International Atlantic Salmon Research Board

ICR(12)9

Research Proposal for Consideration by IASRB – 2012
Genetic stock identification of salmon caught in the Faroes fishery

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RESEARCH PROPOSAL FOR CONSIDERATION BY IASRB - 2012

Genetic stock identification of salmon caught in the Faroes fishery.

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Background

Fish from both Northern and Southern European stock complexes migrate through the southern Norwegian Sea as post-smolts and as 1SW and MSW adults, and were exploited in the long-line fishery that operated within the Faroes EEZ in the 1980s and 1990s. No fishery has operated at Faroes for at least 10 years, but ICES is asked to provide annual catch advice to NASCO for the fishery, and a management decision has been agreed each year. In recent years ICES has developed a risk-framework for the provision of this advice (ICES, 2011 & 2012), but this development is constrained, in part, by lack of data on the composition of the stocks exploited by the fishery. The only suitable data currently available come from a limited number of tag returns in homewaters (~100) from adult salmon tagged in the fishery area in the 1990s (Hansen and Jacobsen 2003). This restricts the ability of ICES to provide advice based on smaller management units as they have recommended.

Both Northern NEAC MSW and Southern NEAC MSW stocks are currently considered to be close to or above full reproductive capacity and so there is potential for there to be an exploitable surplus in the area in the near future. The NASCO agreement on the adoption of a precautionary approach (NASCO 1998), requires the development of a pre-agreed management framework or decision structure for each fishery. There is therefore an urgent need to provide the data to support such a management framework.

Advances in microsatellite DNA profiling methodologies and statistical genetics approaches now make it possible to identify, with good degree of accuracy, salmon caught at sea to their natal region and, in some cases, to their river of origin. The SALSEA-Merge project has facilitated the development of a molecular stock assignment protocol, GRAASP - Genetically-based Regional Assignment of Atlantic Salmon Protocol, based on a suite of 14 microsatellites. The GRAASP database comprises 26,813 Atlantic salmon individuals from 467 locations, in 284 rivers, encompassing 370,000 pieces of genetic information representing ~ 85% of the non-Baltic European salmon production. The GRAASP tool is capable of delivering both broad and medium scale regional assignment. At the broad geographical scale, it currently recognises three regional assignment units (RAUs), namely, Iceland, Northern Europe and Southern Europe. Furthermore, at the finest supportable scale, it can distinguish 17 geographically cohesive regional subdivisions or RAUs (see Figure 1). Several high resolution microsatellite databases for genetic stock identification are now available in Ireland (the Beaufort NGSI panel), UK (Scotland-

FASMOP), UK (N. Ireland), UK (England & Wales, ASAP), Norway and France that may allow, in many instances, river specific assignments.

