International Atlantic Salmon Research Board

SAG(14)6

Final Project Report for
Genetic stock identification of salmon caught in the Faroes fishery

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Genetic stock identification of salmon caught in the Faroes fishery

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Abstract

A study was undertaken to extract DNA from historical scale samples taken from Atlantic salmon caught in the Faroes long-line fishery and perform genetic assignments with the aim of estimating the historical stock composition of the catch. Approximately 750 samples were selected from each of two periods comprising the 1983/84 and 1984/85 seasons and the 1993/94 and 1994/95 seasons, with scales being selected from all months in which samples were collected. DNA from the samples collected in the 1980s was found to be severely degraded, with most of the longer microsatellite alleles failing to amplify. These samples could not therefore be used and the analysis had to be based upon the later period. DNA was extracted from 656 scale samples collected during two fishing seasons, 1993/4 and 1994/5 and assigned using 14 microsatellites markers compared to a baseline established from 467 site locations, in 284 rivers, encompassing 370,000 pieces of genetic information representing rivers responsible for ~ 85% of the non-Baltic European salmon production.

At the highest hierarchical level, genetic exclusion analytical techniques and conformation analysis identified 16% of the total samples as being of North American continental origin and 84% as European. At the next hierarchical level, 62% of the European fish were identified as coming from the northern Europe (Russia, Finland, Norway and Sweden), 37% from southern European (UK and Ireland, France and Spain) and 1% from Iceland. These proportions were scaled to the distribution of commercial catches in the Faroes fishery in an average season between 1983/84 and 1990/91. This analysis indicated that about 56% of the catch in an average year might originate from northern European countries, 26% from southern European countries, 1% from Iceland and 16% from North America. These proportions were further broken down by both region (to 17 regional assignment units) and by the month of the fishery samples.

This project was funded by:

- *International Atlantic Salmon Research Board of NASCO*
- *The Norwegian Environment Agency*
- *Department for Environment, Food and Rural Affairs (UK)*) (part of Cefas contract SF0257)
- *Inland Fisheries Ireland*
- *Marine Scotland*

1. Introduction

Salmon from rivers in both northern and southern Europe were exploited as one-sea-winter (1SW) and multi-sea-winter (MSW) adults in the long-line fishery that operated within the Faroes Exclusive Economic Zone (EEZ) in the 1980s and 1990s (Jacobsen *et al.*, 2012). No salmon fishery has operated in Faroes waters since 2001, but ICES (2013) has advised that the both the northern Northeast Atlantic Commission (NEAC) MSW and southern NEAC MSW stock complexes have been close to or above full reproductive capacity in some recent years. There is therefore potential for there to be an exploitable surplus in the area in the near future (ICES, 2013). However, NASCO has not agreed an approach for determining a TAC, although 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.

ICES (2013) has recently provided NASCO with proposals for a risk-framework for the provision of catch advice for the Faroes fishery, but this has not yet been formally adopted by the NEAC. ICES has also proposed that the framework should ideally be applied to management units at the country level or smaller but has had limited data on the stock composition of the catches in the fishery. There is therefore an urgent need to obtain such information. Advances in microsatellite DNA profiling methodologies and statistical genetics approaches now make it possible to identify, with a good degree of accuracy, salmon caught at sea to their natal region and, in some cases, to their river of origin (Gilbey et al., In Prep.). The SALSEA-Merge project (Anon, 2011) has facilitated the development of a genetic stock assignment protocol based on a suite of 14 microsatellites. The SALSEA-Merge database comprises 26,813 Atlantic salmon individuals from 467 locations, in 284 rivers, encompassing 370,000 pieces of genetic information representing rivers responsible for ~ 85% of the non-Baltic European salmon production. The assignment 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, and at the finest supportable scale, it can distinguish 17 geographically cohesive regional subdivisions or RAUs (Gilbey et al., In Prep.)(Figure 1). Furthermore, several higher resolution microsatellite databases for genetic stock identification are now available, including for Ireland, Scotland, Northern Ireland, England & Wales, Norway and France that may allow, in some instances, river specific assignments.

The paper reports on the application of this approach to scale samples taken from salmon caught in the commercial and research fisheries operated in the Faroes EEZ in the 1980s and 1990s.

2. Objectives

The overall aim of the project was to identify the origin of salmon caught in the Faroes fishery in the 1980s and 1990s using genetic analysis of scales samples collected from commercial and research catches and to use the results in the development of a risk framework for the provision of catch advice for the fishery.

The specific objectives were:

- 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

3. Materials and Methods

3.1 Selection of scale samples

Scale sampling programmes were conducted during the commercial and research fisheries for salmon that operated within the Faroes EEZ between 1983 and 1997 (Table 1). Over 20,000 samples were collected and have been stored by the Norwegian Institute for Nature Research (NINA) in Trondheim (Table 2). Approximately 750 samples were selected from each of two periods comprising the 1983/84 and 1984/85 seasons and the 1993/94 and 1994/95 seasons (Table 3), with scales being selected from all months in which samples were collected. The samples to be analysed were selected at random from the full archive. All scales had previously been read, and the scale packets indicated whether they had been identified as farmed or wild using the method of Hansen et al., (1999). Where a scale sample to be selected was of farmed origin, the next sample from a wild fish was used in its place. Thus, all samples analysed were believed to be from wild fish.

3.2 DNA extraction and microsatellite analysis

DNA was extracted from two to four scales per sample in 96-well plates using Qiagen DNeasy blood and tissue kits, following the manufacturer's protocol. Each plate included two or more negative control wells. DNA concentration was measured for 15 samples on each plate, averaged, and a working dilution for PCR was prepared with a DNA concentration of approximately 15ng/ul . The following loci were amplified: SSsp3016 (Genbank no. AY372820), SSsp2210, SSspG7, SSsp2201, SSsp1605, SSsp2216 (Paterson et al. 2004), Ssa197, Ssa171, Ssa202 (O'Reilly et al. 1996), SsaD157, SsaD486, SsaD144 (King et al. 2005), Ssa289, Ssa14 (McConnell et al. 1995), SsaF43 (Sanchez et al. 1996), SsaOsl85 (Slettan et al. 1995), MHC I (Grimholt et al. 2002) and MHC II (Stet et al. 2002). These loci were combined into multiplexes as follows:

- Multiplex1: SSsp2210, SSspG7, SsaD144, Ssa202 and SSsp2201
- Multiplex2: Ssa289, Ssa14, SSsp1605, Ssa171, SSsp2216
- Multiplex3: SsaF43, Ssa197, SsaD486, MHC1, MHC2 and SsOSL85

Amplifications were carried out in 15 ul volumes, including 3ul DNA, 3 ul buffer, 1.2 ul MgCl2, 2.4ul dNTPs, 0.5 U Taq DNA Polymerase (Promega), and 0.12 to 0.345 ul of forward and reverse primers.

Reactions were carried out on an ABI9700 thermocycler, and consisted of an initial denaturation step of 15 min at 95°C, followed by 5 cycles of denaturation at 94°C for 30 s, annealing at 55°C for 90 s and extension at 72°C for 60 s. This was followed by 22 cycles of denaturation at 94°C for 30 s, annealing at 57°C for 90 s and extension at 72°C for 60 s. The same protocol was used for all three multiplexes. PCR products were analysed on an ABI 3730 Genetic Analyser and sized by a 500LIZTM size standard.

Initial analysis of the historic scales samples revealed extensive degradation of the DNA such that most microsatellite alleles above 200bp did not amplify. To improve these results, a modified PCR protocol was attempted. In this protocol, several PCR cycles are conducted at a lower annealing temperature to try to amplify fragments present in low concentration, before the annealing temperature was raised to the level specified in the standard protocol.

3.3 Exclusion Analysis

In order to estimate the proportion of North American fish in the samples and exclude them from being assigned to the European baseline, a series of methods were used to identify the North American fish. Initial identification of probable North American origin fish was obtained using individual genotypes at the microsatellite locus *SsaD486.* Scores for *SsaD486* from a separate study that had a mixture of American, Icelandic, and European fish showed several unique alleles at this locus for the American fish all with 176 or more base pairs (IMR unpublished data) (Figure 2). Samples with at least 176 base pairs at this locus were therefore identified as probably of North American origin.

An exclusion analysis was then performed using the method of Vasemägi *et al*. (2001) (see also Ikediashi *et al*., 2012). The baseline used to represent the European salmon range is shown in Figure 3 and included sites that covered the full European (non-Baltic) range of the species. Exclusion of fish belonging to the European baseline was first performed using fish individual assignment probabilities obtained using Monte-Carlo resampling based on the simulation algorithm of Paetkau *et al.* (2004) with a Type I error of 0.01 using the software GENECLASS2 (Piry *et al*., 2004).

Following calculation of the assignment probabilities, the highest score across each of the baseline assignment units (maximum assignment score) was obtained for each fish. Fish with low scores are those which do not assign well to any of the baseline populations, and a cut-off can be defined under which fish can be excluded as not belonging to any of the baseline groups. In order to check whether European fish from sites not represented in the baseline would have been identified as North American in the above analysis, 500 fish were chosen at random from sites not represented in the reduced baseline (Figure 4); this sample included a fish from the Baltic. Baltic salmon have been shown to be the most differentiated group in Europe (Verspoor *et al*., 1999; Nilsson et al., 2001), and importantly the Baltic was not represented in the reduced baseline used.

Cluster analysis of the full scale sample data set was also performed in order to determine in which group the samples belonged based on their genotype and the similarity of the genotypes in the two groups, North American and European. This was performed twice using different clustering algorithms. Firstly clustering was performed using the admixture model with correlated alleles as implemented in STRUCTURE 2.3.3 (Pritchard et al., 2000; Pritchard and Wen, 2004) using three independent runs and the admixture ancestry model with 250,000 Markov chain Monte Carlo (MCMC) replicates after a burn-in of 50,000, and assuming K=2 populations (i.e. North American and European). Loc-Prior was not used and so each individual was free to assign to one of the two populations. Secondly clustering was performed using a Discriminant Analysis of Principal Components (DAPC) approach as implemented in the R package *adegenet* 1.4-0 (Jombart and Ahmed, 2011; R Core Team, 2013). This approach firstly transforms the data using PCA and then performs K-means clustering on the informative PC to again assign individuals to one of K=2 possible clusters. Again no prior information was included in the clustering and all individuals were free to cluster to either of the populations.

A final test of the North American assignments was performed on the following four sets of samples using two genetic markers (*ND-1* and *SS1*) that have been shown to have a high association of different alleles with fish from either North American or European and have been suggested as being effective for discrimination of the continental origin of salmon (Gilbey *et al*., 2005):

1: samples classified as North American by microsatellite SsaD486
2: samples classified by North American by assignment/exclusion
3: Other samples from Faroes classified as European
4: River sample of parr from the Klimkovka river, Kola peninsula.

