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ORIGINAL ARTICLE

Genetic signatures of historical dispersal of fish threatened by biological invasions: the case of galaxiids in South America

Delphine Vanhaecke[1,a], Carlos Garcia de Leaniz[2], Gonzalo Gajardo[3], Jason Dunham[4], Guillermo Giannico[5] and Sofia Consuegra[1,2*]

[1]Institute of Biological, Environmental & Rural Sciences, Aberystwyth University, Aberystwyth SY23 3DA, UK, [2]Department of BioSciences, College of Science, Swansea University, Swansea, UK, [3]Laboratorio de Genética, Acuicultura y Biodiversidad, Universidad de Los Lagos, Osorno, Chile, [4]US Geological Survey, Forest and Rangeland Ecosystem Science Center, Corvallis, OR, USA, [5]Department of Fisheries and Wildlife, Oregon State University, Corvallis, OR, USA

*Correspondence: Sofia Consuegra, Swansea University, College of Science, Department of BioSciences, Singleton Park, Swansea SA2 8PP, UK.
E-mail: s.consuegra@swansea.ac.uk

[a]Present address: Flanders Marine Institute, Wandelaarkaai 7, Oostende B-8400, Belgium

ABSTRACT

Aim The ecological effects of biological invasions are well documented, but little is known about the effects of invaders on the genetic structure of native species. We examined the phylogeography, genetic variation and population structuring of two galaxiid fishes, *Aplochiton zebra* and *A. taeniatus*, threatened by non-native salmonids, and whose conservation is complicated by misidentification and limited knowledge of their genetic diversity.

Location Chile and the Falkland Islands.

Methods We combined microsatellite and mitochondrial DNA (16S rDNA and COI) markers to compare genetic diversity, effective population size and gene flow of *Aplochiton* spp. populations differentially affected by salmonid presence.

Results We identified two 16S rDNA haplotypes among *A. zebra* – one dominant in coastal populations and another dominant in inland populations. Populations living on the island of Chiloé displayed a mixture of coastal and inland haplotypes, as well as high microsatellite diversity, as one would expect if the island had been a refugium during the Last Glacial Maximum, or a contact zone among populations. Microsatellite data revealed strong population structuring, indicative of current isolation patterns, and a negative correlation between the genetic diversity of *A. zebra* and the relative abundance of invasive salmonids.

Main conclusions Our study indicates that population structuring of *A. zebra* reflects the influence of historical patterns of migration, but also the current levels of reduced gene flow among watersheds. Invasive salmonids, known to compete with and prey on native galaxiids, may have had negative impacts on the genetic diversity of *Aplochiton* spp. The low genetic variation found in some populations, coupled with potential biases in abundance estimates due to species misidentification, highlight the urgent need for more research into the conservation status of the two species of *Aplochiton*.

Keywords
***Aplochiton*, biological invasions, gene flow, microsatellites, mtDNA, phylogeography, post-glacial colonization, salmonids.**

INTRODUCTION

Biological invasions represent a major cause of biodiversity loss (Clavero & García-Berthou, 2005), and although they seldom cause wholesale extinctions (Ricciardi *et al.*, 2011), they can trigger ecological changes which can make native species less resilient to subsequent stressors (Parker *et al.*, 1999). Surprisingly, relatively little is known about the genetic impact of invasions (e.g. Strayer *et al.*, 2006; Carroll, 2011), as most studies tend to focus on genetic changes exhibited by the invaders (Monzón-Argüello *et al.*, 2013, 2014a,b), rather than genetic responses of native species

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(Vanhaecke *et al.*, 2012a). This is unfortunate because without genetic data, it may be difficult to get accurate assessments of the conservation status of threatened populations (Traill *et al.*, 2010) or to quantify the impact of biological invasions. For example, genetic data can be applied to detect changes in effective population size, estimate gene flow, or detect range contractions of native species in relation to the presence of invaders (Arenas *et al.*, 2012). Estimates of genetic diversity are also essential for understanding the long-term evolutionary consequences of biological invasions (Strauss *et al.*, 2006), and could perhaps also be used as an early warning of impending impacts, before range shifts or local extirpations take place.

In this study we employed molecular markers to understand how non-native salmonids may have impacted native galaxiid fishes, taking into account historical biogeographical patterns. We focused on two closely related species, *Aplochiton zebra* Jenyns, 1842 and *Aplochiton taeniatus* Jenyns, 1842, inhabiting rivers of Chilean Patagonia and the Falkland Islands: two areas where native galaxiids are threatened by the introduction of non-native salmonids since the 19th century (Garcia de Leaniz *et al.*, 2010; Schröder & Garcia de Leaniz, 2011; Arismendi *et al.*, 2014). *Aplochiton zebra* is considered to be endangered over its entire range (Lattuca *et al.*, 2008; Arismendi *et al.*, 2009) due to its ecological overlap with non-native salmonids (McDowall, 2006, 2010). However, the conservation status of *A. taeniatus* remains unclear (McDowall, 2006) and until recently its range did not include the Falkland Islands, where it had been misidentified as *A. zebra* (Vanhaecke *et al.*, 2012b). This is not surprising because the two species are morphologically very similar, and the limited information available on their ecology and genetic structure makes prioritization of populations for conservation difficult (Vanhaecke *et al.*, 2012b; Alò *et al.*, 2013). *Aplochiton taeniatus* appears to attain larger sizes than *A. zebra* and is considered a specialist that preys mostly on fish, in contrast to *A. zebra* which is considered a generalist that feeds mainly on aquatic invertebrates. The existence of a third species, *A. marinus*, has been suggested, but its taxonomic status remains unclear (Alò *et al.*, 2013).

The distribution of native galaxiids in South America is related to historical pathways of dispersal (Habit *et al.*, 2012). To understand these historical pathways for *Aplochiton* spp. we applied molecular markers with different modes of inheritance, mitochondrial DNA (mtDNA; maternally inherited) and microsatellites (biparentally inherited). This combination of markers allowed us to reconstruct the phylogeography of *Aplochiton* spp. and also to provide insights into the historical and current drivers of genetic structure in relation to the presence of non-native salmonids. We hypothesized that ecological impacts of non-native salmonids (e.g. predation, competition or other processes) could decrease population sizes that would be reflected by reduced microsatellite genetic diversity of *Aplochiton* in rivers and lakes invaded by salmonids, whereas mtDNA genetic variation should reflect the extent of the Last Glacial Maximum (LGM) showing the influence of historical routes of dispersal.

MATERIALS AND METHODS

Sampling

We collected tissue samples from 456 individuals of *Aplochiton* spp. from 20 streams in Chile and 15 streams in the Falkland Islands (Fig. 1; see Appendix S1 in Supporting Information). Given the morphological similarity between *A. zebra* and *A. taeniatus*, molecular analysis was needed to discriminate between both species and their hybrids (Vanhaecke *et al.*, 2012b; Alò *et al.*, 2013). After DNA extraction and genetic barcoding using the Cytochrome c oxidase I gene (COI), samples were classified by species as in Vanhaecke *et al.* (2012b). 341 samples were classified as *A. zebra* (317 from Chile and 24 from the Falklands) and 115 as *A. taeniatus* (61 from Chile and 54 from the Falklands). As a result, sample sizes were unbalanced and reduced in some populations. We analysed the genetic structure of 13 *A. zebra* populations from Chile which had at least 16 individuals per sampling site (Table 1). We used data on catch per unit effort (CPUE, fish min^{-1} m^{-2}) from single-pass electrofishing to derive indices of the relative abundance of *Aplochiton* and salmonids (as in Vanhaecke *et al.*, 2012a), and employed the nonparametric Spearman's rank correlation coefficient (SPSS 19; Armonk, NY, USA) to examine the relationship between CPUE and elevation. Although CPUE from electrofishing surveys is typically a poor indicator of absolute fish abundance, it can be used as a proxy to compare relative species abundance among sites (Bergman *et al.*, 2011), and use of rank-based methods are more appropriate in these cases.

