Cambridge Conservation Initiative, 11th December 2019


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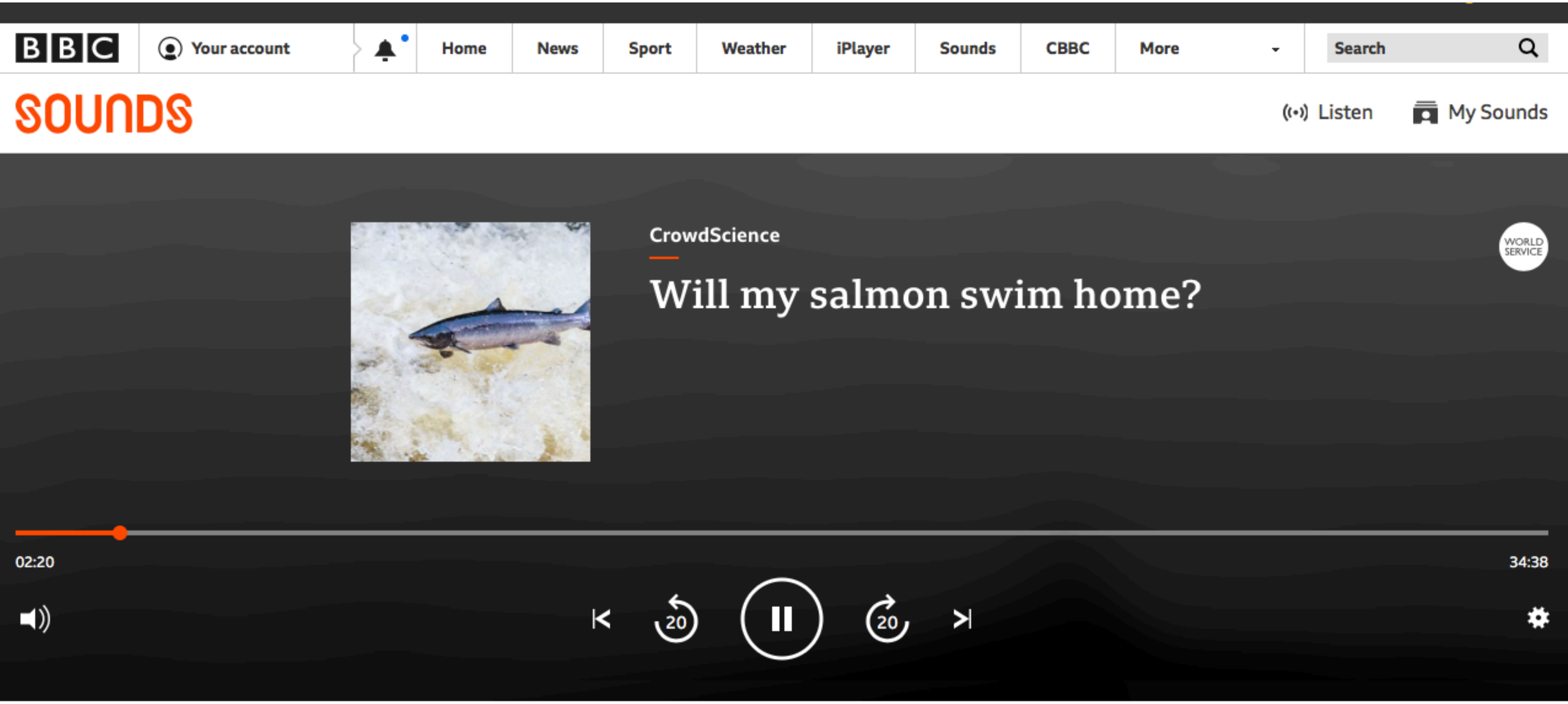
Jamie Stevens
University of Exeter

Conserving genetic diversity in Atlantic Salmon: challenges for the chalk stream populations of southern England

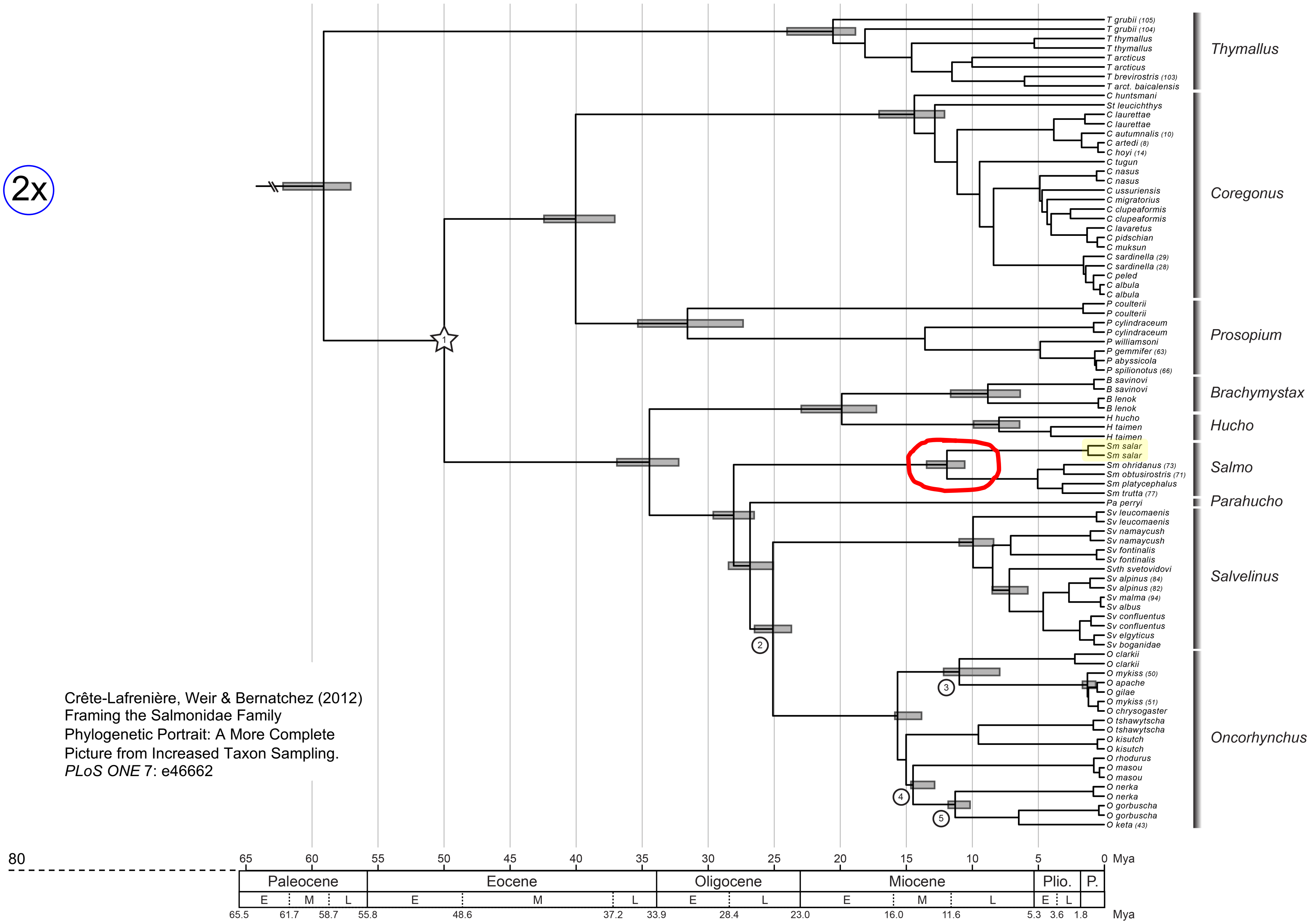
j.r.stevens@exeter.ac.uk



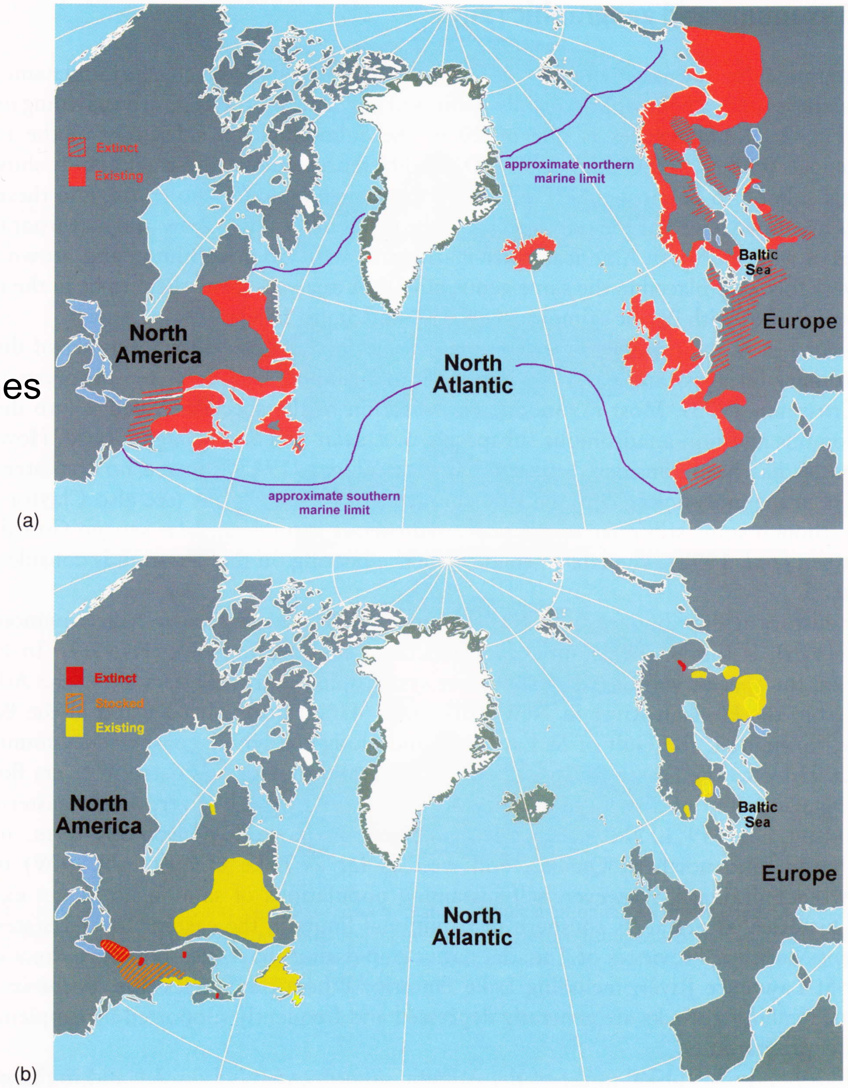
CrowdScience

Will my salmon swim home?

