PROJECT FINAL REPORT

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Note: SALSEA-Merge consists of 5 scientific workpackages where WP 1 and WP 3 concerns genetics. As these two WP's links directly, WP 2, marine data acquisition is reported first, then WP 1 and WP 3 combined thereafter for improved readability and flow in the story.

4.1 Final publishable summary

Foreword

This is the Final Report of project 212529 EU /FP7:

SALSEA-Merge - Advancing Understanding of Atlantic Salmon at Sea: Merging Genetics and Ecology to Resolve Stock-specific Migration and Distribution Patterns.

SALSEA-Merge is the first ever large scale, oceanic Atlantic salmon project focusing on the post-smolt phase of the salmon’s life cycle. The methods developed and the results obtained provide us with a new perspective on managing this iconic species, encompassing both the saltwater and freshwater phases of its unique existence. However, the true significance of the work carried out under SALSEA-Merge and outlined in this report, will only become evident in the future. If a salmon is caught anywhere in the Atlantic Ocean it is now possible to quickly assess its continent of origin and in the case of European salmon, to identify the fish back, with remarkable accuracy, to its region or indeed in some cases, it's river of origin. The scientific connection has now been made between the salmon's oceanic feeding grounds and the remote freshwater streams of its birth. For the first time we can now directly link survival of these fish at sea with the prevailing ecological characteristics of specific migration pathways and feeding zones in the ocean.

It is now clear that, in the future, management of the wild salmon resource will involve not alone a knowledge of adult returns to freshwater and an estimate of spawning stock, but equally a knowledge and understanding of the ecology of the oceans in which the salmon grow to adulthood and mature. The outcomes from SALSEA-Merge also point towards the potential of a predictive salmon management methodology which will base its predictions on a thorough knowledge and understanding of the salmon's oceanic feeding areas. It also points towards a new management regime which will, in equal parts, base its predictions on knowledge and understanding of the fish’s life, both in fresh water and in salt water.

Because of the costs involved in obtaining samples of these fish, scattered as they are across the ocean, it is most unlikely that another single species salmon research programme, of the scale and magnitude of SALSEA-Merge, will be undertaken in the north-east Atlantic. Each year, many large scale surveys of the pelagic ecosystem are undertaken by a broad range of European research vessels. These surveys cover areas frequented by all of the marine stages of the Atlantic salmon and should, we strongly suggest, embrace the concept of the salmon as an integral part of these intricate ecosystems. Given the wealth of knowledge now available regarding the potential location of regional salmon populations, on a temporal scale, throughout the entire north Atlantic, salmon surveys should become an integral part of these studies, as only minor gear modifications are required to routinely include salmon assessments. In general, we expect to see an increasingly holistic approach to marine research and welcome this change, as we believe this is entirely consistent with an ecosystem based model of ocean management.

Since young salmon originate from a totally separate ecosystem, we believe they are indeed the perfect “canary of the ocean” and serve as a living sampler, traversing in a few shorts years the oceans and the freshwater ecosystems and carrying with them as they return back to freshwater, a chemical and biological history of their unique and complex journey. The potential of the salmon as a source of information on the ever changing state of the oceans is now apparent. Given its relatively short life cycle and the large distances it covers across the ocean, it is now clear that salmon have the potential to become an important contributor of invaluable data to the future ecosystem-based management of the oceans.

Jens Christian Holst and Ken Whelan

14th January 2012

Executive Summary

Over the past two decades, an increasing proportion of North Atlantic salmon are dying at sea during their oceanic feeding migration. Arguably the greatest challenge in salmon conservation is to gain insight into the spatial and ecological use of the marine environment by different regional and river stocks. The SALSEA-Merge programme was designed to advance our understanding of oceanic-scale, ecological and ecosystem processes. Through a partnership of 9 European nations, the programme has delivered innovation in the areas of: genetic stock identification techniques, new genetic marker development, fine scale estimates of growth, the use of novel high seas pelagic trawling technology and estimates of food and feeding patterns. In addition it has provided for the first time fine scale migration and distribution models, merging hydrographic, oceanographic, genetic and ecological data.

Research cruises to designated areas in the North- East Atlantic took place in 2008 and 2009. In total, 1,728 post-smolts and 53 adult salmon were captured in 233 trawl tows. The tissues from these fish and associated environmental data collected at sea were combined with a subset of 1,800 tissue samples selected from archival material. A unique, comprehensive biological and environmental database (SALSEA PGNAPES) was developed to facilitate any future analyses.

The SALSEA-Merge programme facilitated the development of a unique molecular assignment protocol – GRAASP: **G**enetically-based **R**egional **A**ssignment of **A**tlantic **S**almon **P**rotocol - based on a suite of 14 microsatellite loci. The database comprised 26, 813 individuals from 467 locations, in 284 rivers, representing ~85% of non-Baltic European salmon production. A total of 3,871 of the 4,151 fish were assigned on a regional basis. Significant temporal and spatial heterogeneity in the distribution of the regional stock groups was found and fish of farm-origin identified, demonstrating the value and power of the tool.

Over 23,000 scales of Atlantic salmon from seven rivers, located in six countries, and smolt age and fine scale growth of 2, 242 sea caught post-smolts were analysed. The average rate of circuli formation in the marine zone of scales was estimated to be 6.3 days per circulus. Both the age structure and the number of marine circuli in the scales suggest that the majority of the post-smolts originated in rivers in southern Europe. Marine growth rates varied among years, with highest growth rates in 2002, followed by 2003 and 2009. The lowest growth rates were in 2008. Growth rates during the first period at sea were lowest for salmon of southernmost origin. Growth indices were linked to prevailing environmental and biological conditions. There was clear evidence found that growth is linked to oceanic conditions for all rivers. The diet of salmon, herring and mackerel was studied for four years (2002, 2003, 2008 and 2009). Although the fish examined fed in close proximity in the ocean, the diet differed between the three species. Salmon showed clear differences in diet among years from 2002-2009. The condition factor of salmon decreased from 2002 to 2009.

The distribution pattern of several specific populations of salmon were spatially mapped at different genetic assignment levels. Likely migration routes were assembled for some individual river stocks such as the Loire Allier (France), the Namsen (Norway) and the Bann River (Northern Ireland). The distribution of post-smolts was clearly linked to ocean currents. South of 61.5°N, the post-smolts are not randomly distributed within the migration path, but are located in areas where the currents are stronger than average. A migration drift model for specific stocks of post-smolts wasdeveloped. When temperature and salinity preferences were included with active swimming behavior, this proved to be important mechanism for changing the migration routes and the post-smolt distribution pattern. Also, inter-annual variation in wind fields, and thus the surface currents, altered the migration pathways. Several key areas in the migration routes, where shifts in the migration direction may occur due to climate change, were also identified. A conceptual ecological model was developed, where the main factors relating to the survival of salmon at sea were identified and described. Important factors that were described include: predators, growth and fisheries, which in turn depend on post-smolt distribution, climate variability and change, specific stocks, and synergetic effects and lifehistory changes.

SALSEA-Merge has for the first time provided a comprehensive overview of the migration and distribution pattern of regional and river specific populations of Atlantic salmon post-smolts in the North-East Atlantic. The study has clearly indicated a need to move away from a paradigm centred on the study of adult survivors to an all-embracing vision of salmon populations which encompasses survival corridors stretching from the most remote spawning burn to the limits of the salmon's migration pathways at sea.

Summary description

Over the past two decades, an increasing proportion of North Atlantic salmon are dying at sea during their oceanic feeding migration. Arguably the greatest challenge in salmon conservation is to gain insight into the spatial and ecological use of the marine environment by different regional and river stocks. The SALSEA-Merge programme was designed to advance our understanding of oceanic-scale, ecological and ecosystem processes. Through a partnership of 9 European nations, the programme has delivered, over the past 43 months, innovation in the areas of genetic stock identification techniques, new genetic marker development, fine scale estimates of growth on a weekly and monthly basis, the use of novel high seas pelagic trawling technology and estimates of food and feeding patterns. In addition it has provided fine scale migration and distribution models, merging hydrographic, oceanographic, genetic and ecological data.

WP 2:

Marine data acquisition

The objective of WP 2 was to provide information on the distribution and relative abundance of salmon post-smolts in three selected areas of the North East Atlantic; to provide samples for genetic assignment (WP3) and integrated ecological analyses (WP 4) from catches of post-smolts and older aged fish between May 2008 and August 2009.

The research objectives of the marine surveys were:

- to assemble archival tissues and scales for combined genetic typing and biological analyses
- develop a marine sampling strategy and protocols
- conduct cruises to collect samples of post-smolts (salmon), to gather stomach contents, macro-plankton and oceanographic information from three key marine areas in the North-East Atlantic
- increase the number of nose tagged fish available for recapture

In WP2, 1,800 tissue samples were selected from the 2,300 historical available to the programme. Background genetic data- analyses were completed on these samples by 2009. A scale reading workshop was held in 2008 to standarise scale reading methodologies. A selection of rivers with a long time series of scale data were chosen for further analyses. Data from several thousand historical recaptures of tagged salmon were assembled as part of an ICES salmon data archive programme. Results were published as three ICES reports and the material was made available to SALSEA-Merge. A total of 100, 000 hatchery reared smolts were tagged with Coded Wire Tags (CWT) and released into a selection of Norwegian rivers. None of these smolts were recaptured in 2008 and 2009, leading to the conclusion that the key feeding areas of the Norwegian fish were not encountered during the surveys. Some 800 000 nose tagged smolts were released annually in 2008 and 2009 by other ICES countries (predominantly in Ireland) and 41 of these were recaptured.

After initial technology transfer and standardisation of sampling methods between the partners, cruises to the designated areas (2.4–2.6) took place in 2008 and 2009. In total, 1,728 post-smolts and 53 adult salmon were captured in 233 trawl tows, representing a mean catch of 3.4 post-smolts per trawl hour. All salmon were weighed, measured, dissected and sexed on board. A selection of these fish was extensively sampled. The tissue and associated environmental data collected at sea were distributed in 2008 and 2009 to the partners in WP 3, 4 and 5 respectively. Ancillary material collected during the cruises was stored for use in future projects, outside the scope of the SALSEA-Merge programme. The coordinated SALSEA efforts made it possible to survey large parts of the feeding areas of young salmon during the full summer feeding season, giving an exceptional insight into the migration and distribution patterns of the species. For the first time, the northernmost feeding areas were consistently sampled. Of particular value was the recovery of 41 Coded Wire nose Tagged post-smolts, originating from several countries, allowing estimation of migration speeds and routes from these countries. These high resolution migration data formed an important input into the development of the migration models in WP5. The PGNAPES database format, used by ICES, was tested by one of the partners, and with some adaptations, this format was used to assemble all of the data collected on the individual research cruises and stored by the involved institutes. However, an additional task of merging the existing cruise database with the other SALSEA generated databases was considered essential and hence was carried out during 2010. The databases containing data from WP 4 (scale analyses and images, growth data and stomach analyses) were linked to the SALSEA PGNAPES data base. The database is designed such that subsets can be chosen for analyses using standard queries. This database is compatible with the genetic database (developed as a deliverable of WP 3). WP 2 has therefore generated a unique, comprehensive biological and environmental database which will facilitate any future analyses of the material collected over the course of the SALSEA-Merge programme. The WP 2 has achieved its primary milestones and deliverables.

WP 1 and WP 3:

Development of genetic identification methodology and identification of stock origin of samples

The overall objective of WP 1 and WP 3 was to develop a genetic methodology for the identification of European Atlantic salmon caught at sea to their region, and possibly river, of origin. WP1 would focus on developing an assignment database covering a large portion of the European smolt production while WP 3 would focus to assign the fishes caught at sea based on the method developed in WP 1.

Existing information on potential molecular genetic markers was reviewed and a molecular assignment protocol – GRAASP: **G**enetically-based **R**egional **A**ssignment of **A**tlantic **S**almon **P**rotocol - based on a suite of 14 microsatellite loci was developed and validated by 12 European genetic research laboratories. Existing and new genetic data were calibrated and integrated in a purpose built electronic database to create the assignment baseline, with calibration errors of ~1%. The unique database created initially encompassed 32,002 individuals from 588 rivers. In parallel, work was carried out to assess the potential for enhancing the resolution and cost-effectiveness of the GRAASP in the future using additional microsatellite loci, or mitochondrial and nuclear single nucleotide polymorphisms (SNPs). The baseline data for the microsatellite-based GRAASP was used to identify the natural evolutionary regional stock groupings for assignment. It was optimised for assignment to region/river of origin with regard to sample composition, and an analytical framework for statistical assignment optimised and validated using 967 “blind” samples of known origin. The final optimized and quality controlled database comprised 26,813 individuals from 467 locations, in 284 rivers encompassing over 375,000 pieces of genetic information, representing ~85% of non-Baltic European salmon production. Employed within the molecular assignment protocol **GRAASP**, it was capable of delivering both broad and medium scale regional assignment of the majority of fish with a high degree of accuracy. In WP3 it was applied to assign the region/river of origin of marine samples captured in the NE Atlantic between 1996 and 2007, including 2,290 archival tissues and 1,861 samples collected as part of the SALSEA-Merge project. A total of 3,871 of the 4,151 fish were assigned. Significant temporal and spatial heterogeneity in the distribution of the regional stock groups was found and fish of farm-origin identified, demonstrating the value and power of the tool, for marine studies. Individual assignments were merged with ecological data in WP5. Toward this end, the GRAASP database is now publically available for assignment and will allow the data base of assigned fish to be extended using adult archival material and new sample collections like fishery bycatch and fish caught in scientific surveys. Additionally, the work carried out on GRAASP enhancement using other molecular markers (mtDNA SNPs & nSNPs) shows there exists a very substantial capacity to increase the resolution and cost-effectiveness of the GRAASP in the future. Such analysis has the potential to increase the quality and extent of the insights that can be gained from knowledge of the region and river of origin of fish, caught at different locations and times in the marine environment.

WP4:

Biological analysis of samples

Contemporary digital scale reading techniques were used to analyse fine scale growth of adult salmon from selected rivers and post-smolts collected in the North East Atlantic. A workshop was held in Trondheim in September 2008 to train researchers from four centres in the use of the new scale reading techniques, and to ensure the use of standardized scale analysis procedures between laboratories. Following the workshop a blind test was conducted to ensure standardized scale reading.. The growth data with the corresponding digital images have been split into two parts, and stored in two different electronic databases.

Over 23,000 scales of Atlantic salmon from seven rivers located in six countries have been analysed with the new scale reading technique. Most scales are from 1970 to the present, with some limited information for one stock extending back to earlier periods. In stark contrast to the temporal pattern seen for the Scandinavian and Icelandic rivers, the Burrishoole data (Ireland) indicated strong temporal variation over time with most recent values being the lowest in time series. In the absence of a direct measure of marine survival for each river, standardised survival indices were calculated from at least one river in close proximity to the rivers in this study, where survival data were available. Annual growth indices for the Burrishoole and Nordurá (Iceland) systems were positively correlated with the indices of survival, but this was not the case for the other rivers. In addition, significant positive correlations were shown between survival indices and monthly PSG indices for July, October, November and December for the Repparfjord (Norway), and Burrishoole in September and October. Recruitment estimates (Pre-fishery Abundance, PFA) for the northern and southern components of the North-Eastern Atlantic salmon stock were calculated annually. Growth and recruitment correlated with PFA in several comparisons, but annual growth indices showed negative correlations with recruitment for the Hofsá (Iceland) and Nordurá, and positive correlations with the Burrishoole. Annual growth indices generally correlated with SST, while there were some correlations with specific months in the first year in the ocean for migrating post-smolts. Significant positive correlations were found between annual growth indices and the Winter NAO index for Repparfjord and Teno (Finland/Norway), but negative correlations were found with the Burrishoole data. The lack of temporal synchrony between these rivers, which are widely located across western Europe, may suggest very different post-smolt feeding areas which are influenced by different oceanic conditions and biological parameters. Growth is, however, clearly linked to oceanic conditions (either SST or NAO or both) for all rivers. Further investigation is also warranted to identify key periods and locations where these factors influence growth rates specifically and this will provide insights into how fish from different geographic origins are influenced by broader oceanic conditions.

Smolt age and fine scale growth of 2, 242 post-smolts collected by surface trawls covering a large area of the Northeast Atlantic in 2002, 2003, 2008 and 2009 were analysed. The predominant smolt age of wild post-smolts was two years, followed by one and three year old fish, and a few four year old fish. The average rate of circuli formation in the marine zone of scales was estimated to be 6.3 days per circulus. Both the age structure and the number of marine circuli in the scales suggest that the majority of the post-smolts originated in rivers in southern Europe. Applying intercirculi distances in scales as a proxy for variable growth rate suggests that marine growth rates varied among years, with highest growth rates in 2002, followed by 2003 and 2009, and the lowest growth rates in 2008. Furthermore, the first marine intercirculi distances were narrowest in one year old smolts, successively increasing with smolt age, indicating that growth rates during the first period at sea were lowest for salmon of southernmost origin. Growth indices were linked to prevailing environmental and biological conditions.