DNA extraction and genotyping

DNA was extracted using the Wizard® SV 96 DNA Purification. All samples were amplified for 13 microsatellite loci (Aggarwal *et al.*, 2011) and mtDNA COI (Vanhaecke *et al.*, 2012b), and those individuals identified as hybrids (Vanhaecke *et al.*, 2012b) were removed from the dataset. To estimate the repeatability of scoring, between 11 and 71 individuals were rescored for each marker and allele sizes were compared. Potential errors in genotyping were estimated using MICRO-CHECKER (van Oosterhout *et al.*, 2004), with the exception of microsatellites Aze2, Aze4 and Aze5 that have a complex motif.

A region of 479 bp of the 16S rDNA gene of the mtDNA was amplified in 96 *A. zebra* samples using the universal primers 16S rRNAr and 16S rRNAbr (Palumbi *et al.*, 1991). Both strands were sequenced on an ABI 3100 DNA Analyzer (Applied Biosystems, Foster City, CA, USA) and sequences were aligned using BIOEDIT 7.0.9 (Hall, 1999).

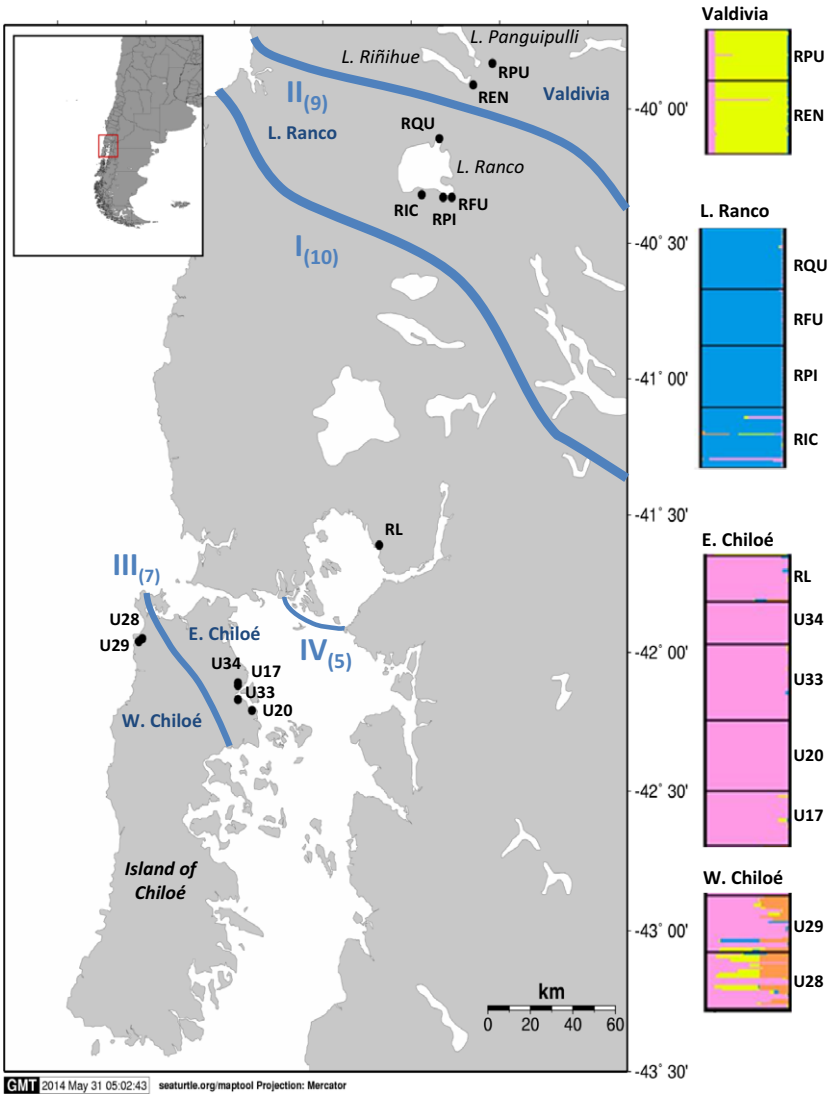

Figure 1 Representation of genetic barriers (left) between galaxiid fish populations (*Aplochiton zebra*) in Chile identified using BARRIER 2.2, based on 11 microsatellites using Monmonier's algorithm. Blue lines represent the main barriers to gene flow, ranked from 1st to 4th (number of loci supporting the barrier is indicated in brackets next to ranking), thickness of the line represents bootstrapping support. Plot of individual assignment (right) based on 11 microsatellites using TESS with $K = 4$, averaged from 100 runs using CLUMPP and represented using DISTRUCT. Each bar constitutes an individual fish with colours representing the probability of membership to each cluster.

Microsatellite analyses: genetic variation

Linkage disequilibrium between microsatellite loci was computed using GENEPOP (Raymond & Rousset, 1995) and all markers were tested for F_{ST} deviation from neutral expectations using FDIST in ARLEQUIN 3.5.1.2 (Excoffier & Lischer, 2010). Observed and expected heterozygosity (*Ho*, *He*) estimates and tests for Hardy–Weinberg equilibrium were conducted in TFPGA 1.3 (Miller, 1997) and the significance was adjusted by Bonferroni correction for multiple tests (Rice, 1989). Allelic richness (*Ar*) was calculated by FSTAT 2.9.3.2 (Goudet, 1995). Comparisons of genetic diversity (*Ar*, *He*, *Ho*) among populations and geographical groups were also performed in FSTAT using 10,000 permutations. All populations were tested for recent bottlenecks using BOTTLENECK 1.2.02 (Piry *et al.*, 1999) under two models; infinite alleles (IAM) and two-phase (TPM), using a Wilcoxon sign-rank test based on a 1000 iterations. For TPM, ps (frequency of single step mutations) was set to 0.90 with a 10% variance of multistep mutations (Piry *et al.*, 1999). Contemporary effective population size (N_e) was estimated using COLONY 2 (Wang, 2009) from the frequencies of full or half siblings in each population calculated by sibship assignment analysis. N_e was calculated by three runs of medium length with the full likelihood option, only for populations with a minimum sample size of 20. We also used a new implementation of the LD method included in NEESTIMATOR 2 (Do *et al.*, 2014), using allele frequencies > 0.02 to minimize potential bias caused by rare alleles (Waples & Do, 2008).

Microsatellite analyses: population structuring

Pairwise genetic differentiation (F_{ST}) between populations was computed in TFPGA and significance values were obtained by 10,000 permutations. Pairwise genetic distances (D_{est}) (Jost, 2008) were also calculated in SMOGD (Crawford, 2010). Population genetic structuring was examined using analysis of molecular variance (AMOVA) implemented in ARLEQUIN (10,000 permutations). To identify the most

Table 1 Characteristics and location of study rivers, sample size of *Aplochiton zebra* (*n*) in Chile, presence of different species and relative abundance (CPUE, fish min^{-1} m^{-2}) of native *A. zebra* and salmonids(*).