https://www.bbc.co.uk/sounds/play/w3csz1tn



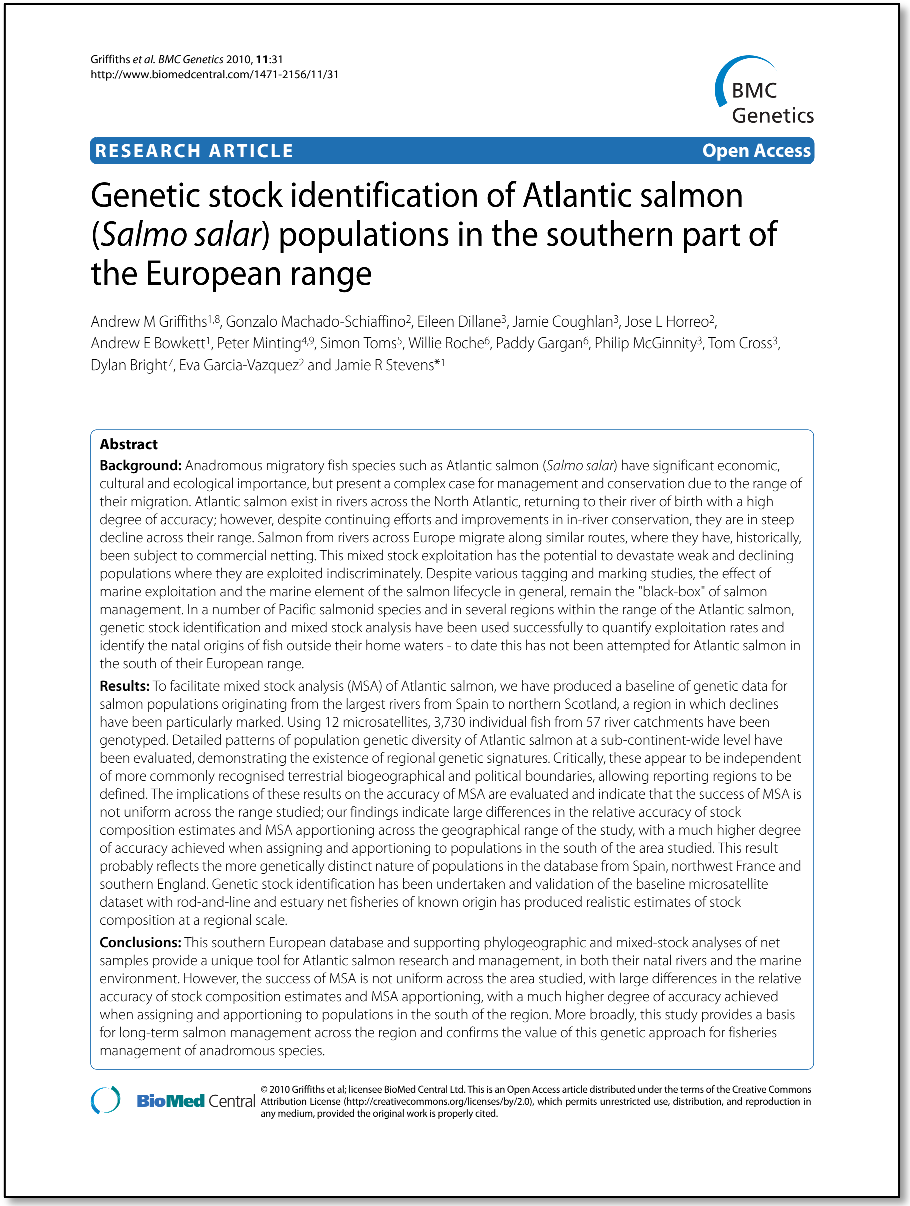
Crête-Lafrenière, Weir & Bernatchez (2012)
Framing the Salmonidae Family
Phylogenetic Portrait: A More Complete
Picture from Increased Taxon Sampling.
PLoS ONE 7: e46662



29 chromosomes

27 chromosomes

Fig. 2.4 The approximate distribution of wild anadromous (a) and non-anadromous (b) populations of Atlantic salmon in the North Atlantic region. In some southern parts of the species range where wild salmon are shown to still exist, some populations have gone extinct and others have severely depleted populations. In some areas where wild anadromous populations are shown to be extinct (e.g. the Baltic Sea), rivers have populations sustained by stocking (based on MacCrimmon and Gots 1979; IBSFC and HELCOM 1999).



Griffiths *et al. BMC Genetics* 2010, **11**:31
http://www.biomedcentral.com/1471-2156/11/31

BMC Genetics

RESEARCH ARTICLE **Open Access**

Genetic stock identification of Atlantic salmon (*Salmo salar*) populations in the southern part of the European range

Andrew M Griffiths[1,8], Gonzalo Machado-Schiaffino[2], Eileen Dillane[3], Jamie Coughlan[3], Jose L Horreo[2],
Andrew E Bowkett[1], Peter Minting[4,9], Simon Toms[5], Willie Roche[6], Paddy Gargan[6], Philip McGinnity[3], Tom Cross[3],
Dylan Bright[7], Eva Garcia-Vazquez[2] and Jamie R Stevens*[1]

Abstract

Background: Anadromous migratory fish species such as Atlantic salmon (*Salmo salar*) have significant economic, cultural and ecological importance, but present a complex case for management and conservation due to the range of their migration. Atlantic salmon exist in rivers across the North Atlantic, returning to their river of birth with a high degree of accuracy; however, despite continuing efforts and improvements in in-river conservation, they are in steep decline across their range. Salmon from rivers across Europe migrate along similar routes, where they have, historically, been subject to commercial netting. This mixed stock exploitation has the potential to devastate weak and declining populations where they are exploited indiscriminately. Despite various tagging and marking studies, the effect of marine exploitation and the marine element of the salmon lifecycle in general, remain the "black-box" of salmon management. In a number of Pacific salmonid species and in several regions within the range of the Atlantic salmon, genetic stock identification and mixed stock analysis have been used successfully to quantify exploitation rates and identify the natal origins of fish outside their home waters - to date this has not been attempted for Atlantic salmon in the south of their European range.

Results: To facilitate mixed stock analysis (MSA) of Atlantic salmon, we have produced a baseline of genetic data for salmon populations originating from the largest rivers from Spain to northern Scotland, a region in which declines have been particularly marked. Using 12 microsatellites, 3,730 individual fish from 57 river catchments have been genotyped. Detailed patterns of population genetic diversity of Atlantic salmon at a sub-continent-wide level have been evaluated, demonstrating the existence of regional genetic signatures. Critically, these appear to be independent of more commonly recognised terrestrial biogeographical and political boundaries, allowing reporting regions to be defined. The implications of these results on the accuracy of MSA are evaluated and indicate that the success of MSA is not uniform across the range studied; our findings indicate large differences in the relative accuracy of stock composition estimates and MSA apportioning across the geographical range of the study, with a much higher degree of accuracy achieved when assigning and apportioning to populations in the south of the area studied. This result probably reflects the more genetically distinct nature of populations in the database from Spain, northwest France and southern England. Genetic stock identification has been undertaken and validation of the baseline microsatellite dataset with rod-and-line and estuary net fisheries of known origin has produced realistic estimates of stock composition at a regional scale.

Conclusions: This southern European database and supporting phylogeographic and mixed-stock analyses of net samples provide a unique tool for Atlantic salmon research and management, in both their natal rivers and the marine environment. However, the success of MSA is not uniform across the area studied, with large differences in the relative accuracy of stock composition estimates and MSA apportioning, with a much higher degree of accuracy achieved when assigning and apportioning to populations in the south of the region. More broadly, this study provides a basis for long-term salmon management across the region and confirms the value of this genetic approach for fisheries management of anadromous species.

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Conseil International pour l'Exploration de la Mer

ICES Journal of Marine Science (2018), 75(2), 662–674. doi:10.1093/icesjms/fsx184

Original Article

A microsatellite baseline for genetic stock identification of European Atlantic salmon (*Salmo salar* L.)

