P<0.05$; Spain vs United Kingdom: $F_{ST}=0.0448$, $R_{ST}=0.0613$, $P<0.05$). This could be interpreted in two ways: (i) there was a third refuge in UKSouth, from which salmon colonised the whole of the United Kingdom and Ireland; (ii) the United Kingdom and Ireland were a contact zone for Atlantic salmon colonising out of the different refugia in Spain and France, the test being significant because the UK and Ireland populations are comprised of salmon descended from both refugia.

mtDNA RFLP analysis

RFLP analysis of the *ND1* region of mtDNA revealed a total of four composite haplotypes (AAAA, AABA, BBBA and BBBB), all of which have been observed previously in populations from northwest Europe (Nielsen *et al.*, 1996; Verspoor *et al.*, 1999; Nilsson *et al.*, 2001). The majority of populations exhibited varying frequencies of all four haplotypes, with only one population fixed for a single haplotype (Ulla; BBBB). All four haplotypes are thought to have been widely distributed before the last glacial period (Nilsson *et al.*, 2001), but due to their frequency distributions, the AAAA and AABA haplotypes have been previously termed 'Baltic' haplotypes, while the BBBB and BBBA haplotypes were termed 'Atlantic' haplotypes (Nilsson *et al.*, 2001); for continuation we will also refer to this nomenclature in this study, although it is important to remember that this does not reflect their true origins, rather the nomenclature simply reflects their comparative dominance within the two regions. The Spanish populations were dominated by 'Atlantic' haplotypes (BBBB; BBBA; 97.5%), while the French populations were dominated by 'Baltic' haplotypes (AAAA; AABA; 80%). Overall, the United Kingdom was largely dominated by the 'Atlantic' haplotypes; however, southern UK populations exhibited a higher proportion of 'Baltic' haplotypes compared with northern UK populations. Genetic diversity, expressed as haplotype and nucleotide diversity, was highest in the United Kingdom, specifically the UKSouthwest group and lowest in Spain (Table 2); a significant reduction in genetic diversity was observed in Spain compared with the United Kingdom ($P<0.05$). All other comparisons were nonsignificant.

The unweighted pair-group method using arithmetic averages population tree, constructed from Nei's (1987) D_A distance (Figure 4), revealed the division of populations into three clusters: one dominated by French populations exhibiting high frequencies of the 'Baltic' haplotypes, which also contained the geographically proximate Avon; one largely Spanish clade dominated by high frequencies of the 'Atlantic' haplotypes, with two rivers from other regions (Dart and Boyne), which show similarly high frequencies of the 'Atlantic' haplotypes; and a third clade containing the majority of UK and Irish samples, which have a more equal distribution of both the 'Atlantic' and 'Baltic' haplotypes. Hierarchical analysis for these three broad regions revealed that 34.37% of genetic diversity lay among the three regions, 8.74% lay among populations within each region and 56.89% resided within populations.

ND1 sequence analysis

A 1155 bp region of the mtDNA sequence was obtained from 182 salmon. In total, 22 bases were polymorphic and 20 haplotypes were identified (EMBL accession numbers: HF586486–HF586505). The number of haplotypes per population ranged from one to eight (average = 3.85), with two Spanish populations being fixed for a single haplotype; nine haplotypes were found only in a single

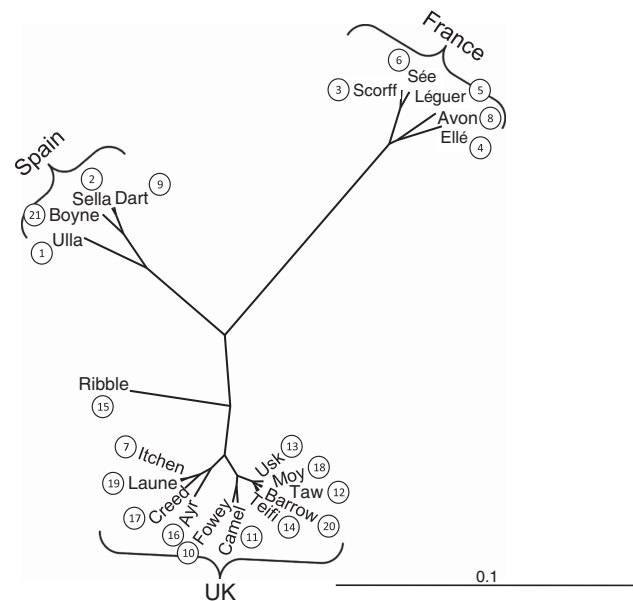


Figure 4 Unweighted pair-group method using arithmetic averages phylogenetic tree generated from mtDNA RFLP data.

individual (Supplementary Information, Supplementary Figure 2 and Supplementary Table 4).