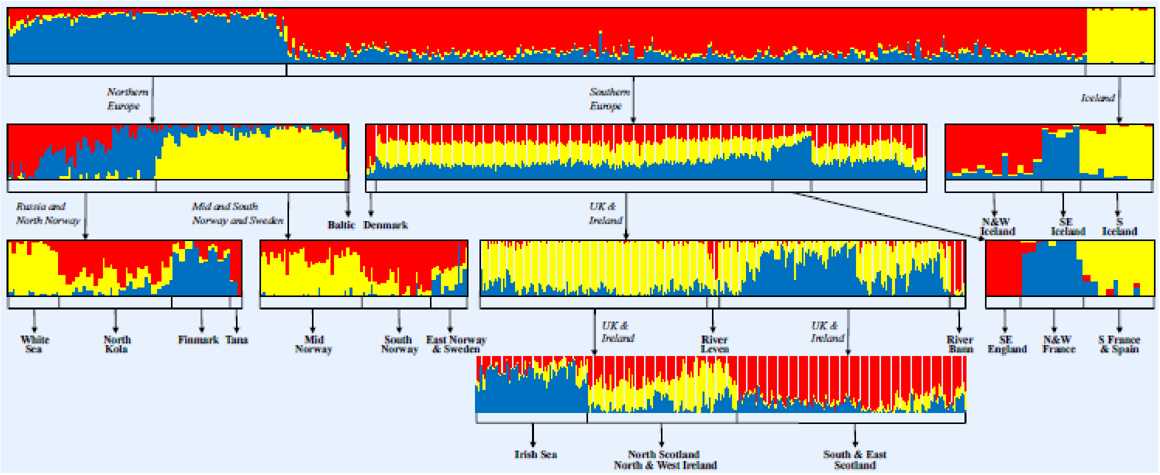

Figure 1. Hierarchical organisation of 17 GRAASP Regional Assignment Units (RAUs).

Sampling of both commercial and research catches in the Faroes EEZ was undertaken in a number of years between 1985 and 2000, and assignment of these samples should therefore provide a basis for establishing a baseline stock composition for the fishery. ICES (2012) has proposed that changes from this baseline over time might be estimated by weighting the regional contributions by their changes in pre-fishery abundance.

Objective

The overall aim of the project will be to provide the basis for assigning potential catches in a fishery at Faroes to their regions of origin in the NEAC area. The specific objectives are:

- To catalogue the scale samples collected from salmon caught in the Faroes fishery between 1984 to 2000;
- To identify a selection of scales that will best represent the likely stock composition during a baseline period or periods;
- To use GRAASP to provide country/region of origin assignments for the selected scales;
- To report to NASCO and ICES on the results of the study, the estimated changes in stock composition in the Faroes area within the fishing season and over time and how the finding can be used in the provision of catch advice for the NEAC area.

Work Plan

The project will be co-ordinated and carried out by the proposers.

Genetic typing of the samples will be undertaken at the Institute of Marine Research, Bergen, Norway, led by Vidar Wennevik, using an ABI3730XL 48 capillary system. Fish would be screened for the IMR microsatellite salmon marker panel, which is a combination of the GRAASP and the Norwegian panels. It is anticipated that in the order of 1,500 samples will be analysed with the final number of samples processed depending on available funding and on the method of DNA extraction utilised (with high quality scales in sufficient quantities to allow for multiple extractions, a cheaper extraction method can be employed than if there has been some DNA degradation during storage or if the quantity of scales is limited).

The GRAASP genotypes will be used by the Marine Scotland Genetics Unit at the Freshwater Fisheries Laboratory, led by Dr Gilbey, to provide regional assignments to SALSEA Level 1- Level 4 groupings. Attempts will also be made to assign fish to the sub-SASLEA levels utilising both the GRAASP and other available datasets.

A workshop will be held to consider the results and finalise a combined report detailing the assignments, and the relevant levels of confidence at the various geographical levels of resolution, and the implications for fishery management.

Should the project proposal outlined here be funded, selecting the scales samples will begin immediately, genotyping can commence in October 2012 with scored genotypes available for assignment analysis by January 2013. The assignment analysis will be completed by March 2013.

The results of the assignment will be used in developing catch advice for the NEAC area by the ICES Working Group on North Atlantic Salmon in April 2013.

The analysis of the marine distribution and the implications of the results will be led by Ted Potter, Jan Arge Jacobsen and Lars Petter Hansen. The results of the assignments will be presented in a final report, which will be submitted to the funding agency by June 2013.

Projected Costs

Genotyping (IMR, Norway: ~1500 scale sets at £13 per fish	£20,000
Assignments (Marine Scotland): Assignment of genotype data, statistical and GIS analysis of assignments data and report writing:	£9,500
Workshop (Location TBA): Two day workshop and the associated travel expenses for participants:	£4,000.
Total cost:	**£33,500**

References

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Hansen, L.P. and Jacobsen, J.A. 2003. Origin, migration and growth of wild and escaped farmed Atlantic salmon, *Salmo salar* L., in oceanic areas north of the Faroe Islands. *ICES Journal of Marine Science* 60: 110–119