John Gilbey[1,*], Jamie Coughlan[2], Vidar Wennevik[3], Paulo Prodöhl[4], Jamie R. Stevens[5],
Carlos Garcia de Leaniz[6], Dennis Ensing[7], Eef Cauwelier[1], Corrine Cherbonnel[8], Sofia Consuegra[6,9],
Mark W. Coulson[10,11], Tom F. Cross[2], Walter Crozier[7], Eileen Dillane[2], Jonathan S. Ellis[5,‡],
Eva García-Vázquez[12], Andrew M. Griffiths[5], Sigurdur Gudjonsson[13], Kjetil Hindar[14], Sten Karlsson[14],
David Knox[1], Gonzalo Machado-Schiaffino[12,§], Dorte Meldrup[15], Einar Eg Nielsen[15],
Kristinn Ólafsson[16], Craig R. Primmer[17,¶], Sergey Prusov[18], Lee Stradmeyer[1], Juha-Pekka Vähä[17,**],
Alexey Je. Veselov[19], Lucy M. I. Webster[10,‡‡], Philip McGinnity[2,†], and Eric Verspoor[1,11,†]

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[4]*Institute for Global Food Security, School of Biological Sciences, Queen's University, Belfast BT9 7BL, UK*
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[6]*Department of Biosciences, Swansea University, Swansea, UK*
[7]*Agri-Food and Biosciences Institute Northern Ireland, Fisheries and Aquatic Ecosystems Branch, Newforge Lane, Belfast BT9 5PX, UK*
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[14]*Norwegian Institute for Nature Research (NINA), PO Box 5685 Torgard, 7485 Trondheim, Norway*
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[17]*Department of Biology, University of Turku, 20014 Turku, Finland*
[18]*Knipovich Polar Research Institute of Marine Fisheries and Oceanography, 6 Knipovich Street, Murmansk 183763, Russia*
[19]*Institute of Biology, Karelian Research Institute, Pushkinskaya 11, Petrozavodsk 10 185610, Russia*

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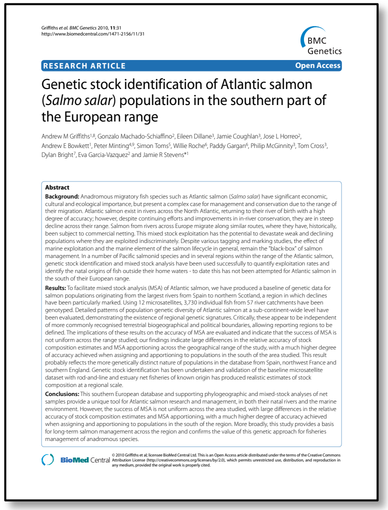
§*Present address: Department of Biology, University of Konstanz, 78457 Konstanz, Germany.*
¶*Present address: Department of Biosciences and Biotechnology Institute, University of Helsinki, 00014 Helsinki, Finland.*
[‡‡]*Present address: Science and Advice for Scottish Agriculture, Roddinglaw Road, Edinburgh EH12 9FJ, UK.*

We dedicate this paper to the memory of our co-author Kristinn Ólafsson who died 22 March 2017, aged 39. Kristinn's contribution to the paper was seminal and crucial, both in leading the technical development of the screening protocols for the SALSEA panel of microsatellites, and in the generation of the Icelandic component of the baseline. He is sorely missed by us, his colleagues, and friends, and his passing is a loss to the European fisheries science community. Though only in the early stages of his career, his contribution to European fisheries science was already highly significant, and well beyond just the SALSEA-MERGE project.

The Atlantic salmon arc project

ASAP



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BMC Genetics

RESEARCH ARTICLE **Open Access**

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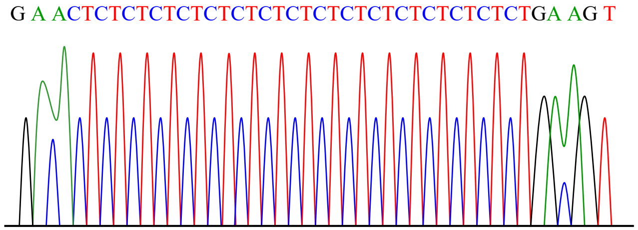
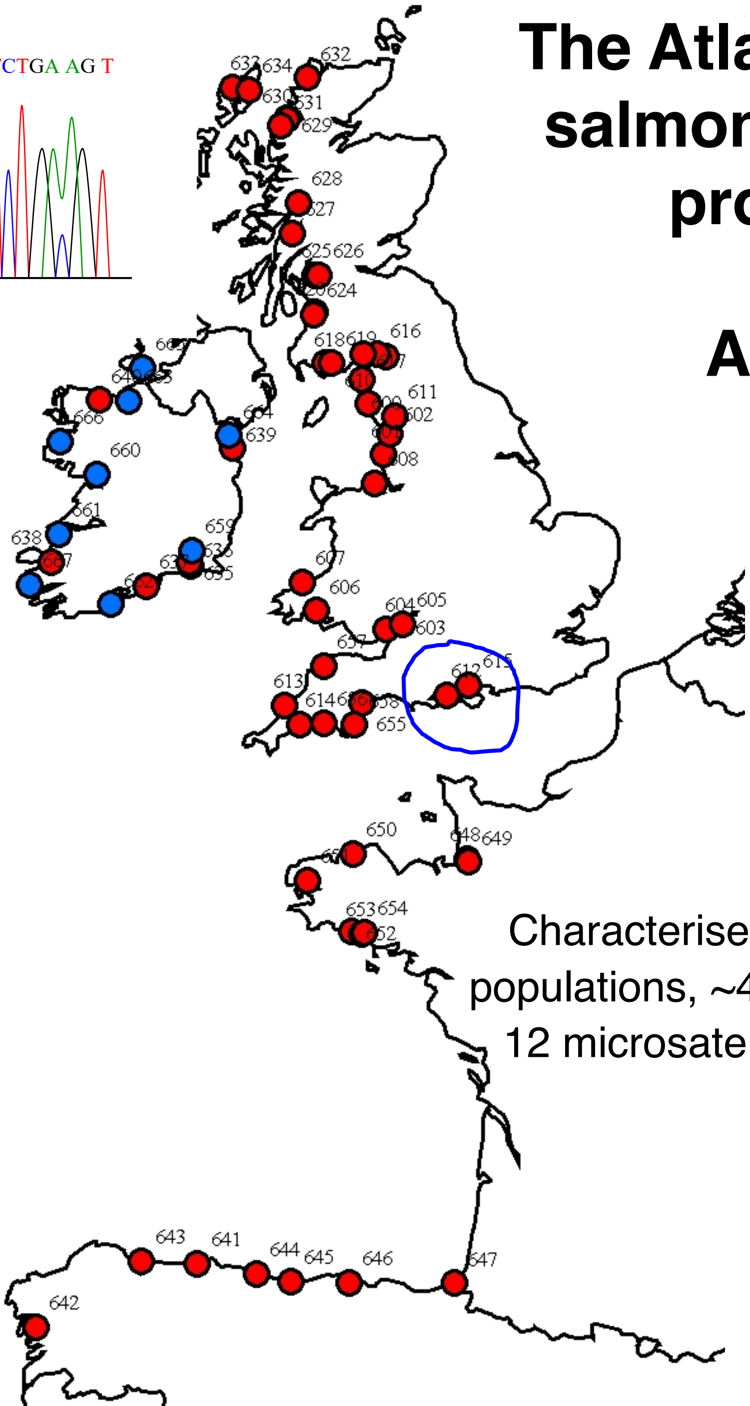