Principal coordinates analysis of pairwise F_{ST} values of the sequence data reiterated the three groupings defined by mtDNA RFLP analysis (Figure 4): Spain plus the River Dart; France plus the River Avon; and the remaining British and Irish populations (Supplementary Information and Supplementary Figure 3). All subsequent results are based on these three groupings. F_u 's F_s was -1.158 ($P=0.294$) and 0.270 ($P=0.518$) for the French and Spanish groups, respectively, but was significantly negative for the British and Irish group (-10.589 , $P=0.0004$). A negative value indicates evidence for a history of population expansion.

Parameter estimates were consistent across the three runs in the IM analysis (Supplementary Information and Supplementary Table 5). Divergence time estimates between the French and British group and between the Spanish and British group were $\sim 16\,000$ – $20\,000$ years. The divergence time estimate for the Spanish and French group was much longer, at around $63\,000$ years (Figure 5). Estimates using other salmonid-derived mtDNA mutation rates (*ND4*, 9.7×10^{-9} (Wilson and Turner, 2009), and whole mtDNA genome, 1.537×10^{-8} , (Jacobsen *et al.*, 2012)) produced more recent divergence estimates; critically, however, all divergence times for the Spanish and French groups pre-date the last glacial maximum (Supplementary Information and Supplementary Figure 4).

DISCUSSION

The high genetic diversity observed in Britain and Ireland, particularly in the SouthwestUK, suggests that Atlantic salmon did not colonise this region following the last glacial retreat from salmon expanding out of a single Iberian refuge in northern Spain (that is, H_0 is rejected). Rather, the results are consistent with there being a second, cryptic western refuge for Atlantic salmon in northwest France (that is, H_{1A} is accepted) with colonisation of Britain and Ireland from both refugia.

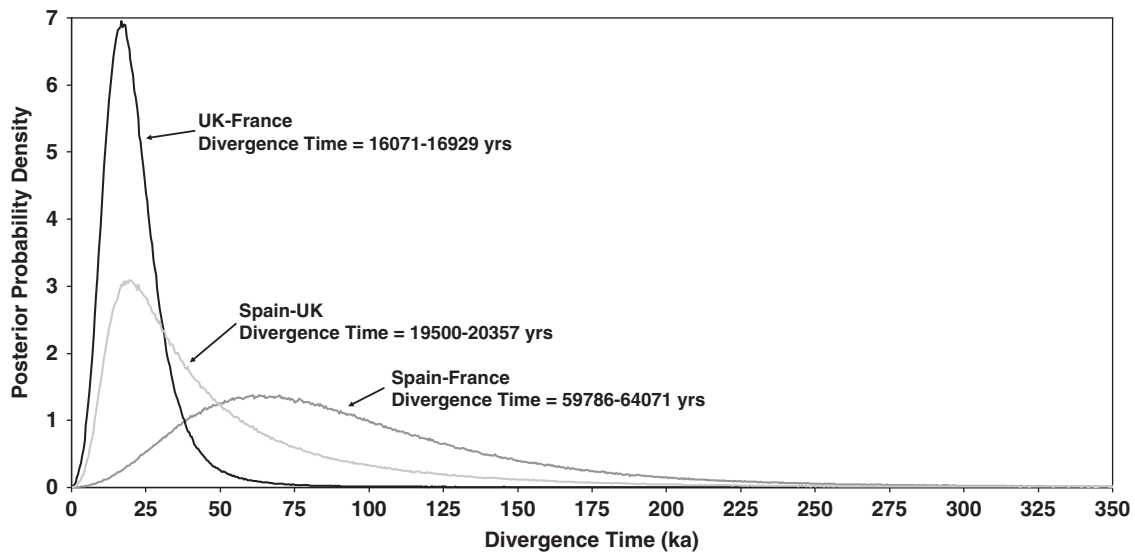


Figure 5 Estimate of divergence times from IMA2 using an *ND1*-derived divergence rate of 5.7×10^{-9} substitutions per site per year (Doiron *et al.*, 2002).