The diet of salmon, herring and mackerel was studied for four years (2002, 2003, 2008 and 2009). Although the fish examined fed in close proximity in the ocean, the diet differed between the three species. The main food of herring and mackerel was *Calanus finmarchicus*, and secondly euphausids and gastropods, respectively. The salmon's main food items were juvenile fish and amphipods of the genus *Themisto*. Salmon also showed clear differences in diet among years from 2002-2009. In 2009, when Themisto and fish were less dominant in their diet, salmon post-smolts appeared to have a broader diet and were feeding more on small prey. Forage ratios north of 62°N decreased from 2002 to 2008. Forage ratios in 2008 and 2009 were very similar. Forage ratios of salmon were higher than for the other two species. Also condition factor of salmon decreased from 2002 to 2009, and there was a positive relationship between forage ratio and the condition factor. It seemed that the observed stomach content and the condition of the fish were related, although growth will be the result of the feeding over the whole feeding season. Comparing forage ratio to the observations of growth of salmon, there was a close relationship between forage ratio and the salmon's growth. A possible implication of these results is that stomach content, measured at a given time, is representative for the feeding of salmon during its whole feeding season and can be used to study growth in relation to diet and feeding intensity. Similar to the salmon, condition factor and forage ratio of herring and mackerel did not differ much between 2008 and 2009.

WP 5:

Merge and analyse genetic, biological and oceanographic data

Data generated from the other WPs were combined into a comprehensive Geographical Information System (GIS). Distributions of several specific stocks or populations, collected during the marine surveys and from historical archives, were spatially mapped at different genetic assignment levels. The spatial overlaps of the different stock groups were identified and the distribution maps for the different months clearly indicate the northward movements of the post-smolts. Likely migration routes were assembled for some individual river stocks such as the Loire Allier (France) and the Bann River (Northern Ireland). Relationships between the post-smolt distributions with other parameters were analyzed using data from the marine surveys in 2008 and 2009. The analysis showed that the captured post-smolts were mainly in water with temperatures within 9-12 ^{o}C and salinities larger than 35 ‰.

Ambient sea surface temperature (SST) was calculated along the migration routes of several different specific stocks. The results showed that the southern European stocks entered the sea in warmer sea water conditions than the more northern stocks. The SST in the feeding areas varied between a minimum of ~7.6 ^{o}C in the late 1960s and a maximum of ~10.2 ^{o}C in the 2000s. The distribution of post-smolts was clearly linked to ocean currents. The majority of the post-smolts were caught in pathways of the northward flowing Atlantic Water, from the North East Atlantic to the northern Norwegian Sea. South of 61.5^{o}N, the post-smolts are not randomly distributed within the migration path, but are located in areas where the currents are stronger than average. The relationship between sea temperatures and growth rate during the last month before capture was tested for post-smolts captured in the Norwegian Sea, using circuli spacings at the edge of scales of fish. In 2008, the growth rate increased with decreasing temperatures and increased with the latitude where the post-smolts were captured. This suggests that growth increased with latitude, indicating increased food availability to the north. This was more pronounced in 2008 compared with 2009.

A migration drift model for specific stocks of post-smolts was developed. Within the model both oceanographic (ocean currents, temperature and salinity) and biological (growth) information were merged to provide likely migration routes for both southern and northern European stock groups. Simulations of both passive drift, with the ocean currents and active swimming were included. Information from recaptured tagged post-smolts showed that the post-smolts had an active swimming speed which in many cases was similar to the speed of the ocean currents. When temperature and salinity preferences were included in the active swimming behavior this proved to be an important mechanism for changing the migration routes and the post-smolt distribution. Also, inter-annual variation in wind fields, and thus the surface currents, altered the migration pathways. Several key areas in the migration routes where shifts in the migration direction may occur due to climate change were also identified. A conceptual ecological model was developed where the main factors relating to the survival of salmon at sea were identified and described. Important factors that were described include: predators, growth, and fisheries. These parameters in turn depend on the post-smolt distribution, climate variability and change, specific stocks, and synergetic effects and life history changes.

Main results/foregrounds

WP 2: Marine data acquisition

The collection and assembly of marine samples for analysis along with associated ecological data

Objectives

To provide information on distribution and relative abundance of salmon as well as providing samples for genetic assignment (WP3) and integrated ecological analyses (WP 4) from catches of post-smolts and older aged fish. To collect contemporary samples of post-smolts, and associated critical oceanographic information, in three key marine areas between May and August, 2008 and 2009, from which high resolution estimates of marine growth, body condition, key prey species in diet, and stock origin can be determined, in addition to assembling available archival material and data.

Assemble archival material residing in individual partner laboratories to set a background for contemporary data collected at sea

The material consists of both incidental catches of post-smolts at pelagic surveys and from specific expeditions for surveying salmon distribution. At IMR (1) biological samples have been taken from most of these catches over the last 15 years, and samples intended for later genetic analysis have been preserved from many of them. An inventory of these IMR samples has been compiled for use by the wider SALSEA team**.** Approximately 1800 of the 2300 available samples of post-smolt and adult salmon mostly from oceanic regions captured on surveys covering 1999 - 2006 (Figure 3.1) were considered as suitable to take forward for genetic analysis in WP 3 where results of the analyses are reported.

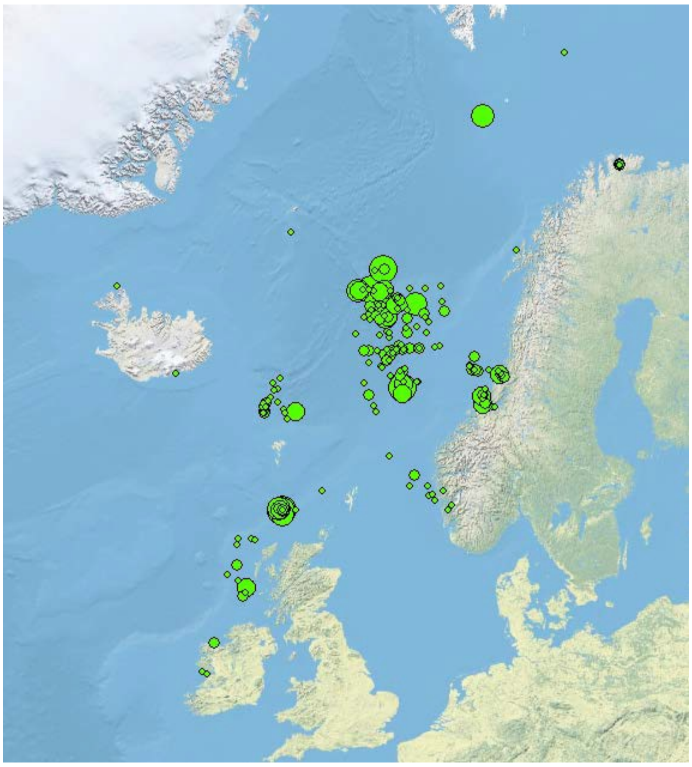
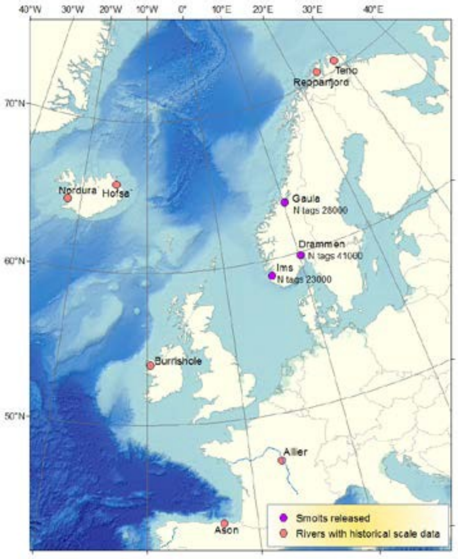
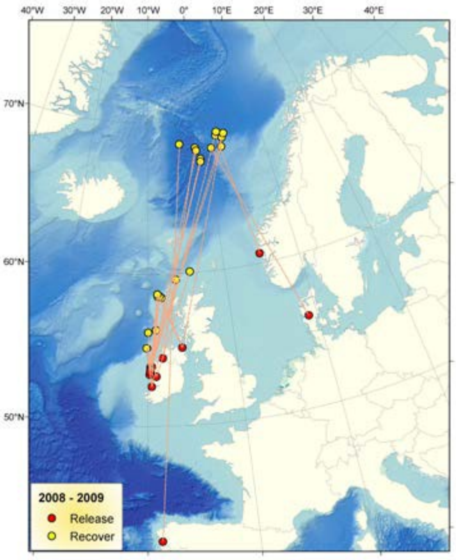


Figure 3.1: *Archival tissues for genetic analyses: Locations for marine samples analysed.*

The partners involved in growth analyses (WP4) established and agreed upon which selection of rivers (Figure 3.2) with archival scale material was to be used in the growth and scale analyses. The basic criteria for the selection were length of time series and number of samples for analyses.

A considerable amount of unexploited historical information from conventional tagging studies from 1960s onwards (CWT, Floy, Carlin etc) that resided in participant laboratories was assembled by ICES workshops. This material was made available to SALSEA-Merge and was of use in designing the cruises in WP 2, contributing to spatial model development in WP 5. The material was also valuable for developing a standard format for recording tags as well as using GIS as a tool for presenting the geographical distribution of recaptured salmon and describing distribution of salmon of different origins and ages in time and space. The 2007- 2009 reports are available on the ICES homepage.





Strategic coded wire tag release to support stock ID and modelling

With the support from SALSEA, in 2008 and 2009 close to 50 000 salmon smolts were tagged annually by Partner 4 with coded wire tags (CWT) in three rivers in Norway (Figure 3.2). At the same time close to 800 000 CWT smolts were released by national agencies in Ireland, Iceland, UK, Germany, France, Spain, Sweden and Denmark. No CWT tagged post-smolts from the SALSEA CWT releases in Norway were captured during the SALSEA expeditions, although a relatively large number of them survived to return as adults to their home rivers. On the other hand 39 CWTs of southern origin (Ireland, UK , Spain) and 2 "northern" tags (Denmark, Norway) were recovered during the expeditions (Figure 3.3). The absence of captures of Norwegian SALSEA tagged fish during the SALSEA expeditions suggests that the feeding areas for post-smolts of these Norwegian stocks were not encountered. It has been suggested from the "historical" age data from scale samples, that post-smolts from south Europe (Spain, France Ireland and UK) are the dominating component in the samples from Central Norwegian Sea. Data from the assignment exercises under SALSEA (WP 3) largely confirm these observations. The coded wire tag recaptures provide unique records of the specific migration routes and run timings of known origin groups of migrating salmon from these countries. These high resolution migration data have been an important input into the migration models in WP5.

Figure 3.2, upper: *River locations. Red dots: rivers with long time series of archival scale material selected for age and growth analyses in WP 4, Mauve dots: Coded wire tagging (CWT) in Norway-sites for the SALSEA strategic CWT releases of smolts in 2008 and 2009. Numbers indicate the total of coded wire tagged fish released in each river.*

Figure 3.3, lower: *Locations for origin at release, and recapture at sea of Coded Wire Tagged (CWT) post-smolts during SALSEA surveys in 2008 and 2009.*

Preparation and planning for cruises to collect contemporary salmon data at sea

Three co-ordination meetings and workshops were organised in 2008 to develop standard operating procedures (SOPs) for sampling fish, plankton, oceanographic and meteorological data. Training on the use of gears at MI (2) was obtained from IMR (1) personnel with previous experience of using plankton and post-smolt salmon trawls. In addition individual planning meetings were held by the partner institutes IMR (1), MI (2) and FAMRI (15).

Two meetings to assess cruise effectiveness were organised in 2008 and 2009. However, an additional task of merging existing cruise and other databases was considered essential and hence was carried out during 2010. The databases containing data from WP3 (genetic analyses and assignments) and WP 4 (Scale analyses and images, growth data) were linked to the SALSEA PGNAPES data base from which selections of subsets for analysis can be made using standard queries. A description of this "SALSEA-Merge PGNAPES" database is given in Deliverables report. At present the database is located on a sharepoint site hosted by Marine Laboratory, Scotland.

Expeditions to areas of known salmon distribution to collect salmon samples and associated biological and physical environmental data

Expeditions to collect contemporary post-smolt samples were carried out in 2008 and 2009 to three different areas by the three partners involved. Area 1, West of Ireland – Northwest Scotland was surveyed by the Marine Institute (MI, Ireland, partner 2) with two ships, the R/V Celtic Voyager and the RV Celtic Explorer, in May 2008, and May and June in 2009. Area 2, Mid Norwegian Sea - North of Faroes – East of Iceland was surveyed by the Faroes Marine Research Institute (FAMRI, Faroes, partner 15) with the RV Magnus Heinasson in June/July 2008 and 2009.

Area 3, North Norwegian – western Barents – east Greenland Sea was surveyed by the Institute of Marine Research (IMR, Norway, partner 1) using the MS Eros in 2008 and MS Eros and MS Libas in 2009. The areas surveyed are presented in Figure 3.4 and main cruise activities are summarized in Table 3.1.

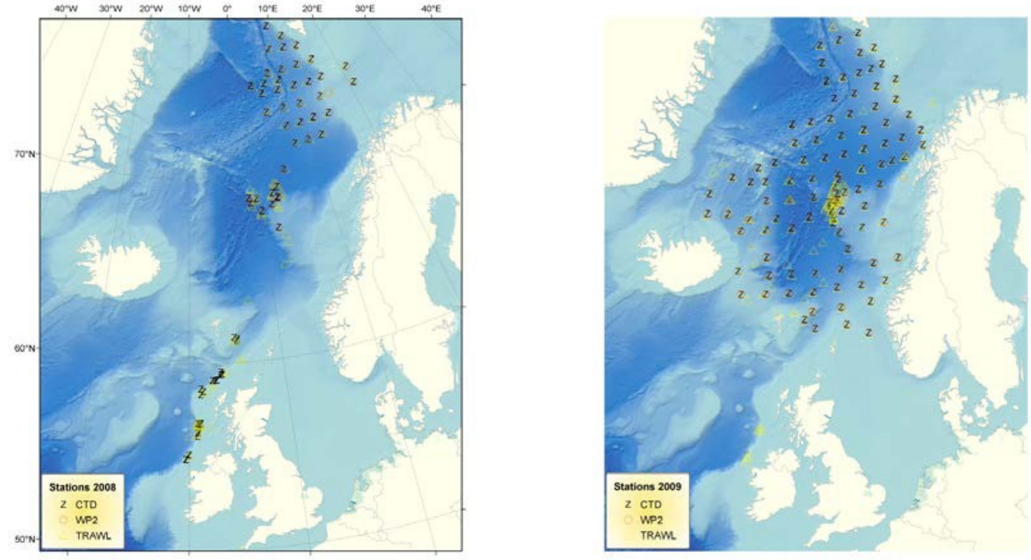


Figure 3.4 *Expeditions in 2008 (left panel) and 2009 (right panel). Southern area covered by RV Celtic Voyager and RV Celtic Explorer (expedition 1, partner 2), Mid-Norwegian sea by RV Magnus Heinasson (Expedition 2, partner 15), northern area by MS Eros (Expedition 3, partner 1). Sites for monitoring salinity/temperature/density (CTD casts, Z), plankton sampling with nets WP2 or MIK (O) and post-smolt trawl tows (triangle, yellow) indicated.*

Of particular importance is that, for the first time, a considerable part of the salmon distribution areas could be sampled during the summer season when salmon would be expected to be present, and that the northernmost area was included and consistently sampled.

Table 3.1: *Summary of no of stations sampled by Partners 1, 2 and 15 to Survey Areas 1 (West of Ireland & Scotland and South Norwegian Sea), 2 (Mid-Norwegian Sea) and 3 (orth Norwegian Sea) between mid- May and beginning of August in 2008 1nd 2009. CTD profiles include logging of depth, temperature, salinity, density and fluorescense (for details consult Annex 1, WP 2).*

		STATION TYPE							
PARTICIPANT		**TRAWL**		**CTD -PROFILES**		**PLANKTON NET**		**KRILL TRAWL**	
COUNTRY (PARTNER/ AREA SURVEYED)	**Vessel**	**2008**	**2009**	**2008**	**2009**	**2008**	**2009**	**2008**	**2009**
IRELAND (2/1)	**R/V CELTIC EXPLORER**	27	15	18	6	7	6		
	R/V CELTIC VOYAGER	10	7	8	1	2	1		
FAROES (15/2)	**R/V MAGNUS HEINASSON**	32	45	10	8	13		2	1
NORWAY (1/3)	**M/S EROS**	31	68	31	47	31	47	22	2
	M/S LIBAS		61		44		91	.	
SUM STATION		**100**	**196**	**67**	**106**	**53**	**153**	**24**	**3**

The sampling methods were in essence analogous for all three expeditions. All post-smolt sampling was carried out using the post-smolt trawl (Fig.3.4b). To be effective for post-smolts, the trawl is towed in arches with speed exceeding 3 knots at the very surface (upper floats must not slide under water).