The first three sets were selected at random from the Faroes samples previously analysed.

3.4 Individual Assignments

Individual assignments for all fish were performed using the Bayesian assignment method implemented in the GENECLASS2 software package (Rannala and Mountain, 1997; Piry *et al*., 2004) using an assignment threshold of 0.05. Individual assignments are performed at the site level with assignment to sites within an assignment unit being summed (i.e. assignment back to the region rather than individual sites is examined, and scores are summed across sites within a region). Individual assignment allows the origin of individual fish to be estimated together with an associated assignment score which can then be used as a cut-off value. Fish falling under a specified assignment score value can be removed from the analysis giving a trade-off between assignment accuracy and numbers of fish assigned.

3.5 Mixed Stock Analysis

Proportions of fish from the different reporting units were determined using the conditional maximum likelihood method as implemented in the ONCOR software package (Millar, 1987; Kalinowski *et al*., 2007). The Expectation–Maximization (EM) algorithm was used to estimate mixture proportions, and iteration continued until the total change of mixture proportions from one iteration to the next (summed across all stocks) was less than 10^{-6}. Genotype probabilities were calculated using the method of Rannala and Mountain (1997). Confidence intervals of assignment proportions were obtained by bootstrapping both the baseline and the mixture samples. Mixture samples were bootstrapped by resampling individuals with replacement from the individuals in the mixture file. Baseline genotypes were bootstrapped by resampling alleles from baseline samples using the method of Rannala and Mountain (Equations 23 - 25 of Rannala and Mountain, 1997). Analysis was performed separately for each month represented in the samples and fish have been assigned to the hierarchical reporting units at four Levels (1-4) as defined by the SALSEA-Merge project (Gilbey et al., In Prep.), but particular attention was given to levels 1 and 3.

4. Results

4.1 DNA extraction and sequencing

Initial analysis of samples from November/ December 1983 and January 1984 revealed extensive degradation of the DNA and most microsatellite alleles above 200bp failed to amplify. Even for the best individuals, peaks were almost completely absent from the longer microsatellites, indicating degraded or fragmented DNA. Results from a sample of 94 scales collected in November 1993 were better, but the DNA was still very fragmented, and the long alleles tended to be missing. The proportion of samples providing useable DNA for 18 microsatellites varied from zero to 100% (accepting some poor quality peaks) (Table 5). Based on just the 14 SALSEA-Merge marker panel, about 95% of the November 1993 samples provided useable DNA for 6 loci, but this decreased to only about 10% of samples scoring for 11 loci (Table 6).

There was an indication that the longer alleles in the samples were more prone to degradation although one short microsatellite (*Ssa14*) also seemed to perform badly in the Nov. 1993 samples. Figure 5 shows a comparison of the size distributions of these loci with the SALSEA baseline allele size data set, distinguishing between group (A) which are the three 'problematic' loci from the first analysis and group (B), the remaining (working) loci. Evaluation of the loci genotypes shows the allele frequency distributions at all the loci in the scales and SALSEA baseline data were not significantly different (T-tests and Chi-sq test $p > 0.05$), confirming that the 'problematic' loci do not show any greater deviation from the size distributions in the SALSEA dataset than the better performing loci.

The application of the modified PCR protocol to the Nov. 1993 sample increased average scoring of microsatellites from 61% to 88% (Table 5) but did not significantly improve the scoring for the 1983/84 samples. Considering the above analysis, the decision was made to concentrate the DNA extraction and sequencing on the later period (1993/94 and 1994/95) and to use the modified PCR protocol for all samples included in the analysis. The full set of samples used in the assignment analyses is detailed in Table 7, and the proportion of scale samples that provided useable DNA for 18 microsatellites in the SALSEA and Norwegian marker panels is shown in Table 5. The average scoring for microsatellites for the sample months between Feb 1994 and Mar 12995 varied between 72% and 99%.

4.2 Identification of North American fish

Initial identification of probable NA origin fish based on the *SsaD486* microsatellite locus, revealed 61 fish with alleles with at least 176 base pairs, which were therefore initially identified as being of probable North American origin. Examination of the assignment probabilities (Figure 6) reveals that all but one of these fish had assignment probabilities of 0 or 0.01. There were also a number of other fish, not previously identified as NA which also had this very low probability of belonging to any of the baseline populations used. As such a

probability cut-off of 0.01 was identified and any fish with a maximum assignment probability less than this was classed as NA. The proportion of NA fish identified in the monthly samples varied between 7% and 13% in the 1993/94 season (Table 8) and between 16% and 29% in the 1994/95 season, with overall proportions of 11% and 22% in the two seasons respectively and 16% overall. Of the total of 105 fish identified as North American, 61 were identified by *SsaD486* (and confirmed by exclusion analysis) and 44 were identified only by the exclusion analysis.

None of the 500 European fish used in the conformation analysis had an assignment score below 0.02 (Figure 7), and so none of these fish would have been classified as North American using the above exclusion analysis; this includes the Baltic fish. The conformation analysis therefore suggests that the original exclusion and identification of the North American fish is likely to be robust.

In all cases, the original identification of the North American fish as classified by the exclusion analysis was also confirmed by both the STRUCTURE and *adegenet* cluster analysis, and in all three cases the techniques classified the same fish into the same North American and European groups.

In the final conformation analysis, the results show that tests based on the *ND-1* and *SS1* markers are not 100% diagnostic for separating European and North American salmon. While all the samples previously identified as North American fish were classified as North American, some fish previously identified as European and some juveniles from the Klimkovka river were also classified as North American based on these two markers. In addition, the *SS1* marker did not work well for the European Faroes samples, possibly because it requires good DNA quality. Nevertheless, these test do not indicate that any of the samples previously classified as North Americans had been incorrectly assigned.

4.3 Individual Assignments

The North American fish were removed from the analysis, and the European assignments continued using just the 551 European fish. Individual assignments for all fish with assignment scores at all assignment levels are presented in Appendix 3. It should be noted that simply summing individual assignments at different cut-off levels to try to estimate fishery stock proportions should not be undertaken due to the differential exclusion of more difficult to assign regions giving rise to bias if this is attempted.

4.4 Mixed Stock Analysis

Proportions of fish in the different reporting units are detailed for Level 1 to Level 4 assignments in in Tables 9 to 12 respectively and in Figure 7. The Level 1 and Level 3 assignments were also conducted by month across both fishing seasons (Tables 9 and 11). The results are also summarised across all months in Table 13. It should be noted that in Tables 8 – 11 some reporting unit estimates have confidence intervals which cross the zero value and as such it cannot be said with statistical confidence that the proportions of these stocks are significantly different from zero. In the summaries presented in Figure 8 and Table 13 these reporting units have therefore been omitted.

4.5 Catch composition

The scales samples analysed in this study were collected in November, December, February and March. This did not reflect the normal pattern of the fishery, which generally extended from November until April or May, and followed a similar pattern each year with catches increasing from November to December, and then again from January to February before declining at the end of the season (Table14). The possible composition of the catch at Faroes can be estimated by scaling the genetic assignments to the mean catch in each month for the 1983/84 to 1990/91fishing seasons taking account of the uncertainties in both the assignments and the catch distribution. At this stage only a preliminary analysis has been completed which does not include the uncertainty in these estimates. The genetic assignments have been scaled to the catch by applying the November and December samples to the same months in the commercial catch, the February

samples to the catches in January and February and the March samples to the catches between March and the end of the fishing season.

Applying this approach gave the same estimate of the proportion on North American fish in the catches as in the samples, 16.2%, varying between 12% in December and 19% in March to June (Table 15). The Level 1 and Level 3 assignments were therefore applied to the European portion of the catch in each month (Tables 16 and 17). The Level 1 assignments suggest that about 56% of an average commercial catch would have originated from rivers in northern NEAC, 27% in southern NEAC and 0.5% in Iceland. The Level 3 assignments provide a further breakdown of these proportions.

5. Discussion

The aim of this study was to conduct genetic stock identification analysis on scale samples collected from salmon caught in the commercial and research fisheries at Faroes to provide estimates of the likely stock composition of the catch during any future fishery in the area. Samples were chosen from two baseline periods and included samples that covered the full commercial fishing season (1983/84 and 1984/95) and samples collected during the period when tagging studies were undertaken (1993/94 and 1994/95). It was hoped that this would provide information on the temporal stability of the catch composition and a means to validate some of the results from tag recoveries. However, the scale sampling programmes were not conducted on a systematic basis, and so the samples are not fully representative of the catches in the commercial fisheries for the same periods (Tables 1 and 2). Furthermore, it was not possible to take account of the spatial distribution of the fishery or the sampling because no data were available on where vessels were operating or the location of capture of the sampled fish. There were also no years in which samples were collected every month that commercial fishing took place and in many years few samples were collected in the autumn months (Nov-Dec). Jacobsen *et al.* (2012) reported differences in the origin of stocks caught in the autumn and winter (Jan onwards) months and so efforts were made to ensure adequate samples were analysed from these two periods.

It is known from tagging returns that a proportion of the salmon caught in the Faroes fishery originate from North American rivers (Jacobsen *et al.,* 2012). The analysis identified 16% of the samples as being of North American origin, with the proportions varying between 7% in December 1993 and 29% in February 1995. This partly reflected a large difference in the proportions between the two seasons, with 10.7% of the samples being North American in the 1993/94 season compared to 22.0% in the 1994/95 season. In comparison, 7% of the recaptures of salmon tagged in the Faroes fishery in the 1993/94 season were recaptured in Canada (Hansen and Jacobsen (2003)). However the tagging results do not necessarily reflect the stock composition of all the tagged fish because the survival rate for return to homewaters and the probability of recapture is likely to vary among areas. ICES (2007) has also reported the recapture in the Faroes fishery of about six salmon tagged as smolts in Canada in the 1970s and 1980s, however it is not possible to use these results to estimate the proportion of North American fish in the total catch because of differences in tagging programmes in different countries. This study therefore provides the first direct measure of the proportion of North American salmon in catches within the Faroes EEZ.

At level 1, the genetic assignment discriminated between salmon stocks from Iceland and northern and southern Europe. The latter groups are essentially the same as the Northern and Southern stock complexes defined by ICES (2013), with the exclusion of Icelandic stocks. Overall, 62% of the European fish were assigned to the northern region and 37% to the southern region. Proportions of northern and southern fish are seen to vary both within and, to an extent, between fishing seasons, but there is a tendency for the proportion of northern fish present in the fishery to increase in March compared to the other months. The higher incidence of northern fish in the fishery is in broad agreement with the recapture of tagged smolts in the Faroese fishery reported by Jacobsen *et al*. (2001), with 68% originating from the northern region and 32% from the southern region, and by adult tagging studies conducted by Hansen & Jacobsen (2003) who reported

that northern countries (Norway, Russia and Sweden) accounted for 65% of the fish caught in the fishery while southern countries (UK, Ireland, Denmark and Spain) accounted for 35%.