Genetic diversity and differentiation

The genetic diversity of 21 populations of Atlantic salmon in northwest Europe as revealed by microsatellite analysis (12 loci, 289 alleles) was found to be comparable with that reported for other regions (King *et al.*, 2001; Tonteri *et al.*, 2005; Säisä *et al.*, 2005). Expected heterozygosity ($H_e = 0.808$) was consistent with that reported for populations from Britain and Ireland by Säisä *et al.* (2005) ($H_e = 0.812$) and higher than that reported for other regions (Baltic: $H_e = 0.73$ (Säisä *et al.*, 2005); northern Europe: $H_e = 0.56$ (Tonteri *et al.*, 2005); North America: $H_e = 0.60$ (King *et al.*, 2001)). The genetic divergence of salmon populations in northwest Europe, as measured using F_{ST} estimates, was lower in this study (Global $F_{ST} = 0.0436$) than previously reported for populations in northwest Europe ($F_{ST} = 0.12$ (Bourke *et al.*, 1997); $F_{ST} = 0.114$ (King *et al.*, 2001)). However, the sampling range of this study was restricted compared with those of Bourke *et al.* (1997) and King *et al.* (2001). Within northwest Europe, genetic diversity was found to be highest in UKSouthwest ($A_r = 12.276$, $H_e = 0.86$) and lowest in UKSouth ($A_r = 7.396$, $H_e = 0.767$), although this latter estimate was still higher than previously reported for other regions (King *et al.*, 2001; Säisä *et al.*, 2005; Tonteri *et al.*, 2005). Genetic divergence was highest between UKSouth and Spain ($F_{ST} = 0.114$) and lowest between the UKSouthwest and UKNorthwest/Ireland ($F_{ST} = 0.026$).

The genetic diversity of matrilineal Atlantic salmon populations in west/northwest Europe as revealed by PCR-RFLP of mtDNA and measured using average haplotype diversity estimates (Global $H = 0.509$) was found to be comparable to that observed in previous studies (British Isles and Spain $H = 0.507$ (Nilsson *et al.*, 2001), higher than that reported for the Atlantic as a whole or the Baltic ($H = 0.478$, $H = 0.217$, respectively; Nilsson *et al.*, 2001), but lower than that reported for northern Europe ($H = 0.543$; Asplund *et al.*, 2004)). In terms of PCR-RFLP variability within west/northwest Europe, genetic diversity was found to be highest in UKSouthwest ($H = 0.647$) and lowest in Spain ($H = 0.166$). Lower diversity in Spanish populations compared with those from the British Isles in PCR-RFLP mtDNA studies has been reported previously by Verspoor *et al.* (1999) and Consuegra *et al.* (2002).

All four composite mtDNA haplotypes observed in this study have been described previously (Nielsen *et al.*, 1996) and are known to be

widespread across Europe (Verspoor *et al.*, 1999; Nilsson *et al.*, 2001; Asplund *et al.*, 2004). The consensus is that the evolution of these haplotypes predates the Pleistocene glaciations and hence all haplotypes were probably widespread before the last glacial maximum (Nilsson *et al.*, 2001; Asplund *et al.*, 2004; Säisä *et al.*, 2005). Thus, the effects of the last glacial period would primarily be observed by lineage sorting through random drift, initially in the differing frequency distributions of these mtDNA haplotypes in different refugial populations, and subsequently in mixing of these haplotypes in postglacial processes, such as processes of secondary contact.

The dominance of the 'Atlantic' (BBBB and BBBA) mtDNA haplotypes in Spain and high frequency of these haplotypes in Britain and Ireland has been noted previously (Verspoor *et al.*, 1999; Consuegra *et al.*, 2002; Ciborowski *et al.*, 2007; Campos *et al.*, 2008). However, the dominance of the 'Baltic' (AAAA and AABA) haplotypes in northwest France has not been observed before, although none of the previous studies had sampled from this region.

