Contrasting population genetic structure among freshwater-resident and anadromous lampreys: the role of demographic history, differential dispersal and anthropogenic barriers to movement

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Abstract

The tendency of many species to abandon migration remains a poorly understood aspect of evolutionary biology that may play an important role in promoting species radiation by both allopatric and sympatric mechanisms. Anadromy inherently offers an opportunity for the colonization of freshwater environments, and the shift from an anadromous to a wholly freshwater life history has occurred in many families of fishes. Freshwater-resident forms have arisen repeatedly among lampreys (within the Petromyzontidae and Mordaciidae), and there has been much debate as to whether anadromous lampreys, and their derived freshwater-resident analogues, constitute distinct species or are divergent ecotypes of polymorphic species. Samples of 543 European river lamprey Lampetra fluviatilis (mostly from anadromous populations) and freshwater European brook lamprey Lampetra planeri from across 18 sites, primarily in the British Isles, were investigated for 13 polymorphic microsatellite DNA loci, and 108 samples from six of these sites were sequenced for 829 bp of mitochondrial DNA (mtDNA). We found contrasting patterns of population structure for mtDNA and microsatellite DNA markers, such that low diversity and little structure were seen for all populations for mtDNA (consistent with a recent founder expansion event), while fine-scale structuring was evident for nuclear markers. Strong differentiation for microsatellite DNA loci was seen among freshwater-resident L. planeri populations and between L. fluviatilis and L. planeri in most cases, but little structure was evident among anadromous L. fluviatilis populations. We conclude that postglacial colonization founded multiple freshwater-resident populations with strong habitat fidelity and limited dispersal tendencies that became highly differentiated, a pattern that was likely intensified by anthropogenic barriers.

Keywords: anadromy, barriers to migration, Lampetra, life history, microsatellite, speciation

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Introduction

Although the abandonment of migration remains a poorly understood aspect of evolutionary biology, there is evidence to suggest that this phenomenon might act as an initiator for adaptive radiation (Bell & Andrews 1997; Winker 2000; Räsänen & Hendry 2008; Langerhans & Riesch 2013). Differences in life history traits between resident and migrant individuals can be thought of as adaptive behaviours that act to increase growth, survival rate, fecundity and egg quality. This is reflected in the fitness outcomes of both life history strategies, with residency favoured when the cost of migration exceeds the benefits of doing so, particularly in terms of growth potential and mortality risk before reproduction (Fryxell & Sinclair 1988; Bell & Andrews

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Anadromy, which involves reproduction in freshwater and the majority of growth in the marine environment, is a distinctive migratory trait that is recognized in 18 fish families and 120 species (McDowall 1997; Chapman et al. 2011). Anadromy inherently offers an opportunity to colonize previously unexploited freshwater environments, and the shift from an anadromous to a wholly freshwater life history has occurred repeatedly in many taxa of fishes (e.g. Petromyzontiformes, Salmonidae, Gasterosteidae; Potter 1980; Taylor et al. 1996; Lucas & Baras 2001). Glacial cycles may have supported the evolution of wholly freshwater forms by either blocking migration routes and preventing anadromy or, upon deglaciation, making available new habitats and food resources that are inaccessible through freshwater but easily reached by anadromous fish (Bell & Andrews 1997; Lee & Bell 1999).

The extent to which anadromy is obligatory varies among species. Many populations of anadromous fishes contain a component that does not migrate to sea and instead remains in freshwater where they mature and spawn. In some cases, they may subsequently move little, but in other cases migrate between distinct freshwater habitats (potamodromy), often reproducing with their anadromous conspecifics (Lucas & Baras 2001; McDowall 2001). 'Partial migration' is the term coined for this resident-migratory dimorphism within populations (Chapman et al. 2011), and it is widespread in mammals, invertebrates, birds (Lundberg 1988; Jahn et al. 2010) and fishes (Olsson & Greenberg 2004; Brodersen et al. 2008; Kerr et al. 2009; Chapman et al. 2012).

Incipient speciation in these systems may be promoted through both allopatric and sympatric mechanisms (Chapman et al. 2011). Reduced gene flow between migrants and freshwater-residents breeding in allopatry could promote differentiation by genetic drift or local adaptation. Conversely, population differentiation is limited by the large-scale dispersal capacity of migrants, resulting in a greater chance of panmixia (Hoarau et al. 2002; Coltman et al. 2007). Migratory populations that exhibit philopatry, or habitat fidelity, however, can maintain discrete genetic differences between populations within species. For example, anadromous Atlantic salmon (*Salmo salar*) undergo extended oceanic migrations, yet exhibit significant local adaptation and substantial reproductive isolation between populations owing to precise philopatry and a high homing fidelity to their natal river or tributary (Taylor 1991).

In contrast to anadromous salmonids, anadromous lampreys (Petromyzontiformes) generally show very low interpopulation differentiation across geographically distant river systems (Almada et al. 2008; Goodman et al. 2008) and have been shown to use pheromones released by stream dwelling larvae as partial cues to find suitable spawning habitats (Fine et al. 2004). An evolutionary trend among lampreys is the occurrence in most genera of 'paired species' (Zanandrea 1959), whereby larvae are morphologically indistinguishable, while the adults of two putative species adopt either a nonparasitic freshwater-resident or a parasitic life history which can be either potamodromous or anadromous.