Previous studies based on tag returns have reported a small component of Icelandic fish being present in the fishery (e.g. 27 of a total of 2651 tags reported in Jacobsen *et al.,* 2012 and 1.2% recaptured from Iceland in Jacobsen *et al.* 2001). The present analysis confirms that the proportion of Icelandic fish in the catch was very small (<1%), with all the Icelandic fish being caught in the autumn months, as was the case with the Icelandic recaptures reported by Jacobsen et al. (2001).

Turning to the Level 4 assignment units, around 5% of the total fish stocks are assigned each to the White Sea and N Kola in Russia and to Finnmark. The 10% of Russian fish is a smaller proportion than the 20% reported by Hansen & Jacobsen (2003). It should also be noted that during the analysis of marine samples carried out under the SALSEA project a number of fish were assigned as being from these northern regions but these were later identified (from scale analysis) as being probably of farmed origin (Anon, 2011). However, fish identified as being farm escapees were excluded from this study based on scale reading and so there should be few if any, such fish in the samples.

There is considerable variation in the proportions of fish originating from different regions within and between each of the fishing seasons. However, it is not possible to say whether this is due to real differences in stock composition between the two seasons or is simply a reflection of different spatial fishing effort between the two years. Jacobsen *et al*. (2001) also reported such variation, observing that during the years 1991-1995 the proportion of fish from the northern region was on average 34% in Nov-Dec compared to 66% in Jan-Mar based on the recapture of salmon tagged as smolts. Jacobsen *et al.* (2012) reported both spatial and temporal segregation of stocks of different origin based on tag returns, and unless effort was matched temporally and spatially for both the seasons over which the current data extends, which is unlikely, it is difficult to make definitive statements on changes within or between years.

Nevertheless, ICES requires an estimate of the likely composition of any catch in the Faroes area in order to develop catch advice for NASCO. The assignments from this study provide the most detailed estimates of the likely stock composition currently available, but they need to be scaled to the likely distribution of the catch between months of the fishing season, taking account of uncertainty in both the assignments and the expected catches (Tables 14, 15 and 16). The catch composition estimated in this way has been compared with the estimates currently used by ICES, and the relative production (the maturing and non-maturing 1SW pre-fishery abundance) from each country (Table 17). ICES currently assumes a roughly 50:50 split of the catch between northern and southern NEAC and only a very small contribution from North America. This study suggests that the northern NEAC proportion should be slightly higher (~56%) and the southern NEAC proportion is substantially lower (27%), with the majority of the balance being made up by North American fish (16%) which, up until now, have been largely ignored in the assessments. The results also show that the composition of the catch is likely to differ significantly from the relative productivity (pre-fishery abundance) of contributing stocks. The significant numbers of North American fish in the samples suggests that there may be a need to reconsider the basis for providing management advice for this fishery. Further analysis of these results will be considered by the ICES Working Group on North Atlantic salmon in 2015 and will be taken into account in the provision of catch advice for the Faroes fishery.

Taking into consideration the above caveats the usefulness of the present analytical techniques should not be underestimated. Techniques such as those reported allow all fish sampled in the fishery (where samples are of sufficient quality) to be assigned to their regions of origin with good confidence. This compares with the relatively small numbers of the tags recovered in tagging experiments and the difficulty in comparing recapture rates from different tagging programmes. Further, if factors such as temporal and spatial locations can be factored into future analysis, these will allow the patterns of stock composition within and between years to be examined in greater detail. Together with incorporation of information such as scale ages and

tagging data the techniques would seem to show great promise for the examination of both historical data, and perhaps or even greater usefulness, contemporary samples if/when the fishery is again opened. Indeed, using baselines such as that presented here, together with finer-scale regional baselines and new baselines using markers such as Single Nucleotide Polymorphisms (SNPs) may allow river level assignments and management on a finer scale as happens at present with species of salmonid in the Pacific (Beacham et al., 2004; Beacham et al., 2008; Dann et al., 2013). SNP analysis may also provide better results from degraded and fragmented DNA, as the intact fragment lengths required for SNP analysis are shorter than those required for analysis of microsatellite loci.

6. Acknowledgements

The authors would like to thank the International Atlantic salmon Research Board, the Department of the Environment (Norway), the Department for Environment, Food and Rural Affairs (UK), the Inland Fisheries Institute (Ireland) and Marine Scotland for funding this study.

7. References

Anon. 2011. Advancing understanding of Atlantic salmon at sea: merging genetics and ecology to resolve stock-specific migration and distribution patterns. 79 pp.

Beacham, T., Lapointe, M., Candy, J., Miller, K., and Withler, R. 2004. DNA in Action: Rapid Application of DNA Variation to Sockeye Salmon Fisheries Management. Conservation Genetics, 5: 411-416.

Beacham, T. D., Winther, I., Jonsen, K. L., Wetklo, M., Deng, L., and Candy, J. R. 2008. The Application of Rapid Microsatellite-Based Stock Identification to Management of a Chinook Salmon Troll Fishery off the Queen Charlotte Islands, British Columbia. North American Journal of Fisheries Management, 28: 849-855.

Dann, T. H., Habicht, C., Baker, T. T., and Seeb, J. E. 2013. Exploiting genetic diversity to balance conservation and harvest of migratory salmon. Canadian Journal of Fisheries and Aquatic Sciences, 70: 785-793.

Gilbey, J., Coughlan, J., Wennevik, V., Prodohl, P., McGinnity, P., Cauwelier, E., Cherbonnel, C., et al. In Prep. A microsatellite baseline for genetic stock identification of European Atlantic salmon (Salmo salar L.).

Gilbey, J., Knox, D., O'Sullivan, M., and Verspoor, E. 2005. Novel DNA markers for rapid, accurate, and cost-effective discrimination of the continental origin of Atlantic salmon (Salmo salar L.). ICES Journal of Marine Science: Journal du Conseil, 62: 1606-1616.

Grimholt U., Drablos F., Jorgensen S.M., Hoyheim B. & Stet R. J.M. (2002) The major histocompatibility class I locus in Atlantic salmon (Salmo salar L.): polymorphism, linkage analysis and protein modelling. Immunogenetics 54, 570–581.

Hansen, L. P., Jacobsen, J. A., and Lund, R. A. 1999. The incidence of escaped farmed Atlantic salmon, Salmo salar L., in the Faroese fishery and estimates of catches of wild salmon. – ICES Journal of Marine Science, 56: 200–206.

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

ICES. 2007. Report of the Workshop on the Development and Use of Historical Salmon Tagging Information from oceanic areas (WKDUHSTI), 19–22 February 2007, St. John's, Canada. ICES CM 2007/DFC:02. 64 pp. ICES. 2012. Report of the Working Group on North Atlantic Salmon (WGNAS). ICES CM 2012/ACOM:09. 321 pp.

ICES. 2013. Report of the Working Group on North Atlantic Salmon (WGNAS). ICES CM 2013/ACOM:09. 380 pp.

Ikediashi, C., Billington, S., and Stevens, J. R. 2012. The origins of Atlantic salmon (Salmo salar L.) recolonizing the River Mersey in northwest England. Ecology and Evolution: 11.

Jacobsen, J. A., Lund, R. A., Hansen, L. P., O'Maoileidigh, N. 2001. Seasonal differences in the origin of Atlantic salmon (*Salmo salar* L.) in the Norwegian Sea based on estimates from age structures and tag recaptures. Fisheries Research, 52: 169-177.

Jacobsen, J. A., Hansen, L. P., Bakkestuen, V., Halvorsen, R., Reddin, D. G., White, J., Ó Maoiléidigh, N., et al. 2012. Distribution by origin and sea age of Atlantic salmon (Salmo salar) in the sea around the Faroe Islands based on analysis of historical tag recoveries. ICES Journal of Marine Science: Journal du Conseil, 69: 1598-1608.

Jombart, T., and Ahmed, I. 2011. adegenet 1.3-1: new tools for the analysis of genome-wide SNP data. Bioinformatics.

King T.L., Eackles M.S. & Letcher B.H. (2005) Microsatellite DNA markers for the study of Atlantic salmon (Salmo salar) kinship, population structure, and mixed-fishery analyses. Molecular Ecology Notes 5, 130–132.

Kalinowski S.T, Manlove K.R., Taper M.L. (2007) ONCOR: a computer program for genetic stock identification. Department of Ecology, 310 Lewis Hall, Montana State University. Available from http://www.montana.edu/kalinowski/Software/ONCOR.htm,

McConnell S.K., Oreilly P., Hamilton L., Wright J.N. & Bentzen P. (1995) Polymorphic microsatellite loci from Atlantic salmon (Salmo salar) - genetic differentiation of North-American and European populations. Canadian Journal of Fisheries and Aquatic Sciences 52, 1863–1872.

Millar, R. B. 1987. Maximum Likelihood Estimation of Mixed Stock Fishery Composition. Canadian Journal of Fisheries and Aquatic Sciences, 44: 583-590.

NASCO. 1998. North Atlantic Salmon Conservation Organisation. Agreement on the adoption of a precautionary approach. Report of the 15th annual meeting of the Council. . CNL(98)46. 4 pp.

Nilsson, J., Gross, R., Asplund, T., Dove, O., Jansson, H., Kelloniemi, J., Kohlmann, K., et al. 2001. Matrilinear phylogeography of Atlantic salmon (Salmo salar L.) in Europe and postglacial colonization of the Baltic Sea area. Molecular Ecology, 10: 89-102.

Olafsson, K., Hjorleifsdottir, S., Pampoulie, C., Hreggvidsson, G. O., and Gudjonsson, S. 2010. Novel set of multiplex assay (SalPrint15) for efficient abalysis of 15 microsatellite loci of comtemporary samples of the Atlantic salmon (Salmo salar). Molecular Ecology Resources., 10: 533-537.

O′Reilly P.T., Hamilton L.C., McConnell S.K. & Wright J.M. (1996) Rapid analysis of genetic variation in Atlantic salmon (Salmo salar) by PCR multiplexing of dinucleotide and tetranucleotide microsatellites. Canadian Journal of Fisheries and Aquatic Sciences 53, 2292–2298.

Paetkau, D., Slade, R., Burden, M., and Estoup, A. 2004. Genetic assignment methods for the direct, real-time estimation of migration rate: a simulation-based exploration of accuracy and power. Molecular Ecology, 13: 55-65.