Refugial locations for Atlantic salmon in northwest Europe

The British/Irish ice sheet extended to around 52°N at the time of the last glacial maximum, with permafrost extending over most of Britain and Ireland, except the far southwest corner of England (Murton and Lautridou, 2003). South of the ice sheet, the Iberian Peninsula (northern Spain and Portugal) has been widely accepted as a refuge for Atlantic salmon since bone relics dating back 40 000 years were uncovered in a cave in this region (Consuegra *et al.*, 2002). The initial hypothesis set out in this study was to ascertain whether this was the sole source of contemporary Atlantic salmon populations in northwest Europe; results from this study suggest that this is highly unlikely, and there is evidence to propose that there was a distinct second refuge for Atlantic salmon in northwest France. Supporting evidence comes from both microsatellite and mtDNA data. Separation of the French populations from the Spanish populations is depicted in the clustering and phylogenetic analysis, where the French populations formed a distinct cluster in the STRUCTURE analysis and distinct groupings on both the microsatellite and mtDNA population trees. Furthermore, the allele size permutation test of microsatellite data indicated that French and Spanish populations were separated before the last glacial maximum, although some caution may be required in

interpreting the results from the allele size permutation test, as recent work has shown that the F_{ST} estimator used in the calculations may be downwardly biased in cases of high heterozygosity (Meirmans and Hedrick, 2011), as was the case in this study. This result, however, was also supported by the analysis of divergence times with IMA2. This analysis indicated divergence times between populations in the two proposed refugia (Spain and France) to be considerably older (~60 000 years) than were the divergence estimates of populations from Britain and Ireland with either of the continental refugial populations (Britain/Ireland–France ~16 000 years; Britain/Ireland–Spain ~20 000 years).

Hence, these regions (France and Spain) and the salmon within them appear to have been distinct during the last glacial period. The discontinuity of mtDNA haplotype frequencies also corroborates this theory. In line with previous studies (Verspoor *et al.*, 1999; Consuegra *et al.*, 2002; Ciborowski *et al.*, 2007; Campos *et al.*, 2008), modern Spanish populations are dominated by 'Atlantic' haplotypes, although the high frequency of a distinctive *HaeIII* variant in Pleistocene salmon samples from northern Spain (Consuegra *et al.*, 2002) appears more characteristic of contemporary Baltic populations, suggesting that Pleistocene salmon populations within the region may have differed somewhat from those found today. Contemporary French populations, however, are dominated by 'Baltic' haplotypes. This indicates that modern French populations are unlikely to be related to contemporary Spanish populations, but may be a relic of forms distributed more widely in the west of Europe during the Pleistocene era. To our knowledge, northwest France has never been stocked with fish from the Baltic region, and due to the current migratory behaviour of Baltic salmon, whereby very few fish pass the Danish strait into the North Sea and Atlantic Ocean, it seems improbable that northern France would have been colonised naturally by Baltic salmon. Therefore, it seems likely that the high frequencies of these 'Baltic' haplotypes exhibited by salmon populations in northwest France are due to lineage sorting through random drift. Thus, it appears that French populations were isolated from those in Spain during the last glacial period, over which time populations between the two regions differentiated genetically. Such a finding accords with the results from another biogeographic study within the region; Larmuseau *et al.* (2009) identified a similar distinct differentiation between a population of sand gobies from the Gironde river in western France and those from the Atlantic rivers of Portugal and Spain.

Thus, the data suggest that at least two refugia for Atlantic salmon were present in western Europe during the last glacial period, one in northern Spain (Iberian Peninsula) and one in northwest France, and there is increasing evidence that many species existed further north of the well-recognised southern refugia, in sheltered areas experiencing stable microclimates (Stewart and Lister, 2001). Northwest France may have been once such location and evidence emerging from a number of marine species over the past few years (Provan *et al.*, 2005; Hoarau *et al.*, 2007; Olsen *et al.*, 2010; Panova *et al.*, 2011) suggests that the Brittany coast and the area of Hurd Deep in the western English Channel may have been a refuge during the last glacial maximum. In a recent review, it was proposed that species whose current northerly range extends to 60°N or further would potentially have been able to persist in northerly refugia; this seemingly reflects the ecological and physiological adaptations these animals have to survive these conditions (Bhagwat and Willis, 2008). For example, the bullhead (*Cottus gobio*), a cold adapted freshwater fish, seems to have persisted in a refuge in the southern British Isles (Hanfling *et al.*, 2002). In the case of Atlantic salmon, their current distribution

extends to over 70°N in the Barents and Kara Seas (MacCrimmon and Gots, 1979) and they can exhibit high tolerance to extreme cold conditions; hence, it is plausible that Atlantic salmon could have persisted in the conditions in northern France during the late glacial period.