Characterised ~180 populations, ~4000 fish, 12 microsatellite loci

MDS plot - salmon population genotypes analysed in ASAP

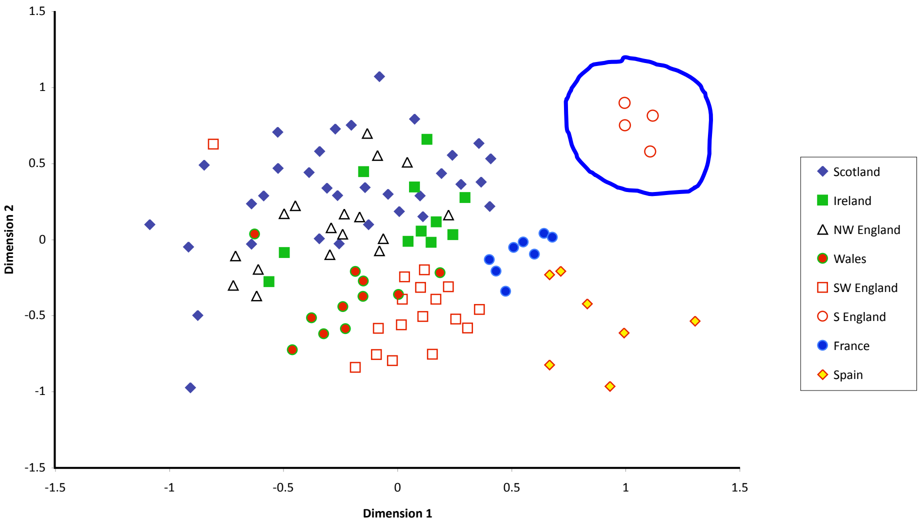
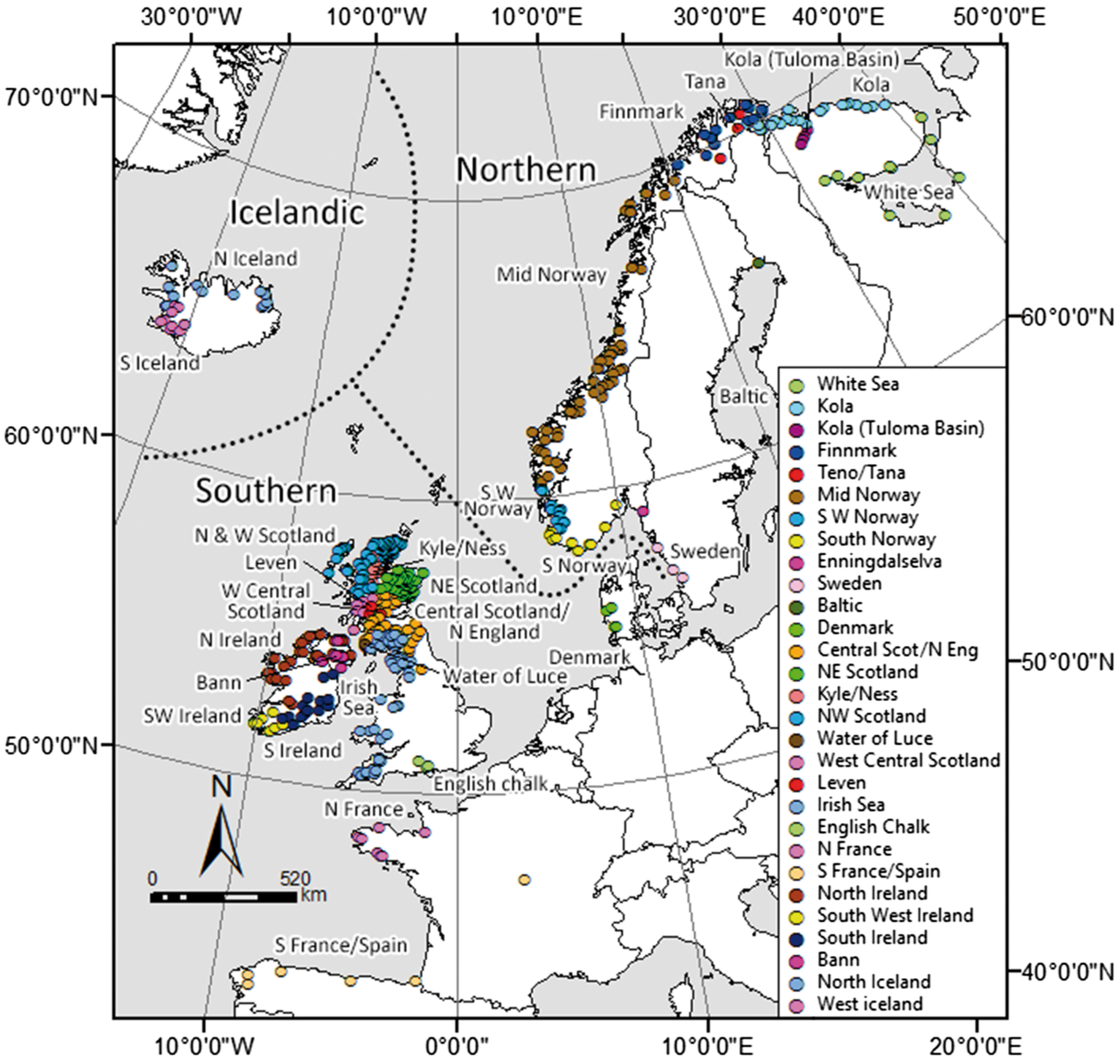


Figure 1. Map of sampling region. Points represent sample sites and/or river mouths.

SALSEA



ICES Journal of Marine Science, Volume 75, Issue 2, March-April 2018, Pages 662–674, https://doi.org/10.1093/icesjms/fsx184

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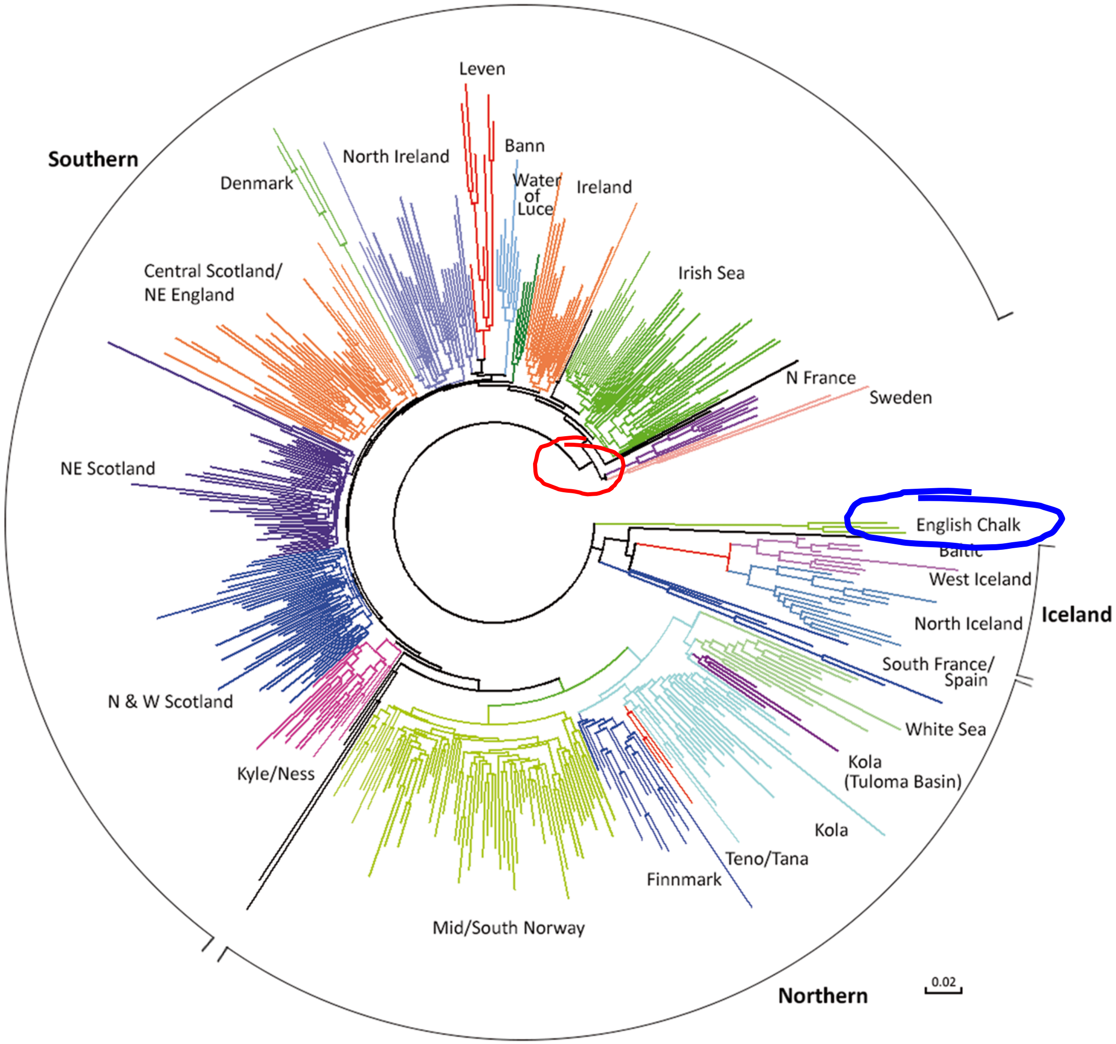
Figure 2. Neighbour-joining phylogenetic tree of sample sites based on D_A distances calculated from microsatellite genotypes (14 loci; major clusters coloured).

SALSEA



ICES Journal of Marine Science, Volume 75, Issue 2, 2018, Pages 662–674, https://doi.org/10.1093/icesjms/fsx184