Paterson S., Piertney S.B., Knox D., Gilbey J. & Verspoor E. (2004) Characterization and PCR multiplexing of novel highly variable tetranucleotide Atlantic salmon (Salmo salar L.) microsatellites. Molecular Ecology Notes 4, 160–162.

Piry, S., Alapetite, A., Cornuet, J. M., Paetkau, D., Baudouin, L., and Estoup, A. 2004. GENECLASS2: A software for genetic assignment and first-generation migrant detection. Journal of Heredity, 95: 536-539.

Pritchard, J. K., Stephens, M., and Donnelly, P. 2000. Inference of Population Structure Using Multilocus Genotype Data. Genetics, 155: 945-959.

Pritchard, J. K., and Wen, W. 2004. Documentation for STRUCTURE software, version 2. Available from: http://pritch.bsd.uchicago.edu.

Rannala, B., and Mountain, J. L. 1997. Detecting immigration by using multilocus genotypes. Proceedings of the National Academy of Science, USA., 94: 9197-9201.

R Core Team, 2013. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. http://www.R-project.org

Sanchez J.A., Clabby C., Ramos D., Blanco G., Flavin F., Vazquez E. et al. (1996) Protein and microsatellite single locus variability in Salmo salar L (Atlantic salmon). Heredity 77, 423–432.

Slettan A., Olsaker I. & Lie O. (1995) Atlantic salmon, Salmo salar, microsatellites at the SsOSL25, SsOSL85, SsOSL311, SsOSL417 loci. Animal Genetics 26, 281–282.

Stet R.J.M., de Vries B., Mudde K., Hermsen T., van Heerwaarden J., Shum B.P. et al. (2002) Unique haplotypes of co-segregating major histocompatibility class II A and class II B alleles in Atlantic salmon (Salmo salar) give rise to diverse class II genotypes. Immunogenetics 54, 320–331.

Vasemägi, A., Gross, R., Paaver, T., Kangur, M., Nilsson, J., and Eriksson, L. O. 2001. Identification of the origin of an Atlantic salmon (Salmo salar L.) population in a recently recolonized river in the Baltic Sea. Molecular Ecology, 10: 2877-2882.

Verspoor, E., McCarthy, E. M., Knox, D., Bourke, E. A., and Cross, T. F. 1999. The phylogeography of European Atlantic salmon (Salmo salar L.) based on RFLP analysis of the ND1/16sRNA region of the mtDNA. Biological Journal of the Linnean Society, 68: 129-146.

Table 1 Catch of salmon by number by month in the Faroes fishery between 1983/84 to 1996/97

Season	Fishery	Month								Grand Total
		11	12	1	2	3	4	5	7	
83/84	Com.	8,680	24,882	12,504	26,396	32,712	12,486	6,849		124,509
84/85	Com.	5,884	20,419	14,493	24,380	26,035	25,471	19,095		135,777
85/86	Com.	1,571	27,611	13,992	50,146	25,968	21,209	14,057		154,554
86/87	Com.	1,881	19,693	5,905	15,113	32,241	21,053	39,153	1,365	136,404
87/88	Com.	4,259	27,125	5,803	9,387	9,592	4,203	4,642		65,011
88/89	Com.	17,019	24,743	2,916	4,663	12,457	31,698			93,496
89/90	Com.	13,079	40,168	5,533	11,282	11,379	29,504	570		111,515
90/91	Com.	6,921	28,972	3,720	7,996	6,275	3,557			57,441
Mean	Com.	7,412	26,702	8,108	18,670	19,582	18,648	10,546	171	109,838
		7%	24%	7%	17%	18%	17%	10%	0%	
91/92	Res.		3,842		931	3,039	652			8,464
92/93	Res.	1,282	334			3,799				5,415
93/94	Res.	*876*	*560*		*178*	*458*				*2,072*
94/95	Res.	*437*	*382*		*456*	*688*				*1,963*
95/96	Res.		282							282
Mean	Res.	519	1,080	-	313	1,597	130	-	-	3,639
		14%	30%	0%	9%	44%	4%	0%	0%	
Grand Total		69,301	245,715	72,974	169,599	184,226	168,481	94,912	1,536	1,006,741

Table 2 Summary of scale samples collected in the Faroes commercial and research salmon fisheries between 1980 and 1997 (samples without month have been omitted)

Season	Fishery	Month								Total autumn	Total winter	Grand Total
		11	12	1	2	3	4	5	7	Nov-Dec	Jan-Jul	
80/81	Com.					187				0	187	187
81/82	Com.		85		391	532	244			85	1167	1252
82/83	Com.			97	469	387	542			0	1495	1495
83/84	Com.		286	416	355	35	80		28	286	914	1200
84/85	Com.	60		80	209	217	39	193		60	738	798
85/86	Com.		38	283	162		86	255		38	786	824
86/87	Com.					370	252			0	622	622
87/88	Com.	87		204	187	183	133			87	707	794
89/90	Com.	175		207						175	207	382
90/91	Com.		99							99	0	99
91/92	Res.		700			223	200			700	423	1123
92/93	Res.	216	375			3436				591	3436	4027
93/94	Res.	464	841		295	330				1305	625	1930
94/95	Res.	450	235		171	958				685	1129	1814
95/96	Res.		271							271	0	271
96/97	Res.					33				0	33	33
Grand Total		1452	2930	1287	2239	6891	1576	448	28	4382	12469	16851

Table 3 Numbers of scale samples selected for initial genetic analysis by fishing season and month.

		Month						
Period	Year	11	12	1	2	3	4	Total
1	83/4		90	90	90	35	80	385
	84/5	60		80	90	90	39	359
2	93/4	90	110		90	90		380
	94/5	90	90		90	110		380

Table 4 Hierarchical split of assignment reporting regions as defined using the SALSEA baseline.

Level 1	**Number of rivers**	**Level 2**	**Number of rivers**	**Level 3**	**Number of rivers**	**Level 4**	**Number of rivers**
Iceland	17	Iceland NW	8	Iceland NW	8	Iceland NW	8
		Iceland S	4	Iceland S	4	Iceland S	4
		Iceland SE	5	Iceland SE	5	Iceland SE	5
North	117	Mid & South Norway & Sweden	66	E Norway & Sweden	14	E Norway & Sweden	14
				Mid Norway	27	Mid Norway	27
				S Norway	25	S Norway	25
		Russia & North Norway	50	Finmark	13	Finmark	13
				N Kola	26	N Kola	26
				Tana	1	Tana	1
				White Sea	10	White Sea	10
		Sweden Baltic	1	Sweden Baltic	1	Sweden Baltic	1
South	163	Denmark	2	Denmark	2	Denmark	2
		UK Ireland France & Spain	161	N & W France	8	N & W France	8
				S France & Spain	5	S France & Spain	5
				South England	3	South England	3
				UK Ireland	145	Bann/Levin	2
						Irish Sea	34
						N Scotland N&W Ireland	62
						S&E Scotland	47

Table 5 The proportion of scales samples collected in November and December 1993 that provided useable DNA for 18 microsatellites in the SALSEA and Norwegian marker panels.

Marker	Size range (bp)	*Nov 1993 Std. PCR*	Nov 1993 Mod. PCR	*Dec. 1993 Std. PCR*	Feb 1994 Mod. PCR	Mar 1994 Mod. PCR	Nov. 1994 Mod. PCR	Dec. 1994 Mod. PCR	Feb. 1995 Mod PCR	Mar 1995 Mod. PCR
SP2201	223-391	*8*	75	*97*	74	81	86	99	71	74
SP2210	96-176	*93*	100	*100*	99	100	98	100	89	91
SPG7	103-227	*92*	88	*100*	87	93	96	100	70	76
SsaD144	106-270	*73*	99	*99*	99	100	91	100	94	88
Ssa202	202-326	*66*	95	*99*	28	63	74	97	63	64
SsaD157	271-434	*0*	54	*29*	61	27	63	91	64	63
SP1605	216-268	*20*	37	*99*	95	94	88	100	67	72
SP2216	186-282	*18*	94	*22*	69	92	96	98	63	22
Ssa171	193-271	*0*	96	*98*	93	93	82	99	78	58
Ssa14	132-144	*49*	100	*99*	95	91	84	98	95	66
Ssa289	100-136	*100*	99	*99*	98	100	96	100	96	92
SP3016	66-154	*100*	98	*98*	100	100	100	100	95	95
Ssa197	152-276	*88*	100	*99*	99	100	99	100	61	54
SsaD486	160-192	*100*	98	*99*	100	100	98	100	93	90
SsaF43	99-131	*100*	100	*97*	100	100	100	100	79	72
SSOSL85	169-227	72	86	*99*	98	94	83	99	65	58
MHC1	118-170	99	98	*99*	86	98	100	100	26	52
MHC2	210-400	15	60	*98*	94	76	78	97	21	43
Mean		61	88	91	88	89	90	99	72	68

Table 6 Number and proportion of samples providing useable DNA for different numbers of loci from the SALSEA-Merge panel.

Number of scored loci	Number of samples	Proportion of all samples
6	89	94.7
7	79	84
8	64	68.1
9	42	44.7
10	26	27.7
11	9	9.6

Table 7 Numbers of scale samples selected for final genetic analysis and assignment by fishing season and month.

Season	Month						Total
	Nov	Dec	Jan	Feb	Mar	Apr	
1993/4	89	94	-	91	73	-	347
1994/5	84	94	-	70	61	-	309

Table 8 Classification of fish North America of Europe using all exclusion techniques.

Season	**Origin**	**Sampling month**				**Totals**
		Nov	**Dec**	**Feb**	**Mar**	
93/94	American	12	7	10	8	37
		13%	7%	11%	11%	11%
	European	77	87	81	65	310
		87%	93%	89%	89%	89%
94/95	American	18	15	20	15	68
		21%	16%	29%	25%	22%
	European	66	79	50	46	241
		79%	84%	71%	75%	78%
All seasons	American	30	22	30	23	105
		17%	12%	19%	17%	16%
	European	143	166	131	111	551
		83%	88%	81%	83%	84%
	Totals	173	188	161	134	656

Table 9 Proportions of fish in Level 1 assignments as estimated by maximum conditional likelihood (95% CI in brackets).