In earlier studies, the southern North Sea has been proposed as the most likely location of a second refuge for Atlantic salmon in northwest Europe (Verspoor *et al.*, 1999; Asplund *et al.*, 2004; Säisä *et al.*, 2005). No indication of this was observed in this study, but our research focused on a more westerly region. An investigation centred on drainages of the North Sea would be necessary to explore this theory, although this would be difficult since many of the North Sea drainages are now extinct of salmon.

Colonisation of Britain and Ireland

A second objective for this study was to reconstruct the colonisation pathway of Atlantic salmon from these source populations into Britain and Ireland. Results are consistent with the hypothesis that Britain and Ireland are a secondary contact zone for Atlantic salmon expanding out from the Spanish and French refugial populations.

Evidence from the allele size permutation test, comparing populations within Britain and Ireland, indicated that stepwise mutations had not contributed to the differentiation of populations within the region, suggesting that these populations are likely to be descended from the same refugial population(s). Moreover, when populations from Britain and Ireland were compared with the potential source populations of France and Spain, the allele size permutation tests revealed a significant contribution of stepwise mutations to the observed differentiation. We interpret this as evidence that salmon from both France and Spain were successful in colonising Britain and Ireland. Analysis of divergence times in IMA2 suggested similar divergence times for populations from Britain and Ireland with France (~16 000 years) and with Spain (~20 000 years); these are broadly consistent with a pattern of recolonisation since the last glacial maximum, that is, approximately 20 000 years ago (particularly given the wide confidence intervals on such estimates; Supplementary Information and Supplementary Table 5).

Given our findings, it is possible to speculate on the colonisation route of Atlantic salmon out of these refugial populations through the exploration of matrilineal haplotype frequencies. The French populations were largely dominated by the 'Baltic' haplotypes, whereas the Spanish populations were dominated by the 'Atlantic' haplotypes. Within Britain, the highest frequency of 'Baltic' haplotypes was in the region geographically most proximate to France, namely SouthUK. The proportion of 'Baltic' haplotypes then decreased in SouthwestUK, where the frequency distribution of the 'Baltic' and 'Atlantic' haplotypes were most closely balanced, and decreased northwards in Britain and Ireland, where the 'Atlantic' haplotypes began to dominate once more. This suggests that as the ice retreated, salmon from the French refuge first recolonised rivers in SouthUK, while salmon from the Spanish refuge moved into SouthwestUK and Ireland, where the two lineages came into secondary contact; ultimately, it appears that salmon from the Spanish refuge came to dominate more in the northern regions. Although speculative, perhaps similarities between refugial environments and recolonised regions, and potential associated local adaptations, can help explain the distribution of contemporary haplotypes.

CONCLUSIONS

The use of multiple classes of molecular markers has proved highly effective in resolving the phylogeographic history of Atlantic salmon

in a region which to date has received little focused attention. In addition to the well-established refuge in the Iberian Peninsula, a cryptic western refuge in northwest France also seems to be likely, with subsequent colonisation of Britain and Ireland occurring from both refugia.

The clear distinction of the populations of northwest France from those in Spain has not been observed in previous studies. To protect effectively these two ancient lineages, it would be necessary to locate the boundary between the two refugia—an obvious avenue for future research. The ability to reliably identify such variation is important to safeguard the genetic diversity of the species, especially in these small populations existing in somewhat atypical warmer environments at the extreme southern edge of the species' European range.

DATA ARCHIVING

All mtDNA *ND1* sequences were deposited in EMBL with accession numbers HF586486–HF586505. Microsatellite data and mtDNA RFLP haplotype data were deposited in Dryad doi: 10.5061/dryad.0hj6g.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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Supplementary Information accompanies this paper on Heredity website (<http://www.nature.com/hdy>)