Nonparasitism has arisen repeatedly among lampreys (Docker 2009) and even within species (Espanhol et al. 2007), suggesting that feeding type is plastic and nonparasitic lineages may be polyphyletic. Reduced gene flow within freshwater only (i.e. freshwater-residents; Maitland et al. 2011) and its nonparasitic freshwater-resident derivative the European brook lamprey (*Lampetra fluviatilis* L. 1758) and its nonparasitic freshwater-resident derivative the European brook lamprey (*Lampetra planeri* Bloch 1784), together with several *L. fluviatilis* populations that comprise potamodromous individuals that migrate within freshwater only (i.e. freshwater-residents; Maitland et al. 1994; Inger et al. 2010). We used a combination of *mtDNA* and microsatellite nuclear DNA markers to test the hypothesis that the postglacial expansion of anadromous *L. fluviatilis* during the Holocene prompted the establishment of multiple freshwater-resident *L. planeri* populations that subsequently became genetically differentiated. We also investigated the possibility that anthropogenic barriers are isolating lamprey populations and provide a robust quantitative assessment of this. In some freshwater fishes, the fragmentation of habitats by dams can promote genetic differentiation between the upstream and downstream populations resulting from the reduction of gene flow, often compounded by founder effects and subsequent genetic drift (Yamamoto et al. 2004; Palkovacs et al. 2008). Population divergence and dispersal at local to catchment scales were examined enabling inference about population connectivity and evolutionary viability, which may
indicate important applications in conservation management (Latta 2008) and enhance our understanding of the systematics of these ancient fish.

Methods

Sampling and DNA isolation

Tissue samples were collected across a total of 18 sites (Fig. 1, Table S1, Supporting information). Unlike, for example, in some Baltic regions (Sjöberg 2011), there is no evidence or likelihood of historical stocking or translocation of lampreys at any of these sites. MtDNA loci were examined in \( n = 108 \) individuals from six sites including two paired sites (i.e. where *Lampetra planeri* and *Lampetra fluviatilis* were obtained from the same river; Table S1, Supporting information, Table 1, Fig. 1). For microsatellite loci, 543 samples were collected from 18 sites, including seven paired sites (PS; Table S1, Supporting information, Fig. 1). One of these paired sites also included a freshwater-resident *L. fluviatilis* population (PS7; Loch Lomond, Scotland, Table S1, Supporting information). Three additional sites for *L. fluviatilis* were also included in the analysis (sites 9, 17, 18, Table S1, Supporting information, Fig. 1); one of which is a freshwater-resident population of *L. fluviatilis* in the River Bann (site 17). In Loch Lomond (PS7 in Table S1, Supporting information; Scotland), all three ‘ecotypes’ (i.e. *L. planeri*, *L. fluviatilis* and freshwater-resident *L. fluviatilis*) are truly sympatric; however, in all other paired sites, *L. planeri* samples were obtained upstream (within the same river) of anadromous *L. fluviatilis* populations, which were usually separated by migration barriers (Table S2, Supporting information). It should also be noted that the location from which the River Swale *L. planeri* samples were obtained is a spawning site for both *L. planeri* and sometimes *L. fluviatilis*.

Samples were obtained by hand-netting, electro-fishing and the utilization of static double-funnel traps to capture spawning, and upstream-migrating lampreys (Table S1, Supporting information). Both *L. fluviatilis* and *L. planeri* were sampled where they were found to be locally abundant prior to the spawning period and so were, in most cases, captured in the vicinity of their

Fig. 1 Map showing location of sampling sites 1–18 (see Table S1, Supporting information for detail). Inset is a detailed map of part of the Ouse subcatchment of the Humber catchment, showing sampling locations. Only sampled rivers are shown.
Table 1 Diversity indices for MtDNA ATPase

<table>
<thead>
<tr>
<th>Population</th>
<th>Site no.</th>
<th>Country</th>
<th>N</th>
<th>H</th>
<th>π</th>
<th>h</th>
<th>D</th>
<th>Dp</th>
<th>Fs</th>
<th>Fsp</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bann (Lf Res)</td>
<td>17</td>
<td>N. Ireland</td>
<td>20</td>
<td>3</td>
<td>0.0002 ± 0.0003</td>
<td>0.1947</td>
<td>-1.5128</td>
<td>0.059</td>
<td>-1.1801</td>
<td>0.015</td>
</tr>
<tr>
<td>Scheldt (Lf)</td>
<td>18</td>
<td>Belgium</td>
<td>20</td>
<td>10</td>
<td>0.0012 ± 0.0009</td>
<td>0.7105</td>
<td>-2.0976</td>
<td>0.006</td>
<td>-8.7029</td>
<td>0</td>
</tr>
<tr>
<td>Nidd (Lf)</td>
<td>12</td>
<td>Wales</td>
<td>12</td>
<td>2</td>
<td>0.0001 ± 0.0002</td>
<td>0.1176</td>
<td>-1.1639</td>
<td>0.125</td>
<td>-0.7484</td>
<td>0.092</td>
</tr>
<tr>
<td>Dee (Lf)</td>
<td>17</td>
<td>Wales</td>
<td>17</td>
<td>2</td>
<td>0.0006 ± 0.0006</td>
<td>0.3500</td>
<td>-1.8399</td>
<td>0.015</td>
<td>-1.7904</td>
<td>0.014</td>
</tr>
<tr>
<td>Dee (Lf)</td>
<td>13</td>
<td>Wales</td>
<td>17</td>
<td>2</td>
<td>0.0003 ± 0.0004</td>
<td>0.2206</td>
<td>-0.4913</td>
<td>0.264</td>
<td>0.0353</td>
<td>0.255</td>
</tr>
<tr>
<td>All</td>
<td>108</td>
<td></td>
<td>16</td>
<td></td>
<td>0.0007 ± 0.0006</td>
<td>0.4907</td>
<td>-2.1898</td>
<td>0</td>
<td>-18.4452</td>
<td>0</td>
</tr>
</tbody>
</table>