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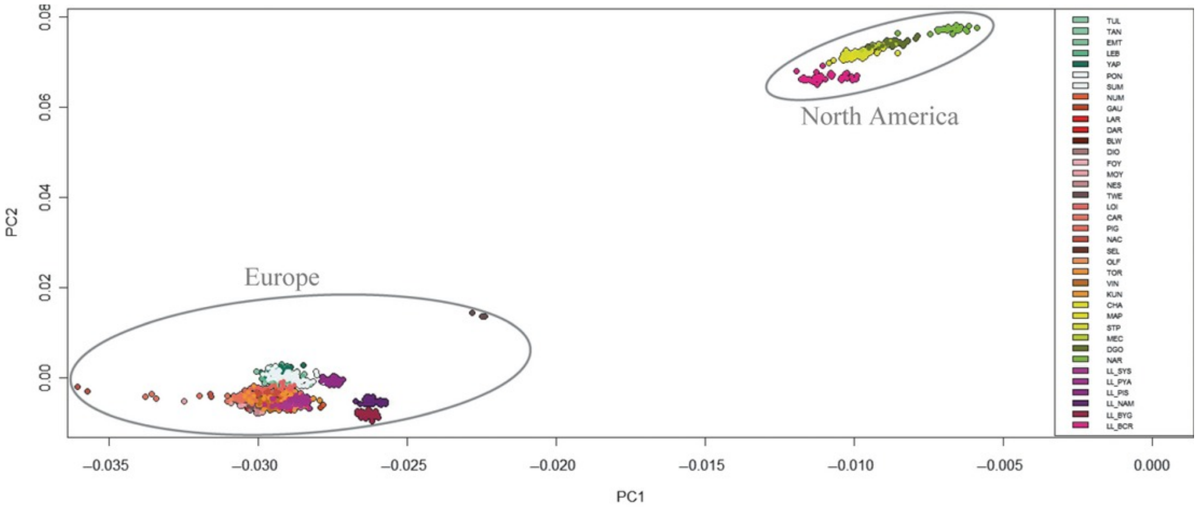
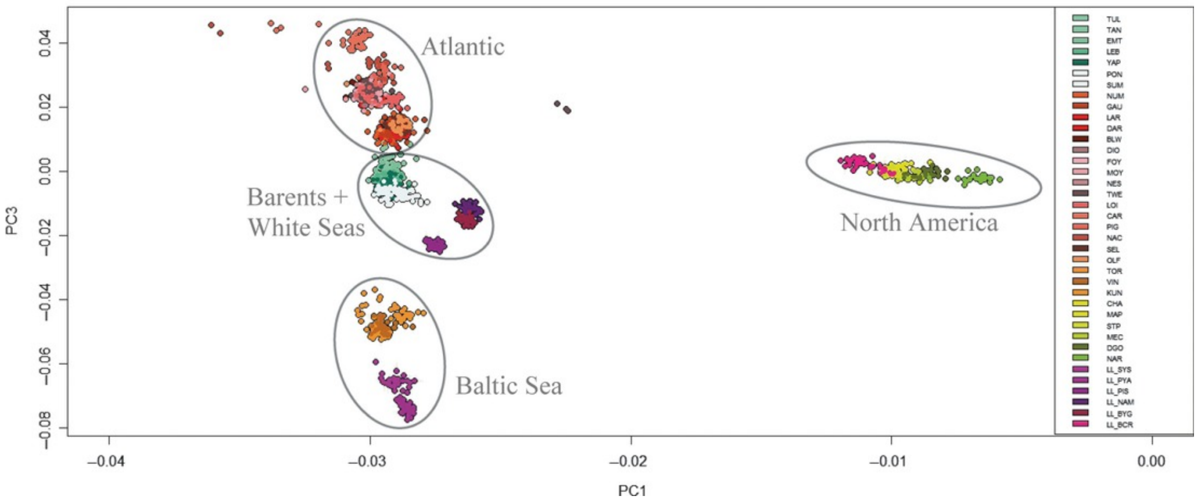
SNP-array reveals genome-wide patterns of geographical and potential adaptive divergence across the natural range of Atlantic salmon (Principal components analysis)

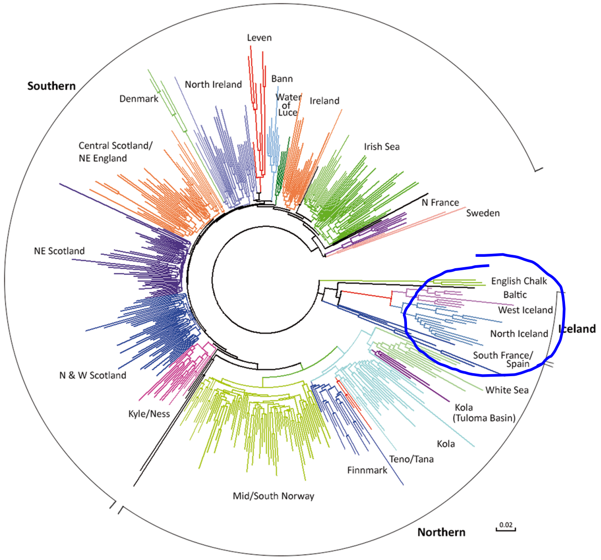


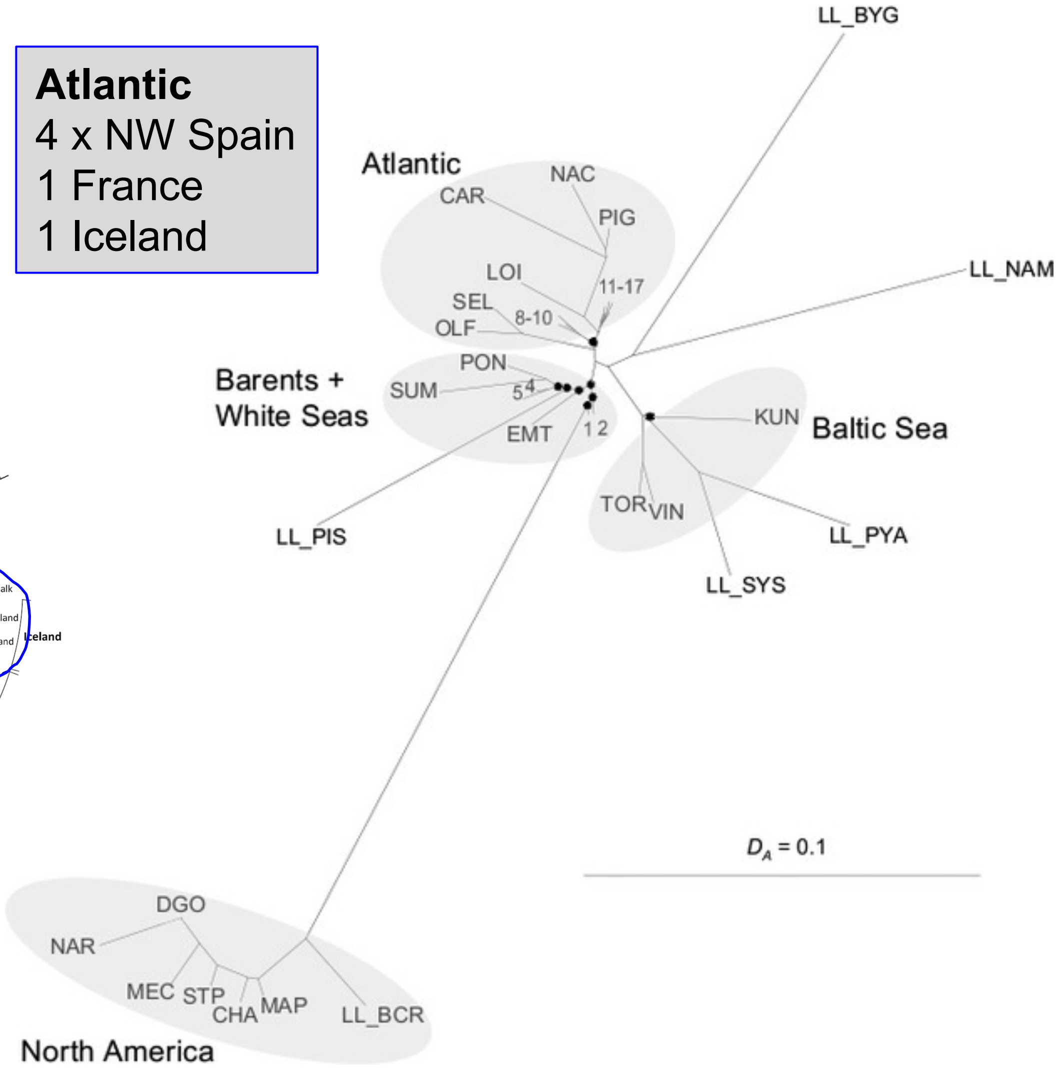


Bourret V. *et al.* (2013) Molecular Ecology, Volume: 22, Pages: 532-551, First published: 12 September 2012, DOI: (10.1111/mec.12003)

SNP-array reveals genome-wide patterns of geographical and potential adaptive divergence across the natural range of Atlantic salmon (*Salmo salar*)

Atlantic
4 x NW Spain
1 France
1 Iceland





Bourret V. *et al.* (2013) Molecular Ecology, Volume: 22, Pages: 532-551, First published: 12 September 2012, DOI: (10.1111/mec.12003)

Chalk cliffs of southern England…

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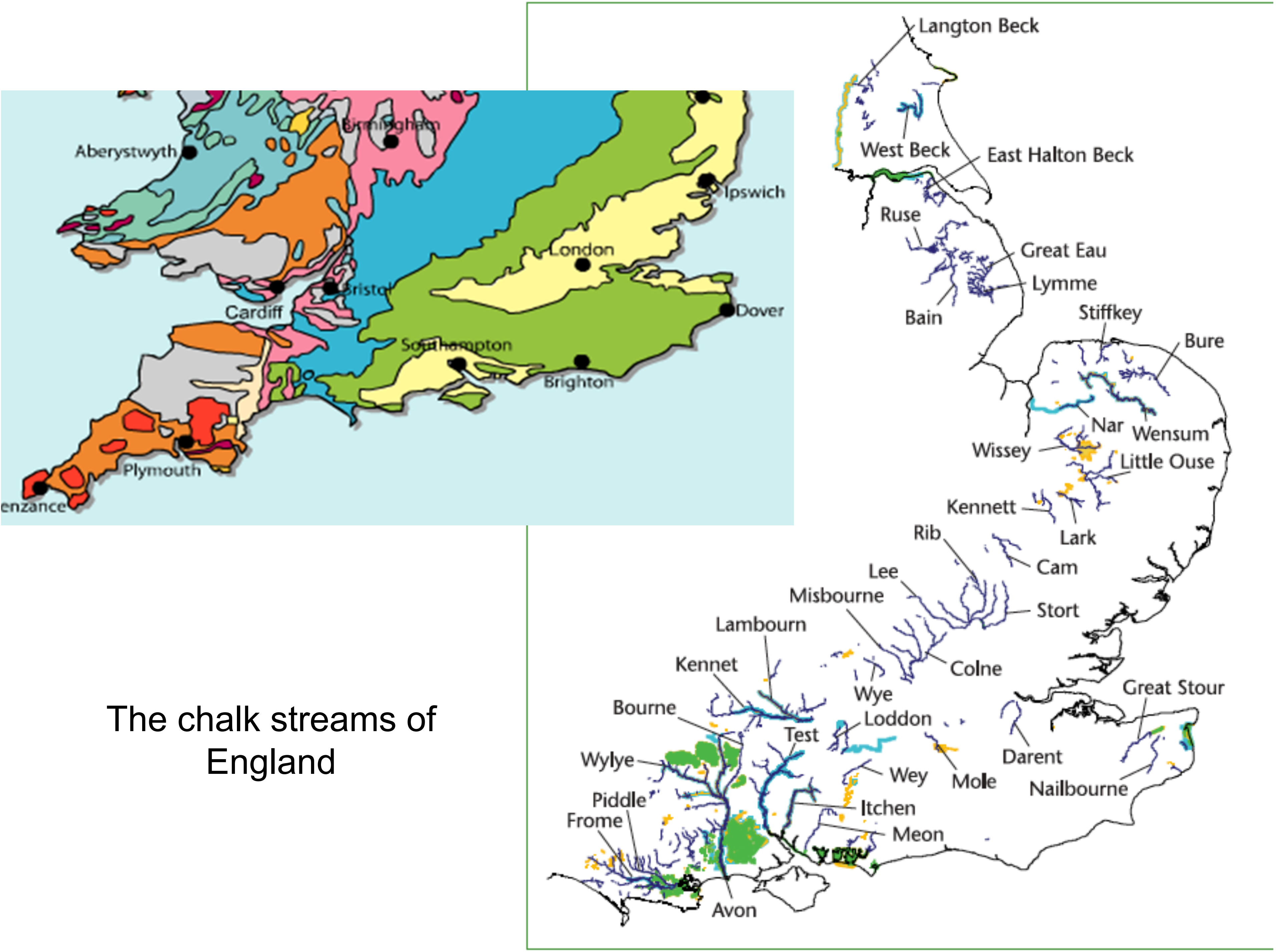