	Nov_93		Dec_93		Feb_94		Mar_94	
North	0.6591	(0.4696, 0.7102)	0.6425	(0.4258, 0.6932)	0.3974	(0.2745, 0.5004)	0.8105	(0.6435, 0.8652)
South	0.3280	(0.2768, 0.5000)	0.3234	(0.2661, 0.5366)	0.6026	(0.4971, 0.7166)	0.1895	(0.1280, 0.3492)
Iceland	0.0130	(0.0000, 0.0390)	0.0341	(0.0000, 0.0805)	0	(0.0000, 0.0000)	0	(0.0000, 0.0062)
	Nov_94		Dec_94		Feb_95		Mar_95	
North	0.3676	(0.2191, 0.4603)	0.4125	(0.2851, 0.5523)	0.8431	(0.5783, 0.8963)	0.8431	(0.6030, 0.8888)
South	0.6028	(0.4756, 0.7354)	0.5875	(0.4391, 0.7023)	0.1569	(0.0921, 0.3926)	0.1569	(0.1086, 0.3601)
Iceland	0.0296	(0.0000, 0.0758)	0	(0.0000, 0.0000)	0	(0.0000, 0.0307)	0	(0.0000, 0.0000)
	Nov all Years		Dec all years		Feb all years		Mar all years	
North	0.4915	(0.3973, 0.5594)	0.5408	(0.4252, 0.6068)	0.5564	(0.4114, 0.6369)	0.8369	(0.7050, 0.8712)
South	0.4877	(0.4132, 0.5824)	0.4421	(0.3807, 0.5645)	0.4436	(0.3611, 0.5699)	0.1631	(0.1283, 0.2894)
Iceland	0.0207	(0.0000, 0.0489)	0.0171	(0.0000, 0.0301)	0	(0.0000, 0.0038)	0	(0.0000, 0.0000)

Table 10 Proportions of fish in Level 2 assignments as estimated by maximum conditional likelihood (95% CI in brackets).

	Nov_93		Dec_93		Feb_94		Mar_94	
Denmark	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
UK Ireland France & Spain	0.328	(0.2571, 0.5072)	0.3234	(0.2817, 0.5081)	0.6026	(0.4981, 0.7343)	0.1895	(0.1181, 0.3269)
Iceland S	0	(0.0000, 0.0000)	0.0115	(0.0000, 0.0345)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
Iceland NW	0.013	(0.0000, 0.0519)	0.0226	(0.0000, 0.0574)	0	(0.0000, 0.0000)	0	(0.0000, 0.0214)
Mid & South Norway & Sweden	0.6144	(0.4421, 0.6777)	0.5606	(0.3585, 0.6032)	0.3107	(0.1911, 0.4184)	0.4503	(0.2606, 0.5508)
Russia & N Norway	0.0447	(0.0000, 0.1054)	0.0819	(0.0228, 0.1635)	0.0867	(0.0257, 0.1739)	0.3602	(0.2293, 0.4761)
Sweden Baltic	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
	Nov_94		Dec_94		Feb_95		Mar_95	
Denmark	0	(0.0000, 0.0000)	0.0133	(0.0000, 0.0253)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
UK Ireland France & Spain	0.6028	(0.5161, 0.7670)	0.5742	(0.4477, 0.6691)	0.1569	(0.0818, 0.3607)	0.1569	(0.0830, 0.3309)
Iceland S	0.0144	(0.0000, 0.0302)	0	(0.0000, 0.0000)	0	(0.0000, 0.0245)	0	(0.0000, 0.0000)
Iceland NW	0.0152	(0.0000, 0.0757)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
Mid & South Norway & Sweden	0.3329	(0.1580, 0.4375)	0.3535	(0.2409, 0.4765)	0.6786	(0.4239, 0.7689)	0.4168	(0.2852, 0.5387)
Russia & N Norway	0.0347	(0.0000, 0.0916)	0.059	(0.0204, 0.1287)	0.1644	(0.0415, 0.2614)	0.4263	(0.2349, 0.5249)
Sweden Baltic	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
	Nov all Years		Dec all years		Feb all years		Mar all years	
Denmark	0	(0.0000, 0.0000)	0.0046	(0.0000, 0.0178)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
UK Ireland France & Spain	0.4877	(0.3889, 0.5943)	0.4375	(0.3735, 0.5581)	0.4436	(0.3594, 0.5351)	0.1631	(0.1285, 0.3139)
Iceland S	0.0063	(0.0000, 0.0143)	0.006	(0.0000, 0.0181)	0	(0.0000, 0.0023)	0	(0.0000, 0.0000)
Iceland NW	0.0145	(0.0000, 0.0350)	0.0111	(0.0000, 0.0239)	0	(0.0000, 0.0058)	0	(0.0000, 0.0000)
Mid & South Norway & Sweden	0.4695	(0.3521, 0.5402)	0.4751	(0.3447, 0.5251)	0.4495	(0.3130, 0.5364)	0.4442	(0.2937, 0.5309)
Russia & N Norway	0.022	(0.0026, 0.0788)	0.0657	(0.0296, 0.1265)	0.1069	(0.0419, 0.1661)	0.3928	(0.2721, 0.4756)
Sweden Baltic	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
Denmark	0	(0.0000, 0.0000)	0.0046	(0.0000, 0.0178)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)

Table 11 Proportions of fish in Level 3 assignments as estimated by maximum conditional likelihood (95% CI in brackets).

	Nov_93		Dec_93		Feb_94		Mar_94	
Denmark	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
South England	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0.0123	(0.0000, 0.0370)	0	(0.0000, 0.0000)
Uk Ireland	0.3174	(0.2584, 0.4744)	0.2889	(0.2527, 0.4766)	0.561	(0.4225, 0.7137)	0.1895	(0.1045, 0.3266)
N & W France	0.0106	(0.0000, 0.0415)	0	(0.0000, 0.0000)	0.0292	(0.0000, 0.0560)	0	(0.0000, 0.0154)
S France & Spain	0	(0.0000, 0.0000)	0.0345	(0.0000, 0.0690)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
Iceland S	0	(0.0000, 0.0000)	0.0115	(0.0000, 0.0348)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
Iceland NW	0.013	(0.0000, 0.0390)	0.0226	(0.0000, 0.0460)	0	(0.0000, 0.0000)	0	(0.0000, 0.0121)
S Norway	0.1698	(0.0574, 0.3081)	0.1787	(0.0441, 0.2449)	0.1626	(0.0364, 0.2644)	0.1183	(0.0383, 0.2328)
Mid Norway	0.2829	(0.1393, 0.3991)	0.2361	(0.0987, 0.3379)	0.0876	(0.0231, 0.2203)	0.2635	(0.1010, 0.3981)
Finmark	0	(0.0000, 0.0431)	0.0364	(0.0000, 0.0871)	0.0387	(0.0000, 0.0805)	0.0807	(0.0172, 0.1869)
E Norway & Sweden	0.1618	(0.0142, 0.2120)	0.1458	(0.0225, 0.1978)	0.0605	(0.0000, 0.1551)	0.0685	(0.0000, 0.1267)
N Kola	0.0101	(0.0000, 0.0780)	0.034	(0.0061, 0.0960)	0.0129	(0.0000, 0.0756)	0.0638	(0.0291, 0.2238)
Tana	0.0346	(0.0000, 0.0566)	0	(0.0000, 0.0185)	0	(0.0000, 0.0275)	0.0118	(0.0000, 0.0839)
White Sea	0	(0.0000, 0.0263)	0.0115	(0.0000, 0.0460)	0.0351	(0.0000, 0.0740)	0.2038	(0.0484, 0.2371)
Sweden Baltic	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
	Nov_94		Dec_94		Feb_95		Mar_95	
Denmark	0	(0.0000, 0.0000)	0.0133	(0.0000, 0.0256)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
South England	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
Uk Ireland	0.6028	(0.5112, 0.7485)	0.5656	(0.4187, 0.6694)	0.1569	(0.1400, 0.3892)	0.1569	(0.0862, 0.3627)
N & W France	0	(0.0000, 0.0152)	0.0087	(0.0000, 0.0252)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
S France & Spain	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
Iceland S	0.0144	(0.0000, 0.0303)	0	(0.0000, 0.0000)	0	(0.0000, 0.0364)	0	(0.0000, 0.0000)
Iceland NW	0.0152	(0.0000, 0.0606)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
S Norway	0.0671	(0.0052, 0.2178)	0.1332	(0.0423, 0.2328)	0.2018	(0.0358, 0.3175)	0.0561	(0.0000, 0.1764)
Mid Norway	0.2556	(0.0890, 0.2984)	0.1372	(0.0511, 0.2394)	0.3638	(0.1565, 0.5763)	0.2396	(0.0471, 0.3397)
Finmark	0	(0.0000, 0.0578)	0.0135	(0.0000, 0.0587)	0.012	(0.0000, 0.0916)	0.1902	(0.0389, 0.2961)
E Norway & Sweden	0.0102	(0.0000, 0.0596)	0.0832	(0.0182, 0.1764)	0.1131	(0.0000, 0.1983)	0.1211	(0.0095, 0.2638)
N Kola	0.0286	(0.0000, 0.0592)	0.0201	(0.0000, 0.0514)	0.0738	(0.0000, 0.1222)	0.0629	(0.0000, 0.2227)
Tana	0.0061	(0.0000, 0.0301)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0.021	(0.0000, 0.0665)
White Sea	0	(0.0000, 0.0148)	0.0254	(0.0000, 0.0760)	0.0786	(0.0000, 0.1414)	0.1522	(0.0443, 0.2277)
Sweden Baltic	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)

Table 12 Proportions of fish in Level 4 assignments as estimated by maximum conditional likelihood (95% CI in brackets).