Watershed	Code	River name	*n*	Latitude	Longitude	Elevation (m)	Origin	Species present	CPUE	
									A. zebra	Salmonids
West Chiloé	U28	N/A	22	−41.95	−74.02	10	Coastal	AZ, AT	0.00151	0
	U29	N/A	21	−41.96	−74.04	18	Coastal	AZ	0.05786	0
East Chiloé	U17	N/A	20	−42.12	−73.48	10	Coastal	AZ, GM, OM*	0.00040	0.0002
	U20	N/A	26	−42.21	−73.40	9	Coastal	AZ, GM, OM*	0.00108	0.0005
	U33	N/A	25	−42.17	−73.48	4	Coastal	AZ, AT, GM, OM*, SS*	0.00140	0.0022
	U34	N/A	16	−42.11	−73.48	11	Coastal	AZ, AT, BB, GM, OM*	0.00800	0.0010
Reloncaví	RL	Lenca	17	−41.61	−72.68	13	Pre-Andean	AZ, GM, OM*, ST*	0.00110	0.0014
Valdivia	REN	Blanco	30	−39.91	−72.15	139	Andean	AZ, OM*, ST*	0.00646	0.0068
	RPU	Punahue	21	−39.83	−72.04	195	Andean	AZ, OM*, ST*	0.00137	0.0075
L. Ranco	RPI	Pitreño	30	−40.33	−72.32	82	Central Valley	AZ, GP, PT, TA, BA, CA, OM*	0.00774	0.0062
	RQU	Quiman	27	−40.11	−72.34	118	Central Valley	AZ, GP, OM*, SS*, ST*	0.00135	0.0068
	RFU	Futangue	30	−40.33	−72.27	71	Central Valley	AZ, GP, PT, OM*	0.00767	0.0007
	RIC	Iculpe	30	−40.32	−72.44	89	Central Valley	AZ, GP, TA, PT, OM*, OT*, ST*	0.00933	0.0049

AZ, *Aplochiton zebra*; AT, *Aplochiton taeniatus*; GM, *Galaxias maculatus*; BB, *Brachygalaxias bullocki*; BA, *Basilichthys australis*; CA, *Cheirodon australe*; TA, *Trichomycterus areolatus*; PT, *Percichtys trucha*; GP, *Galaxias platei;* OM, *Oncorhynchus mykiss*; ST, *Salmo trutta*; SS, *Salmo salar*; OT, *Oncorhynchus tshawytscha.*

plausible spatial driver of genetic variation, two analyses were carried out, grouping the populations by (1) region: West Chiloé Island, North East Chiloé Island (including Reloncavi), Lake Ranco and Valdivia (Fig. 1), or (2) origin: freshwater (Lake Ranco and Valdivia populations) versus coastal (Chiloé and Reloncavi populations).

Population structuring was further analysed taking into account the spatial distribution of genotyped individuals using TESS 2.3.1 (Chen *et al.*, 2007). We ran 100 replicates per *K* (2–15) using an admixture model, 500 sweeps of burn-in, and a running period of 2100 sweeps with the interaction parameter (Ψ) fixed at 0.6. The maximum number of clusters (K_{max}) was inferred from changes in the deviance information criterion (DIC) (Spiegelhalter *et al.*, 2002). The results from the replicates were averaged using the software CLUMP (Jackobsson & Rosenberg, 2007) and the output was represented using DISTRUCT 1.1 (Rosenberg, 2004).

Isolation by distance (IBD) among all populations, and between coastal and freshwater groups, was estimated with a Mantel test (10,000 permutations) on genetic distance measured by $F_{ST}/(1-F_{ST})$ and geographical distance (km) using the ZT software (Bonnet & Van de Peer, 2002). To identify barriers to gene flow among *A. zebra* populations, we used the Monmonier's (1973) maximum difference algorithm implemented in BARRIER 2.2 (Manni *et al.*, 2004). Geographical coordinates for each sampling location were connected by Delaunay triangulation and the analysis was conducted using two matrices of genetic distance (D_{est} and F_{ST}, described above). To assess the robustness of the barriers, analyses were also run for 100 bootstrapped F_{ST} matrices and for each microsatellite locus separately (Hemmer-Hansen *et al.*, 2007). Barriers supported by high bootstrap values (> 65%) were ranked (I–IV) according to the number of loci supporting them, strong support being inferred when more than 10 loci supported the presence of a barrier.

We used approximate Bayesian computation (ABC) implemented in DIYABC 2.0.3 (Cornuet *et al.*, 2008) to reconstruct the potential colonization routes of *A. zebra* using microsatellite data. We compared three simple colonization scenarios based on the mtDNA groupings (Chiloé, Lake Ranco, Valdivia and the Falklands). The potential scenarios involved a two-step colonization of Lake Ranco/Valdivia and Chiloé/Falklands (Scenario 1), a sequential colonization of Lake Ranco, Valdivia and the Falklands (Scenario 2) and the possibility of admixture between Valdivia and Chiloé (Scenario 3). Priors were considered to be uniformly distributed and we used the default settings for mutation rates. We simulated 300,000 data sets per scenario and considered the following summary statistics: mean number of alleles per locus, mean gene diversity, mean size variance, mean M ratio (the ratio between the number of alleles and the range of allele sizes) within each population and pairwise F_{ST} values between populations. Effective population sizes were considered to vary between 10 and 100,000 for three Chilean populations and between 10 and 50,000 for the Falklands. Confidence in the scenario with the highest posterior probability was estimated by comparing simulated and observed summary statistics, and by calculating type I and II error rates (Cornuet *et al.*, 2008).

Mitochondrial DNA (mtDNA) analysis: genetic diversity and population structuring

For mtDNA, the number of haplotypes (*h*), haplotype diversity (H_D) and nucleotide diversity (π) were calculated in DNASP 5 (Librado & Rozas, 2009). AMOVA was conducted in ARLEQUIN to estimate population structuring, using the same groups as for the microsatellite analyses.

Nonparametric Spearman's rank correlations between genetic diversity (microsatellite heterozygosity and allelic

richness, mtDNA haplotype and nucleotide diversity) of *A. zebra* populations and salmonid abundance (as estimated by CPUE) were carried out using SPSS 19 to test for potential effects of salmonid presence on *A. zebra* genetic diversity.

RESULTS

Relative abundance (CPUE) of *A. zebra* and salmonids

We found salmonids in all but two of the study rivers (U28 and U29; Table 1). The relative abundance of salmonids (estimated by CPUE, fish min^{-1} m^{-2}) ranged from 0 (West Chiloé) to 0.0075 (R. Punahue, Valdivia) and, as expected for cold-water fishes, CPUE increased significantly with elevation (Spearman's $r_s = 0.718$; $P = 0.003$). The relative abundance of *A. zebra* was not correlated with elevation and was highest in site U29, on the west coast of the island of Chiloé, an area free from fish farming and not yet invaded by salmonids (Young *et al.*, 2010).