MtDNA analysis was performed on only a subset of the 543 lampreys and 18 sites used for the microsatellite analysis. The 'Site No.' column corresponds to the site numbers in Fig. 1 and Table S1 (Supporting information).

N = Sample size, H = number of haplotypes, π = nucleotide diversity, h = haplotype diversity, D = Tajima’s D, Dp = Tajima’s D P-value, Fs = Fu’s F, Fsp = Fu’s F P-value, and Lf = *L. fluviatilis*, Lp = *L. planeri*, and Lf Res = freshwater-resident population of *L. fluviatilis*.

Amplification and genotyping of microsatellites

Thirteen recently developed polymorphic microsatellite loci were used to examine genetic differentiation among and between all *L. fluviatilis* and *L. planeri* populations. Eight microsatellite primers developed for European *Lampetra* (Lp-003, Lp-006, Lp-009, Lp-018, Lp-027, Lp-028, Lp-046 and Lp-045; Gaigher et al. 2013), one primer set developed for *Lampetra richardsoni* (Lri-5; Luzier et al. 2010), and four microsatellite primers developed in this study (using the protocol described in White et al. 2010) and optimized for European *Lampetra* species (Lamper_1, Lamper_2, Lamper_3, Lamper_4) were included (Table S3, Supporting information).

Microsatellite loci were multiplex amplified using a Qiagen Multiplex kit. Thermal cycler conditions were as follows: initial denaturation at 95 °C for 15 min; followed by 35 cycles of denaturation at 94 °C for 30 s, annealing temperature 60 °C for 90 s and extension at 72 °C for 60 s; and followed by a final extension at 60 °C for 30 min. PCR products were genotyped on a 3730 ABI DNA Analyser (DBS genomics Durham University).

Amplification and sequencing of mitochondrial DNA

The PCR primers ATPfor and ATPrev (Espanhol et al. 2007) were used to amplify 838 bp of the mitochondrial gene ATPase subunits 6 and 8. This locus was chosen to facilitate comparison with previous data from Espanhol et al. (2007) and Mateus et al. (2011). Each 20 μL reaction contained 1.2 μL (final conc. 1.5 μM) MgCl2, 2 μL dNTPs (2.0 mM), 0.2 μL of each primer (10 mM), 4 μL of Colorless GoTaq® Reaction Buffer (Promega), 0.1 μL GoTaq DNA polymerase (Promega) and 1 μL of template DNA. Cycle conditions were as follows: initial denaturation at 94 °C for 3 min, followed by 30 cycles of; denaturation at 94 °C for 1 min, annealing temperature 57.1 °C for 1 min and extension at 72 °C for 2 min; and followed by a final extension at 72 °C for 2 min. The resulting PCR products were purified using the Qiagen PCR Purification kit and sequenced using an ABI PRISM 3730 DNA Analyser (DBS genomics Durham University).
indicating positive or balancing selection (using a forced neutral mean $F_{ST}$, a confidence interval of 0.99 and false discovery of 0.1), and no loci with evidence for selection were found.

**Genetic diversity and structure**

MitDNA sequences were aligned manually using **GENEMO** vR6 (Biomatters). The program **DNASP** 10.4.9 (Rozas et al. 2003) was then used to calculate mitochondrial DNA polymorphism estimated as haplotypic diversity (Nei & Tajima 1981) and nucleotide diversity (Nei 1987). To determine the level of genetic differentiation between pairs of populations, $F$-statistics (Weir & Cockerham 1984) were calculated for mtDNA and microsatellite DNA loci using **ARLEQUIN** version 3.5. Significance was tested using 1000 permutations. **ARLEQUIN** was also used to calculate Fu’s $F$, Tajima’s $D$ and mismatch distributions. We estimated the putative time of population expansion from the mismatch distribution using the statistic $\tau$; Rogers & Harpending (1992). Substitution rate was estimated after Ho et al. (2007) who suggest an average of ~50% per site per million years for the control region, based on recent evolutionary time frames, although of course this varies among species. The substitution rate for the control region can be ten times faster than the rest of the mitochondrial genome (McMillan & Palumbi 1997). Therefore, 5% per site per million years was used as a rough estimate for ATPase. Mutation rates of 1% and 10% per million years were also used to illustrate the effect that the rate of divergence will have in the expansion times. The relationship between haplotypes was investigated using a median-geance will have in the expansion times. The relationship also used to illustrate the effect that the rate of divergence was estimated after Ho et al. (1996) which gives a visual representation of individual genotype clustering. A test for a positive association between genetic $F_{ST}/(1 – F_{ST})$ and geographic distances [Isolation by distance (IBD)] based on microsatellite DNA loci was carried out using a Mantel test (10 000 permutations) in **GENEPOP** v4.2. Geographic distances were calculated between sample sites using linear referencing tools in Quantum GIS (Lisboa). A Mantel test was also carried out to test for association between genetic distances and number of physical barriers (defined as any anthropogenic feature larger than 0.5 m height at base river level which reaches the full width of the river) between sample sites. The 0.5 m value was subjective, based on the fact that many structures of this height or greater generate discrete water level differences (upstream–downstream) at base flows, on published and unpublished data on the impact of different height potential barriers on lamprey movement (L. fluviatilis, Lucas et al. 2009; L. planeri, M. C. Lucas personal observation), and on our ability to identify potential barriers in field surveys and databases. Only river systems for which information on barriers was available were utilized in the Mantel tests (including the Dee, Wear and all rivers within the Ouse subcatchment, excluding the Swale due to the low sample size attained for L. planeri).