	Dec_93		Nov_93		Feb_94		Mar_94	
Denmark	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
South England	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0.0123	(0.0000, 0.0370)	0	(0.0000, 0.0000)
Irish Sea	0.0209	(0.0000, 0.0887)	0.0811	(0.0000, 0.1542)	0.0285	(0.0026, 0.1806)	0.0152	(0.0000, 0.1166)
S&E Scotland	0.165	(0.1000, 0.3065)	0.1963	(0.1339, 0.3734)	0.301	(0.2003, 0.4394)	0.1279	(0.0302, 0.2117)
N & W France	0	(0.0000, 0.0000)	0.0106	(0.0000, 0.0386)	0.0292	(0.0000, 0.0680)	0	(0.0000, 0.0156)
S France & Spain	0.0345	(0.0000, 0.0690)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
Iceland S	0.0115	(0.0000, 0.0345)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
Iceland NW	0.0226	(0.0000, 0.0460)	0.013	(0.0000, 0.0390)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
N Scotland N&W Ireland	0.084	(0.0144, 0.2021)	0.04	(0.0000, 0.1421)	0.2066	(0.0586, 0.2800)	0.0465	(0.0073, 0.1433)
L4 BannLev	0.019	(0.0000, 0.0458)	0	(0.0000, 0.0263)	0.0249	(0.0000, 0.0514)	0	(0.0000, 0.0311)
S Norway	0.1787	(0.0609, 0.2859)	0.1698	(0.0614, 0.2737)	0.1626	(0.0276, 0.2340)	0.1183	(0.0306, 0.2496)
Mid Norway	0.2361	(0.1220, 0.3351)	0.2829	(0.1531, 0.3902)	0.0876	(0.0238, 0.1663)	0.2635	(0.1231, 0.3782)
Finmark	0.0364	(0.0000, 0.0944)	0	(0.0000, 0.0647)	0.0387	(0.0000, 0.0747)	0.0807	(0.0000, 0.1552)
E Norway & Sweden	0.1458	(0.0259, 0.1961)	0.1618	(0.0131, 0.2496)	0.0605	(0.0000, 0.1234)	0.0685	(0.0000, 0.1085)
N Kola	0.034	(0.0000, 0.0955)	0.0101	(0.0000, 0.0821)	0.0129	(0.0000, 0.0569)	0.0638	(0.0341, 0.2205)
Tana	0	(0.0000, 0.0233)	0.0346	(0.0000, 0.0645)	0	(0.0000, 0.0247)	0.0118	(0.0000, 0.0824)
White Sea	0.0115	(0.0000, 0.0347)	0	(0.0000, 0.0259)	0.0351	(0.0000, 0.0771)	0.2038	(0.0577, 0.2592)
Sweden Baltic	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
	Dec_94		Nov_94		Feb_95		Mar_95	
Denmark	0.0133	(0.0000, 0.0371)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
South England	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
Irish Sea	0.097	(0.0125, 0.1751)	0.092	(0.0122, 0.1663)	0.0668	(0.0000, 0.1297)	0.0214	(0.0000, 0.1285)
S&E Scotland	0.2744	(0.1644, 0.3974)	0.4206	(0.2300, 0.5178)	0.0825	(0.0404, 0.2887)	0.0651	(0.0000, 0.2151)
N & W France	0.0087	(0.0000, 0.0258)	0	(0.0000, 0.0151)	0	(0.0000, 0.0000)	0	(0.0000, 0.0160)
S France & Spain	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0145)	0	(0.0000, 0.0000)
Iceland S	0	(0.0000, 0.0000)	0.0144	(0.0000, 0.0303)	0	(0.0000, 0.0293)	0	(0.0000, 0.0000)
Iceland NW	0	(0.0000, 0.0000)	0.0152	(0.0000, 0.0611)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
N Scotland N&W Ireland	0.1816	(0.0706, 0.2749)	0.0902	(0.0250, 0.2686)	0.0076	(0.0000, 0.1369)	0.0704	(0.0000, 0.2105)
L4 BannLev	0.0126	(0.0000, 0.0633)	0	(0.0000, 0.0184)	0	(0.0000, 0.0412)	0	(0.0000, 0.0137)
S Norway	0.1332	(0.0195, 0.2237)	0.0671	(0.0013, 0.2181)	0.2018	(0.0517, 0.3784)	0.0561	(0.0000, 0.1881)
Mid Norway	0.1372	(0.0569, 0.2378)	0.2556	(0.0794, 0.3255)	0.3638	(0.1741, 0.4858)	0.2396	(0.0655, 0.3810)
Finmark	0.0135	(0.0000, 0.0577)	0	(0.0000, 0.0457)	0.012	(0.0000, 0.1031)	0.1902	(0.0617, 0.3073)
E Norway & Sweden	0.0832	(0.0044, 0.1638)	0.0102	(0.0000, 0.0803)	0.1131	(0.0000, 0.1891)	0.1211	(0.0000, 0.2100)
N Kola	0.0201	(0.0000, 0.0621)	0.0286	(0.0000, 0.0612)	0.0738	(0.0000, 0.1182)	0.0629	(0.0000, 0.2228)
Tana	0	(0.0000, 0.0000)	0.0061	(0.0000, 0.0444)	0	(0.0000, 0.0000)	0.021	(0.0000, 0.0889)
White Sea	0.0254	(0.0000, 0.0862)	0	(0.0000, 0.0000)	0.0786	(0.0000, 0.1600)	0.1522	(0.0248, 0.2217)
Sweden Baltic	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)

Table 12 (cont'd) Proportions of fish in Level 4 assignments as estimated by maximum conditional likelihood (95% CI in brackets).

	Nov all Years		Dec all years		Feb all years		Mar all years	
Denmark	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
South England	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0.0076	(0.0000, 0.0229)	0	(0.0000, 0.0000)
Irish Sea	0.0679	(0.0140, 0.1280)	0.0209	(0.0000, 0.0887)	0.0329	(0.0148, 0.1322)	0.0203	(0.0000, 0.0833)
S&E Scotland	0.3497	(0.2368, 0.4328)	0.165	(0.1000, 0.3065)	0.2358	(0.1606, 0.3603)	0.0831	(0.0425, 0.1733)
N & W France	0.0024	(0.0000, 0.0305)	0	(0.0000, 0.0000)	0.0157	(0.0000, 0.0365)	0	(0.0000, 0.0158)
S France & Spain	0	(0.0000, 0.0000)	0.0345	(0.0000, 0.0690)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)
Iceland S	0.0063	(0.0000, 0.0140)	0.0115	(0.0000, 0.0345)	0	(0.0000, 0.0018)	0	(0.0000, 0.0000)
Iceland NW	0.0145	(0.0000, 0.0419)	0.0226	(0.0000, 0.0460)	0	(0.0000, 0.0017)	0	(0.0000, 0.0000)
N Scotland N&W Ireland	0.0678	(0.0284, 0.1591)	0.084	(0.0144, 0.2021)	0.141	(0.0430, 0.1963)	0.0597	(0.0167, 0.1407)
L4 BannLev	0	(0.0000, 0.0139)	0.019	(0.0000, 0.0458)	0.0106	(0.0000, 0.0455)	0	(0.0000, 0.0250)
S Norway	0.1198	(0.0389, 0.2400)	0.1787	(0.0609, 0.2859)	0.181	(0.0839, 0.2544)	0.0876	(0.0405, 0.1770)
Mid Norway	0.3074	(0.1628, 0.3580)	0.2361	(0.1220, 0.3351)	0.1937	(0.1222, 0.3143)	0.273	(0.1431, 0.3134)
Finmark	0	(0.0000, 0.0315)	0.0364	(0.0000, 0.0944)	0.037	(0.0000, 0.0644)	0.1299	(0.0471, 0.2045)
E Norway & Sweden	0.0423	(0.0070, 0.1337)	0.1458	(0.0259, 0.1961)	0.0748	(0.0128, 0.1218)	0.0836	(0.0105, 0.1549)
N Kola	0.0063	(0.0000, 0.0542)	0.034	(0.0000, 0.0955)	0.0151	(0.0000, 0.0621)	0.0689	(0.0225, 0.1653)
Tana	0.0157	(0.0000, 0.0339)	0	(0.0000, 0.0233)	0	(0.0000, 0.0137)	0.0155	(0.0000, 0.0514)
White Sea	0	(0.0000, 0.0221)	0.0115	(0.0000, 0.0347)	0.0548	(0.0225, 0.0846)	0.1785	(0.0771, 0.2086)
Sweden Baltic	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)	0	(0.0000, 0.0000)

Table 13 Proportions of fish in the four assignment hierarchical levels as estimated by conditional maximum likelihood across all months. Note only stocks where CI estimates are not across zero for all months are shown.

Level 1		
	North	**South**
Mean	0.62	0.37
St Dev	0.2	0.2

Level 2			
	UK Ireland France & Spain	**Mid & South Norway & Sweden**	**Russia & N Norway**
Mean	0.37	0.46	0.16
St Dev	0.2	0.14	0.15

Level 3							
	Uk Ireland	**S Norway**	**Mid Norway**	**Finmark**	**E Norway & Sweden**	**N Kola**	**White Sea**
Mean	0.35	0.14	0.23	0.05	0.1	0.04	0.06
St Dev	0.19	0.05	0.09	0.06	0.05	0.03	0.08

Level 4									
	Irish Sea	**S&E Scotland**	**N Scotland N&W Ireland**	**S Norway**	**Mid Norway**	**Finmark**	**E Norway & Sweden**	**N Kola**	**White Sea**
Mean	0.05	0.2	0.09	0.14	0.23	0.05	0.1	0.04	0.06
St Dev	0.03	0.12	0.07	0.05	0.09	0.06	0.05	0.03	0.08

Table 14 Classification of fish North America of Europe using all exclusion techniques scaled to the mean annual catch composition in the Faroes commerical fishery between 1983/84 and 1990/91.

		Sampling month									
	Origin	**Nov**	**Dec**		**Feb**	**Mar**				**Totals**	**%**
All scales	American	30	22		30	23				105	16%
		17%	12%		19%	17%					
	European	143	166		131	111				551	84%
		83%	88%		81%	83%					
	Origin	**Nov**	**Dec**	**Jan**	**Feb**	**Mar**	**Apr**	**May**	**Jun**	**Totals**	**%**
Mean annual commercial catch		7,412	26,702	8,108	18,670	19,582	18,648	10,546	171	109,838	
		8%	27%	8%	19%	20%	19%	11%	0.2%		
		Nov	**Dec**		**Jan-Feb**	**Mar-Jun**					
Estimated catch comp.	American	1,285	3,125		4,990	8,401				17,801	16%
	European	6,126	23,577		21,789	40,545				92,037	84%
	Prop. NA	17%	12%		19%	17%					

Table 15 Proportions of fish in Level 1 assignment units scaled to the mean annual catch composition in the Faroes commerical fishery between 1983/84 and 1990/91.

Assignment of scales	**Nov**	**Dec**	**Jan-Feb**	**Mar-Jun**	**Total**
North	49%	54%	56%	84%	
South	49%	44%	44%	16%	
Iceland	2.1%	1.7%	0.0%	0.0%	
Av. Com. Catch European	**6,126**	**23,577**	**21,789**	**40,545**	**109,838**
North	3,011	12,750	12,123	33,932	61,817
South	2,988	10,423	9,666	6,613	29,690
Iceland	127	403	-	-	530
America	1,285	3,125	4,990	8,401	17,801
Composition of av. Catch	**Nov**	**Dec**	**Jan-Feb**	**Mar-Jun**	**Total**
North	41%	48%	45%	69%	56%
South	40%	39%	36%	14%	27%
Iceland	1.7%	1.5%	0.0%	0.0%	0.5%
America	17%	12%	19%	17%	16%

Table 16 Proportions of fish in Level 3 assignment units scaled to the mean annual catch composition in the Faroes commerical fishery between 1983/84 and 1990/91.