Microsatellite genetic diversity and population genetic structuring of *A. zebra*

Scoring repeatability was 94 ± 6% on average (per allele). No large allele drop outs were identified, although null alleles were detected in two populations for markers Aze3 and Aze11, and in five populations for Aze14. Aze14 was therefore excluded from further analyses. Microsatellites Aze6 and Aze13 were in linkage disequilibrium in one of the 13 populations analysed (RPU, $P = 0.00045$). None of the markers displayed evidence of being under selection. Significant deviations from Hardy–Weinberg equilibrium were found for microsatellite Aze9 in one population (U29, $P = 0.0002$) and Aze14 in two populations (REN, RPU $P = 0.0001$), in both cases due to an excess of homozygotes (see Appendix S1). F_{IS} was high for locus Aze4 in all populations (Appendix S1), and was also excluded from analyses.

Inland and coastal populations did not differ in genetic diversity (see Appendix S2; coastal: $Ar = 9.03$; $Ho = 0.65$; $Hs = 0.74$ and inland: $Ar = 8.93$; $Ho = 0.72$; $Hs = 0.76$; $P = 0.393$). Effective population size (N_e) estimated using COLONY was generally low for *A. zebra* and ranged between 47 (RPU) and 127 (U29). Confidence intervals were very wide, particularly those obtained by the LD method probably due to small sample sizes (Table 2); we therefore only considered those confidence intervals obtained from COLONY for further analyses. Neither genetic diversity, nor effective population size (N_e), were significantly associated with elevation (Spearman rank correlation $P = 0.237$). We found a negative correlation between microsatellite genetic diversity of *A. zebra* and the relative abundance of salmonids (*He*: $r = -0.48$, $P = 0.048$; *Ar*: $r = -0.52$, $P = 0.030$). Only the population with the lowest effective population size (RPU) showed significant evidence of genetic bottleneck after strict Bonferroni correction under the IAM model ($P = 0.0012$).

Table 2 Effective population size (N_e) and 95% confidence intervals estimated with COLONY (full likelihood score method) and NEESTIMATOR (linkage disequilibrium, LD method) for populations with sample size (n) of at least 20 individuals and based on 11 microsatellites.

	COLONY				NEESTIMATOR	
	n	N_e	0.05	0.95	N_e	CI (Jackknife method)
U28	22	66	35	205	40.6	(22.7, 122.0)
U29	21	127	44	∞	∞	(78.6, ∞)
U17	20	84	37	∞	∞	(88.5, ∞)
U20	26	71	39	190	31.3	(19.3, 63.2)
U33	25	54	31	115	608.4	(68.5, ∞)
REN	30	83	47	173	172.2	(47.0, ∞)
RPU	21	47	25	129	49.3	(25.5, 223.5)
RPI	30	58	34	101	332.6	(85.3, ∞)
RQU	27	71	41	136	∞	(102.0, ∞)
RFU	30	64	39	115	226.5	(60.7, ∞)
RIC	30	72	40	137	194.2	(64.5, ∞)

The genetic diversity of *A. zebra* in the Falkland Islands, estimated by pooling samples from all populations (due to limited numbers of individuals in local collections) was similar to that in Chile ($n = 22$, $Ar = 7.5$, $He = 0.72$, $Ho = 0.61$).

Pairwise F_{ST} comparisons of population differentiation ranged between 0 and 0.066 (see Appendix S3), and F_{ST} values showed a highly significant pattern of differentiation ($P < 0.001$) among geographical regions (West Chiloé, East Chiloé, Reloncavi, Valdivia and Lake Ranco) but non-significant differences within them (Appendix S3). The only significant F_{ST} within a region was between coastal populations U33 and U20 on the East Coast of Chiloé. D_{est} values ranged between 0 and 0.264 and generally showed similar patterns as F_{ST}, with low to zero values within regions and high differentiation among regions (Appendix S1b).

AMOVA revealed that 4.6% of genetic variation could be explained by differences among the four geographical regions considered ($F_{CT} = 0.046$; $P < 0.001$), 0.8% of variation was explained by differences among populations within locations ($F_{SC} = 0.008$; $P < 0.001$) and 94.7% of variation was distributed within populations ($F_{ST} = 0.054$; $P < 0.001$). In contrast, dividing the populations into inland or coastal groups only explained 1.97% of genetic variation between groups ($P = 0.01$).

Individual assignment analysis (using TESS) supported regional genetic clusters with a most likely $K = 4$ (Fig. 1). All populations displayed very uniform genotype clustering except for sites U28 and U29 on the west coast of Chiloé, which were the populations with the highest degree of admixture (average Q membership coefficients ranged between 16% and 59%). The Mantel test revealed significant patterns of isolation by distance (IBD) among all 13 *A. zebra* populations in Chile ($r = 0.490$; $P = 0.001$; Fig. 2), and also in coastal ($r = 0.680$; $P = 0.002$) and inland populations ($r = 0.860$; $P = 0.044$) considered separately. Results from

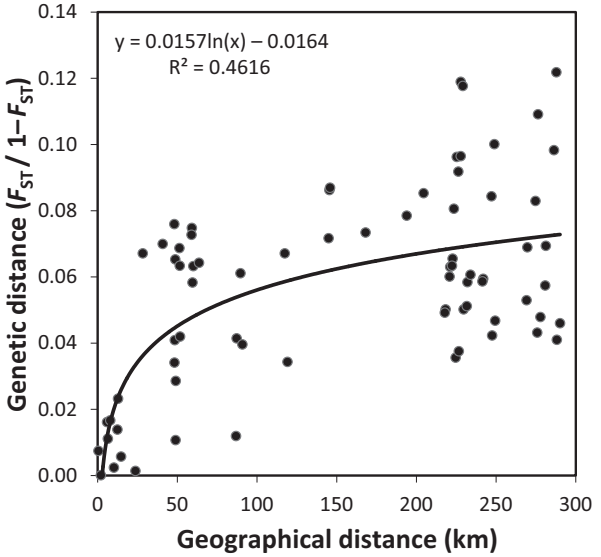

Figure 2 Relationship between geographical distance (km) and genetic distance ($F_{ST}/1-F_{ST}$) for 13 fish populations of *Aplochiton zebra* in Chile ($y = 0.0157 \ln(x) - 0.0164$, $R^2 = 0.462$).

BARRIER supported the population structuring identified by TESS. Two strong barriers were identified based on matrices of pairwise F_{ST} and D_{est} differentiation: barrier I, which separated inland from coastal populations and was supported by 10 of the 11 loci; and barrier II, which separated the two freshwater drainages of Lake Ranco and Valdivia and was supported by 9 of the 11 loci (Fig. 1, Appendix S2). Two weaker barriers included barrier III, which separated East- and West Chiloé (supported by seven loci), and barrier IV which separated River Lenca (coastal mainland) and Chiloé Island (supported by five loci), but these were not strongly supported by pairwise F_{ST} values based on all loci combined. The most likely colonization scenario identified by DIYABC was one where there was population mixture between Chiloé and Valdivia, followed by a more recent split of the Falklands populations from Chiloé (see Appendix S3, scenario 3).

mtDNA diversity and population structuring of *A. zebra*

The sequencing of 479 bp of the mtDNA 16S rDNA region in 98 *A. zebra* revealed three parsimoniously informative sites, one of which was a non-synonymous substitution (A/G). Based on this difference, we identified four haplotypes that could be included in either haplogroup 1 (base site 148 = G; H1 with $n = 51$ and H2 with $n = 2$) or haplogroup 2 (base site 148 = A; H3 with $n = 2$ and H4 with $n = 43$; GenBank accession numbers: JF437635–JF437642). Haplogroup 1 tended to be more common in inland populations (Valdivia, L. Ranco) than haplogroup 2, which characterized most of the coastal fish in Chiloé and the Falklands individuals (Fig. 3, Table 3). Grouping populations according to regional location indicated that West Chiloé had the highest genetic diversity ($H_D = 0.56$, $\pi = 0.001$) and Valdivia the lowest ($H_D = 0$, $\pi = 0$; Table 3). For COI we had previously identified six unique haplotypes defined by five mutations amongst *A. zebra* (Vanhaecke *et al.*, 2012b), the highest variability corresponding to East Chiloé.