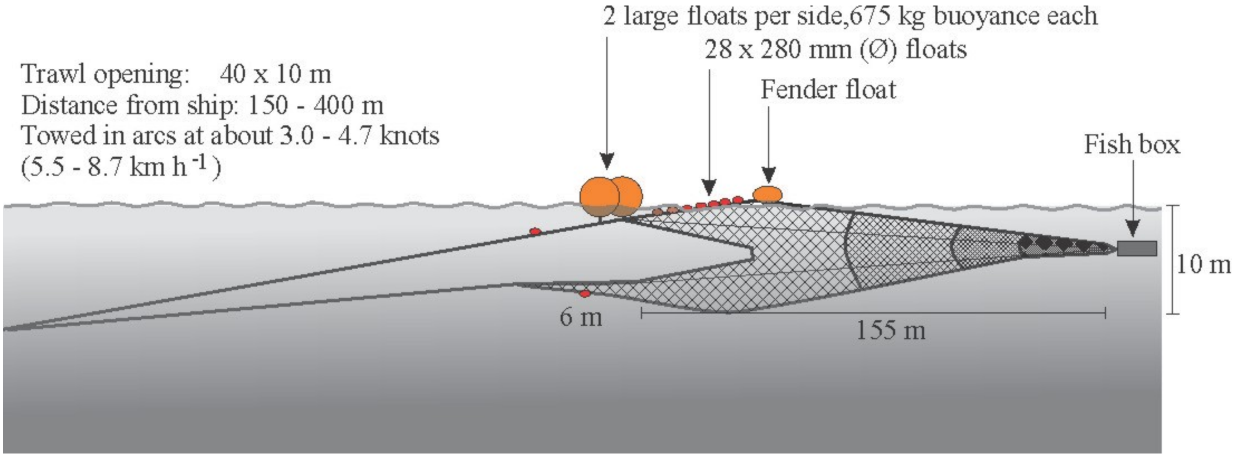


Figure 3.4b *Schematic drawing of the special post-smolt trawl developed by (partner 1) expeditions. A very similar design was used by all partners.*

A total of 898 post-smolts, at a mean catch rate of 5,1 post-smolt per trawl hour, 662 post-smolts at a catch rate of 5.7 and 168 post-smolts at a catch rate of 1,55 per hour were captured in area 1, 2 and 3 respectively. Hydrographic data were collected from vertical CTD-profiles (salinity, temperature, density and fluorescence) taken from 0 to 500 m. Continuous thermo-salinograph logging at 5 m depth of temperature, salinity and fluorescence along the ships transects was undertaken. Other relevant information, such as meteorological observations from the ship, satellite data (e.g. SST) etc. were also collected and stored in the cruise database. Acoustic Doppler Current Profiler (ADCP) measurements were collected continuously from the Celtic Explorer in 2008 and 2009. These data were post- processed and assembled into the SALSEA PGNAPES data base, and have been and used for analyses in WP 5.

Horizontal and vertical macro-plankton net (206 plankton nets and 27 Krill trawl hauls) tows were undertaken at selected trawl stations (Figure 3.4). The results of the Krill trawl tows are reported in D 4.3, while other plankton samples in accordance with the DoW were fixed in formalin and made available for laboratory analysis later. The number and nature of these plankton tows can be found in Table 3.1.

Acoustic Doppler Current Profiler (ADCP) monitoring data are available from the Celtic Explorer in 2008 and 2009. A first assessment of acoustic data was carried out on board for preliminary information on distributions and abundance of plankton per unit area/volume

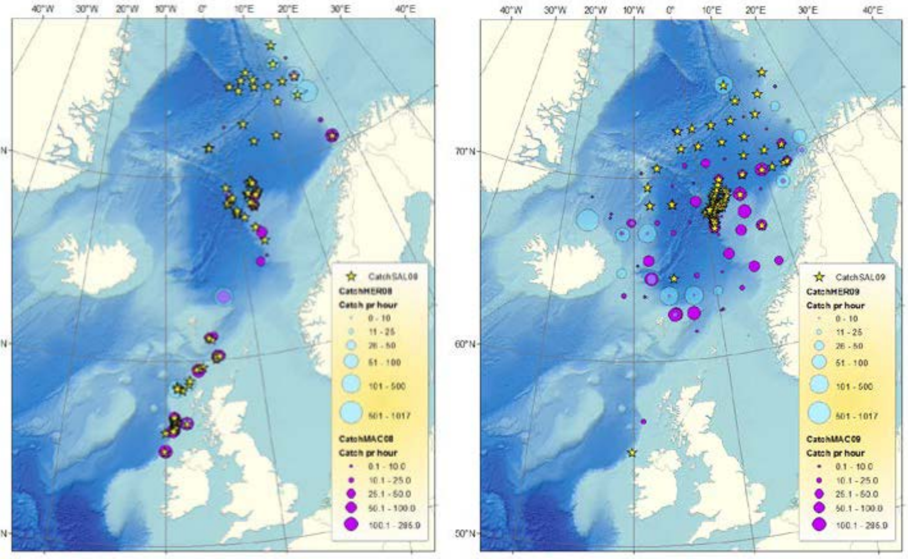


Figure 3.5: *Catch (kgs) per h (CPUE) of other pelagic species during SALSEA expeditions in 2008 (left) and 2009 (right). Trawl stations where salmon were caught indicated with stars.*

as well as co-occurring fish and potential predators. These data need specialist post-processing outside the scope of the SALSEA resources. Post-smolts have been observed to mainly reside in the upper 5-6 m (Holm et al 2000), i.e. well above the layers sampled by the multi beam transducers and in future projects, will be used to carry out further in-depth analyses of the stored information in the macro-plankton database. Due to technical problems on board the other ships, ADCP data were not collected.

Figure 3.5 shows the distribution of the herring, mackerel and post-smolts caught during the expeditions. The distribution of the three species largely overlap, but especially in the northernmost area, salmon occur independently of the two others, however, often together with considerable numbers of lumpfish which is a common occurrence over the total survey area. Figure 3.6 presents the catch (nr. per trawl h) of salmon in 2008 and 2009. A full sampling protocol was adopted for the surveys (**D.2.3**). All of the 1,728 post-smolt and 52 adult salmon captured were sacrificed and a full range of biological samples was taken. Stomach, gill arch, viscera samples were retained from virtually all fish for parasites studies as well as samples being retained for lipid content analysis.

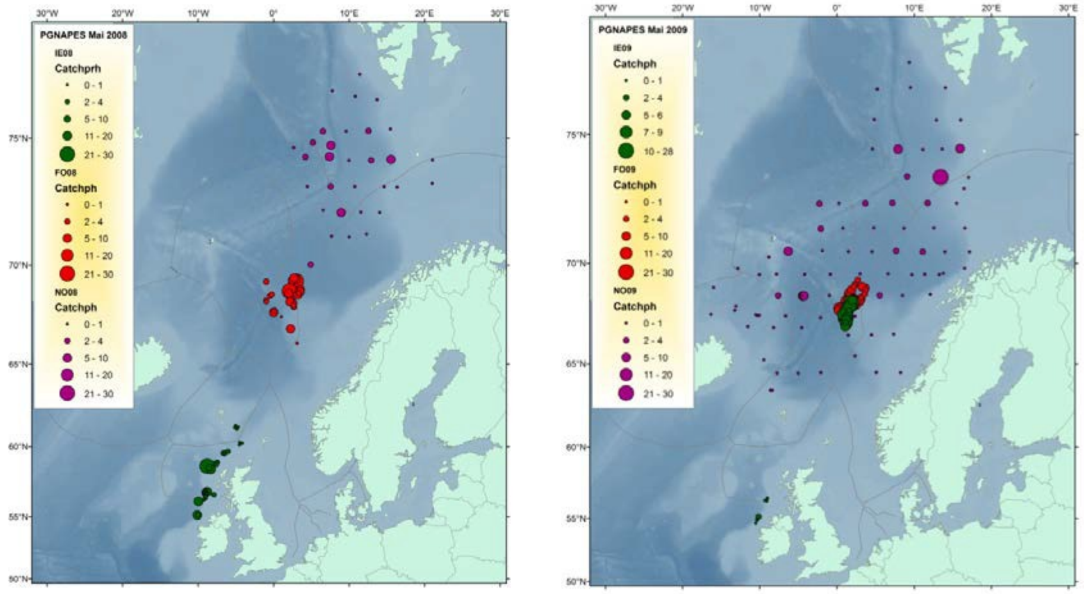


Figure 3.6: *Catches of post-smolts per trawl hour (CPUE) at expeditions 1, MI, Ireland (partner 2, green), 2, FAMRI, Faroes (partner 15, red) and 3, IMR, Norway (partner 1, mauve). Size of catch corresponds to size of dot. For explanation see legends in figure.*

Tissues for genetic analyses and scales for growth and age studies were carried over to WPs 3 and 4 respectively, and in addition, approximately 50 samples of herring, mackerel and other species were retained per survey for further analyses of stomach contents, condition and lipid and parasites for future studies. Stomach samples were analysed by IMR (1) or FAMRI (15). Results on condition and growth data are reported in WP4, while stomach contents are detailed in the Final Plankton Report appended to Deliverable 4.3 of WP4.

WP 1:

Development of genetic identification methodology

The overall WP1 objective was to develop a genetic methodology for the identification of European Atlantic salmon caught at sea to their region, and possibly river, of origin. Existing information on potential molecular genetic markers was reviewed. This was achieved by the integration of existing and new genetic data on an optimized set of microsatellite DNA loci, from across the European range of the species, into an optimal electronic database. Using recognised statistical tools, placed in a bespoke microsatellite based analytical framework, a molecular assignment protocol – **GRAASP**: **G**enetically-based **R**egional **A**ssignment of **A**tlantic **S**almon **P**rotocol - was developed and validated. The GRAASP allows assignment of fish at both broad and medium scale regional assignment. Further molecular marker loci were assessed which have the potential to improve the tool, to enable exploitation of new more cost-effective emerging genetic technologies and to increase assignment resolution to small scale regions or individual rivers and tributaries.

GRAASP represents the operational culmination of an integrated, progressive series of work activities linking 12 European genetic research laboratories in a unique, large-scale transnational collaborative endeavour. The GRAASP baseline was used within the SALSEA-Merge programme to generate initial insight into the marine biology of European Atlantic salmon post-smolts and is now in the public domain, to be exploited by all researchers and managers, for the determination of the origin of Atlantic salmon captured at sea. The demonstrated assignment power of the molecular genetic approach embodied by GRAASP will allow it to become a standard biological tool for informing Atlantic salmon management.

A review was carried out of the assembled catalogue of data bases on molecular genetic variation in European Atlantic salmon existing in 2007 (Garcia de Leaniz et al., unpublished manuscript). This concluded that, within the context of technological constraints and partner laboratory analysis capabilities, the GRAASP should build on the information base for an existing set of microsatellite loci (“Virginia Panel”), identified by salmon researchers at an international meeting in 2004 as optimal for baseline population genetic studies of the species. An assignment power analysis of existing data found that a subset of 14 of the 15 loci was a sufficient basis for regional assignment as well as the most cost-effective and efficient approach to exploit existing data toward this end (Figure 3.7). At this stage no immediate potential was indicated for improving assignment power using known mitochondrial DNA variants, though it was recognized this source of molecular markers probably had potential to contribute to GRAASP in the future.

The initial meta-analysis identified the data gaps and defined the challenges and technical issues required to assemble a baseline of information on European Atlantic salmon stocks for these loci to achieve comprehensive assignment. The challenge was to achieve baseline coverage of rivers spanning the full European distributional range and representing at least 80% of European production. The existing trans-range river coverage for each of the microsatellites in the suite chosen is given in Table 3.2; of the ~2300 European salmon rivers (Figure 3.8), data for each of the chosen microsatellites was available for 100 rivers stocks or less, with most rivers analysed for less than 6 of the 14, but in some regions full data sets were already available for small numbers of rivers. Existing recreational and commercial catch data indicated that to achieve ~85% coverage of salmon production, it would be necessary to have genetic information on the 450 most productive rivers. To achieve this required extending existing river analyses to the full set of microsatellite loci and substantially extending existing geographical coverage as well as integrating existing and new data bases produced by individual national laboratories. The later situation necessitated inter-calibration of genotypes and standardization of genotype nomenclature to create a single unified data base.

Figure 3.7: *Relationship between A) number of loci and B) number of alleles used in individual assignment simulations and the accuracy of assignment obtained using the full Irish data-set. Assignments are to Region (Irish River Board; solid line, filled diamonds), District (Irish Fishery District; short dashed line, open squares), river (short/long dashed line, filled triangles), and exact match to population (long dashed line, open circles).*

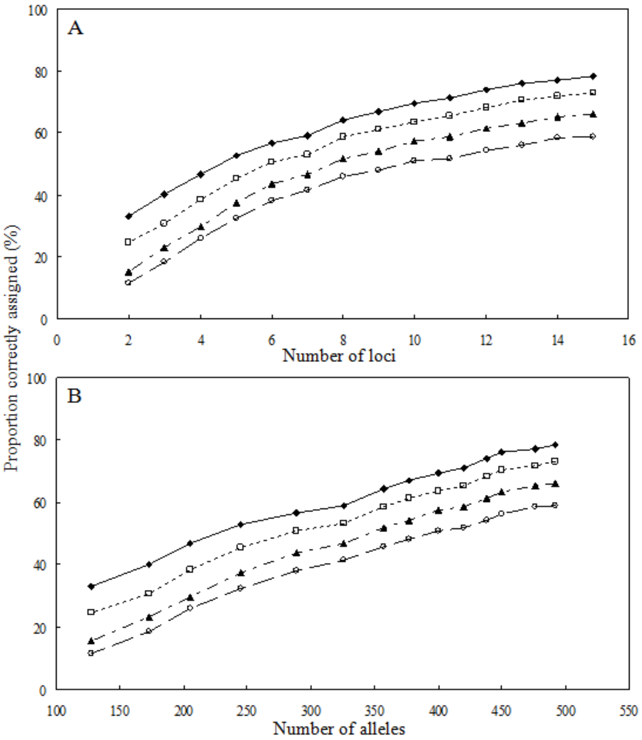
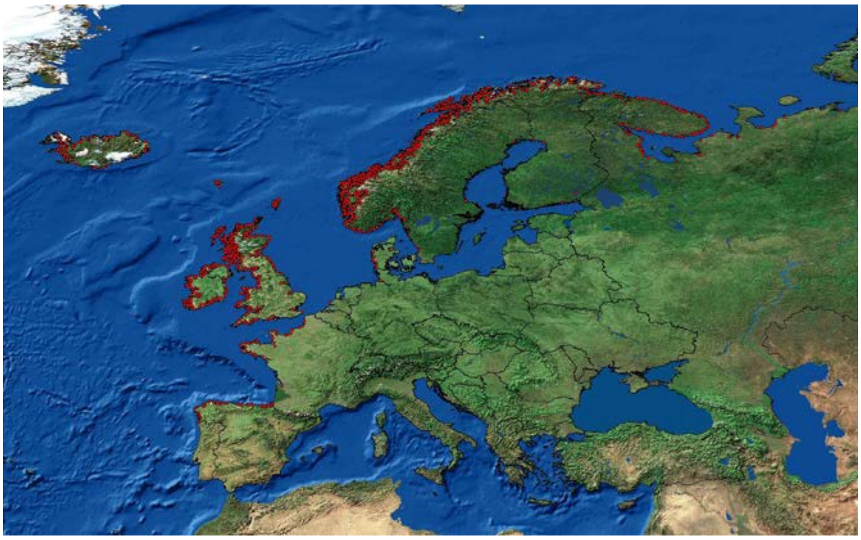


Table 3.2: *The SALSEA-14 set of microsatellites = "Virginia" Panel of microsatellites minus SsaD486.*

Locus name	No. repeat bases	Max Size range	Max no. Alleles	No. Rivers screened
Ssa197	4	135-279	30	186
Ssa 202	4	200-320	18	166
Ssa171	4	193-285	32	126
SSsp2210	4	104-164	15	98
SSsp2216	4	202-305	18	98
SSsp1605	4	222-254	14	97
Ssa 14	2	138-152	4	80
Ssa 289	2	107-132	8	80
SsaF43	2	99-131	13	71
SSsp2201	4	259-371	21	68
SSspG7	4	112-214	24	57
~~SsaD486~~	~~4~~	~~162-210~~	~~7~~	~~35~~
SsaD144	4	112-298	35	34
SSsp3016	4	70-130	?	1

Figure 3.8: *Map Distribution of salmon rivers in the NE Atlantic region excluding the Baltic Sea.*



A key requirement for the development of the GRAASP was an electronic data base capable of storing and retrieving the large set of trans-European microsatellite and other genetic data (potentially millions of individual genotypes) required for robust assignment (http://www2.imr.no/salsea/admin/). The GRAASP data base was created using the widely employed PostgreSQL data base development software, the web interface developed in Cake PHP, a rapid development framework allowing tracking of changes to the system as the development progressed. All the components use open source software. This allows licence-free public distribution of all or part of the system. The National Oceanic and Atmospheric Administration GAPS (Genetic Analysis of Pacific Salmonids) database was studied and used as a starting point for the GRAASP data base development, and modified and enhanced to accommodate the specific data needs of the SALSEA project; the relational schema of the SALSEA database is shown in Figure 3.9. The database will accept genotypes derived all classes of genetic markers making it adaptable to accommodate enhancement of the GRAASP baseline with new marker types as marker technology advances to allow fine-scale regional or river-specific assignments. Efficient, user-friendly data entry protocols using a web browser have been implemented, encompassing data quality control procedures to ensure accurate genotypes, river ID, sample history and source laboratory. The database allows data searching by loci, regions, countries, rivers, sample sites, and data extraction in formats required for genetic assignment programmes (e.g. GENECLASS, Cbayes) as wells as data export in standardized or laboratory specific nomenclature in spread sheet format. There is an option to view geographical data on a map (e.g. based on the Google maps plug-in or ArcView shape file formats), both for baseline and marine samples (Figure 3.10). The open nature of the database structure has allowed it to be exploited for two further EU projects (Celtic Sea Trout Project, Atlantic Aquatic Resources C). An agreement is in place for the public use of the final GRAASP baseline data set.