**MIGRATE-N** (v 3.2.6) was used to estimate levels of historical gene flow between populations (Beerli & Felsenstein 2001; Beerli 2006; Beerli & Palczewski 2010). Pairwise comparisons were carried out between putative species (i.e. L. fluviatilis and L. planeri) at six locations (Wear, Dee, Lomond, Nidd, Ure, Derwent), of which the latter three are all tributaries in the same river catchment, where samples from both species were available. To implement Bayesian inference in MIGRATE-N, the Brownian motion approximation was selected with an MCMC search of 100 000 burn-in steps followed by 5 000 000 steps with parameters recorded every 100 steps; exponential prior on theta (min: 0, mean: 30, max: 60); and an exponential prior on migration (min: 0, mean: 650 max: 1300). **MIGRATE-N** was run...
with parameter values starting from $F_{ST}$-based estimates, and the distribution of parameter values was compared across runs to ensure overlap of 95% CI. BAYE-SASS 1.3 (Wilson & Rannala 2003) was used to estimate the magnitude and directionality of contemporary gene flow between *L. fluviatilis* and *L. planeri*. Pairwise comparisons were carried out for the same six locations that were used in the MIGRATE-N analysis. In contrast to MIGRATE-N, BAYESASS estimates all pairwise migration rates rather than a user-defined migration matrix and provides unidirectional estimates of migration for each population pair. BAYESASS does not assume a migration-drift equilibrium, an assumption that is frequently violated in natural populations (Whitlock & McCauley 1999). A total of 10 000 000 MCMC iterations were run of which 1 000 000 were for the burn-in. All other options were left at their default settings. Five to 10 runs with a different starting point were performed for each population pair and results are given as means. The program TRACER version 1.5 (Rambaut & Drummond 2007) was used as a method to qualitatively assess MCMC convergence.

Results

**MidDNA**

ATPase subunits 6 and 8 were sequenced and haplotypes determined for 108 lampreys (*Lampeia fluviatilis* and *Lampeia planeri*) from six sampling sites (Table 1). Over all populations, haplotype and nucleotide diversity were low, with freshwater-resident populations of both *L. planeri* and *L. fluviatilis* generally exhibiting lower haplotype and nucleotide diversity than the anadromous *L. fluviatilis* populations. Both Tajima’s $D$ and Fu’s $F$ were negative and highly significant (Table 1), consistent with a population expansion (e.g. after a bottleneck) or a selective sweep. Using the value of $tau$, which was 0.673 (Fig. S1, Supporting information), an expansion time of 16 263 (10 182–26 952; 95% CI) years ago was calculated using the mutation rate of $0.028 \pm 0.00524$ to $0.02537$. $F_{ST}$ values between *L. fluviatilis* and *L. planeri* populations ranged from 0.011 to 0.185. Average allelic richness per locus ranged from 2.43 (Lp_003) to 14.9 (Lamper_4). Average $F_{IS}$ per site ranged from −0.095 to 0.11945. When the freshwater-resident *L. fluviatilis* populations were not included, the $F_{ST}$ values ranged from −0.00524 to 0.02537. $F_{ST}$ values between *L. fluviatilis* and *L. planeri* populations ranged from 0.011 to 0.1854. Average allelic richness per locus ranged from 2.43 (Lp_003) to 14.9 (Lamper_4). Average $F_{IS}$ per site ranged from −0.095 [Wear (L. planeri)] to 0.028 [Lomond (anadromous *L. fluviatilis*)].

In COLONY, tests for the proportion of putative full-siblings (as an indicator of close kin) in populations of either species showed this to be rare, 0% in some cases for both species, and no higher than 0.74%. One randomly chosen individual of each full-sibling pair was excluded, and analysis was repeated. There were no differences that affected inference in the results with full-siblings included or excluded, so all individuals were included in the analysis.

**Structure** analyses consistently identified *L. planeri* populations as being separate from *L. fluviatilis* populations (anadromous and freshwater-resident) and from each other (Fig. 4). The only exception was the small sample of *L. planeri* on the Swale compared to the *L. fluviatilis* population downstream on the same river (Fig. S2a, Supporting information). Figure 4a shows the most likely population structure among 12 sampling locations in England and Wales (excluding the Scottish Loch Lomond system) incorporating both species, where $K = 6$ showed the highest LnP(D) (Fig. S3, Supporting information). *Lampeia fluviatilis* samples appear as a single mixed population. Representing a higher
hierarchical level, $AK = 2$ primarily supports separation of $L.\ fluviatilis$ and $L.\ planeri$ (Figs S3 and S4, Supporting information). Figure S4c (Supporting information) shows a comparison across all populations where $K = 9$ [the highest $LnP(D)$ outcome]. There were several peaks for $DK$ at $K = 2, 5$ and $8$ (Fig. S4d, Supporting information), but the maximum $LnP(D)$ result ($K = 9$) was most informative, distinguishing all $L.\ planeri$ and $L.\ fluviatilis$ freshwater-resident populations (with the exception of the $L.\ planeri$ population in the Swale).