AMOVA by geographical region (West Chiloé, East Chiloé and Reloncavi, Lake Ranco and Valdivia) using 16S rDNA revealed that most (56.7%) of the genetic variation could be explained by differences among regions ($\Phi_{CT} = 0.567$; $P < 0.001$), 44.3% was explained by differences within populations ($\Phi_{ST} = 0.557$; $P < 0.001$), while the amount of variation explained by differences among populations within groups was negligible (i.e. high genetic uniformity within regions; $\Phi_{SC} = -0.023$; $P = 0.746$). When populations were divided into coastal and inland groups, genetic variation between groups accounted for 54% ($\Phi_{CT} = 0.539$; $P = 0.001$), differences within populations accounted for 35.9% ($\Phi_{ST} = 0.641$; $P < 0.001$) and 8% was explained by differences among populations within groups ($\Phi_{SC} = 0.219$; $P = 0.002$).

For COI, 5.4% of genetic variation could be explained by differences among groups ($P = 0.04$), 89% by differences within populations ($P < 0.001$), and 5.5% by differences among populations within groups ($P = 0.102$). When populations were divided into coastal and inland groups, genetic variation between groups accounted for 6.2% ($P = 0.001$), differences within populations accounted for 87% ($P < 0.001$) and differences among populations within groups accounted for 6.3% ($P = 0.039$).

In contrast to microsatellite diversity, we did not find a significant correlation between relative salmonid abundance and measures of *A. zebra* mtDNA diversity (haplotype diversity: $r = -0.54$, $P = 0.055$; nucleotide diversity: $r = -0.45$, $P = 0.127$).

Genetic diversity of *Aplochiton taeniatus*

Analysis of genetic diversity was carried out in those populations of *A. taeniatus* with sufficient sample size following DNA barcoding and species identification: River Huicha from Chiloé ($n = 28$) and North Arms from East Falklands ($n = 30$). Comparisons were performed using those nine microsatellites that were variable for both species (Vanhaecke *et al.*, 2012b). Allelic richness (Ar) of *A. taeniatus* in North Arms ($Ar = 2.8$) was significantly lower than in Chiloé ($Ar = 9.2$, $P = 0.016$) although they did not differ significantly in Ho (0.27 vs. 0.46, $P = 0.11$). In addition, *A. taeniatus* in the Falklands (but not in Chiloé) displayed evidence of a recent population bottleneck under the two mutation models considered (IAM, $P = 0.004$; TPM, $P = 0.019$) and a shifted allelic frequency distribution compared to the expected L-shaped distribution as well as deviation from Hardy–Weinberg equilibrium ($P < 0.001$). Estimates of effective population size of *A. taeniatus* were very low in the Falklands ($N_e = 26$; 95% CI = 19–47) and low in Chiloé ($N_e = 49$; 95% CI = 29–100).

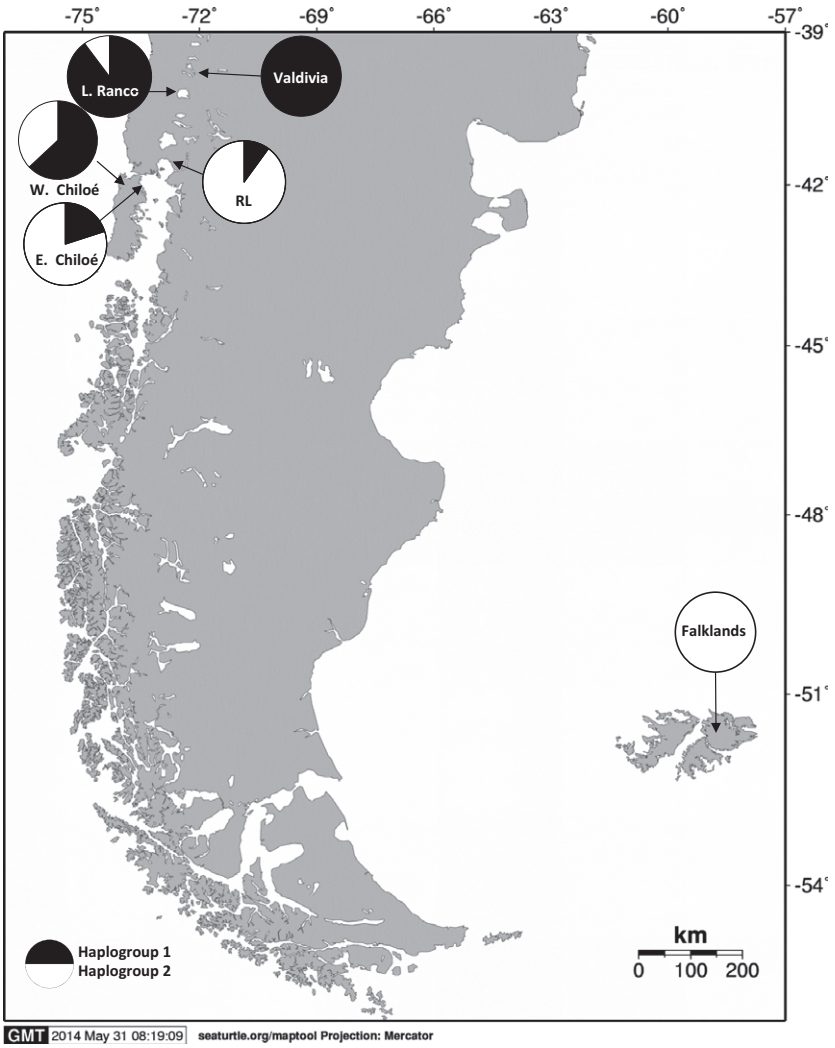

Figure 3 Distribution of mitochondrial 16S rDNA haplogroups of galaxiid fish (*Aplochiton zebra*) in the sampling regions: Valdivia, L. Ranco, West Chiloé, East Chiloé (including Seno Reloncavi) and Falkland Islands.

DISCUSSION

Non-native salmonids are known to impact native galaxiids by displacing, out-competing, and preying upon them (Arismendi *et al.*, 2009; Young *et al.*, 2009; Garcia de Leaniz *et al.*, 2010). However, the potential genetic impact of salmonids on galaxiids remains largely unknown (but see Vanhaecke *et al.*, 2012a). Our estimates of relative salmonid abundance in Chilean streams were similar to those of previous studies that found salmonids were absent in some coastal rivers of Chiloé and were most abundant in areas with greater numbers of fish farms that could serve as sources for invaders (Young *et al.*, 2010; Consuegra *et al.*, 2011; Monzón-Argüello *et al.*, 2014b).