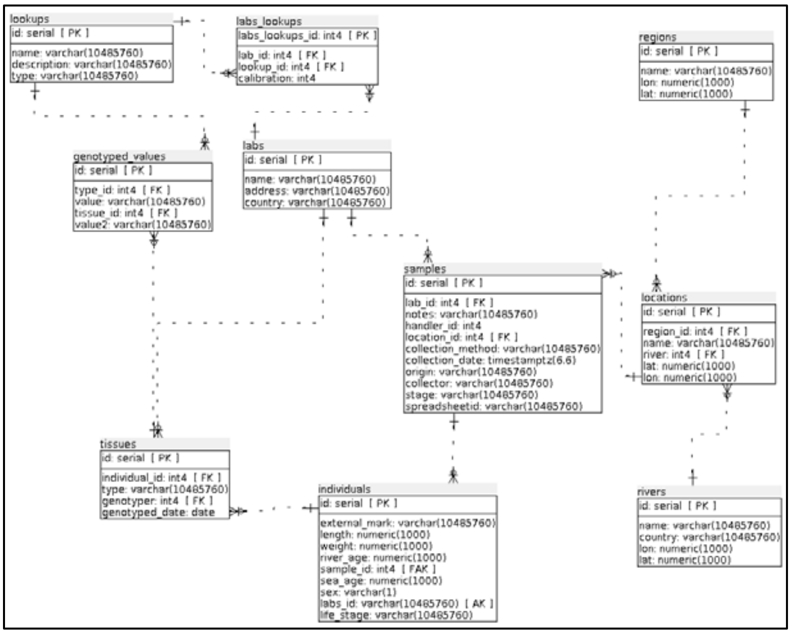


***Figure 3.9:** The relational schema of the SALSEA-Merge GRAASP genetics database.*

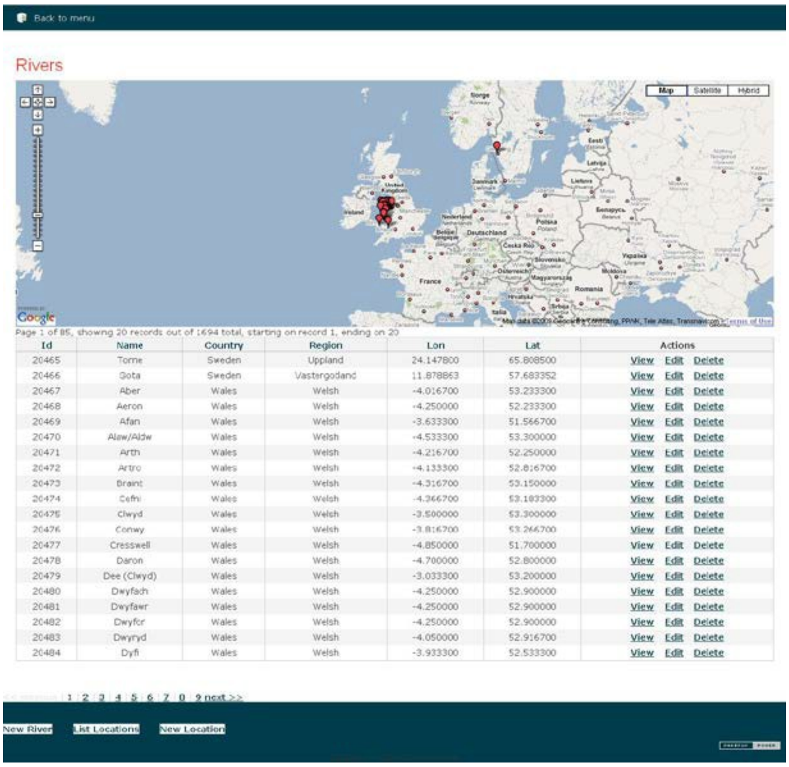


***Figure 3.10:** Optional Google maps based interface for viewing meta-data on GRAASP baseline information.*

Rivers

Page 1 of 85, showing 20 records out of 1694 total, starting on record 1, ending on 20

Id	Name	Country	Region	Lon	Lat	Actions
20465	Torne	Sweden	Uppland	24.147800	65.808500	View Edit Delete
20466	Gota	Sweden	Vastergodand	11.878863	57.683352	View Edit Delete
20467	Aber	Wales	Welsh	-4.016700	53.233300	View Edit Delete
20468	Aeron	Wales	Welsh	-4.250000	52.233300	View Edit Delete
20469	Afan	Wales	Welsh	-3.633300	51.566700	View Edit Delete
20470	Alaw/Aldw	Wales	Welsh	-4.533300	53.300000	View Edit Delete
20471	Arth	Wales	Welsh	-4.216700	52.250000	View Edit Delete
20472	Artro	Wales	Welsh	-4.133300	52.816700	View Edit Delete
20473	Braint	Wales	Welsh	-4.316700	53.150000	View Edit Delete
20474	Cefni	Wales	Welsh	-4.366700	53.183300	View Edit Delete
20475	Clwyd	Wales	Welsh	-3.500000	53.300000	View Edit Delete
20476	Conwy	Wales	Welsh	-3.816700	53.266700	View Edit Delete
20477	Cresswell	Wales	Welsh	-4.850000	51.700000	View Edit Delete
20478	Daron	Wales	Welsh	-4.700000	52.800000	View Edit Delete
20479	Dee (Clwyd)	Wales	Welsh	-3.033300	53.200000	View Edit Delete
20480	Dwyfach	Wales	Welsh	-4.250000	52.900000	View Edit Delete
20481	Dwyfawr	Wales	Welsh	-4.250000	52.900000	View Edit Delete
20482	Dwyfor	Wales	Welsh	-4.250000	52.900000	View Edit Delete
20483	Dwyryd	Wales	Welsh	-4.050000	52.916700	View Edit Delete
20484	Dyfi	Wales	Welsh	-3.933300	52.533300	View Edit Delete

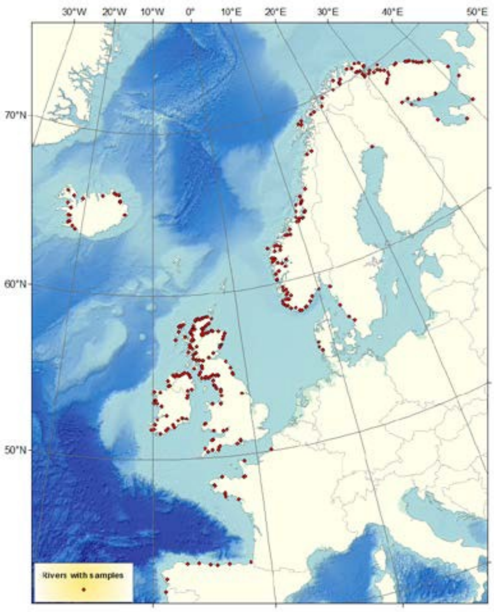
1 2 3 4 5 6 7 8 9 next >>

The integration of microsatellite data from multiple laboratories into a single baseline data base required the inter-calibration of overlapping microsatellite data sets and development a standardized nomenclature (Ellis et al. 2010). The 14 microsatellite loci were calibrated and standardized across 12 laboratories. Inconsistencies were observed, particularly due to differences between migration of fragments and actual allelic size (size-shifts) but inter-laboratory calibration was successful. Standardization also allowed an assessment of the degree and partitioning of genotyping error (see Table 3.3). Notably, the global allelic error rate was reduced from 0.05 ± 0.01 prior to calibration to 0.01 ± 0.002 afterwards. Most errors were found to occur during analysis (i.e. when sizing alleles; mean proportion of analytical error across loci 0.75 and 0.58, before and after calibration respectively). No evidence was found of an association between the degree of error and allelic size range of a locus, number of alleles, or repeat type, nor was there evidence that genotyping errors were more prevalent when a laboratory analysed samples outside of the usual geographic area they encounter. Conversion rules for each laboratory were formulated to achieve a single integrated data-base using a common synthetic GRAASP nomenclature.

Table 3.3: *Observed inter-laboratory error rates for each locus across 12 laboratories before and after calibration.*

Locus	Allelic error e_a	Locus error e_l	Locus error after calibration
Ssa14	**0.0029**	**0.0049**	**0.0049**
Ssa171	**0.0051**	**0.0093**	**0.0093**
Ssa197	**0.0071**	**0.0120**	**0.0052**
Ssa202	**0.0056**	**0.0072**	**0.0072**
Ssa289	**0.0022**	**0.0035**	**0.0035**
SsaD144	**0.0065**	**0.0098**	**0.0098**
SsaD157	**0.0092**	**0.0175**	**0.0175**
SsaD486	**0.0011**	**0.0021**	**0.0021**
F43	**0.0449**	**0.0800**	**0.0454**
SSsp2201	**0.0155**	**0.0280**	**0.0204**
SSsp2210	**0.0084**	**0.0138**	**0.0131**
SSsp2216	**0.0056**	**0.0011**	**0.0085**
SSsp3016	**0.0087**	**0.0137**	**0.0128**
SSspG7	**0.1503**	**0.1807**	**0.0231**
Ssol85	**0.0040**	**0.0059**	**0.0059**

The final baseline for the GRAASP was created using existing data, extending the locus set to the full 14 microsatellites for already screened river samples, as well as expanding spatial coverage to the required number of rivers using archival and new material. These activities involved contributions by all 12 research groups. The data set, before quality control, encompassed 32 002 individuals from 588 rivers (Figure 3.11). After quality control this was reduced to 26 813 individuals from 467 locations in 284 rivers for a total of over 375 000 pieces of genetic information. The rivers represent an estimated 85+% of all wild salmon produced in European rivers (excluding the Baltic Sea). The distribution of rivers encompassed in the final baseline is shown in figure 3.12. A description of the baseline has been submitted for publication (Gilbey et al. submitted) and an agreement is in place for it to be publicly available for use for the genetic assignment at the end of the SALSEA-Merge Project and at which time a copy of the data base will be lodged with ICES.



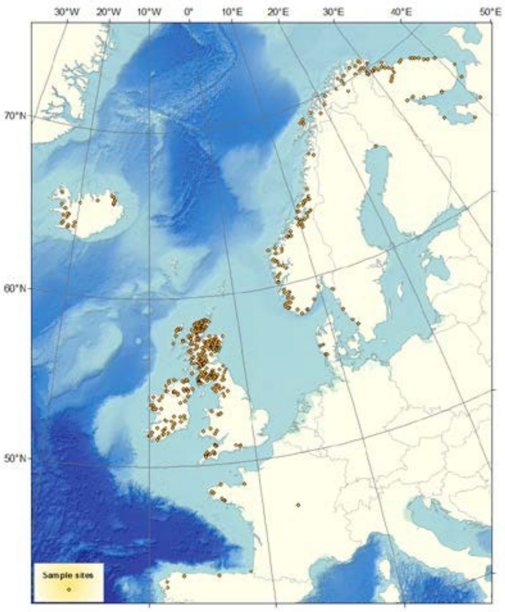


Figure 3.11, left: *The distribution of the rivers included in the final GRAASP baseline database.*
Figure 3.12, right: *The distribution of sample sites in rivers included in the final GRAASP baseline database.*

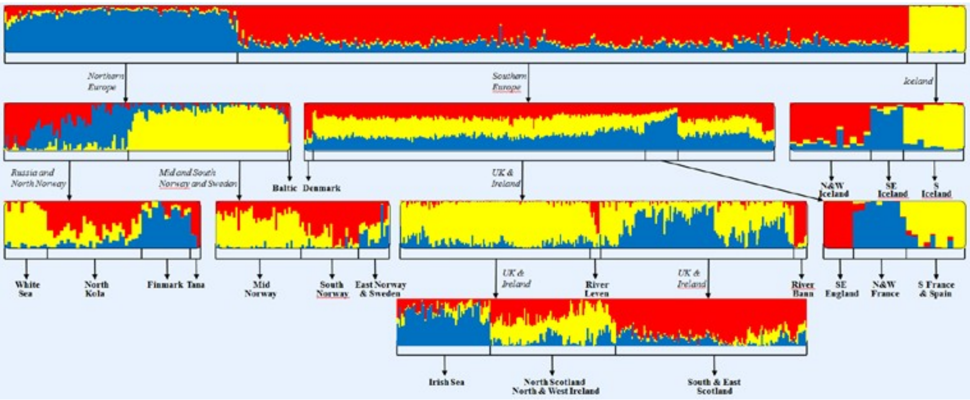
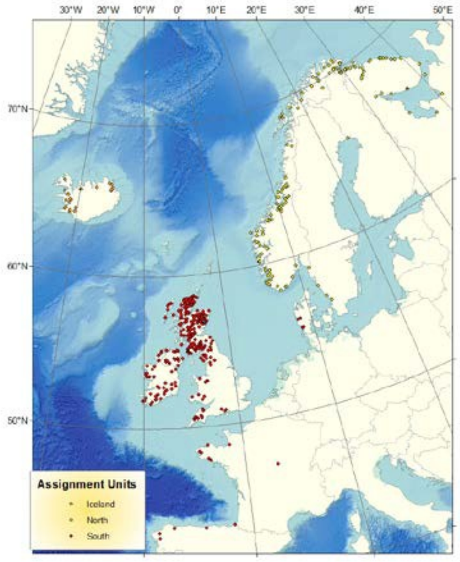
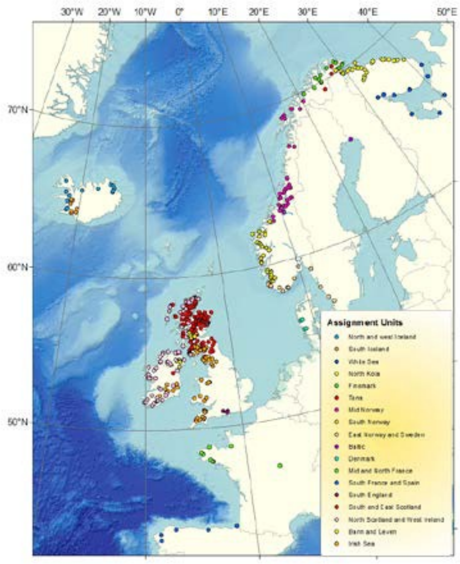


Figure 3.13: *Population structure as estimated from 4 levels of hierarchical STRUCTURE analysis. Populations are represented by vertical lines which are partitioned into shaded segments representing the populations estimated membership of one of the three potential clusters defined in the STRUCTURE run. Arrows represent the hierarchical approach with subsets of populations separated and re-analysed. The subsets are used are delineated below each plot. Text in italics represents clusters which were re-analysed in a subsequent hierarchical STRUCTURE run. Normal bold text represents a finalised cluster within which no further analysis was performed.*





An analysis was carried out to identify the natural phylogenetic regional stock groupings to define the GRAASP assignment units (AUs). The analysis showed hierarchical clustering of river stocks into large-scale and increasing finer-scale regional groups which could be used as AUs. The hierarchical structuring is shown in Figure 3.13. This ranged from 3 AU s at the coarsest level of resolution (Iceland, Northern Europe, and Southern Europe – Figure 3.14) to 17 at the finest supportable geographically cohesive subdivision (Figure 3.15). The size of the regional groups at each level varied. These natural evolutionary and geographical delineations of river stocks were implemented in the GRAASP.

The baseline was established using samples taken over a period of a decade it was necessary to assess the assignment consistency of the GRAASP when using samples collected over wide time frame. The temporal stability of the genetic differences among river stocks based on using samples taken at different times, and potentially different locations within a river, at different seasons, or using different life history stages, was investigated (Nielsen et al., in prep). The meta-analysis undertaken used genetic data from 47 salmon populations from Ireland, Scotland, United Kingdom, Denmark, Norway and Russia (Figure 3.16), the highest number of salmon population investigated in any such study. Significant genetic differentiation was found among temporal samples for 34 of the 47 rivers investigated, but genetic variation among samples within a river stock was low (1.4%) relative to that within samples (95.16%) and among river stocks (3.31%). The number of years between temporal samples varied between one and ten (mean 3) and there was no statistically significant correlation between the number of years between samples and the level of genetic differentiation (Figure 3.17). There was also significant variation among regions in the occurrence of significant temporal variation within river stocks. The analysis demonstrates that such temporal variation needs to be taken into account as regards its implications for assignment accuracy and the need to update the baseline in the future as has been found to be necessary for similar baselines in Pacific salmon species.