When only $L.\ planeri$ populations were compared, the highest likelihood result identified all populations as distinct (Fig. 4b). In this case, $AK$ was 4 (Figs S3 and S4, Supporting information); however, this linked samples from the Nidd with the Dee, and Loch Lomond with the Derwent, in each case populations on opposite sides of British Isles (see Fig. 1; Fig. S4b, Supporting information). When only anadromous $L.\ fluviatilis$ populations were compared, the outcome was $K = 1$ (not shown). The Loch Lomond system (which contains anadromous

Table 2 Matrix of pairwise $F_{ST}$ values for mtDNA analysis of six populations of $Lampetra$

<table>
<thead>
<tr>
<th></th>
<th>Bann (Lf Res)</th>
<th>Dee (Lf)</th>
<th>Nidd (Lp)</th>
<th>Scheldt (Lf)</th>
<th>Nidd (Lf)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dee (Lf)</td>
<td></td>
<td>0.0033</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nidd (Lp)</td>
<td>0.8534</td>
<td></td>
<td>0.7717</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Scheldt (Lf)</td>
<td>0.0074</td>
<td>-0.0001</td>
<td></td>
<td>0.5702</td>
<td></td>
</tr>
<tr>
<td>Nidd (Lf)</td>
<td>-0.0038</td>
<td>0.0024</td>
<td></td>
<td>0.9409</td>
<td></td>
</tr>
<tr>
<td>Dee (Lf)</td>
<td>-0.0258</td>
<td>-0.0196</td>
<td></td>
<td>0.8676</td>
<td>0.0024</td>
</tr>
</tbody>
</table>

Significant $F_{ST}$ values [i.e. all $F_{ST}$ values associated with Nidd (Lp)] are highlighted in grey ($P < 0.0001$).

Lf = Lampetra fluviatilis, Lp = Lampetra planeri and Lf Res = freshwater-resident population of L. fluviatilis.

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L. fluviatilis, freshwater-resident L. fluviatilis and L. planeri populations) was compared to an anadromous L. fluviatilis population (Nidd) and another freshwater-resident population of L. fluviatilis. Table showing the actual values is included in Supporting information (Table S5). Numbers on axes are marked with a square to represent freshwater-resident L. fluviatilis.

The FCA plots support essentially the same clusters as identified in STRUCTURE showing L. fluviatilis as being dominated by one large grouping, with the freshwater-resident populations differentiated (Fig. S5a, Supporting information) and L. planeri populations as all being separated from each other (Fig. S5b, Supporting information). Mantel tests for correlation between genetic and geographic distance showed a significant negative trend for L. planeri populations ($R^2 = 0.2963; P < 0.05$; Fig. 5a) and a weak but significant positive linear relationship for all L. fluviatilis populations ($R^2 = 0.0841; P < 0.05$). However, when freshwater-resident L. fluviatilis populations were excluded (Bann and Loch Lomond), the positive relationship was much stronger ($R^2 = 0.40$, $P < 0.0001$; Fig. 5b). Mantel tests examining correlations between genetic distance and the number of barriers along migration/dispersal routes for L. fluviatilis and L. planeri (populations included as described in methods) showed a highly significant positive correlation ($R^2 = 0.8256$, $P < 0.0001$; Fig. 5c).

Migration rate estimates between species (using MIGRATE-N) ranged from 3.73 to 10.43 migrants/generation from L. fluviatilis to L. planeri, and from 4.18 to 16.28 from L. planeri to L. fluviatilis (Table S6, Supporting information). The six pairwise comparisons all suggested asymmetric gene flow greater in the direction from L. planeri to L. fluviatilis (which apart from Loch Lomond was always in the downstream direction), but 95% confidence intervals were large and overlapping. The BAYESASS analysis indicated low-level contemporary gene flow between the putative species, and some comparisons also suggest the downstream direction from L. planeri to L. fluviatilis (especially in the Derwent; Table S7a,b, Supporting information). It also indicated ongoing gene flow between the three forms in the Loch Lomond system (Table S7b, Supporting information).

Discussion

Population history

This study was based in a geographic region that has undergone profound cyclical changes over the course of the Pleistocene (2.58 Ma–11 700 years ago), with suitable riverine habitat available only during interglacial periods (Hays et al. 1976). For our study sites in the UK, mtDNA failed to show any differentiation between the two putative Lampetra species or among populations, which is consistent with data for some other northern European populations (Espanhol et al. 2007). While this may suggest ongoing gene flow or the incomplete sorting of ancestral polymorphisms, it is also consistent with recent founder events establishing these populations. The network analyses and neutrality tests support this, indicating small founder populations and subsequent expansion. Conversely, for populations in southern Europe where the climate has been more stable over time, there are far higher nucleotide diversities and significant mtDNA phylogeographic structuring (Pereira et al. 2010; Mateus et al. 2011).