The chalk streams of England

A chalk stream – The river Frome

Low energy/nutrient rich

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Characteristic water chemistry and flow…

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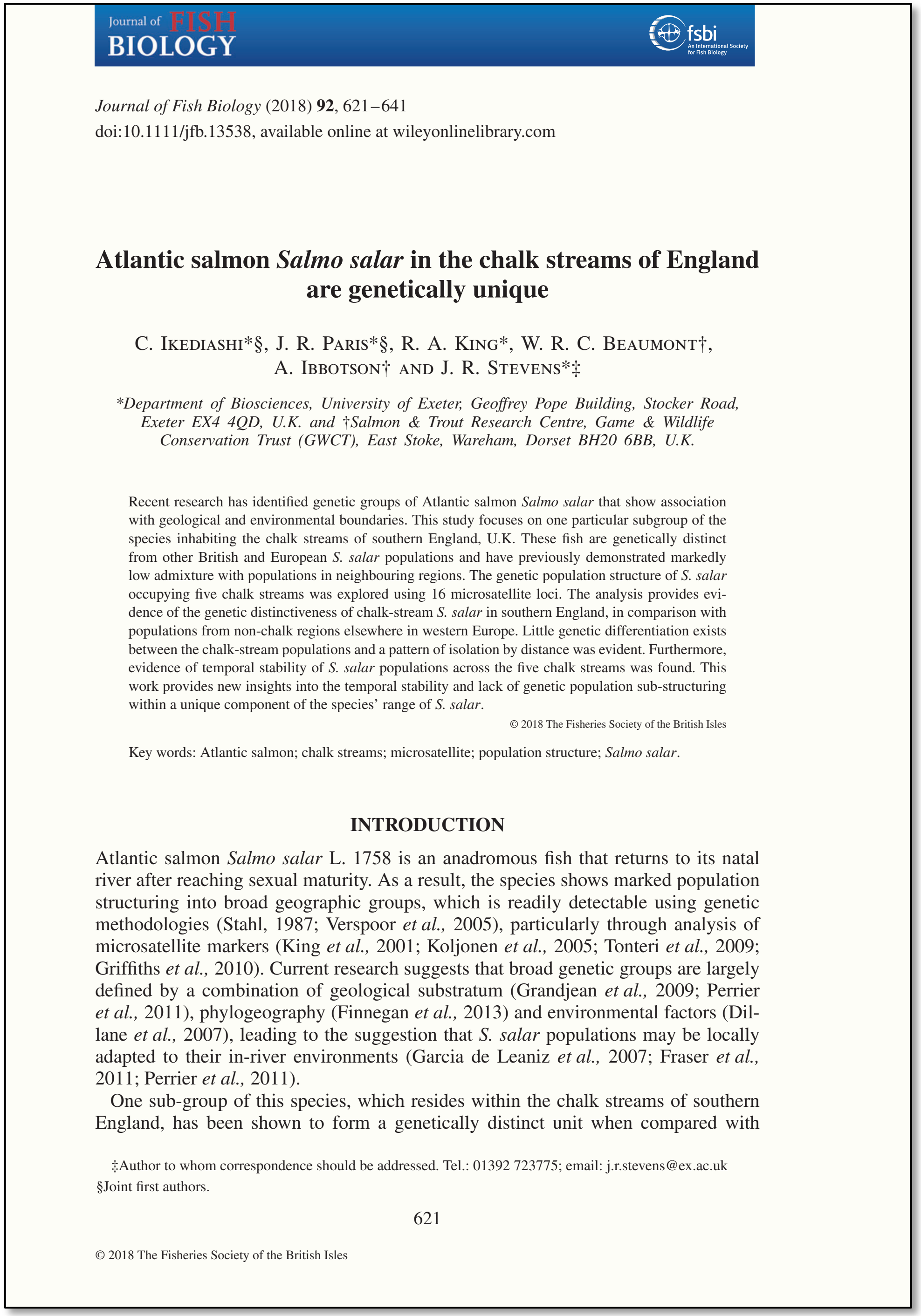

Journal of FISH BIOLOGY

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Journal of Fish Biology (2018) **92**, 621–641
doi:10.1111/jfb.13538, available online at wileyonlinelibrary.com

Atlantic salmon *Salmo salar* in the chalk streams of England are genetically unique

C. Ikediashi*§, J. R. Paris*§, R. A. King*, W. R. C. Beaumont†,
A. Ibbotson† and J. R. Stevens*‡

**Department of Biosciences, University of Exeter, Geoffrey Pope Building, Stocker Road, Exeter EX4 4QD, U.K. and †Salmon & Trout Research Centre, Game & Wildlife Conservation Trust (GWCT), East Stoke, Wareham, Dorset BH20 6BB, U.K.*

Recent research has identified genetic groups of Atlantic salmon *Salmo salar* that show association with geological and environmental boundaries. This study focuses on one particular subgroup of the species inhabiting the chalk streams of southern England, U.K. These fish are genetically distinct from other British and European *S. salar* populations and have previously demonstrated markedly low admixture with populations in neighbouring regions. The genetic population structure of *S. salar* occupying five chalk streams was explored using 16 microsatellite loci. The analysis provides evidence of the genetic distinctiveness of chalk-stream *S. salar* in southern England, in comparison with populations from non-chalk regions elsewhere in western Europe. Little genetic differentiation exists between the chalk-stream populations and a pattern of isolation by distance was evident. Furthermore, evidence of temporal stability of *S. salar* populations across the five chalk streams was found. This work provides new insights into the temporal stability and lack of genetic population sub-structuring within a unique component of the species' range of *S. salar*.

Key words: Atlantic salmon; chalk streams; microsatellite; population structure; *Salmo salar*.

INTRODUCTION

Atlantic salmon *Salmo salar* L. 1758 is an anadromous fish that returns to its natal river after reaching sexual maturity. As a result, the species shows marked population structuring into broad geographic groups, which is readily detectable using genetic methodologies (Stahl, 1987; Verspoor *et al.*, 2005), particularly through analysis of microsatellite markers (King *et al.*, 2001; Koljonen *et al.*, 2005; Tonteri *et al.*, 2009; Griffiths *et al.*, 2010). Current research suggests that broad genetic groups are largely defined by a combination of geological substratum (Grandjean *et al.*, 2009; Perrier *et al.*, 2011), phylogeography (Finnegan *et al.*, 2013) and environmental factors (Dillane *et al.*, 2007), leading to the suggestion that *S. salar* populations may be locally adapted to their in-river environments (Garcia de Leaniz *et al.*, 2007; Fraser *et al.*, 2011; Perrier *et al.*, 2011).