Figure 3.14, upper: *Level 1 Assignment regions.*
Figure 3.15, lower: *Level 4 Assignment regions.*

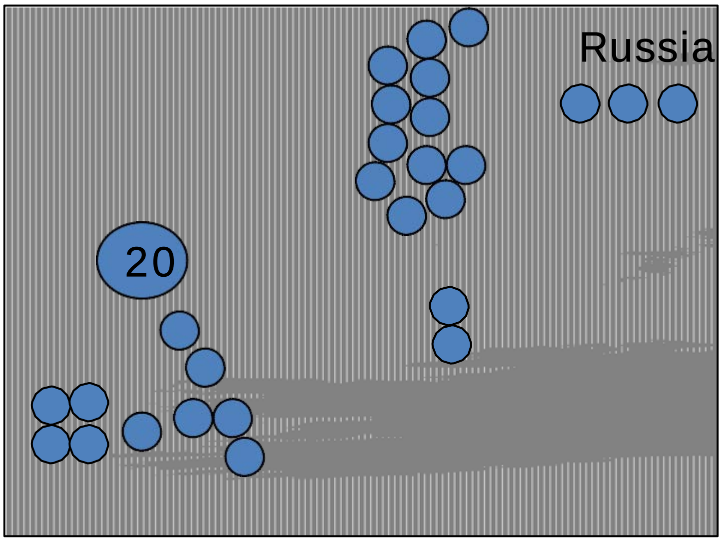


Figure 3.16: *Geographical distribution of samples employed in the temporal genetic stability analysis.*

In light of emerging genetic technologies, further work has carried out to assess the potential of using other molecular loci as part of the GRAASP to make it more cost-effective or increase assignment resolution (Task 1.3). Toward this end, sets of samples were assembled to be used to evaluate within and among river variation and identify region specific genetic markers; assembly of a single set of samples for all purposes and archiving the material proved inefficient and of limited merit. Existing reference sets of tissue and DNA samples assembled by research labs across the North Atlantic were accessed.

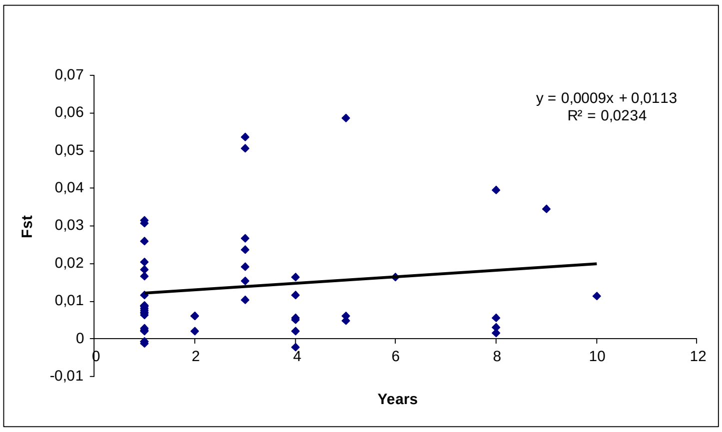


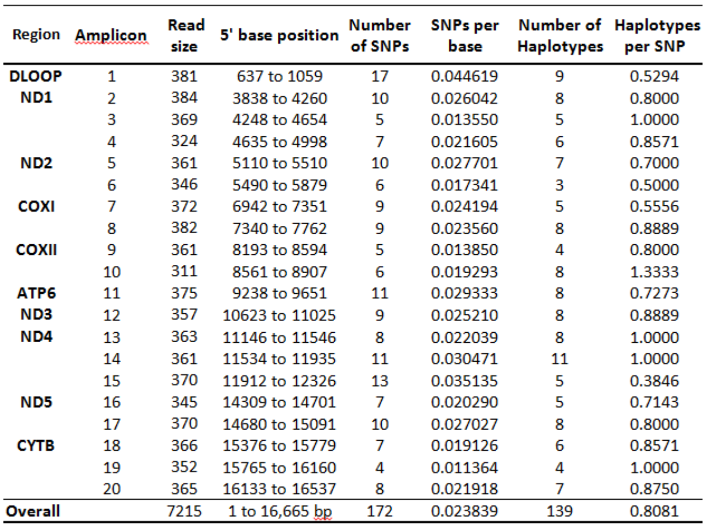
Figure 3.17: *Relationship between FST and number of years between samples.*

The initial data review found that the 14 microsatellite loci initially identified were sufficient for achieving the basic GRAASP objective, reducing the benefits to be gained from the extensive further screening of microsatellites envisaged as necessary to identify a set of loci for this purpose. However, recognising that the suite chosen could potentially be refined to be more efficient and provide higher resolution, a further 49 microsatellites that had particular promise for regional assignment were assessed compared to the standard Virginia15 (SALSEA14+1); the freed resources were redirected to nuclear SNP development, a more promising option for GRAASP enhancement. This assessment (Table 3.4) showed that gains from revising the suite of 14 were found but variable and limited at best, and that SNP markers were more likely to be useful for enhancing GRAASP resolution and cost-effectiveness.

Table 3.4: *Assignment success using different suites of microsatellites.*

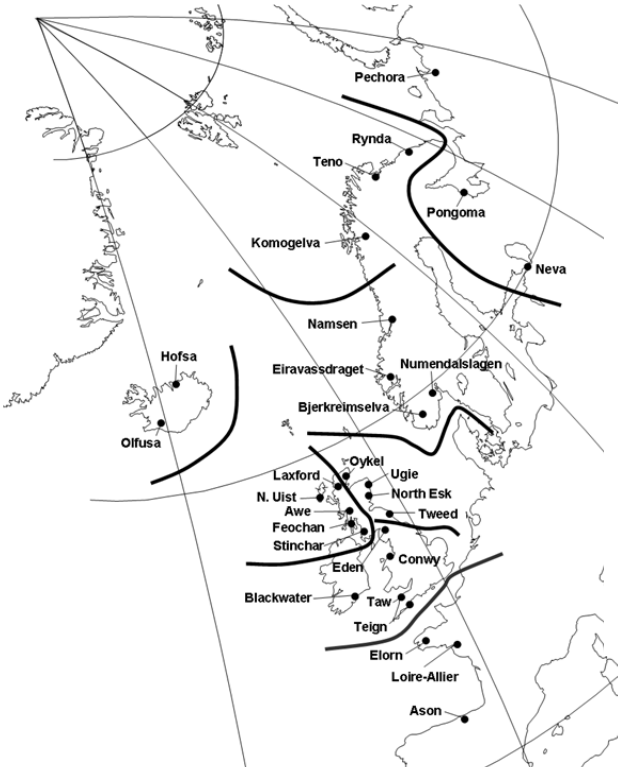
River	**To river**			**To region**		
	All	**Standard set**	**Optimal 15**	**All**	**Standard set**	**Optimal 15**
BlackW	50	25	33	100	59	66
Laxa	100	92	100	100	92	100
MoyTrim	67	33	58	100	83	83
Numedalslågen	70	30	70	90	60	90
Orkla	83	58	50	92	64	50
Shin	92	75	83	92	75	83
Esva	100	67	92	100	67	92
Naatamo/Neiden	75	58	58	100	64	83
Ponoi	50	42	42	100	84	92
Suir	64	55	18	91	82	45

***Table 3.5:** Amplicons sequenced and levels of polymorphism observed.*



Region	Amplicon	Read size	5' base position	Number of SNPs	SNPs per base	Number of Haplotypes	Haplotypes per SNP
DLOOP	1	381	637 to 1059	17	0.044619	9	0.5294
ND1	2	384	3838 to 4260	10	0.026042	8	0.8000
	3	369	4248 to 4654	5	0.013550	5	1.0000
	4	324	4635 to 4998	7	0.021605	6	0.8571
ND2	5	361	5110 to 5510	10	0.027701	7	0.7000
	6	346	5490 to 5879	6	0.017341	3	0.5000
COXI	7	372	6942 to 7351	9	0.024194	5	0.5556
	8	382	7340 to 7762	9	0.023560	8	0.8889
COXII	9	361	8193 to 8594	5	0.013850	4	0.8000
	10	311	8561 to 8907	6	0.019293	8	1.3333
ATP6	11	375	9238 to 9651	11	0.029333	8	0.7273
ND3	12	357	10623 to 11025	9	0.025210	8	0.8889
ND4	13	363	11146 to 11546	8	0.022039	8	1.0000
	14	361	11534 to 11935	11	0.030471	11	1.0000
	15	370	11912 to 12326	13	0.035135	5	0.3846
ND5	16	345	14309 to 14701	7	0.020290	5	0.7143
	17	370	14680 to 15091	10	0.027027	8	0.8000
CYTB	18	366	15376 to 15779	7	0.019126	6	0.8571
	19	352	15765 to 16160	4	0.011364	4	1.0000
	20	365	16133 to 16537	8	0.021918	7	0.8750
Overall		7215	1 to 16,665 bp	172	0.023839	139	0.8081

A study was made of the potential for using mtDNA SNP variation to enhance the resolving power and cost-effectiveness of within continent assignment of European salmon based on microsatellite (Fridjonsson et al. 2011; Verspoor et al., in review). The latest DNA sequencing methods were used to identify variation in 20 mtDNA regions (Table 3.5), encompassing ~43% of this genome in 330 individuals from 29 rivers across Europe (Figure 3.18). High levels of inter-individual and inter-river variation were found,
encompassing 137 different variants (Figure 3.19). An analysis of variance shows evidence of regional differentiation (Table 3.6) paralleling observed microsatellite differentiation. The observations indicate scope for using mtDNA SNPs along with microsatellites for genetically-based assignment of European salmon to region and river of natal origin but further study is needed.



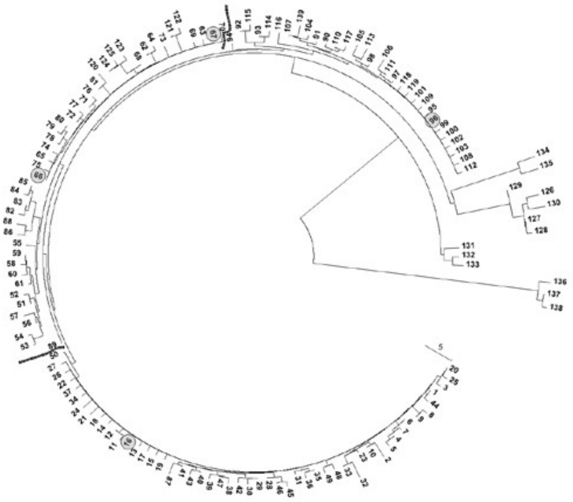


***Figure 3.18, left:** The locations of rivers from which samples were analysed; heavy lines delineate regional stock groupings used for stratified resampling – see text.*

***Figure 3.19, right:** Minimum evolution (ME) tree of the relatedness of the haplotypes based on number of pair-wise differences; the most common haplotypes are highlighted.*

In collaboration with CIGENE, Norway, an arbitrary panel of 388 EST-DNA derived nuclear SNP loci (nSNPs) were assessed for potential utility for regional assignment (Coughlan et al., in prep).

Table 3.6: *Results of AMOVA analysis for within group and among group variation of haplotype frequencies; groups are as delineated in Figure 3.18.*

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Among groups	15	256.682	0.67135 (Va)	16.68
Within groups	13	48.901	0.04287 (Vb)	1.07
Within populations	301	985.680	3.27469 (Vc)	82.09
Total	329	1291.264	3.98891	

Screening conditions were optimised and variation ascertained in an average of 5.5 fish (range 1-26) from 84 rivers across the species range (Figure 3.20 and Table 3.7) plus 9 Irish farm fish and 4 salmon/trout hybrids. The final analysis involved 477 fish and 305 of the 388 SNPs. The analysis reveals substantial population structure and regional grouping similar to that identified using other genetic markers (see above). The regions shown by the STRUCTURE analysis are 1) North America, 2) Iceland, 3) Baltic/Russian/northern Norway, 4) western Norway/Sweden and 5) Denmark/British Isles/France/Spain (Figure 3.21). The nSNPs show ascertainment bias e.g. in terms of different levels of genetic variability within clusters, a useful aspect of the distribution of variation for assignment. The number of nuclear SNPs required for correct assignment to region of origin is indicated to be likely to vary from a few to a few tens of loci (Table 3.8). The study shows that arbitrarily identified nSNPs to be of great potential utility and reliability, at least, for assigning samples to broad geographical region of origin.

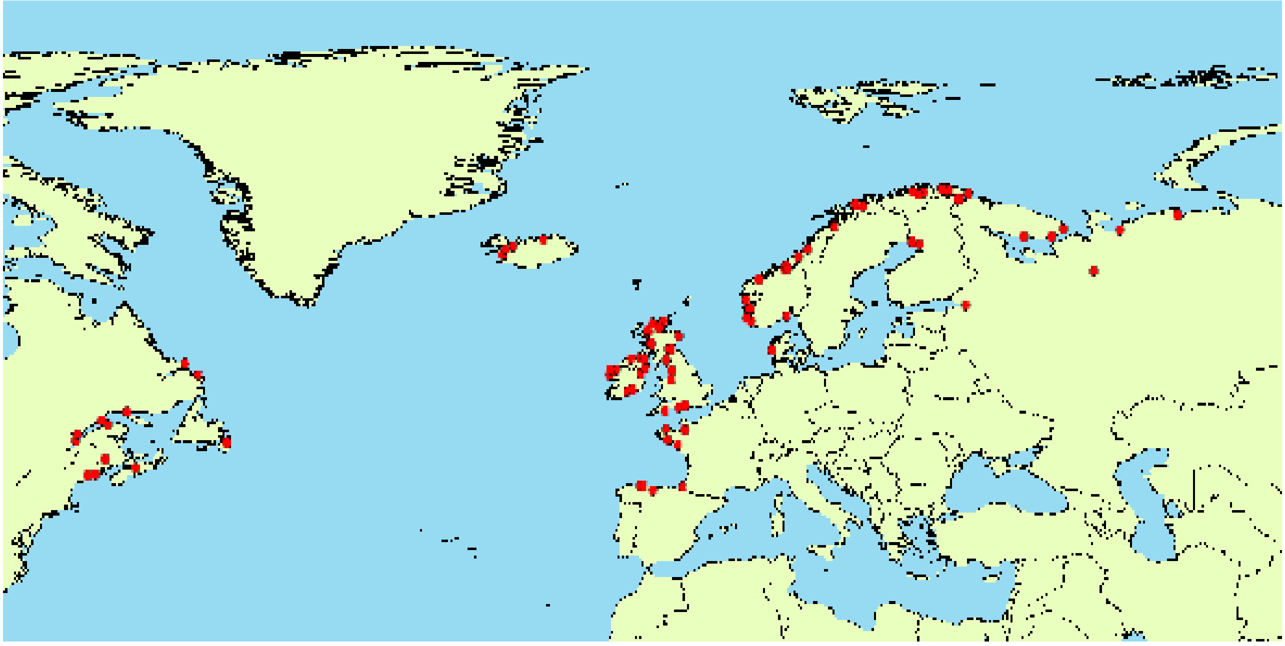


Figure 3.20: *Approximate locations of origin of Atlantic salmon samples used in nSNP study.*

Table 3.7: *Sample details of individuals used in SNP analysis.*

Country	River	n	Country	River	n
Canada	Malbaie	5	Norway	Etneelva	4
Canada	Michael	3	Norway	Figgjo	3
Canada	Sandhill	1	Norway	Komag	4
Canada	Seal Cove	3	Norway	Lakselv	4
Canada	Ste Anne	5	Norway	Langfjordelva	3
Canada	Stewiacke	1	Norway	Laukhalle	4
Canada	St Jean	5	Norway	Loneelva	4
Canada	St John	7	Norway	Naatamo	8
Canada	Ste Marguerite	5	Norway	Neiden	4
Canada	Trinite	5	Norway	Numedalslagen	10
Denmark	Skjern	1	Norway	Orkla	12
England	Dart	3	Norway	Reppasfjord	4
England	Esk	1	Norway	Saltdalselva	5
England	Frome	4	Norway	Skauga	4
England	Itchen	1	Norway	Stordalselva	5
England	Lune	1	Norway	Tana	26
Finland (Baltic)	Simojoki	5	Russia	Pecha	2
France	Allier	5	Russia	Pechora	5
France	Leguer	1	Russia	Ponoi	14
France	Nivelle	6	Russia	Pulonga	2
France	Scourff	3	Russia	Varzuga	14
France	See	5	Russia	Vigda	5
France	Selune	2	Russia (Baltic)	Neva	3
Iceland	Langa	4	Scotland	Almond	5
Iceland	Laxa i Aldal	5	Scotland	Awe	4
Iceland	Laxa I Dolum	11	Scotland	Coulin	5
Iceland	Nupsa	5	Scotland	Don	4
Ireland	Blackwater	15	Scotland	Ewe	1
Ireland	Boyne	5	Scotland	Halladale	8
Ireland	Burrishoole	5	Scotland	Laxford	10
Ireland	Dawros	5	Scotland	Nith	4
Ireland	Fanad (farmed)	9	Scotland	Orchy	6
Ireland	Moy	11	Scotland	Shin	11
Ireland	Owenmore	7	Spain	Esva	12
Ireland	Suir	10	Spain	Narcea	5
Northern Ireland	Bush	7	Spain	Sella	3
Northern Ireland	Glendun	6	Sweden	Altran	5
Northern Ireland	Shimna	7	Sweden	Ura	4
Norway	Åelva	4	Sweden (Baltic)	Tornijoki	13
Norway	Bjerkreimselva	2	USA	Narragus	4
Norway	Bogna	4	USA	Penobscot	5
Norway	Borselv	4	Wales	Dee	7
Norway	Målselv	4	Multiple	Hybrids	4

