

Genetic Analysis Project Update

In July 2010 we reported on the FASMOP (Focusing Atlantic Salmon Management on Populations) Project. One year on, some significant progress has been made.



DNA Samples plus a dye being loaded into an agarose gel, before a current is applied which causes the DNA to move down the gel. An image is then taken under UV light which allows the geneticists to check the quality and quantity of the DNA in preparation for further experiments. (Photo courtesy of Eric Verspoor, Marine Scotland Science).

Background

Most people are familiar with DNA analysis and the way it can be used to confirm parenthood or identify criminals with their crimes. This technology is now being used in fishery management in Scotland to identify the distinctive breeding populations of Salmon – not just to differentiate between fish from one river and those from another – but the different breeding populations that make up a river's stock, so that our management of the fisheries is better

informed. FASMOP is a collaborative venture between Rivers and Fisheries Trusts Scotland (RAFTS), the Scottish Government's Marine Scotland Directorate and all the fisheries Trusts around Scotland, including the Spey Foundation.

FASMOP Project Aims and Funding

The principal aim of FASMOP for the River Spey is the production of a genetic "map" of the Spey catchment, showing the different breeding populations of Salmon that make up the river's stock. A secondary aim is to determine the contribution of the Spey's hatchery stocking to the rod fishery. Once we are in possession of a genetic "map", it may be possible to establish the relative strengths of individual sub-populations in the Spey catchment from further analysis of rod-caught samples.

The core source of funding for the FASMOP project has been that allocated from the Scottish Government / Marine Scotland grant to support the whole fisheries management planning programme across Scotland. Substantial supplementary funds have been pledged from a number of individual Trusts (in particular the Spey, Tweed, Dee and Kyle of Sutherland) to finance larger-scale genetic analysis projects in their areas. The Spey Fishery Board and Spey Foundation are particularly grateful to the H.D.H. Wills Trust and the Robertson Trust for their generous support of the Spey's genetic analysis project.

Initial Results

Initially, the project used a series of 17 Microsatellites as the basis for the genetic analysis. This followed a similar project which genetically mapped the Salmon stocks throughout Ireland. With regard to FASMOP's primary aim – producing genetic "maps" of catchments - early results were mixed; some Rivers showed distinct breeding populations within their stock, while other Rivers (including the Spey and other larger, East Coast Rivers) demonstrated a weaker degree of population distinction and defining distinct population boundaries was much less certain.

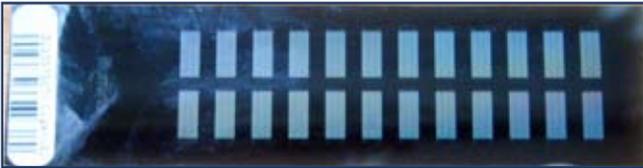
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These weak levels of confidence lacked the clarity to be able to assign fish to their area of origin with an acceptable level of confidence. The microsatellites were producing a picture, but lacked the depth of resolution that appeared necessary when dealing with larger – and potentially more complex – river systems. Further research was going to be necessary if our project aims were to be accomplished and the FASMOP team approached their colleagues at CIGENE in Norway for assistance.

A Closer Look



One of the SNP chips used on FASMOP samples. This chip (which is the size of a microscope slide) has 24 panels (grey boxes), each of which contains the ~6,500 SNPs. A DNA sample is applied to each panel, allowing the geneticists to screen 24 samples against each of the 6,500 DNA markers at a time. (Photo courtesy of Mark Coulson, RAFTS Geneticist).

CIGENE have developed technology that uses Single Nucleotide Polymorphisms (SNPs or “SNiPs”) as an alternative method for genetic analysis. Rather than using 17 Microsatellites, there are some 6,500 SNPs which are applicable to Salmon. Using digital photography as an analogy, the Microsatellites compare to using a 2 Megapixel camera, whereas the SNPs equate to a picture from a 12 Megapixel camera. The increased resolution has allowed us to take a much closer look at the samples we have submitted for genetic analysis. This approach offers the possibility of differentiating between them with a higher degree of certainty in order to create our genetic “map”. While it is too costly to have each of our samples compared to 6,500 SNPs, FASMOP and CIGENE have been working on reducing these to about 200 of the most appropriate SNPs for the Spey and producing a “chip” of these that can then be used for further sample analysis. The data on the initial 6,500 SNPs has now been collected and analysis of the Spey’s samples is underway.

The Hatcheries

Whilst FASMOP and CIGENE were busy researching the most appropriate SNPs for our genetic map, the FASMOP team focused on our secondary aim – determining whether our hatcheries were actually doing any good for the River, rather than merely doing no harm. With finclips taken from all the broodstock used over several years, meticulous breeding records (i.e. details of which males were paired with which females) and

finclips from a large number of rod-caught adults – it is possible to use genetic information from all of these fish to determine whether a proportion of the rod-catch has emanated from our hatcheries. Parent testing for the rod-caught salmon, so to speak! This was an area for which the Microsatellites proved an appropriate vehicle for analysis.

Thanks to the efforts of the Spey’s Ghillies, over 720 rod-caught fish samples had been collated for analysis. From these, 558 had been taken during 2008 and 2009 and enabled us to see if their parents had been part of our broodstock during 2004 and 2005. This was where the meticulous records compiled by our hatchery and research staff came to the fore, allowing us to match fish with absolute confidence.

From the 558 rod-caught samples analysed, 3 of them had emanated from our hatcheries, giving a return rate to the rod fishery of 0.5%. A slightly higher number were caught as broodstock. To put this into perspective, of the 8,626 fish caught during 2009, and on the basis of these genetic results, the hatcheries would have provided about 40 fish. The Board appreciates that this analysis represents a two-year return span for fish emanating from 2004 broodstock, but only one for their equivalent in 2005.

Next Steps

The hatcheries results were presented to the Spey Foundation Committee in February 2011 and to the RAFTS Conference the following month. Since then we have started a thorough review of our stocking policy and practice. This review is ongoing and it is intended that, as far as possible, it should involve all interested stakeholders. We are keen to ensure that any decision taken is properly communicated and widely supported. The Spey Foundation Committee and Board will meet again in August 2011, at which point the numbers to be stocked in 2012 will be decided. It was recognised that this would be premature for any long-term decision on the future of our hatcheries. However, our stocking strategy for next year will be far more targeted than hitherto, and its scope will be determined once we have the results of juvenile surveys later this year. A decision on a longer-term approach will be taken later.

FASMOP will conclude in March 2012 and discussions are underway to determine whether a second genetics project should be conducted. We will report on this in due course.