One sub-group of this species, which resides within the chalk streams of southern England, has been shown to form a genetically distinct unit when compared with

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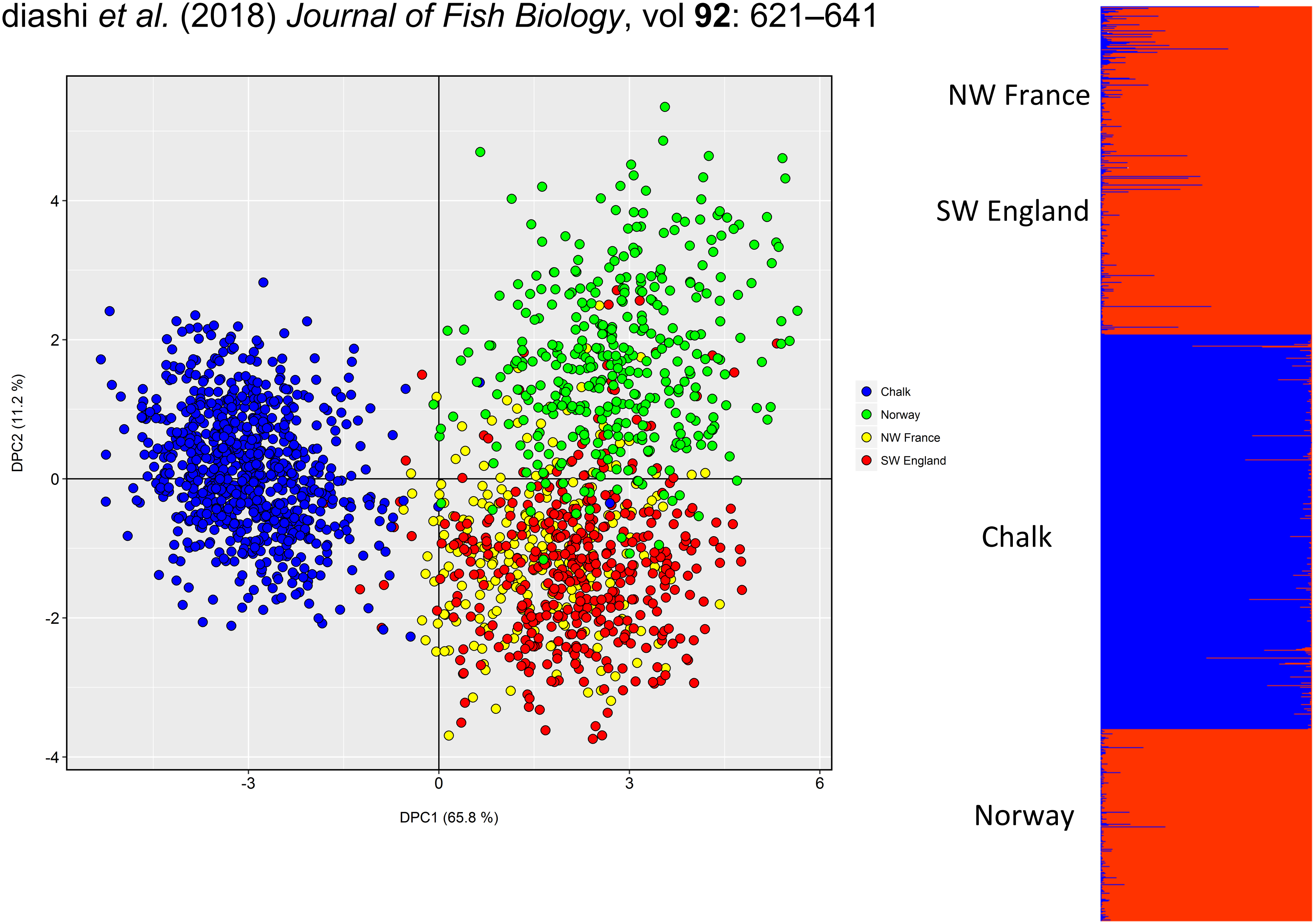
§Joint first authors.

Ikediashi *et al.* (2018) *Journal of Fish Biology*, vol **92**: 621–641



Principle components (L) and STRUCTURE (R) analysis of Atlantic salmon microsatellite data (12 loci)

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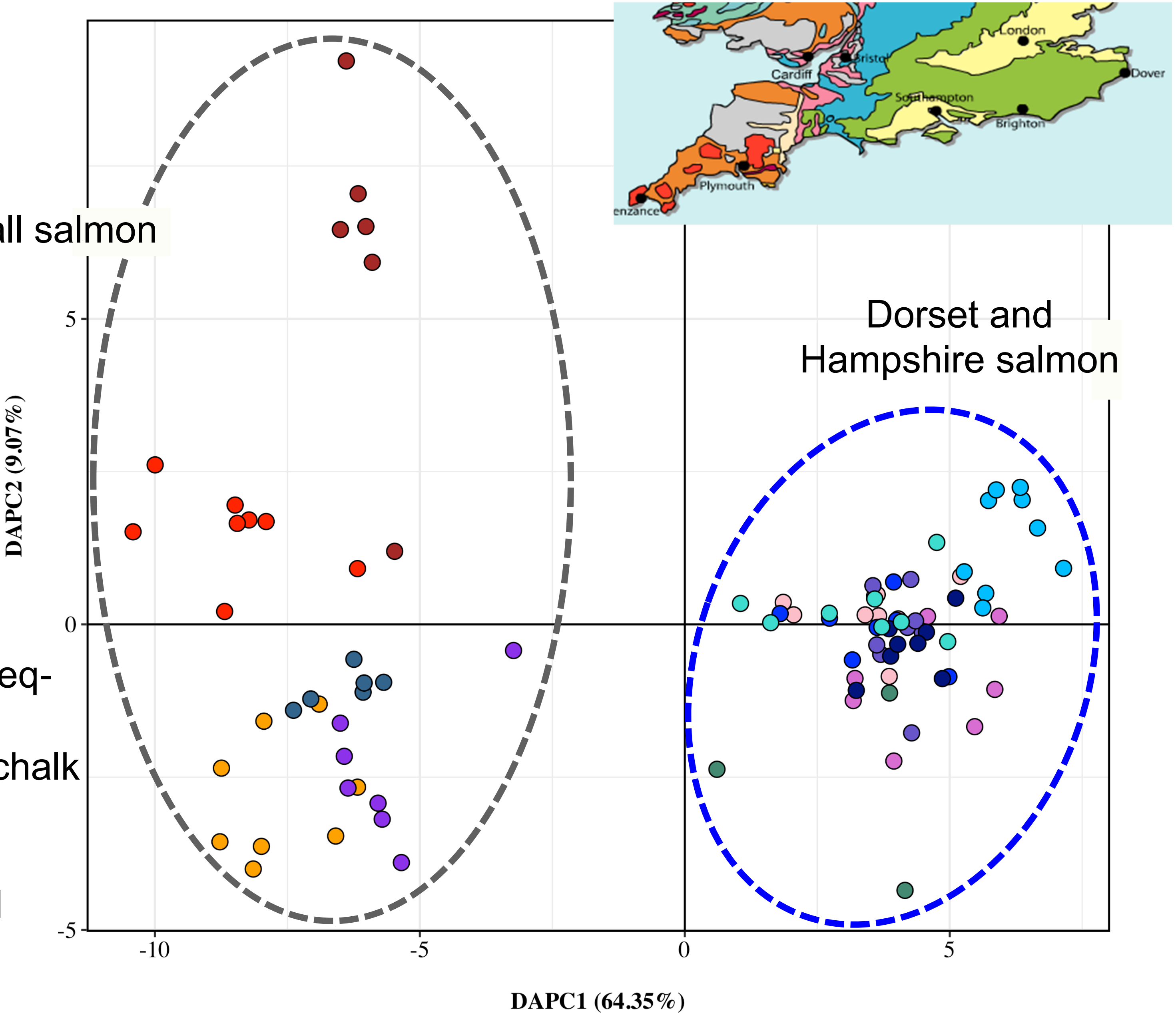


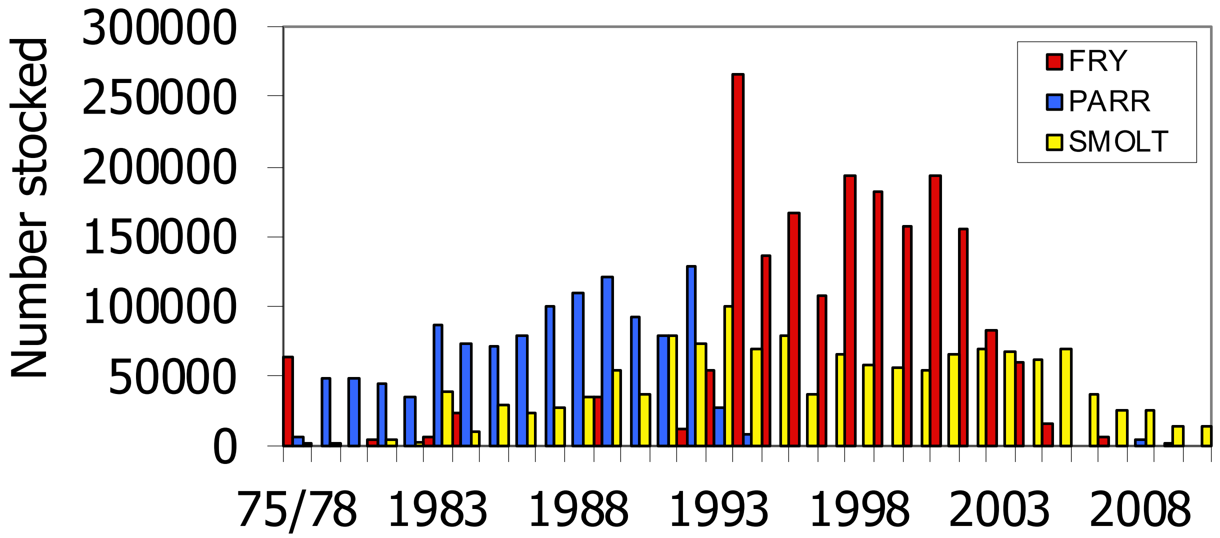
Devon and Cornwall salmon

Dorset and Hampshire salmon

Preliminary RADseq-based analysis of southern English chalk stream salmon (>16,000 SNPs) delivers increased intra-regional resolution

