

The Genetic Analysis Project

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. The project - **Focusing Atlantic Salmon Management on Populations (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.

Background

An increasing number of behavioural and genetic studies have shown that the Atlantic salmon is structured into multiple, distinct breeding populations. In practical terms, a river like the Spey will have a salmon population that is distinct from that of other Scottish Rivers and within the Spey, tributaries such as the Fiddich, Avon and Tromie etc will each hold distinct sub-populations.

Breeding populations are the fundamental units underpinning recruitment and defining the character of a river's salmon stock. Each Atlantic salmon has a unique combination of genetic variants by which it and its offspring can be identified. The analysis of heritable variation in the DNA of salmon can be used to identify the different breeding populations and it is essential to understand a river's population structure for the development of effective stock conservation and management plans. However, such a project will require considerable resources, be time-consuming to undertake and we may not know the results for several years.

Collaboration with Other Projects

In addition to the genetic analysis carried out by the FASMOP project, further genetic analyses are being carried out for all Trusts as part of the EU-funded and NASCO-sponsored SALSEA-MERGE project, which is researching Salmon caught at sea to identify their river of origin, as well as providing information on the marine migration route that is

followed by the Salmon smolts from our rivers. Furthermore, an internal Marine Scotland project (POP MOD) on the development of general predictive models of within-river structuring of Atlantic salmon, by integrating data sets across catchments, will further improve the ability to interpret river specific data sets under FASMOP. These additional analyses will extend the data set available for FASMOP – improving the numbers and sizes of samples analysed and the level of coverage for the system.



Over 6,000 tissue samples have been taken from fish throughout the Spey catchment for the FASMOP Genetic Analysis Project (Photo: Marine Scotland).

Project Aims

The differentiation of one river's Salmon stock from that of another river's will largely come from the SALSEA-MERGE project. FASMOP will focus on:

- **The production of a genetic "map" of the Spey catchment**, showing the different breeding populations of Salmon that make up the river's stock, together with an indication of their strengths and weaknesses in terms of abundance.
- **Providing an indication of Salmon run timings** – useful for management planning, economic exploitation, the Spey's stocking policy and to identify the main rivers within the catchment from which the Spey's Spring running fish originate.

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- **Determining the contribution of the Spey's hatchery stocking to the rod fishery.** With finclips taken from all broodstock over several years, breeding records (i.e. 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 emulated from a hatchery. Parent testing for the rod-caught salmon, so to speak!
- **Potentially assess levels of introgression of escaped farmed salmon with wild fish populations.** The present genetic tools available may allow levels of introgression to be estimated, although new methods to address this issue more precisely are being developed in conjunction with a Norwegian research facility, CIGENE.
- For those rivers that are being re-colonised following the removal of weirs or a reduction in pollution, to identify where the re-colonising fish are coming from. They may have come from a river nearby or be a mixture of salmon that have strayed from multiple catchments.

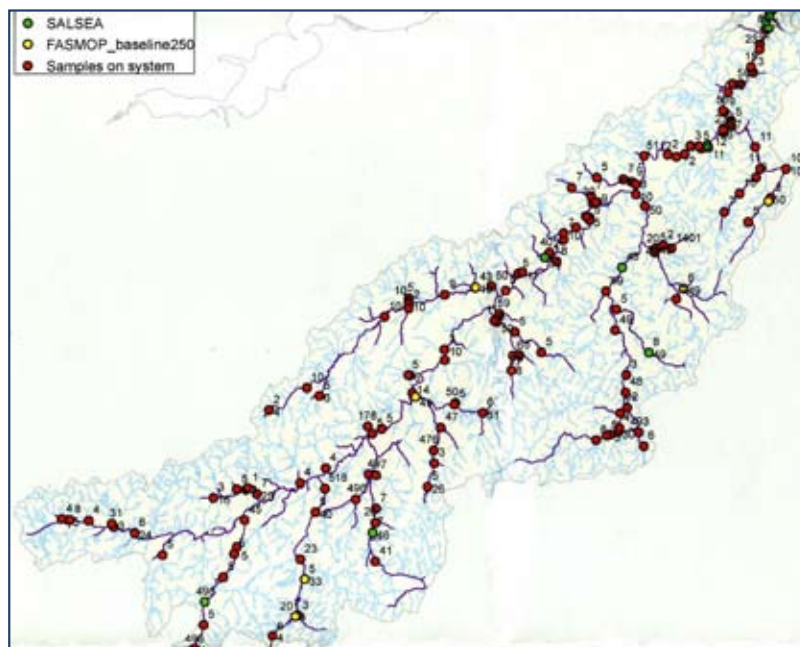
Funding

The core source of funding for the project is that allocated

from the Scottish Government / Marine Scotland grant to support the whole fisheries management planning programme across Scotland. This programme is managed by RAFTS and delivered by its members. 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 is particularly grateful to the HDH Wills Trust and the Robertson Trust for their generous support to the Spey's genetic analysis project.

Conclusion

If we can identify the different fish populations in our rivers, their individual distinct habitats and their relative strengths or weaknesses, we will have a fishery management tool at our disposal, the likes of which we have never had before. Pin-pointing the different fish families will enable us to focus our fishery management planning and stock assessment more precisely on our Salmon breeding populations. It is the logical, crucial and fundamental next step towards new and accurate plans for the management of fish populations throughout Scotland.



A "genetic map" of the Spey's breeding populations of Salmon, together with an indication of their strengths and weaknesses in terms of abundance, is the primary aim for the Spey's Genetic Analysis Project. This map illustrates the locations across the Spey catchment from which fish samples have been collated for analysis.