Espanhol et al. (2007) suggested that Lampetra planeri in Europe may be polyphyletic and have originated within at least two evolutionary lineages, possibly the result of independent divergence events from Lampetra fluviatilis with the repeated loss of anadromy. Pereira et al. (2010) have since found several Portuguese populations of L. planeri which are isolated among themselves and also from the anadromous lamprey population. These populations had only private haplotypes, suggesting that a significant amount of time had passed to establish independent evolutionary histories.
The fact that genetically distinct non-migratory *Lampetra* populations are found in many Portuguese rivers (Pereira et al. 2010; Mateus et al. 2011; 2013a) suggests lamprey were once more abundant and widespread in Iberia. The higher levels of divergence shown in our mtDNA median-joining network that included Portuguese lampreys (Fig. 2), compared to other populations examined across Europe, also suggests that sufficient time may have passed to establish a complex of incipient freshwater-resident species, although further

Fig. 4 STRUCTURE bar plot generated from microsatellite data for three population clusters of lampreys. (a) Comparison between *Lam- petra fluviatilis* and *Lampetra planeri* populations (*K* = 6); (b) *L. planeri* populations (*K* = 6); (c) Loch Lomond populations compared to a population of *L. fluviatilis* from the Humber catchment and freshwater-resident *L. fluviatilis* populations from the R. Bann in N. Ireland (*K* = 3). Please see the open-access online paper for a colour version of this figure.
nuclear DNA data would help resolve this question. Similar processes generating multiple origins have been suggested, for example, in the marine to freshwater transitions of three-spine sticklebacks (Gasterosteus aculeatus; Hohenlohe et al. 2010).

Our study estimates the expansion time of L. planeri and L. fluviatilis populations in the British Isles and northern Europe as 16 236 (10 182–26 952) years ago using tau and a mutation rate of 5% per million years, which roughly coincides with the last glacial maximum (19–26 000 years ago; Clark et al. 2009). The Pleistocene climatic fluctuations impacted much of Europe (Hays et al. 1976; Webb & Bartlein 1992) and significantly influenced the distribution and genetic diversity of plants and animals (Hofreiter & Stewart 2009). In addition to cycles of habitat loss and release as glaciers extended and receded, the ‘refugium theory’ proposes that temperate species survived the glacial maxima in southern refugia and colonized northern latitudes during interglacial periods (Taberlet et al. 1998; Hewitt 2000). The results shown here, coupled with data from the Iberian Peninsula, suggest that southern latitudes served as an important refugium for Lampetra during the Pleistocene glaciations, intermittently acting as a point of dispersal for postglacial expansion (Espanhol et al. 2007; Mateus et al. 2012, 2013b).

Therefore, there may have been a tendency during interglacial periods, while anadromous Lampetra were expanding northwards, for populations at lower latitudes to abandon anadromy and eventually become restricted to freshwater. This is consistent with the findings of a recent study utilizing restriction site associated DNA sequencing (RAD seq.) that identified strong genetic differentiation between sympatric L. fluviatilis and L. planeri in the Iberian Peninsula with numerous fixed and diagnostic single nucleotide polymorphisms (SNPs) between the two putative species, some associated with genes related to osmoregulation (Mateus et al. 2013b). A study using RAD sequencing to compare Pacific lamprey (Entosphenus tridentatus) geographic populations also found evidence consistent with local adaptation (Hess et al. 2013). Our median-joining network in Fig. 2 shows that for the available samples, only clade IV shares a haplotype with the lineage representing the northern expansion, suggesting a possible link between these lineages (with clade IV providing the ancestor of the anadromous group that founded the postglacial population in northern Europe). With expansion into previously unoccupied territory, it is expected that genetic diversity should decrease from the south to the north (Hewitt 2000), consistent with our findings.

**Population structure**

In contrast to mtDNA, we found considerable structure at microsatellite DNA loci between L. fluviatilis and L. planeri populations, especially among populations of L. planeri, but much less among anadromous L. fluviatilis populations. Anadromous lampreys (Lethenteron spp.) in Japan (Yamazaki et al. 2011) and Petromyzon marinus in North America (Bryan et al. 2005) and Europe (Almada et al. 2008) exhibit similar levels of panmixia, with little or no genetic structure, despite their widespread distribution. Spice et al. (2012) found that Pacific
lamprey along the west coast of North America showed low but significant differentiation among locations. However, instead of being philopatric like many other anadromous fish species (McDowall 2001), differentiation was suggested to be due to greater restrictions to dispersal at sea compared to other anadromous lamprey species. The lack of population structure found in our study was, therefore, consistent with the general lack of natal homing seen for other anadromous lamprey species.

The absence of a clear genetic signal for species-level differences between anadromous and freshwater-resident populations is consistent with findings for other paired lamprey species (Espanhol et al. 2007; Hubert et al. 2008; Docker 2009; April et al. 2011; Mateus et al. 2011; Boguski et al. 2012; Docker et al. 2012). Greater differentiation among populations within *L. planeri*, than between *L. planeri* and *L. fluviatilis*, suggests the unexpected pattern of greater gene flow between the putative species than within *L. planeri* (while the greatest gene flow occurs among populations of *L. fluviatilis*). Gene flow between the putative species may be possible owing to a combination of interspecific nest association (Huggins & Thompson 1970; Lasne et al. 2010) and sneaker male behaviour (Malmqvist 1983; Hume et al. 2013). As larvae of both species tend to move downstream through voluntary and involuntary drift behaviour (Hardisty & Potter 1971a; Moser et al. 2015), the distribution and overlap of spawning adults of the two species ultimately depends on a combination of the degree of downstream drift of *L. planeri* from upstream tributaries where they predominate, towards *L. fluviatilis*-dominated zones, and the subsequent upstream movements of freshwater-resident *L. planeri* and anadromous or freshwater-resident *L. fluviatilis* (Hardisty & Potter 1971b; Malmqvist 1980).