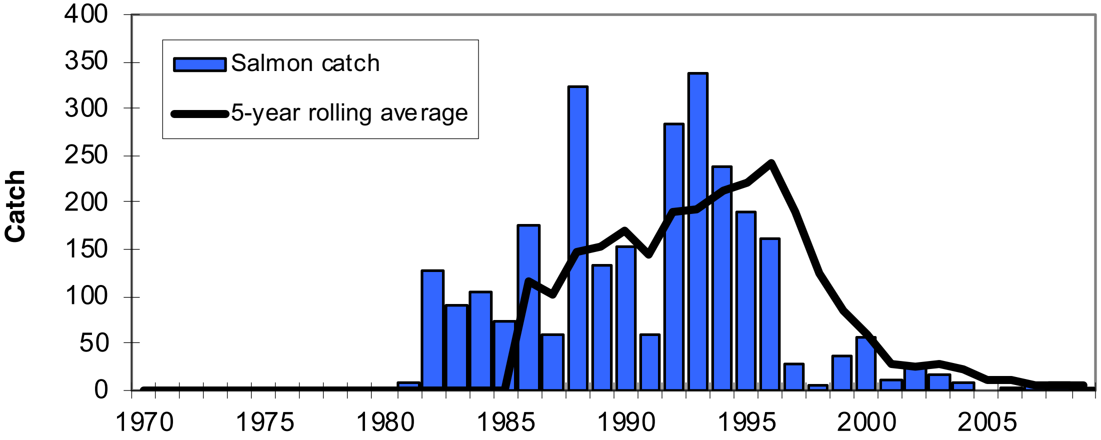
Stevens *et al.* unpublished

Devon & Cornwall incl: Tamar, Dart, Teign, Devon Avon, Exe
Dorset & Hampshire incl: Frome, Piddle, Hampshire Avon, Test, Itchen, Stour



Salmon put into the river Thames

Salmon caught in the river Thames



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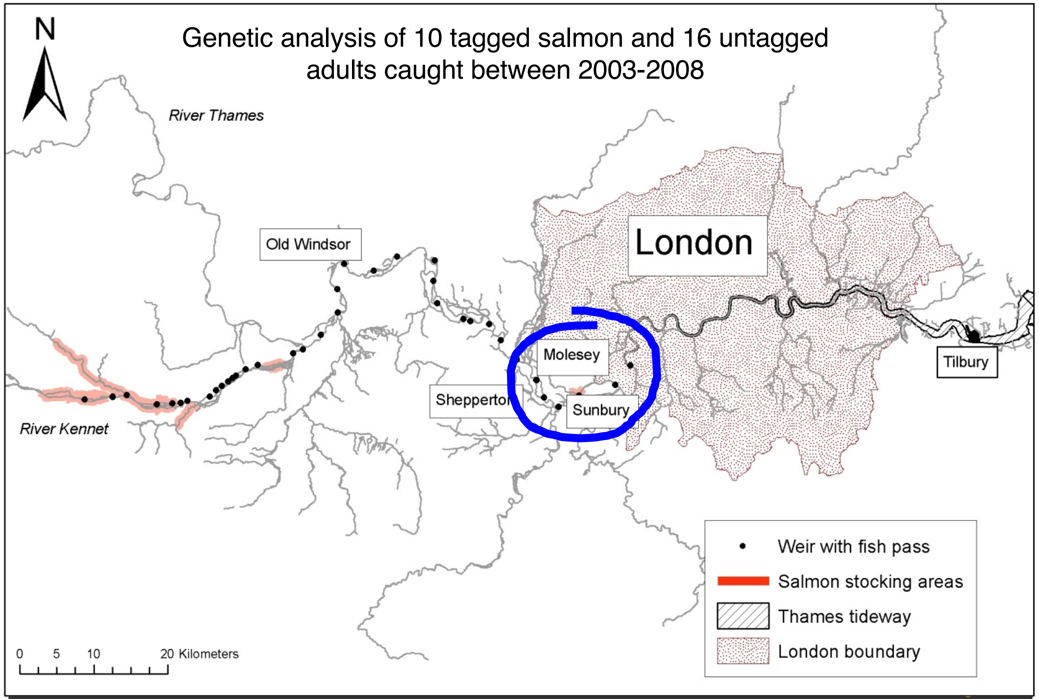
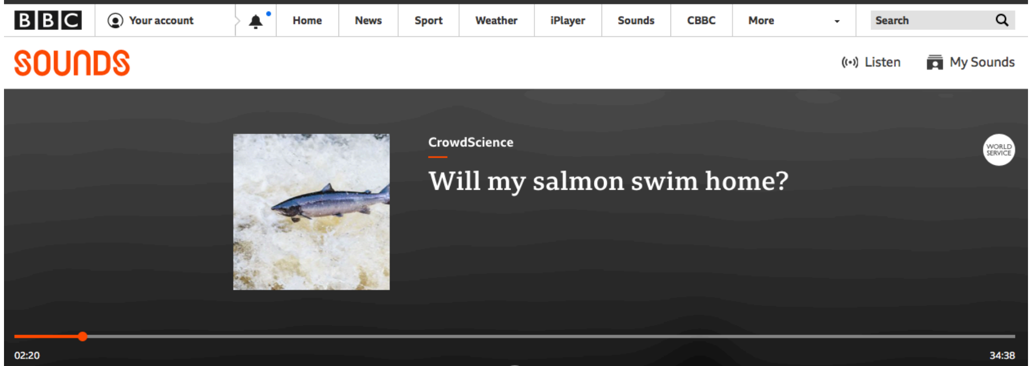
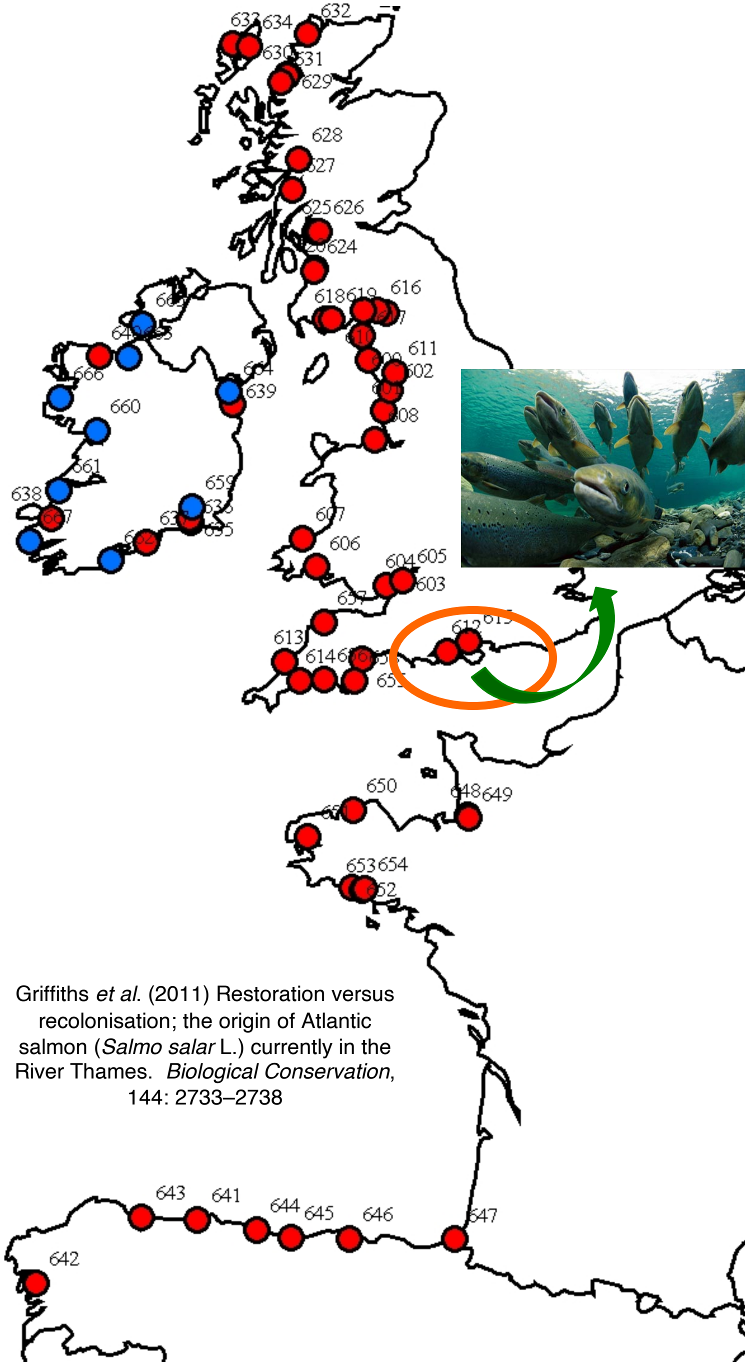
Assignment analysis (based on microsatellite genotypes) identified returning Thames fish (untagged) as strays from southern English chalk-stream rivers


Genetic analysis of 10 tagged salmon and 16 untagged adults caught between 2003-2008



CrowdScience

Will my salmon swim home?



Griffiths *et al.* (2011) Restoration versus recolonisation; the origin of Atlantic salmon (*Salmo salar* L.) currently in the River Thames. *Biological Conservation*, 144: 2733–2738

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Dylan Bright (WRT), Jose Luis Horreo (Oviedo);
Jon Ellis, Andrew Griffiths, Andrew King & Josie Paris (Exeter);
Darryl Clifton-Dey (EA)

EA Fisheries teams: Devon, Cornwall, Southeast and Thames

ATLANTIC AREA
Transnational Programme

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