We used two types of molecular markers with different rates of evolution and modes of inheritance to investigate the drivers of population structuring in *A. zebra*: maternally inherited mtDNA to provide information on historical phylogeographical events (e.g. post-glacial colonization) and biparentally inherited microsatellite loci to infer more recent demographic events influencing patterns of genetic variability (Emerson & Hewitt, 2005). Analyses of the mitochondrial 16S rDNA gene revealed weak population structuring (i.e. high genetic uniformity) within *A. zebra* populations inhabiting freshwater systems, which was unrelated to salmonid presence, and low divergence between inland and coastal populations, including the Falkland Islands. These, along with our analyses of microsatellite variation, suggest that the population structuring of *A. zebra* reflects the signature of historical patterns of colonization since the LGM and current geographical barriers. We also found a negative association between microsatellite genetic diversity of *A. zebra* and estimates of salmonid abundance, but not between mtDNA diversity and salmonid presence. These results suggest that any genetic impacts of salmonids upon *Aplochiton* must have been relatively recent (indicated by microsatellite diversity), and have yet to be reflected in changes in mtDNA diversity.

Unlike the case of the more abundant *Galaxias maculatus*, whose genetic diversity appears to be unaffected by salmonid abundance (Vanhaecke *et al.*, 2012a), our results suggest that invasive salmonids may have caused a decrease in the nuclear genetic diversity of the endangered *A. zebra*; it is important

Table 3 Molecular diversity indices per population based on mitochondrial 16S rDNA and COI genes calculated in Arlequin [sample size (n), number of haplotypes (h), haplotype diversity (H_D) and nucleotide diversity (π)] for each river separately and pooled by region.

	16S rDNA				COI			
River	n	h	H_D	π	n	H	H_D	π
U28	11	3	0.56	0.0013	10	1	0	0
U29	8	2	0.57	0.0012	9	1	0	0
U17	6	3	0.6	0.0014	15	5	0.79	0.0024
U20	5	1	0	0	14	3	0.39	0.0009
U33	5	2	0.4	0.0008	11	4	0.69	0.0018
U34	4	2	0.5	0.0010	7	2	0.29	0.0006
RL	10	2	0.36	0.0007	16	1	0	0
REN	10	1	0	0	30	3	0.25	0.0006
RPU	10	1	0	0	21	1	0	0
RPI	5	2	0.4	0.0008	24	1	0	0
RQU	5	2	0.4	0.0008	18	1	0	0
RFU	4	1	0	0	27	2	0.21	
RIC	5	2	0.4	0.0008	19	1	0	0
Regions								
West Chiloé	19	3	0.56	0.0013	19	1	0	0
East Chiloé and RL	30	3	0.35	0.0008	63	5	0.49	0.0012
Valdivia	20	1	0	0	50	3	0.15	0.0003
Lake Ranco	19	3	0.29	0.0006	88	2	0.07	0.0001
Falkland Islands	10	1	0	0	23	1	0	0

to note, however, that sample sizes were small for some populations, and that results were merely correlational; genetic inferences, therefore, need to be made with caution. An unknown variable related to both salmonid abundance and microsatellite diversity in *Aplochiton* could also explain the associations we observed.

Intraspecific mtDNA sequence divergence can be low in fishes (Hubert *et al.*, 2008), but in species such as *Aplochiton* spp. with diadromous and resident life histories, long-term isolation can cause substantial divergence between populations (McCusker & Bentzen, 2010; McDowall, 2010). We found that one non-synonymous mutation separated coastal from inland populations, with the exception of populations on the west coast of Chiloé that displayed a mixture of both. The populations on Chiloé also displayed the highest haplotype diversity for COI. Population structuring based on mtDNA may reflect the pattern of colonization following the LGM, when freshwater populations are thought to have derived from coastal refugia. A similar pattern of low population structuring has been observed for other diadromous and marine species that retreated to marine refugia during the LGM in this region (Fraser *et al.*, 2010; Zemlak *et al.*, 2010). In contrast, freshwater species occupying recently deglaciated habitats display stronger divergence between separate watersheds, reflecting the recolonization from disconnected freshwater refugia (Ruzzante *et al.*, 2006; Unmack *et al.*, 2009).

Of all the populations examined, *A. zebra* displayed the highest genetic diversity on the island of Chiloé, suggesting that this could have been a refugium for the species during the LGM (approximately 20,000 to 10,000 yr BP), as it has also been suggested for other diadromous and marine species (Fraser *et al.*, 2010; Zemlak *et al.*, 2010). Recolonization from coastal refugia and founder effects could explain the lack of diversity in the most isolated population, such as the Valdivian populations and the Falkland Islands. During the LGM, the Patagonian Ice Sheet spread northwards from the southern tip of Patagonia (54° S) to 38° S, and westwards from the Andes mountains to the Pacific coastline (Cussac *et al.*, 2004); therefore, freshwater species could have migrated from the Andes to the coast and from the south to unglaciated coastal regions in the north, resulting in *A. zebra* from coastal rivers in Chile and the Falkland Islands sharing the same 16S rDNA haplotype. Surface marine currents in the southern coast of Chile move southwards with the Cape Horn Current, around Tierra del Fuego and reach the Atlantic Ocean where the Antarctic Circumpolar Current and the Malvinas Current circumvent the Falkland Islands (Kaiser *et al.*, 2005). Such currents have been found to be important dispersal pathways for Chilean seaweed (Fraser *et al.*, 2010), diadromous *G. maculatus* (Zemlak *et al.*, 2010) and Chinook salmon escaping from Chilean net pens and entering the South Atlantic around Cape Horn (Correa & Gross, 2008). Based on these lines of evidence, a common origin for *A. zebra* in Chile and the Falkland Islands is therefore plausible.

The low mtDNA diversity detected in *Aplochiton* spp. is common among many freshwater fish, which typically display much lower diversity than marine fish (McCusker & Bentzen, 2010). This would explain the genotypic uniformity observed between the River Lenca (mainland Chile) and East Chiloé, connected by the Chiloé Interior Sea, and also the low genetic diversity observed at West Chiloé. In contrast, the strong genetic differentiation observed among landlocked populations suggests that inland populations are less likely to migrate to sea following their recolonization from marine refugia, as observed in other species (Waters *et al.*, 2010). Microsatellite data also indicated highly significant population structuring with four distinct clusters: (1) Valdivia, (2) Lake Ranco, (3) East Chiloé with the River Lenca (i.e. populations inhabiting coastal rivers draining into the Chiloé Interior Sea), and (4) West Chiloé (i.e. populations inhabiting coastal rivers draining into the Pacific Ocean). This level of regional genetic differentiation at microsatellite loci may reflect currently limited gene flow among watersheds and is supported by genetic barriers identified by Barrier and IBD patterns.

In summary, our study of *A. zebra* in Chile and the Falklands indicates that the mtDNA diversity of this species probably reflects the legacy of historical routes of recolonization and migration, whereas the pattern of structuring found at microsatellite loci probably reflects the influence of more recent demographic and isolation processes in the region. Our analysis also indicates that the genetic diversity of *Aplochiton* may have decreased in those populations most affected

by salmonid encroachment, particularly in the case of *A. taeniatus*. Although the possibility of ascertainment bias cannot be totally ruled out with current molecular markers used to study *Aplochiton* spp., the observed low genetic diversity, and the limited information available on their abundance and distribution calls for a more detailed analysis of the conservation status of *A. zebra* and *A. taeniatus* in the face of salmonid invasions.