Both assignment (*BAYESASS*) and coalescent (*MIGRATE-N*) methods suggested directionality in genetic migration, favouring the direction of *L. planeri* to *L. fluviatilis*, although the confidence limits were broad. Asymmetric gene flow occurring in these types of freshwater systems can significantly influence the distribution of genetic variation, with downstream populations typically exhibiting higher genetic diversity than headwater populations (Caldera & Bolnick 2008; Morrissey & de Kerckhove 2009; Julian et al. 2012). Yamazaki et al. (2011) found gene flow to exist at multitemporal scales between 'potentially sympatric' lamprey populations and suggested ongoing gene flow was the result of imperfect size-assortative mating and the plastic determination of life histories. The observed increase in genetic diversity as one moves downstream to the lower reaches of the river could result from historical patterns of colonization, with contemporary dispersal reflecting movement bias, fragmented habitat or the presence of dispersal barriers (Morrissey & de Kerckhove 2009; Dehais et al. 2010). Asymmetric gene flow would be expected if *L. planeri* populations remain primarily resident further up the catchments with occasional migrants moving further downstream to where they may encounter spawning *L. fluviatilis*.

**Connectivity and anthropogenic factors**

Mantel tests for isolation by distance revealed a positive correlation between geographic and genetic distance for anadromous *L. fluviatilis*, and a counterintuitive negative correlation among *L. planeri* populations (Fig. 5). However, while the correlation for *L. fluviatilis* was significant (especially when freshwater-resident *L. fluviatilis* were omitted), and consistent with expectations (implying that long-range dispersal is less common), the correlation with *L. planeri* was weak and showed a broad range of values for a given distance (see Fig. 5a). The *L. planeri* correlation may, therefore, simply reflect a stochastic pattern or ancestral relationships.

The number of anthropogenic barriers between populations was found to be significantly positively correlated with genetic distance, and such barriers have been shown to limit the upstream migration of *L. fluviatilis* (Lucas et al. 2009). Anthropogenic barriers could therefore be amplifying (beyond natural processes) the isolation of *L. planeri* populations by inhibiting the upstream movement of anadromous *L. fluviatilis* and preventing geneflow mediation in this manner between populations. Meldgaard et al. (2003) also detected a statistically significant increase of *F_S* with the number of weirs between grayling (*Thymallus thymallus*) populations in a Danish river system. Similar decreases of genetic diversity from downstream towards upstream populations have been observed in other fish species in relation to anthropogenic barriers (Yamamoto et al. 2004; Caldera & Bolnick 2008; Raeymaekers et al. 2009). Yamazaki et al. (2011) found freshwater-resident nonparasitic lamprey populations in the upper regions of dammed rivers to be genetically divergent from seasonally sympatric, anadromous, parasitic populations. This pattern is consistent with a scenario where barriers amplify the asymmetry of gene flow from upstream towards downstream sites by allowing some passive downstream drift, while obstructing active upstream migration. Spice et al. (2012) also found that larvae from an anadromous population of *E. tridentatus* at a spawning site upstream of nine dams (which only a small number of adults successfully pass each year) exhibited higher
genetic differentiation (i.e. higher $F_{ST}$ values) than most other population comparisons.

When a freshwater-resident lamprey population is physically isolated from anadromous parasitic populations (which may mediate gene flow between freshwater-resident populations), acceleration in genetic divergence may result in the subsequent establishment of allopatric speciation (Yamazaki & Goto 2000). It is probable, however, that freshwater-resident _L. planeri_ populations would have become, and tended to remain, isolated without the added anthropogenic hurdles, as there is a degree of population separation that is due to the natural extent of upstream migration in anadromous _L. fluviatilis_. As previous studies have shown, this is usually limited to higher order channels, and individuals do not generally penetrate the smaller streams even where access is unhindered by barriers (Hardisty & Potter 1971c; Hardisty 1986b).

The system in Loch Lomond offers evidence of the potential for gene flow between morphologically differentiated ecotypes, indicating that where they are found sympatrically, gene flow between _L. fluviatilis_ and _L. planeri_ can occur. This scenario is also supported by the lack of evidence for differentiation between the geographically proximate _L. fluviatilis_ and _L. planeri_ populations on the River Swale, although the sample size for the latter population was small (Fig. S2, Supporting information). Similarly, Docker _et al._ (2012) found no genetic differentiation between silver (_Ichthyomyzon unicuspidis_) and northern brook (_I. fossor_) lampreys occurring sympatriically (also using microsatellite loci), but did find differentiation among parapatric populations. Yamazaki _et al._ (2011) also found a lack of differentiation between sympatric populations of Arctic lamprey (_Lethenteron camtschaticum_) and its nonparasitic derivatives in the Ohno River, Japan.