Composition of av. Catch	Nov	Dec	Jan-Feb	Mar-Jun	Total	%	Approx groups	%
N Kola	39	497	329	2,794	3,659	3.3%	Russia	11.4%
White Sea	-	429	1,194	7,237	8,860	8.1%		
Tana	96	-	-	628	725	0.7%	Finland	0.7%
Finmark	-	622	806	5,267	6,695	6.1%	Norway	44.2%
Mid Norway	1,883	5,095	4,220	11,069	22,268	20.3%		
S Norway	734	3,275	3,944	3,552	11,504	10.5%		
E Norway & Sweden	259	2,834	1,630	3,390	8,112	7.4%		
Sweden Baltic	-	-	-	-	-	0.0%		
Denmark	-	108	-	-	108	0.1%		
Uk Ireland	2,973	9,799	9,158	6,613	28,543	26.0%	UK &	26.1%
South England	-	-	166	-	166	0.2%	Ireland	
N & W France	15	90	342	-	446	0.4%	Frand	0.8%
S France & Spain	-	427	-	-	427	0.4%		
Iceland S	39	141	-	-	180	0.2%	Iceland	0.5%
Iceland NW	89	262	-	-	351	0.3%		
America	1,285	3,125	4,990	8,401	17,801	16.2%	N America	16.2%

Table 17 Comparison of the genetic assignments of the scale samples, the assignments weighted to commercial catches in the Faroes fishery, the stock composition figures for maturing and non-maturing salmon in the Faroes fishery currently used by ICES in the NEAC catch options model, and the estimates of pre-fishery abundance of maturing and non-matruring 1SW salmon derived from the ICES run-reconstruction model. The results are also grouped to approximate the assignment groups (As.Grps.) by combining Norway and Sweden in northern NEAC and all of UK and Ireland in southern NEAC.

	Scale samples			NEAC PFA model (from tags & PFA)					PFA			
Region	Assignment groups	% of samples	% weighted to catch	Country	1SW mat		1SW non-mat		1SW mat		1SW non-mat	
						As.Grps		As.Grps		As.Grps		As.Grps
Northern NEAC	Kola + White Sea	8.1%	11.4%	Russia	11.6%	11.6%	16.3%	16.3%	7.2%	7.2%	10.3%	10.3%
	Tana	0.7%	0.7%	Finland	5.9%	5.9%	5.0%	5.0%	1.9%	1.9%	2.9%	2.9%
	Finmark, Norway & Sweden	50.4%	44.2%	Norway	29.0%	30.9%	29.5%	31.1%	25.2%	26.3%	27.7%	28.2%
				Sweden	1.9%		1.6%		1.1%		0.5%	
Southern NEAC	UK & Ireland	38.5%	26.1%	Scotland	19.5%	45.8%	33.7%	42.8%	19.9%	59.3%	40.6%	55.6%
				Eng&Wls	4.4%		3.4%		5.0%		6.9%	
				N.Ireland	4.6%		1.4%		3.7%		0.9%	
				Ireland	17.3%		4.3%		30.7%		7.2%	
	France & Spain	1.1%	0.8%	France	1.8%	1.8%	0.5%	0.5%	1.9%	1.9%	0.8%	0.8%
	Iceland	1.0%	0.5%	Iceland	4.1%	4.1%	1.8%	1.8%	2.6%	2.6%	1.9%	1.9%
North America			16.2%		0.0%	0.0%	2.5%	2.5%	na	na	na	na

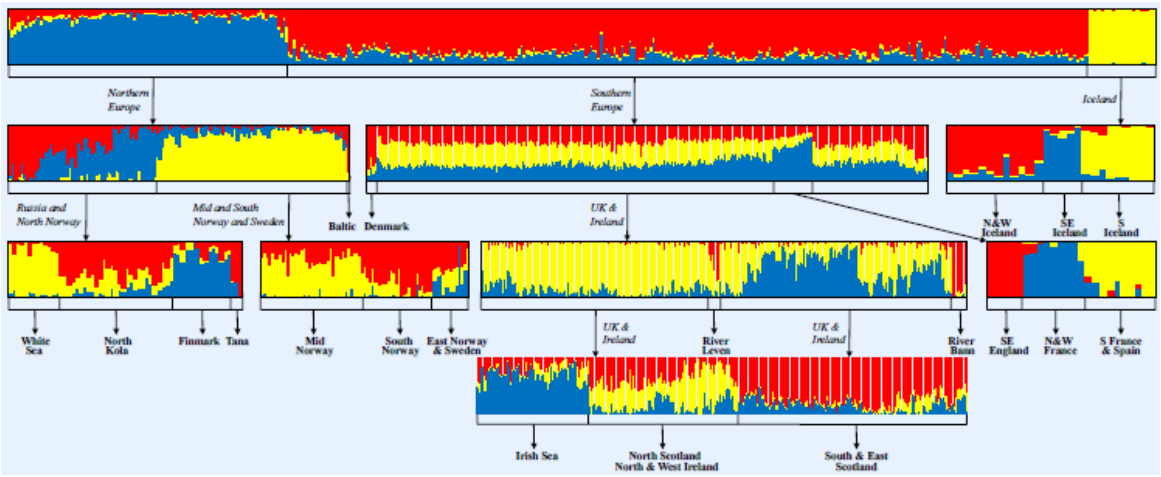


Figure 1. Hierarchical organisation of 17 Regional Assignment Units (RAUs).

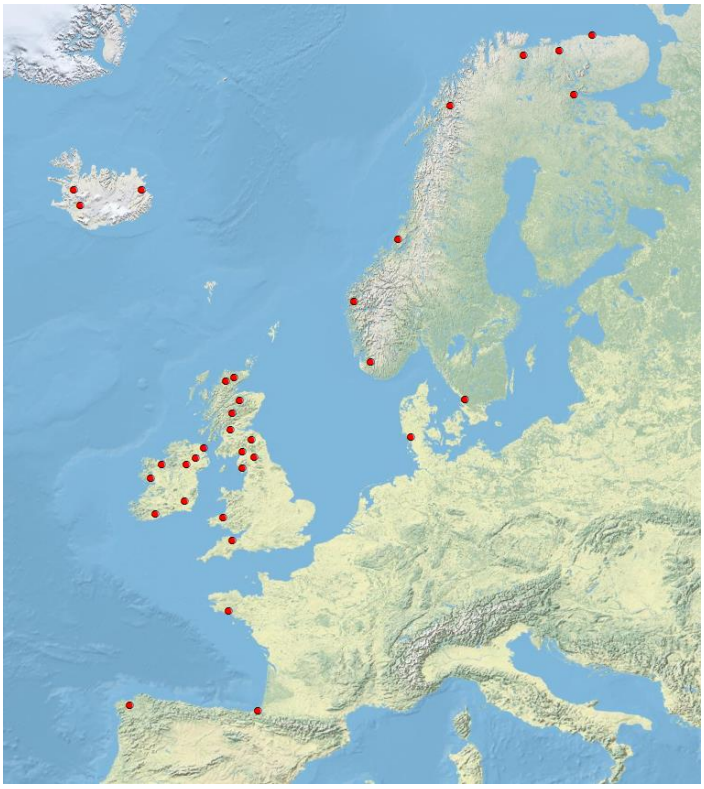


Figure 2 Site locations used in the exclusion analysis of north American fish.

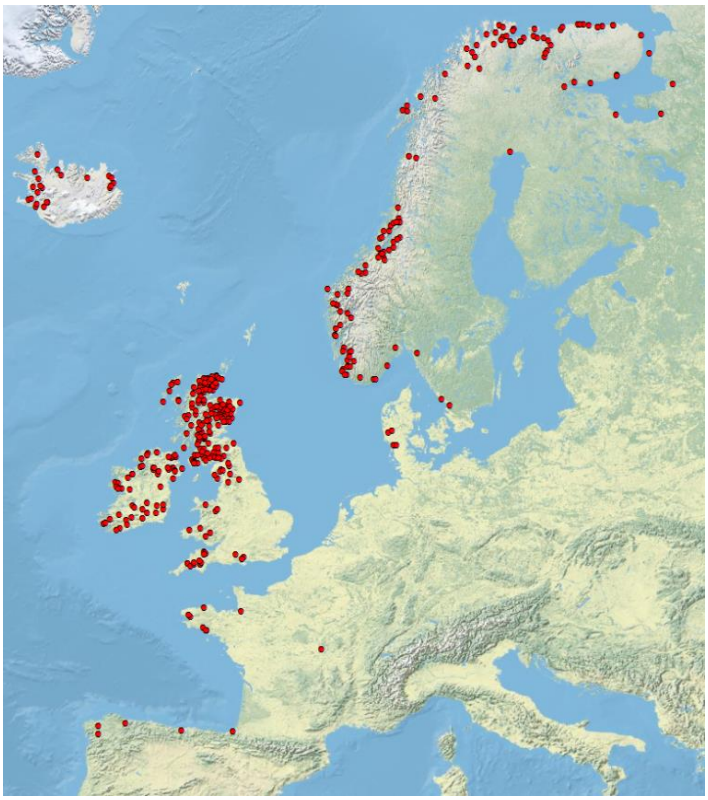
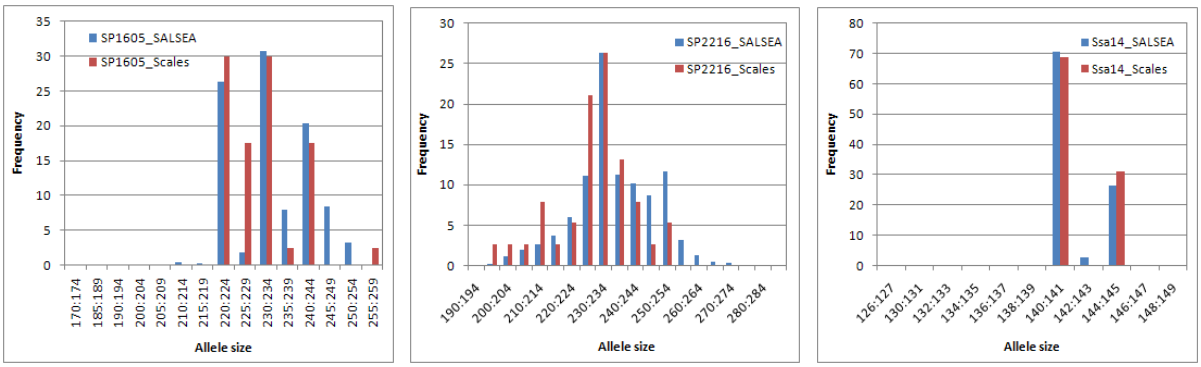


Figure 3 Sites from which 500 fish were chosen at random and used in the exclusion conformation analysis.