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REFERENCES

Aggarwal, R., Allainguillaume, J., Bajay, M. *et al.*; Molecular Ecology Resources Primer Development Consortium (2011) Permanent genetic resources added to molecular ecology resources database 1 August 2010–30 September 2010. *Molecular Ecology Resources*, **11**, 219–222.

Alò, D., Correa, C., Arias, C. & Cárdenas, L. (2013) Diversity of *Aplochiton* fishes (Galaxiidea) and the taxonomic resurrection of *A. marinus*. *PLoS ONE*, **8**, e71577.

Arenas, M., Ray, N., Currat, M. & Excoffier, L. (2012) Consequences of range contractions and range shifts on molecular diversity. *Molecular Biology and Evolution*, **29**, 207–218.

Arismendi, I., Soto, D., Penaluna, B., Jara, C., Leal, C. & León-Muñoz, J. (2009) Aquaculture, non-native salmonid invasions and associated declines of native fishes in Northern Patagonian lakes. *Freshwater Biology*, **54**, 1135–1147.

Arismendi, I., Penaluna, B.E., Dunham, J.B., García de Leaniz, C., Soto, D., Fleming, I.A., Gomez-Uchida, D., Gajardo, G., Vargas, P.V. & León-Muñoz, J. (2014) Differential invasion success of salmonids in southern Chile: patterns and hypotheses. *Reviews in Fish Biology and Fisheries*, **24**, 919–941.

Bergman, P.S., Hansen, M.J. & Nate, N.A. (2011) Relationship between electrofishing catch rate and adult trout abundance in Wisconsin streams. *North American Journal of Fisheries Management*, **31**, 952–961.

Bonnet, E. & Van de Peer, Y. (2002) zt: a software tool for simple and partial Mantel tests. *Journal of Statistical Software*, **7**, 1–12.

Carroll, S.P. (2011) Conciliation biology: the eco-evolutionary management of permanently invaded biotic systems. *Evolutionary Applications*, **4**, 184–199.

Chen, C., Durand, E., Forbes, F. & Francois, O. (2007) Bayesian clustering algorithms ascertaining spatial population structure: a new computer program and a comparison study. *Molecular Ecology Notes*, **7**, 747–756.

Clavero, M. & García-Berthou, E. (2005) Invasive species are a leading cause of animal extinctions. *Trends in Ecology and Evolution*, **20**, 110–110.

Consuegra, S., Phillips, N., Gajardo, G. & Garcia de Leaniz, C. (2011) Winning the invasion roulette: escapes from fish farms increase admixture and facilitate establishment of non-native rainbow trout. *Evolutionary Applications*, **4**, 660–671.

Cornuet, J.-M., Santos, F., Beaumont, M.A., Robert, C.P., Marin, J.-M., Balding, D.J., Guillemaud, T. & Estoup, A. (2008) Inferring population history with *DIY ABC*: a user-friendly approach to approximate Bayesian computation. *Bioinformatics*, **24**, 2713–2719.

Correa, C. & Gross, M.R. (2008) Chinook salmon invade southern South America. *Biological Invasions*, **10**, 615–639.

Crawford, N.G. (2010) SMOGD: software for the measurement of genetic diversity. *Molecular Ecology Resources*, **10**, 556–557.

Cussac, V., Ortubay, S., Iglesias, G., Milano, D., Lattuca, M.E., Barriga, J.P., Battini, M. & Gross, M. (2004) The distribution of South American galaxiid fishes: the role of biological traits and post-glacial history. *Journal of Biogeography*, **31**, 103–121.

Do, C., Waples, R.S., Peel, D., Macbeth, G., Tillett, B.J. & Ovenden, J.R. (2014) NeEstimator v2: re-implementation of software for the estimation of contemporary effective population size (N_e) from genetic data. *Molecular Ecology Resources*, **14**, 209–214.

Emerson, B.C. & Hewitt, G.M. (2005) Phylogeography. *Current Biology*, **15**, R367–R371.

Excoffier, L. & Lischer, H.E.L. (2010) Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. *Molecular Ecology Resources*, **10**, 564–567.

Fraser, C.I., Thiel, M., Spencer, H.G. & Waters, J.M. (2010) Contemporary habitat discontinuity and historic glacial ice drive genetic divergence in Chilean kelp. *BMC Evolutionary Biology*, **10**, 203.

Garcia de Leaniz, C., Gajardo, G. & Consuegra, S. (2010) From best to pest: changing perspectives on the impact of exotic salmonids in the Southern Hemisphere. *Systematics and Biodiversity*, **8**, 447–459.

Goudet, J. (1995) FSTAT (version 1.2): a computer program to calculate F-statistics. *Journal of Heredity*, **86**, 485–486.

Habit, E., Gonzalez, J., Ruzzante, D.E. & Walde, S.J. (2012) Native and introduced fish species richness in Chilean Patagonian lakes: inferences on invasion mechanisms using salmonid-free lakes. *Diversity and Distributions*, **18**, 1153–1165.

Hall, T. (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series*, **41**, 95–98.

Hemmer-Hansen, J., Nielsen, E.E., Frydenberg, J. & Loeschcke, V. (2007) Adaptive divergence in a high gene flow environment: Hsc70 variation in the European flounder (*Platichthys flesus* L.). *Heredity*, **99**, 592–600.

Hubert, N., Hanner, R., Holm, E., Mandrak, N.E., Taylor, E., Burridge, M., Watkinson, D., Dumont, P., Curry, A., Bentzen, P., Zhang, J.B., April, J. & Bernatchez, L. (2008) Identifying Canadian Freshwater Fishes through DNA barcodes. *PLoS ONE*, **3**, e2490.

Jackobsson, M. & Rosenberg, N.A. (2007) CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. *Bioinformatics*, **23**, 1801–1806.

Jost, L. (2008) G_{ST} and its relatives do not measure differentiation. *Molecular Ecology*, **17**, 4015–4026.

Kaiser, J., Lamy, F. & Hebbeln, D. (2005) A 70-kyr sea surface temperature record off southern Chile (Ocean Drilling Program Site 1233). *Paleoceanography*, **20**, 15.

Lattuca, M.E., Battini, M.A. & Macchi, P.J. (2008) Trophic interactions among native and introduced fishes in a northern Patagonian oligotrophic lake. *Journal of Fish Biology*, **72**, 1306–1320.

Librado, P. & Rozas, J. (2009) DnaSP v5: a software for comprehensive analysis of DNA polymorphism data. *Bioinformatics*, **25**, 1451.

Manni, F., Guerard, E. & Heyer, E. (2004) Geographic patterns of (genetic, morphologic, linguistic) variation: how barriers can be detected by using Monmonier's algorithm. *Human Biology*, **76**, 173–190.

McCusker, M.R. & Bentzen, P. (2010) Positive relationships between genetic diversity and abundance in fishes. *Molecular Ecology*, **19**, 4852–4862.

McDowall, R.M. (2006) Crying wolf, crying foul, or crying shame: alien salmonids and a biodiversity crisis in the southern cool-temperate galaxioid fishes? *Reviews in Fish Biology and Fisheries*, **16**, 233–422.

McDowall, R.M. (2010) *New Zealand freshwater fishes: an historical and ecological biogeography*. Springer Netherlands, NY.

Miller, M.P. (1997) *Tools for population genetic analyses (TFPGA) 1.3: a Windows program for the analysis of allozyme and molecular population genetic data*. Computer software distributed by author, Flagstaff, AZ.