The **BAYESASS** analysis suggests that contemporary gene flow is occurring between all three populations in Loch Lomond, consistent with a tendency for interbreeding when there are no environmental barriers to limit connectivity. The divergence of the freshwater-resident _L. fluviatilis_ population would then suggest a period of differentiation in isolation. Therefore, in Loch Lomond, the anadromous strategy is also paralleled by a population component with potamodromous behaviour, with some fish apparently showing migration mostly between the loch and spawning streams. While all three Loch Lomond populations were significantly differentiated from each other (Fig. 3, Table S5, Supporting information), there were also data indicating contemporary gene flow among them, and the anadromous _L. fluviatilis_ and sympatric _L. planeri_ populations both showed evidence of connectivity with the wider _L. fluviatilis_ populations.

**Conclusions**

Alternative life history strategies are common among fishes inhabiting postglacial lakes, often resulting from adaptation to different foraging strategies or environments (Robinson & Parsons 2002). This is one of the best supported mechanisms for speciation in sympathy, for example among cichlid species in Holocene lakes (Barluenga _et al._ 2006). The divergence of multiple independent populations is a common trend in the evolution of diversity for diadromous fish (Schluter & Nagel 1995; Waters & Wallis 2001), and a number of studies have shown the influence of glacial movement within the Holocene on the phylogeographical structure of freshwater fishes (Harris & Taylor 2010; Boguski _et al._ 2012). However, in our study, the geographic scale is small for the extent of differentiation observed. It is apparent that at an initial stage, there was a post-glacial expansion of anadromous _Lampetra fluviatilis_ from southern refugia and the subsequent establishment of multiple freshwater-resident _Lampetra planeri_ populations. These may have been relatively small founder groups that retained some degree of reproductive isolation that was likely intensified, although perhaps not entirely determined, by the anthropogenic introduction of barriers. Moreover, it was ascertained that there is gene flow between _L. fluviatilis_ and _L. planeri_ in both long-term and contemporary timescales and the pattern of gene flow is apparently asymmetric. This has significant implications for the management of _L. planeri_ populations and the extent to which this is underpinned by natural processes will have important evolutionary implications with respect to the mechanisms that generate diversity. Our data emphasizes the importance of founder events in the evolution of diversity among populations and as a frequent component of the speciation process (Templeton 2008). These data also strongly support a scenario of multitemporal and multispatial radiation. In contrast to higher levels of _Lampetra_ divergence present in the Iberian Peninsula, the northern European populations appear to have been established relatively recently, and the process of differentiation is still ongoing. There may be a natural tendency towards speciation in freshwater-resident populations that remain environmentally stable over time, but a dynamic process instead at higher latitudes experiencing a cycle of habitat loss and release.

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M.C.L., A.R.H. and F.S.A.B. designed the study, F.S.A.B. carried out the lab analyses, F.S.A.B. and A.R.H. interpreted the genetic results and drafted the manuscript, M.C.L. and J.B.H. contributed to the writing and editing, J.B.H. provided materials for analysis.

Data accessibility


Supporting information

Additional supporting information may be found in the online version of this article.

Table S1 Numbers collected and location of origin for all genetic samples of Lampetra planeri and Lampetra fluviatilis and by whom they were collected.

Table S2 Number of barriers (distance, km) between sampling locations.

Table S3 Details of microsatellite loci and primers utilised in the study.

Table S4 Table outlining diversity indices for microsatellite loci by population, and by locus.

Table S5 Pairwise \( F_{ST} \) values for 13 microsatellite loci.

Table S6 Migrate-N analysis (Bayesian) showing posterior distributions for six paired sites (95% confidence intervals in brackets).

Table S7 Pairwise estimation of current gene flow, \( M \), between (a) populations of anadromous Lampetra fluviatilis (L) and Lampetra planeri (LP) from within the same river, and (b) populations within Loch Lomond by BAYESSASS.
**Fig. S1** Mismatch distribution (demographic expansion) with Tau 0.673, showing an expansion pattern for the six populations of *Lampetra fluviatilis* and *Lampetra planeri* presented in Table 1.

**Fig. S2** STRUCTURE bar plot generated from microsatellite data showing (a) $\Delta K = 2$ ($\text{LnP}(D) = -2294.8$) where Swale Lp is compared to another *Lampetra planeri* population and *Lampetra fluviatilis* form the same river (b) $\Delta K = 2$ when prior location information is used to analyse the Loch Lomond system which shows the freshwater-resident Lomond population to be differentiated and (c) $\Delta K = 5$ ($\text{LnP}(D) = -4681$) when a location prior is used.

**Fig. S3** Posterior probability of the data ($\text{Ln}[\text{P}(D|K)]$) and values of $\Delta K$ (Evanno et al. 2005) as a function of $K$ (number of clusters), associated with the results shown in Fig. 4 in the main text.

**Fig. S4** (a) Structure for 12 populations where $\Delta K = 2$. (b) Structure for *Lampetra planeri* only where $\Delta K = 4$. (c) Structure for all samples included when $K = 10$ ($Lf = *Lampetra fluviatilis*$, $Lp = *L. planeri*$, $LL = \text{Loch Lomond}$; anad = anadromous; res = resident). (d) $\Delta K$ plot for the structure plot in part c.

**Fig. S5** FCA analysis for (a) *Lampetra fluviatilis* and (b) *Lampetra planeri* population.