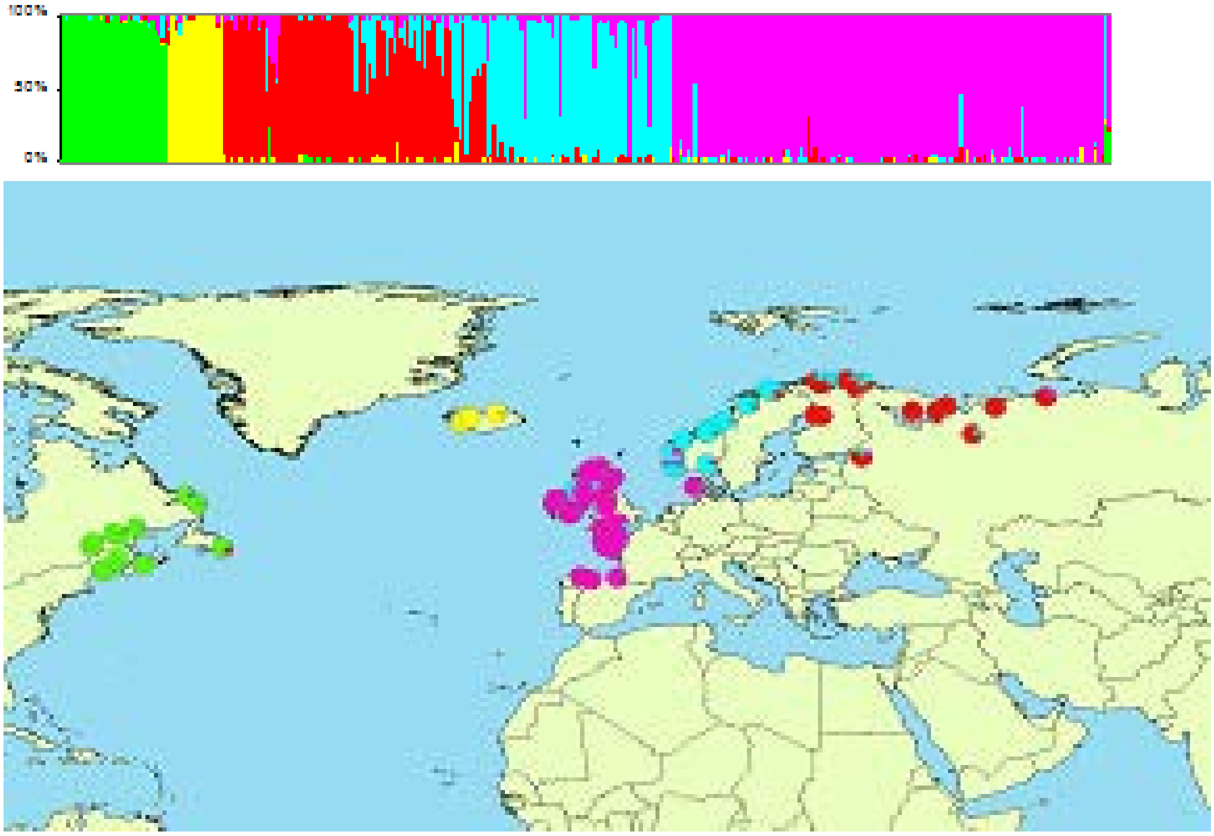
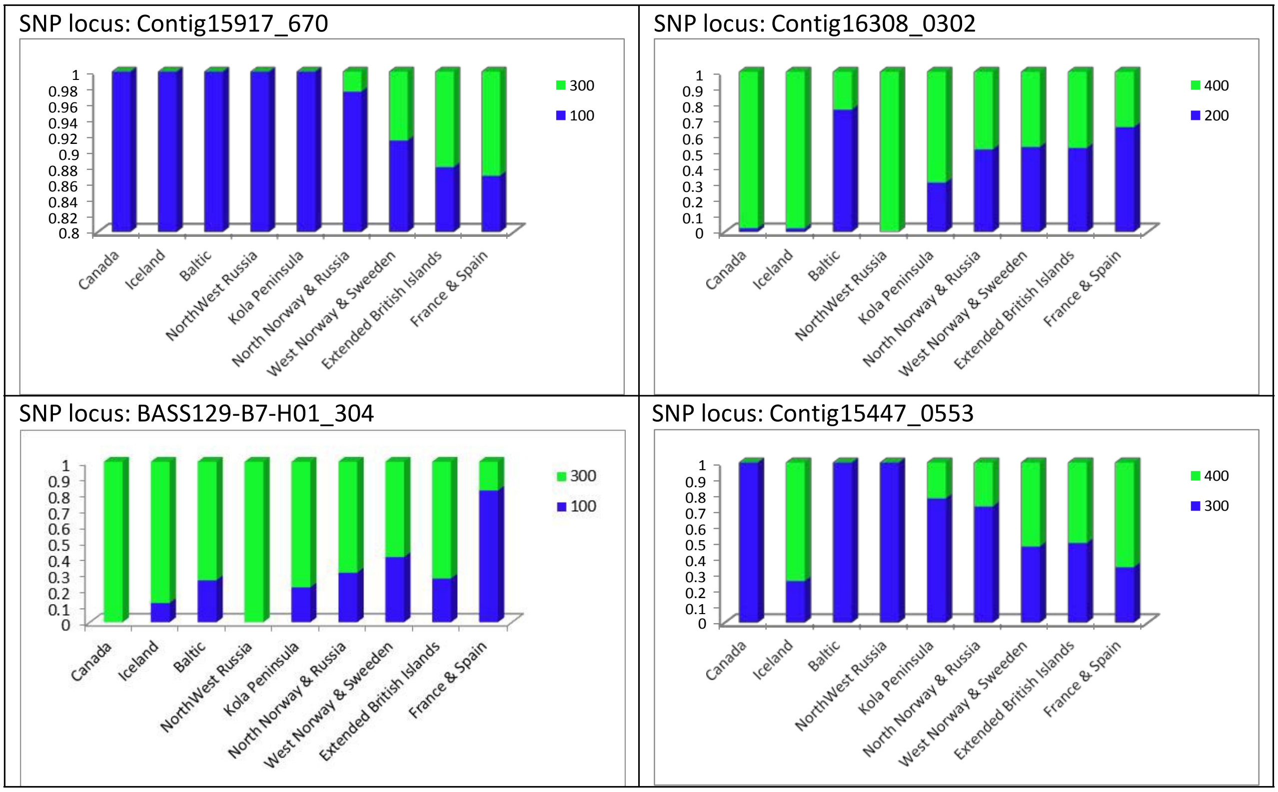


Figure 3.21: *Estimated genetic structure (revealed by STRUCTURE) where each individual is partitioned into five clusters. The map shows the geographical distribution of individual partitioning (averaged for each river).*

Table 3.8: *Number of SNP loci and correct assignment success in terms of discriminating major genetic regions hierarchically.*

# SNP loci	**1**	**5**	**10**	**15**	**20**	**25**	**30**	**305**
North America	98.8							100
Iceland	97.3							100
Baltic	94.4	93.9	97.5					99.2
Kola Peninsula	88.6	88.6	91.2	96.2				99.7
South France/Spain	91.8	92.7	96.5					100
Russia/North Norway	81.1	89.6	92.1	89.1	94.0	94.6	96.2	96.8
West Norway *v* British Isles	76.4	89.4	92.1	94.1	96.1			97.6

The potential for enhancement is likely to be greatest using nSNPs which are subject to selective inter-regional or inter-river differentiation. A literature review identified promising nuclear coding genes (e.g. IDH, MEP, transferrin, and ‘executioner’ caspases), and one, the NADP dependent malic enzyme (MEP) gene complex, chosen for further development work, based on a strong existing case for its selective differentiation. Atlantic salmon expressed DNA sequences from potentially this complex were identified in various genomic databases but re-sequencing of these regions in fish of known MEP-2 genotype failed to resolve the target polymorphism. This work was complimented by screening samples from 84 rivers/locations across the species range for 306 arbitrary EST-DNA (expressed DNA sequences) sequences for patterns of variation among locations suggestive of diversifying selection. Of these, 88 were found to be potentially subject to diversifying selection, of which 41 were suggestive both within and between groups regional river groups across the range, 32 in European samples only, and 15 in comparisons between North America and Europe. Figure 3.22 gives example allelic frequency distributions among samples for these loci; in many cases, these nSNP loci display an obvious “gradient profile” related to geographical origin of samples. The regional clustering seen using these 88 nSNPs are virtually identical to that resolved using all 306 SNPs, and make clear the scope for using such selected loci to develop a more cost effective, useful and precise GRAASP in the future.


SNP locus: Contig15917_670

SNP locus: Contig16308_0302

SNP locus: BASS129-B7-H01_304

SNP locus: Contig15447_0553

Figure 3.22: *Allelic frequency distribution for 4 of the 90 identified SNP loci potentially under the influence of selection.*

The 14 microsatellite-based GRAASP developed for immediate application to marine samples was optimised and validated with respect to mixed stock analysis (MSA) and Individual Assignment (IA) (Task 1.4). This involved addressing 1) the quality, relative number and distribution of samples included in the baseline; 2) the regions for assignment; 3) the statistical method of assignment; and 4) assignment accuracy. A more extensive set of blind samples (967) than originally envisaged (200) was assembled for this purpose by taking out at random a small proportion of fish from the baseline, weighting their selection from rivers according to their relative productivity. Additionally, a further test was carried out by excluding 10% of rivers from the baseline and then testing whether these could still be successfully assigned to the region where they were located. This provided a more stringent test than a straight forward test based on an overall assessment of self-assignment, which tends to overestimate assignment accuracy. The sample composition of the baseline was optimized for data quality by including only samples with 30+ fish for which data was available for most loci for most fish and variant frequencies did not depart from random expectation at more than 6 loci. The regional distribution of rivers used in the final baseline data set compared to the original numbers analysed and considered is set out in Table 3.9.

Assessment of the different software packages available for assignment found that none was universally superior in the current context. However, the most efficient for running large numbers of simulations and assignments was the Baysean approach implemented in the freeware GENECLASS programme and this was used for the GRAASP. Further assessment also showed that assignment of individuals to defined regions was most efficient using the highest combined probability (HCP) across rivers from a region rather than the highest single probability (HSP) of river of origin, with the HCP always allowing the assignment of more fish correctly for a given level of accuracy (Figure 3.23). As such the HSP approach was taken. The effect of using a baseline data set weighted for productivity or a restricted baseline one based on equal regional geographical distribution was also evaluated (Table 3.10). The results of the two approaches were not significantly different and the former was used.

Table 3.9: *The final number of rivers included in the GRAASP data base by country/region before and after quality control.*

Row Labels	Total Rivers collected	Rivers used in baseline after QC
Denmark	6	4
England	38	35
Finland	4	4
France	8	2
France	8	7
Iceland	25	22
Ireland	45	40
Northern Ireland	20	18
Norway	117	101
Russia	37	33
Scotland	260	185
Spain	7	4
Sweden	3	3
Wales	10	9
Grand Total	**588**	**467**

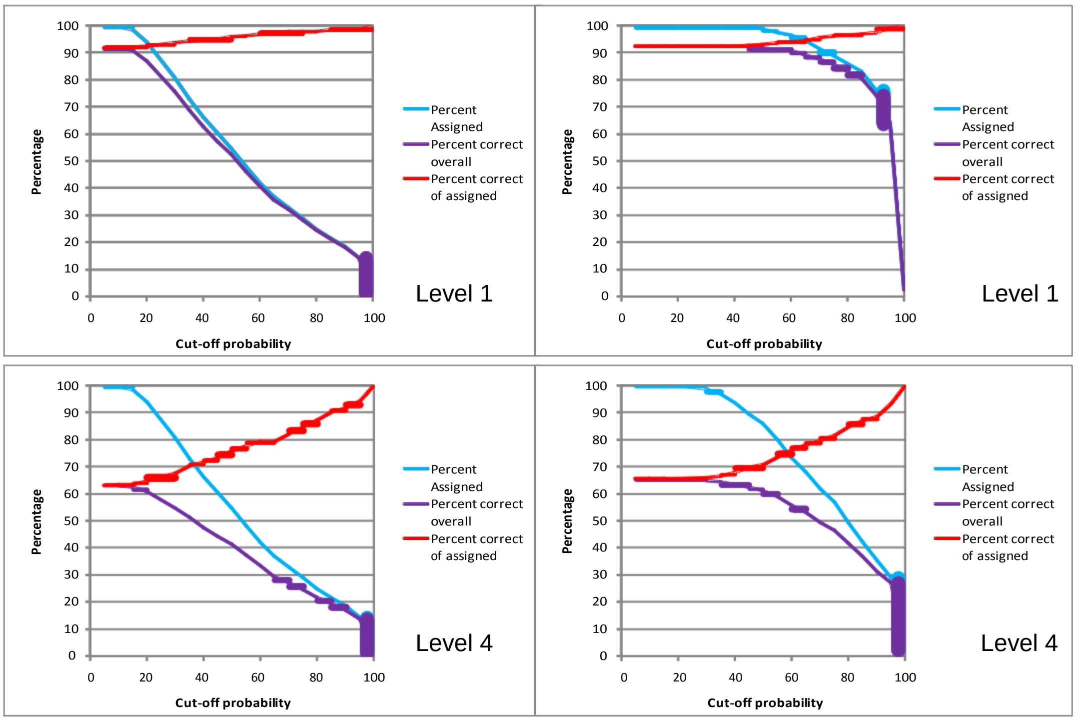


Figure 3.23: *Assignment of individuals to defined regions using the highest single probability (HSP) method, on left, or the highest combined probability (HCP) across rivers method, on right, for the two levels of regional assignment.*

Table 3.10: *Comparison of assignment success of blind samples in respect of Level 1 regions of the full baseline set with relative numbers of rivers in regions weighted by relative productivity and equal numbers of populations per region.*

	Equal baseline	Full baseline	Real origin
L1 North	**360**	**338**	**354**
L1 South	**569**	**594**	**577**
L1 Iceland	**38**	**35**	**36**

WP 3:

Genetic identification of stock origin of samples

The overall objectives of WP3 was to provide a real-life assessment was made of the capacity of the GRAASP to establish the regional origin of marine caught fish and deliver assignments to WP5 to provide new insights into the marine biology of the Atlantic salmon in the Northeast Atlantic. A total of 2290 samples of DNA were assembled from archival samples of tissues and scales collected variously from salmon captured in the NE Atlantic between 1996 and 2007 as part of previous sampling programmes (Table 3.11) and genetically typed for the GRAASP microsatellites, and assigned to region of origin. A further 1729 samples of DNA were assembled and genetically typed from salmon in this region collected specifically as part of the project during the course of marine sampling trips (WP2;Table 3.12) and these were also assigned to region. In total 3871 of the 4151 archival and contemporary marine samples typed provided sufficient genetic information to allow them to be assigned to region of origin using the associated summed assignment scores. The distribution of these samples is shown in figure 3.24. The mean assignment scores for Level 1 and 4 assignments are given in Tables 3.13 and 3.14, respectively. As expected form the blind sample analysis, assignments are made with greater confidence at the higher regional splits, however assignment confidences are still relatively high even at the lowest level 4 splits.

Table 3.11: *The archival samples available for analysis from various historical marine surveys detailed by month and year.*

	Year								
Month	**1996**	**1997**	**2000**	**2001**	**2002**	**2003**	**2004**	**2006**	**2007**
January									
March									
April							121		1
May			142		99	41			71
June	165	259		180	561	289		1	
July			29		30	93			
August						2		44	3
September									
October					36				
November							123		
Grand Total	165	259	171	180	726	425	244	45	75

Table 3.12: *The contemporary collected samples available for analysis from SALSEA-Merge cruises and Icelandic mackerel fishery by-catch detailed by month and year:*

	Year	
Month	**2008**	**2009**
January		1
March		2
April		
May	431	10
June		453
July	382	397
August	44	9
September		
October		
November		
Grand Total	857	872

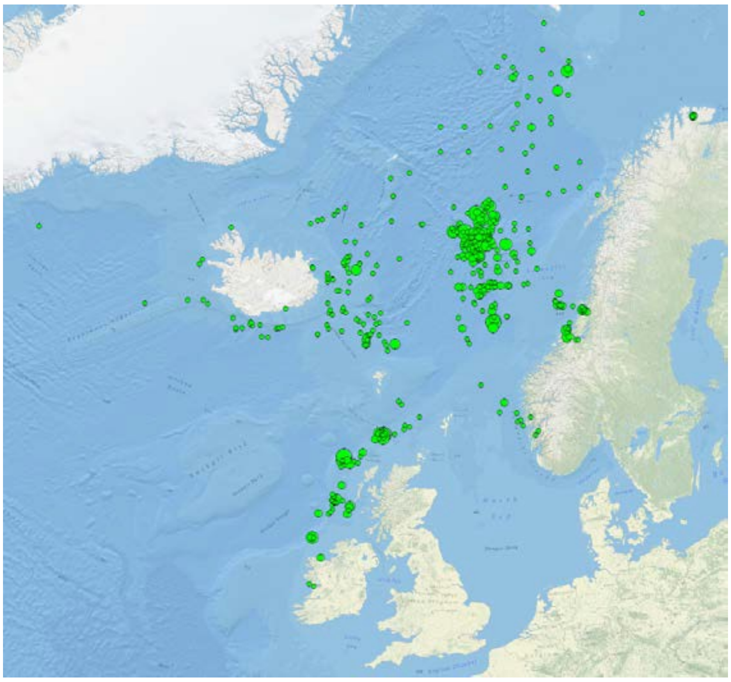


Figure 3.24: Distribution of combined archival and contemporary samples from NE Atlantic assembled for genetic typing.