A) Problematic Loci



B) Normal Loci

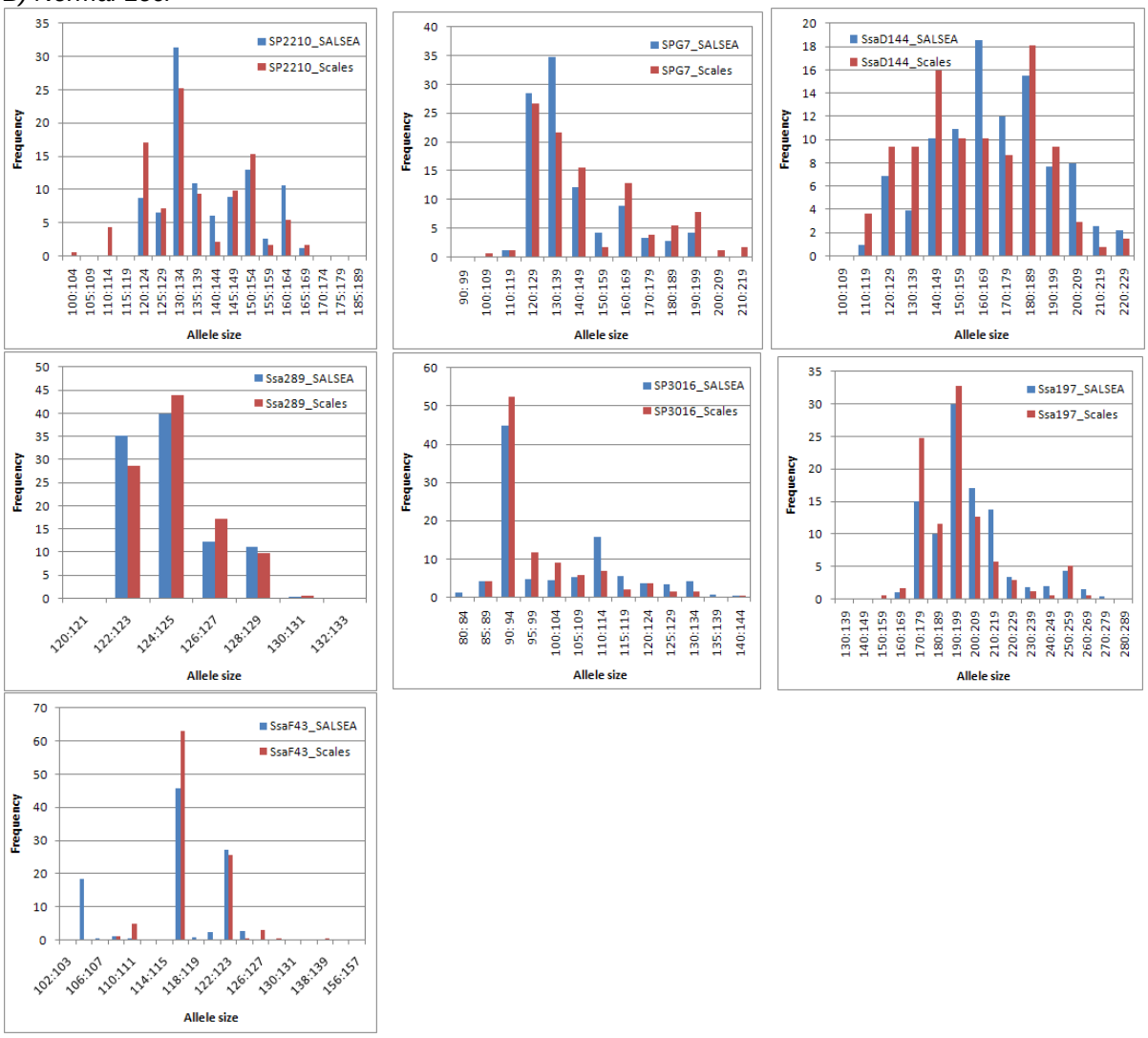


Figure 4 Allele size range proportions in the SALSEA baseline database compared to the scale samples from the fishery.

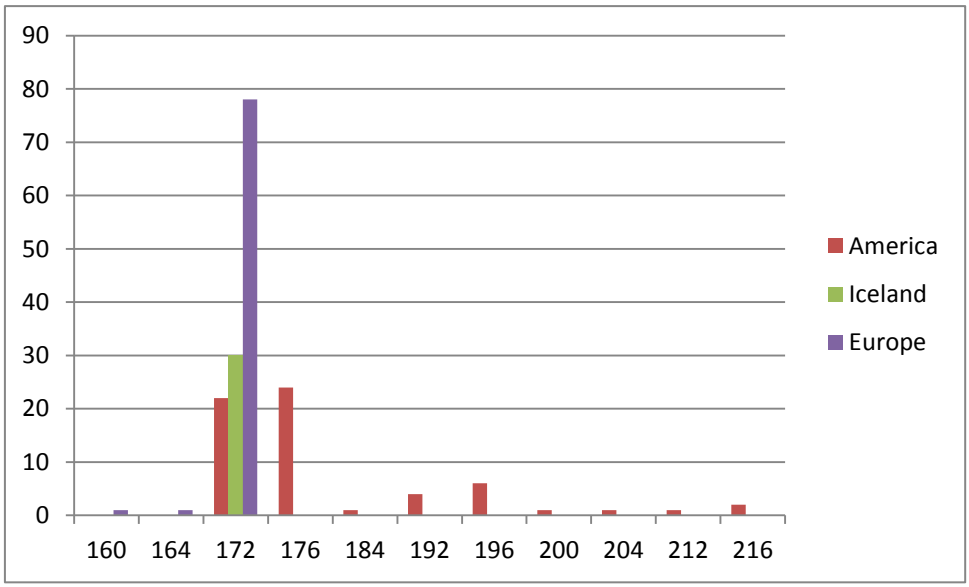


Figure 5 Allele distributions at the SsaD486 microsatellite locus for a sample of American, European and Icelandic salmon samples.

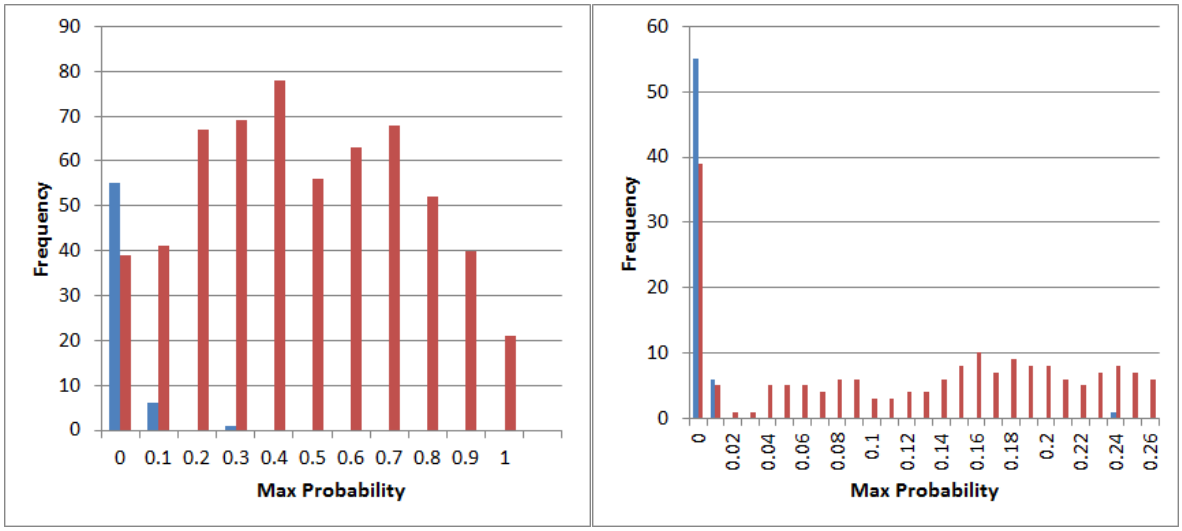


Figure 6 Maximum assignment probabilities of all fish using the reduced SALSEA baseline (note same data in both panels but different x-axis scales). Blue columns are fish identified as putative NA using SsaD486; red columns are all other fish.

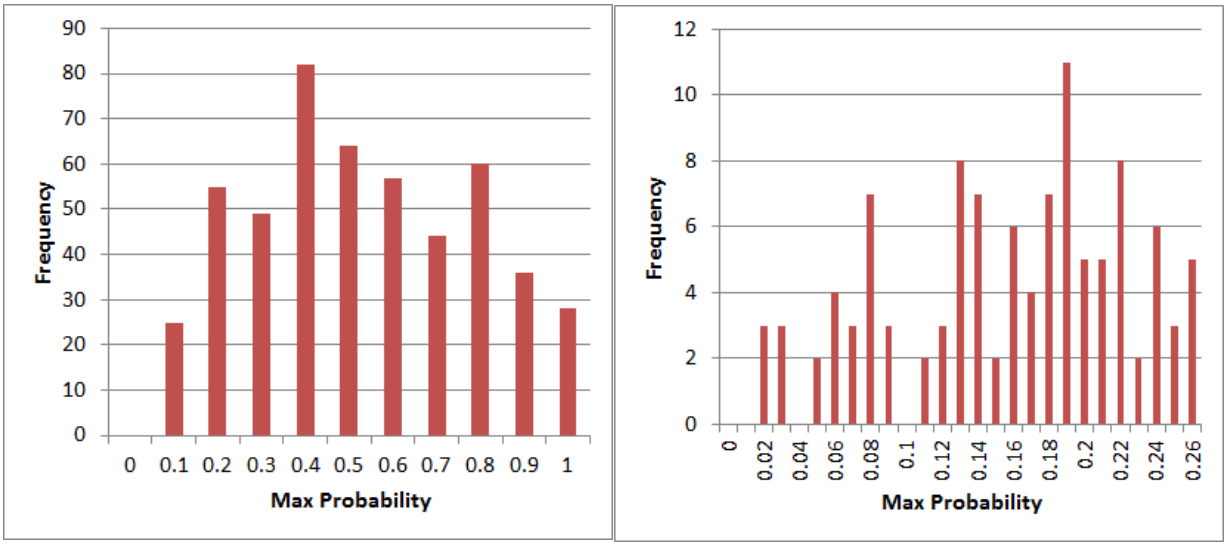


Figure 7 Maximum assignment probabilities of all fish from the conformation set using the reduced SALSEA baseline (note same data in both panels but different x-axis scales).

Figure 8 Proportions of fish in the four assignment hierarchical levels as estimated by conditional maximum likelihood. Note only stocks where CI estimates are not across zero for all months are shown here.