Monmonier, M. (1973) Maximum-difference barriers: an alternative numerical regionalization method. *Geographical Analysis*, **5**, 245–261.

Monzón-Argüello, C., Garcia de Leaniz, C., Gajardo, G. & Consuegra, S. (2013) Less can be more: loss of MHC functional diversity can reflect adaptation to novel conditions during fish invasions. *Ecology and Evolution*, **3**, 3359–3368.

Monzón-Argüello, C., Garcia de Leaniz, C., Gajardo, G. & Consuegra, S. (2014a) Eco-immunology of fish invasions: the role of MHC variation. *Immunogenetics*, **66**, 393–402.

Monzón-Argüello, C., Consuegra, S., Gajardo, G., Marco-Rius, F., Fowler, D.M., DeFaveri, J. & Garcia de Leaniz, C. (2014b) Contrasting patterns of genetic and phenotypic differentiation in two invasive salmonids in the southern hemisphere. *Evolutionary Applications*, **7**, 921–936.

van Oosterhout, C., Hutchinson, W.F., Wills, D.P.M. & Shipley, P. (2004) MICRO-CHECKER: software for identifying and correcting genotyping errors in microsatellite data. *Molecular Ecology Notes*, **4**, 535–538.

Palumbi, S.R., Martin, A.P., Romano, S., McMillan, W.O., Stice, L. & Grabowski, G. (1991) *The simple fool's guide to PCR, ver. 2.0*. Published and distributed by the authors, Honolulu.

Parker, I.M., Simberloff, D., Lonsdale, W., Goodell, K., Wonham, M., Kareiva, P., Williamson, M., Von Holle, B., Moyle, P. & Byers, J. (1999) Impact: toward a framework for understanding the ecological effects of invaders. *Biological Invasions*, **1**, 3–19.

Piry, S., Luikart, G. & Cornuet, J.M. (1999) BOTTLENECK: a computer program for detecting recent reductions in the effective population size using allele frequency data. *Journal of Heredity*, **90**, 502–503.

Raymond, M. & Rousset, F. (1995) GENEPOP (version 1.2): population genetics software for exact tests and ecumenicism. *Journal of Heredity*, **86**, 248–249.

Ricciardi, A., Palmer, M.E. & Yan, N.D. (2011) Should biological invasions be managed as natural disasters? *BioScience*, **61**, 312–317.

Rice, W.R. (1989) Analyzing tables of statistical tests. *Evolution*, **43**, 223–225.

Rosenberg, N.A. (2004) DISTRUCT: a program for the graphical display of population structure. *Molecular Ecology Notes*, **4**, 137–138.

Ruzzante, D., Walde, S., Cussac, V., Dalebout, M., Seibert, J., Ortubay, S. & Habit, E. (2006) Phylogeography of the Percichthyidae (Pisces) in Patagonia: roles of orogeny, glaciation, and volcanism. *Molecular Ecology*, **15**, 2949–2968.

Schröder, V. & Garcia de Leaniz, C. (2011) Discrimination between farmed and free-living invasive salmonids in Chilean Patagonia using stable isotope analysis. *Biological Invasions*, **13**, 203–213.

Spiegelhalter, D.J., Best, N.G., Carlin, B.R. & van der Linde, A. (2002) Bayesian measures of model complexity and fit. *Journal of the Royal Statistical Society B: Statistical Methodology*, **64**, 583–616.

Strauss, S.Y., Lau, J.A. & Carroll, S.P. (2006) Evolutionary responses of natives to introduced species: what do introductions tell us about natural communities? *Ecology Letters*, **9**, 354–371.

Strayer, D.L., Eviner, V.T., Jeschke, J.M. & Pace, M.L. (2006) Understanding the long-term effects of species invasions. *Trends in Ecology and Evolution*, **21**, 645–651.

Traill, L.W., Brook, B.W., Frankham, R.R. & Bradshaw, C.J.A. (2010) Pragmatic population viability targets in a rapidly changing world. *Biological Conservation*, **143**, 28–34.

Unmack, P.J., Bennin, A.P., Habit, E.M., Victoriano, P.F. & Johnson, J.B. (2009) Impact of ocean barriers, topography, and glaciation on the phylogeography of the catfish *Trichomycterus areolatus* (Teleostei: Trichomycteridae) in Chile. *Biological Journal of the Linnean Society*, **97**, 876–892.

Vanhaecke, D., Garcia de Leaniz, C., Gajardo, G., Thomas, C.J. & Consuegra, S. (2012a) Metapopulation dynamics of a diadromous galaxiid fish and potential effects of salmonid aquaculture. *Freshwater Biology*, **57**, 1241–1252.

Vanhaecke, D., Garcia de Leaniz, C., Gajardo, G., Young, K., Sanzana, J., Orellana, G., Fowler, D., Howes, P., Monzon-Arguello, C. & Consuegra, S. (2012b) DNA barcoding and microsatellites help species delimitation and hybrid identification in endangered galaxiid fishes. *PLoS ONE*, **7**, e32939.

Wang, J.L. (2009) A new method for estimating effective population sizes from a single sample of multilocus genotypes. *Molecular Ecology*, **18**, 2148–2164.

Waples, R.S. & Do, C. (2008) LDNE: a program for estimating effective population size from data on linkage disequilibrium. *Molecular Ecology Resources*, **8**, 753–756.

Waters, J.M., Rowe, D.L., Burridge, C.P. & Wallis, G.P. (2010) Gene trees versus species trees: reassessing life-history evolution in a freshwater fish radiation. *Systematic Biology*, **59**, 504–517.

Young, K.A., Stephenson, J., Terreau, A., Thailly, A.-F., Gajardo, G. & Garcia de Leaniz, C. (2009) The diversity of juvenile salmonids does not affect their competitive impact on a native galaxiid. *Biological Invasions*, **11**, 1955–1961.

Young, K.A., Dunham, J.B., Stephenson, J.F., Terreau, A., Thailly, A.F., Gajardo, G. & Garcia de Leaniz, C. (2010) A trial of two trouts: comparing the impacts of rainbow and brown trout on a native galaxiid. *Animal Conservation*, **13**, 399–410.

Zemlak, T., Habit, E., Walde, S., Carrea, C. & Ruzzante, D. (2010) Surviving historical Patagonian landscapes and climate: molecular insights from *Galaxias maculatus*. *BMC Evolutionary Biology*, **10**, 67.

SUPPORTING INFORMATION

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

Appendix S1 Genetic diversity and differentiation among *Aplochiton zebra* populations.

Appendix S2 Barriers to gene flow among *Aplochiton zebra* populations in Chile identified by BARRIER 2.2.

Appendix S3 Alternative scenarios for ABC analysis population colonization of *Aplochiton zebra* in Chile and the Falklands.

DATA ACCESSIBILITY

Alignments of the 16S rDNA results generated in this study are publicly available in figshare, http://dx.doi.org/10.6084/m9.figshare.1423279.

BIOSKETCH

This work was part of the PhD thesis of D.V., supervised by S.C. and C.G.L. on salmonid invasion biology in the Southern Hemisphere.

Author contributions: S.C. and C.G.L. conceived the work; D.V., C.G.L., G.Ga, J.D. and G.Gi collected the samples, D.V. and S.C. analysed the data, all authors contributed to the writing of the manuscript.

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