Table 3.13: *Mean assignment scores for Level 1 regional assignments for blind samples.*

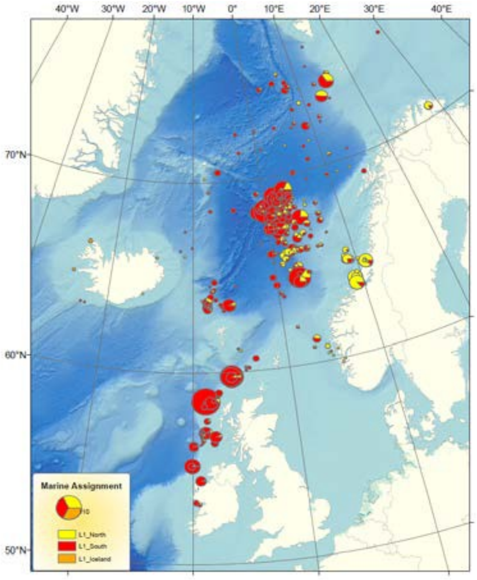
Level 1 regions	Number	Mean assignment score	StDev assignment score
Iceland	11	94.9	8.9
North	705	87.0	15.8
South	3155	91.7	10.8

Table 3.14: *Mean assignment scores for Level 4 regional assignments for blind samples.*

Level 4 regions	Number	Mean assignment score	StDev assignment score
Irish Sea	435	68.6	21.1
Denmark	13	94.9	13.0
Iceland NW	10	94.1	9.2
Iceland S	1	89.5	
E Norway & Sweden	98	69.4	23.7
Finmark	46	61.2	22.3
Mid Norway	277	72.1	20.6
N & W France	39	81.5	21.4
N Kola	69	66.8	20.2
S France & Spain	18	80.4	22.8
S Norway	167	63.1	20.0
South England	4	99.5	0.7
Tana	11	64.3	23.9
White Sea	38	71.9	24.8
Bann and Levin	60	73.1	22.5
N Scotland N&W Ireland	945	69.9	20.1
S&E Scotland	1640	71.3	19.3

The number of archival and contemporary samples analysed, though collectively large, is spatially and temporally patchy and precludes at this point a straight forward or robust analysis of spatial and temporal heterogeneity in the distribution of regional groups; many potential marine feeding areas are poorly represented (e.g. North Norwegian Sea) or not represented at all (e.g. East Greenland, Irminger Sea). It will take the cumulative data over a decade or more to develop a sufficiently comprehensive data base to allow questions to be addressed in a robust manner. However, it is already clear that there are significant spatial/temporal distributional differences among the defined regional groups.

The distribution of Level 1 assignments is shown in Figure 3.25 and 3.26. The distributions for different seasonal periods of the year are shown in Figure 3.27, 3.28 and 3.29. In respect of the Level 1 regional groups, the Southern region is overall significantly over represented relative to expectations based on relative regional productivity (Figure 3.30). The distribution of Level 4 assignments is shown in Figure 3.31 and 3.32. Within the southern regional stock group, subgroups show significant heterogeneity over the sampling years 2002, 2003, 2008 and 2009 (Figure 3.33). Significant temporal distributional shifts among years are also seen in respect of the Level 1 North and South regional groups; the distributions are the same in each case for 3 of the years for both groups but appear to have shifted and become disjointed in 2008 (Figure 3.34). For some rivers, such as the Allier in France, the Bann in Northern Ireland, and the Namsen in Norway, the assignment confidence of fish was sufficient to define distributional patterns for individual rivers (Figure 3.35-3.41). A potential complication of the application of GRAASP to assignment of the origin of wild salmon is the presence of farm fish. Most of these are likely to be of Norwegian origin, are expected to occur variously in marine waters throughout much of the NE Atlantic as a result of escapes from farm operations in the British Isles, Iceland and Norway. The anomalous presence of Level 1 northern genetic types in the marine samples taken to the NW of Scotland and Ireland at times when northern smolts would not yet have migrated into the sea from rivers was indicated by smolt ages consistent with a farm origin. Following inclusion of genetic data on farm fishes (Kevin Glover, unpublished) in the base line, genetic assignments of most of these fish is to farm stocks, demonstrating that this confounding factor can be addressed in any analyses of marine distribution. The apparent anomalous occurrence of the four most western and southern fish assigned as being of Namsen origin can be ascribed to their being of farm origin (Map 3.26), something ascertained once the farm stock data was included in the baseline data set. This is not surprising as the Namsen River stock was one of the main stocks used to establish at least one of the main Norwegian farm strains.



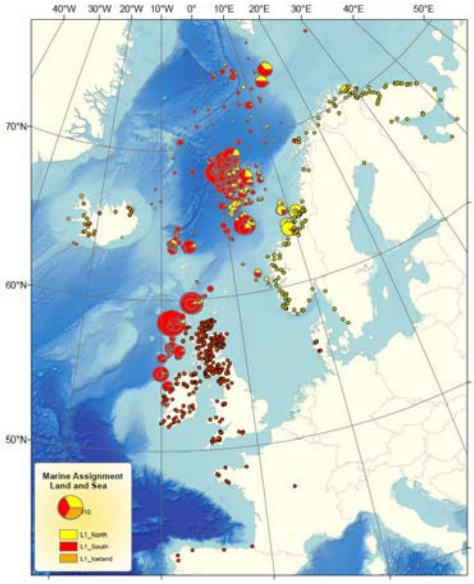


Figure 3.25, ***upper:*** *The distribution of Level 1 assignments; the size of the circles is proportional to the number of fish analysed from each location.*

Figure 3.26, ***lower:*** *The distribution of Level 1 assignments; the size of the circles is proportional to the number of fish analysed from each location.*

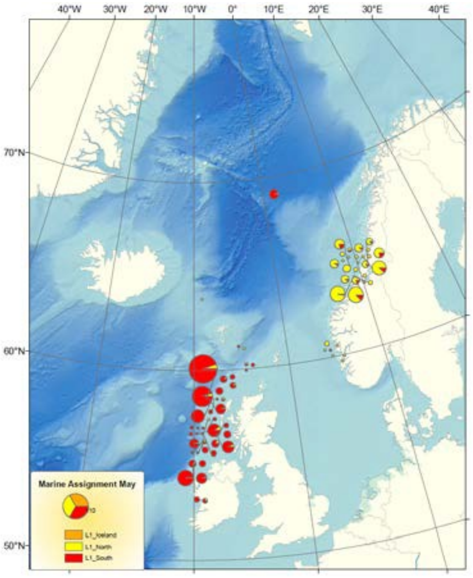


Figure 3.27, left:
The distribution of Level 1 assignments; the size of the circles is proportional to the number of fish analysed from each location.

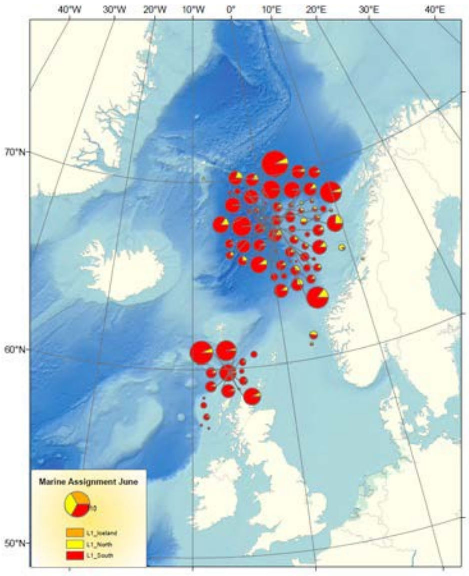
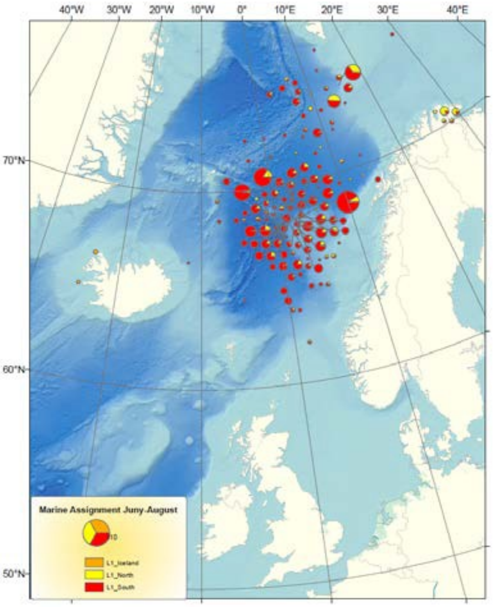


Figure 3.28, right:
The distribution of Level 1 assignments; the size of the circles is proportional to the number of fish analysed from each location.



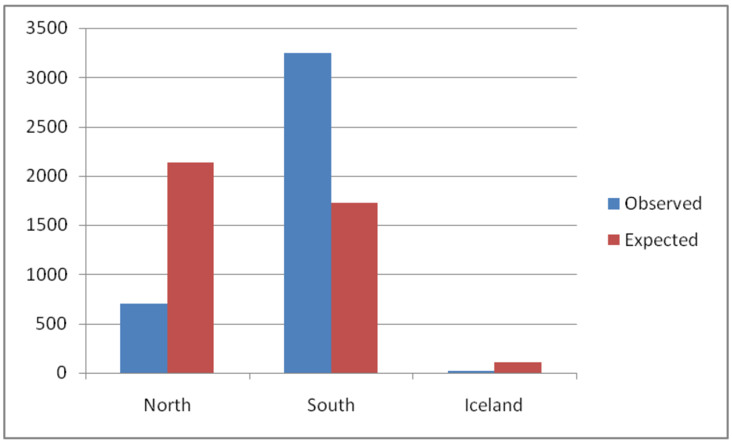
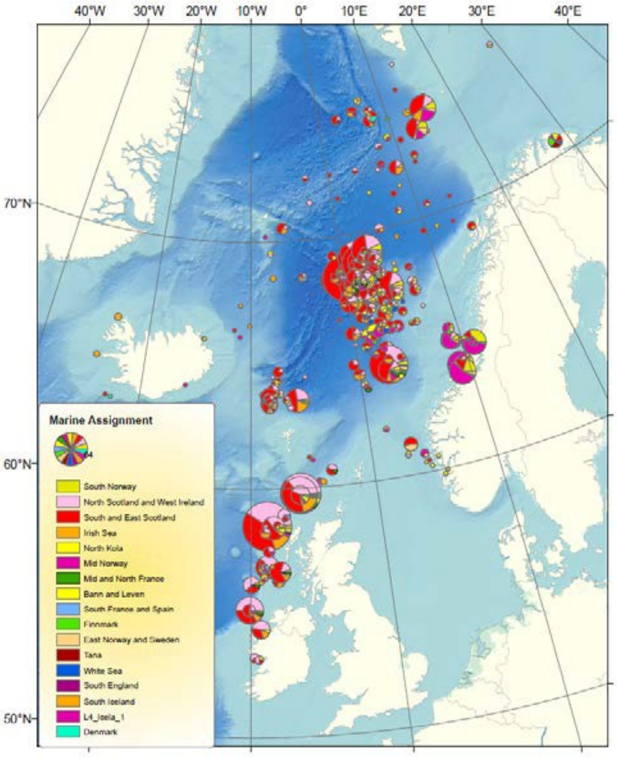


Figure 29, left: *The distribution of Level 1 assignments; the size of the circles is proportional to the number of fish analysed from each location.*

Figure 3.30, right: *The observed numbers of Level 1 regional group fish in all archival and contemporary samples analysed relative to the expected based on regional productivity and assuming that fish are distributed spatially and temporally at random. Difference significant P<0.0001.*



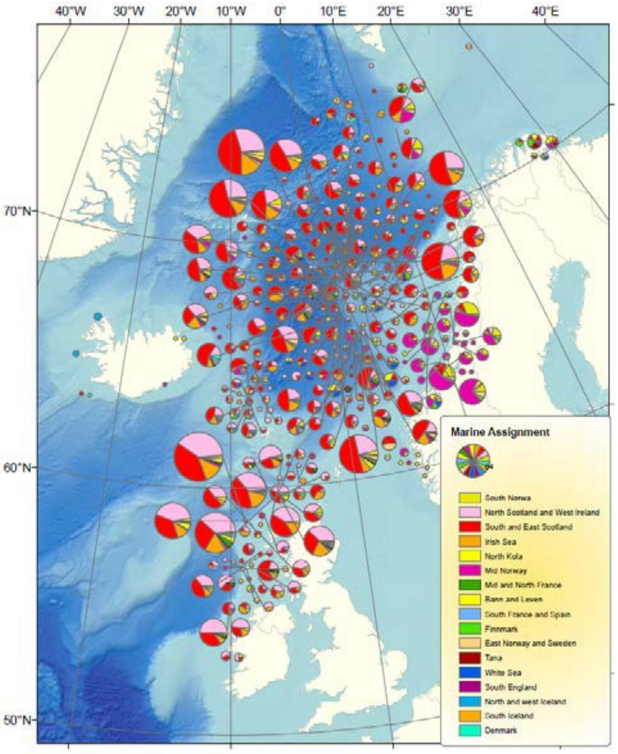


Figure 3.31, left: *The distribution of Level 4 assignments; the size of the circles is proportional to the number of fish analysed from each location.*

Figure 3.32, right: *The distribution of Level 4 assignments; the size of the circles is proportional to the number of fish analysed from each location.*

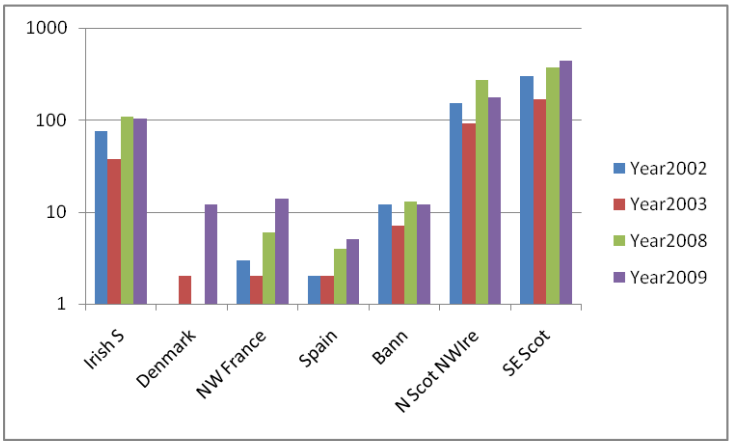


Figure 3.33: *The observed numbers of Level 4 fish with the Level 1 regional group fish in all archival and contemporary samples analysed in the four main collection years. Difference significant P<0.0001.*

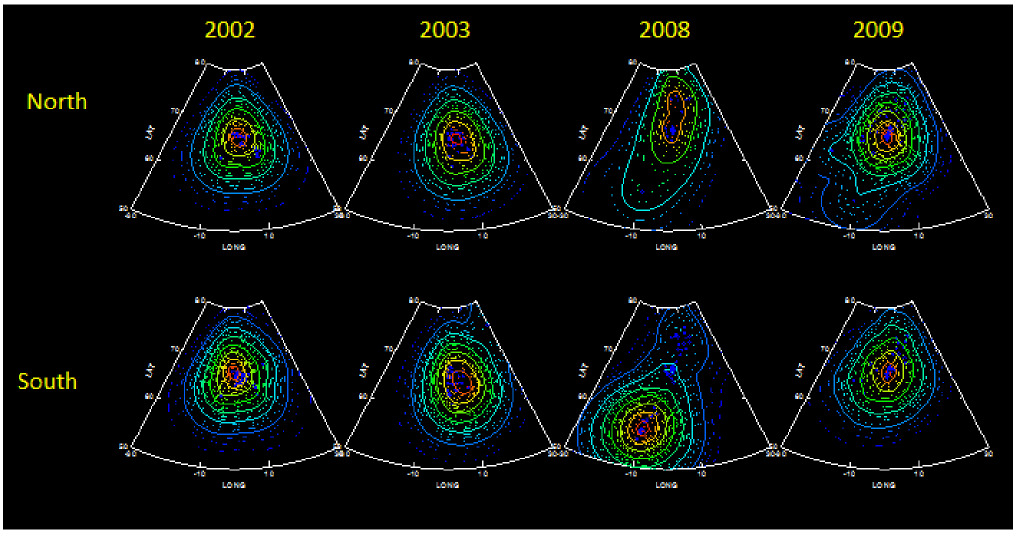
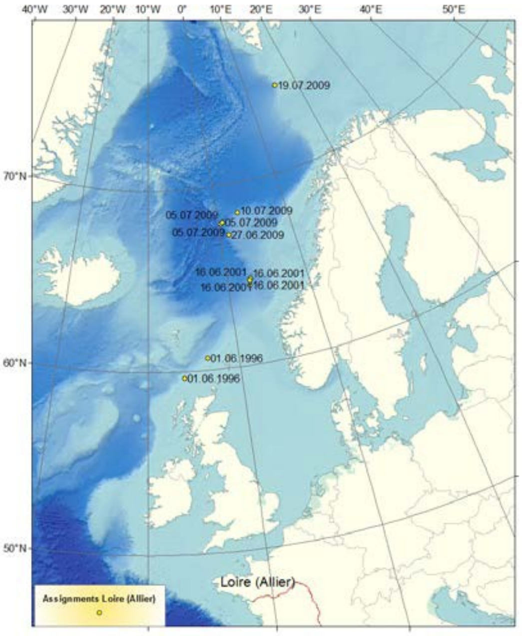


Figure 3.34: *Frequency of occurrence plots for the NE Atlantic region for the North and South Level 1 regional groups for each of the four main collection years for all archival and contemporary samples analysed; based on Krieging analysis.*



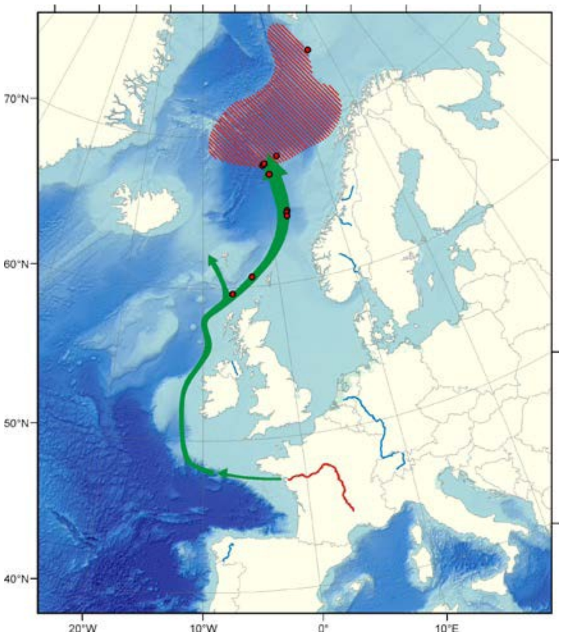
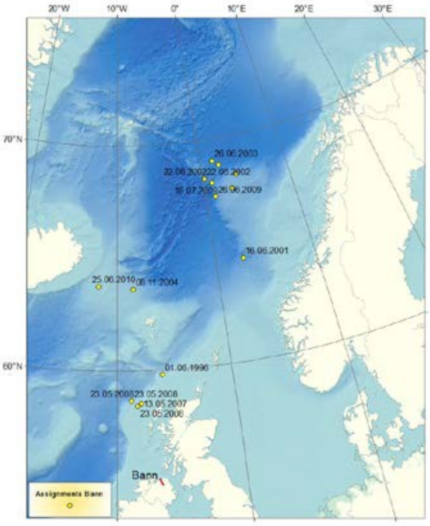


Figure 3.35, left: *The distribution of Allier River assigned fish from all samples analysed.*
Figure 3.36, right: *The distribution of Allier River assigned fish showing the implied migration route.*



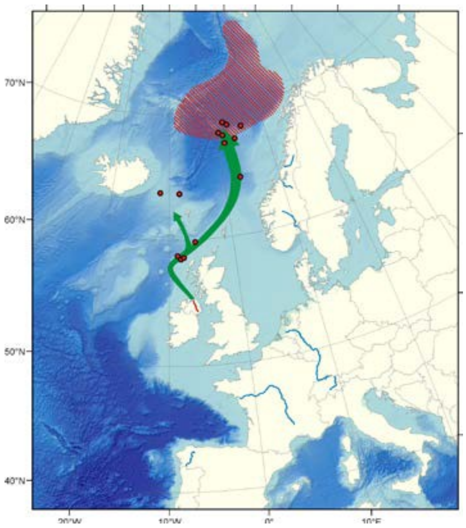
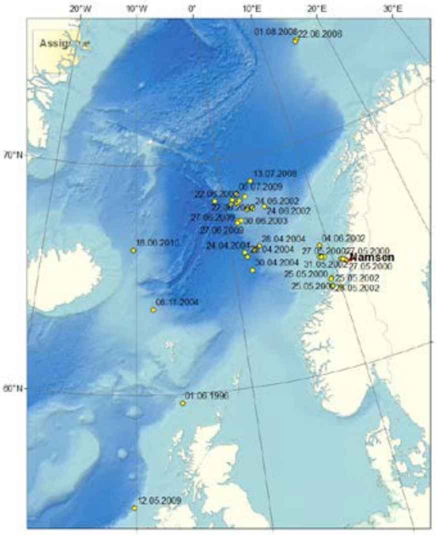


Figure 3.37, left: *The distribution of River Bann fish from all samples analysed.*

Figure 3.38, right: *The distribution of River Bann assigned fish showing the implied migration route.*

These assignments of actual marine samples clearly show the GRAASP developed is able to identify behavioural heterogeneity and confirms that the GRAASP delivers a useful and powerful new molecular genetic tool to help advance understanding of the species' marine ecology. Toward this end, the GRAASP database is now publically available for assignment and a manuscript describing the data base submitted for publication to make its availability known to salmon researchers and biologists. This should allow the existing database of assigned fish to be substantially extended as more material becomes available from other archives and new sample collections (e.g. on-going Icelandic mackerel and herring fisheries). At the same time, it is clear from the work carried out on mitochondrial and nuclear SNP markers in WP1 that there is likely to be a very substantial capacity to increase the resolution and cost-effectiveness of the GRAASP to increase the quality and extent of the insights gained.



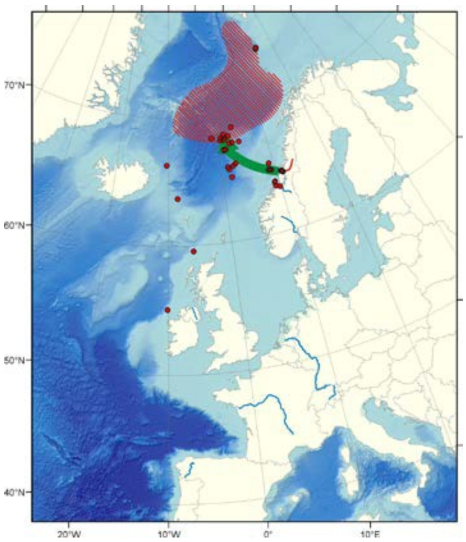


Figure 3.39, left:
The distribution of River Namsen fish from all samples analysed.
Figure 3.40, right:
The distribution of River Nansen assigned fish showing the implied migration route.

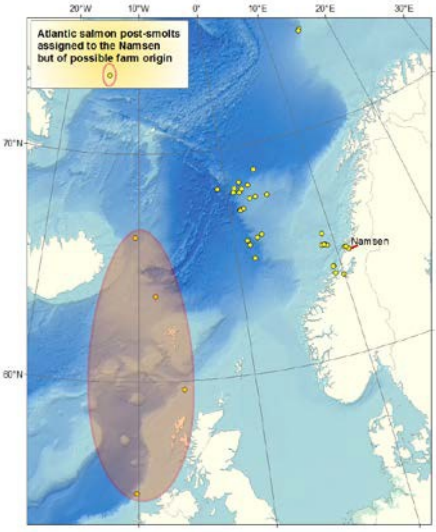


Figure 3.41: *The distribution of River Namsen origin fish with the fish subsequently determined to be of farm origin shown by the red elipse.*

WP 4:
Biological Analysis of Samples

Implementation of new digital scale reading methodology

As part of the SALSEA-Merge project, scales of post-smolts of Atlantic salmon collected from the cruises as well as historical scale material of adult salmon from several rivers, have been analysed by using contemporary digital scales reading techniques. Recent developments in digital analysis hardware and software have resulted in significant advances in this area. Analyses have been conducted in four leading European laboratories (participants 2, 4, 10 and 14), and appropriate equipment and software have been installed in these laboratories.

In images of salmon scales, the spacing between circuli was automatically measured for the marine zone and an aggregate length was recorded for the freshwater zone. These measurements must then be checked manually to ensure correct identification of individual circuli. Circuli spacings are used to quantify marine growth, with narrow spacings indicating periods of decreased growth and wider spacings representing periods with increased growth. A sum value of all circuli spacings from the first marine circuli to the winter annulus represents the total post-smolt growth for each individual (Figure 3.42). A workshop was held in Trondheim in September 2008 to train researchers from the four centres in the correct use of the new scale reading techniques, in the use of the new imaging equipment purchased for the project, and to ensure the use of standardized scale analysis procedures between laboratories. A report from this workshop is available (http://www.nasco.int/sas/salseamerge_ecological.htm). Following the workshop, when the necessary equipment had been installed in all laboratories, and initial training was provided in the ImagePro software, a blind test to ensure standardized scale reading was conducted.

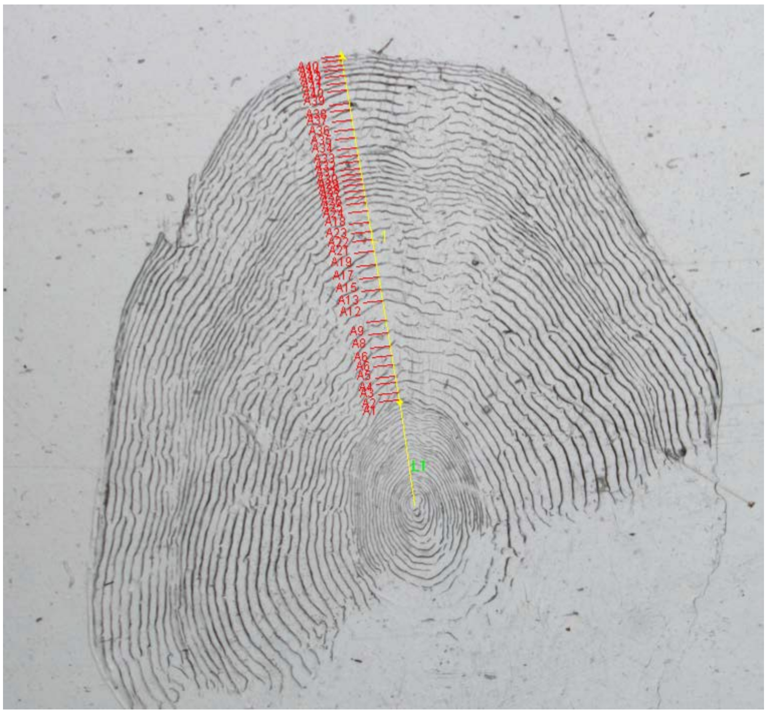


Figure 3.42 *Image of a salmon scale, with length measurement of the freshwater zone (L1) obtained by the Measurement window, and detailed growth data (A1-A40) obtained from the marine zone by the Caliper window of the Image-Pro Plus program.*

Obtaining biological information from scale reading

Reading of scale material from WP2

Over 23,000 scales of Atlantic salmon from seven rivers, located in six countries have now been analysed with the new scale reading technique (Table 3.15). Most scales are from 1970 to present, with some limited information for one stock extending back to earlier periods. The number of circuli laid down in the marine zone of the scales in specific periods as well as the distance between the circuli were measured, and this information is made available for further analyses in WP5.

Reading of scale samples collected in expeditions

In total, 864 post-smolts and 18 older salmon were caught at the trawl surveys in 2008, and the corresponding numbers for 2009 were 858 post-smolts and 28 older salmon. In addition, scales samples of 233 post-smolts collected at a trawl survey in the North-East Atlantic in 2002, and 234 post-smolts collected on a similar survey in 2003 were included in this project. Because of heavy scale losses in the trawl, many scale samples were taken on places not standardized for scale sampling, and in some cases scales were completely missing. Growth data derived from these scales had to be treated with caution. For individuals with missing scales, and in cases when the smolt age could not with certainty be determined from the scales, otoliths were also used for age determination. Scale samples were available for 813 and 765 post-smolts from 2008 and 2009, respectively. In addition, otoliths of 364 post-smolts from 2008 and 310 from 2009 were analysed.

Table 3.15: *Rivers where fine scale marine growth rate from scales of adult Atlantic salmon have been analysed by image analysis, periods when scales were collected, and total numbers of samples analysed.*

Country	River	Period	No. of years	Samples analysed
Norway	River Repparfjordelva	1932, 35-38, 40, 42-44, 46-48, 55, 59-2008	63	4080
Finland	River Teno, old data	1939, 72-2005	35	11565
	River Teno, new data	1976-78, 81, 86-88, 91, 96-98, 01, 06-08	15	1415
Iceland	River Nordurá	1988-2008	21	1956
	River Hofsá	1987-2008	21	1741
Ireland	River Burrishoole	1968-2008	47	2200
France	River Allier	2008-2010	3	52
Spain	River Ason	2000, 02-03	3	55

Establishment digital scale library

The growth data with the corresponding digital images have been split into two parts, and stored in two different electronic databases. During the project it became obvious that, due to the wealth of material available to the researchers, the disk space required to store the digital scale images was considerably larger than expected. A disk space of 17 GB was needed to store the images of the Atlantic salmon scales and otoliths from the surveys. Further, scale images of adult Atlantic salmon from just one of the rivers (4080 samples from the River Repparfjordelva) required 27 GB of disk storage capacity. Reducing the file size of the images will not solve the space problem, because some information may then be lost. Since 100 GB of disk space is rather unwieldy it was decided not to gather all of the images together in one storage unit. Further, growth data and scale images collected during the surveys fit well as an integrated part of the electronic database of biological information of marine samples from the surveys, while the data from the historical scale samples of adult fish from the selected salmon stocks do not fit into this database.

The growth data derived from scale samples of Atlantic salmon collected during the surveys, with the corresponding scale images, are included as an integrated part of the SALSEA_PGNAPES database. This Access database contains two tables relating to salmon growth ("SALMON_Scales" and "SALMON_Circuli_growth"). An overview of the database, relationships between the two growth tables and the remainder of the database, and a detailed description of the two tables related to fish growth, are given in Deliverable D 2.4. For each individual, one of the field names in "SALMON_Scales" contains the file name of the corresponding scale image (which is stored as a *.tif file), and another field name contains the name of the otolith image (if available). A link has been made available between the field name of each image, and the corresponding image. Hence, by accessing the table "SALMON_Scales", and double clicking on the file name of the scale image, the corresponding scale image pops up.

The second part of deliverable D 4.1 is a database of digital scale images and growth data derived from scales of adult salmon. The information on individual fish and growth data derived from scale analyses of over 23,000 individuals from seven rivers, located in six countries (see Table 3.15) are stored in a common database. References to the corresponding scale images along with the results of the growth indices derived from the scale analyses which is required for the second part of deliverable D 4.2, are also included. The digital scale images are currently stored locally at each of the four laboratories.

Determination of growth indices from scale readings

Determination of growth indices from historical scale samples from selected rivers

Peyronnet et al. (2007, 2008) and Friedland et al. (2008) have linked marine growth, survival and recruitment of Atlantic salmon in their first year at sea to ocean climate and conditions (SST, NAO, AMO and abundance of indicator plankton species). In this study, some of these relationships were examined for several new time series of post-molt growth representing other stocks from the North Atlantic. Over 23,000 scales of Atlantic salmon from seven rivers located in six countries have been analysed using contemporary digital scale reading techniques (Table 4.2.1). Circuli spacings were used to quantify marine growth, with narrow spacings indicating periods of decreased growth and wider spacings representing periods with increased growth.

In stark contrast to the temporal pattern seen for the Scandinavian and Icelandic rivers (Figure 3.43), the Burrishoole data (Ireland) indicate strong temporal variation over time, with most recent year's values being the lowest in the time series. There was no correlation between the temporal trend for the Burrishoole and other rivers examined. In the absence of direct measure of marine survival for each river, standardised survival indices were calculated for at least one river in close proximity to the rivers in this study where survival data were available (ICES 2011). Annual growth indices (PSG and/or circuli count) for the Burrishoole and Nordurá were positively correlated with the indices of survival (Table 3.16), but this was not the case for the other rivers. In addition, significantly positive correlations were shown between survival indices and monthly PSG indices for July, October, November and December for the Repparfjord, and Burrishoole in September and October (Table 3.17). Recruitment estimates (Pre-fishery Abundance, PFA) for the Northern and Southern components of the North Eastern Atlantic salmon stock are calculated annually (ICES 2011). Growth and recruitment correlated with PFA in several comparisons, but annual growth indices showed negative correlations with recruitment for the Hofsá and Nordurá, and positive correlations with the Burrishoole.

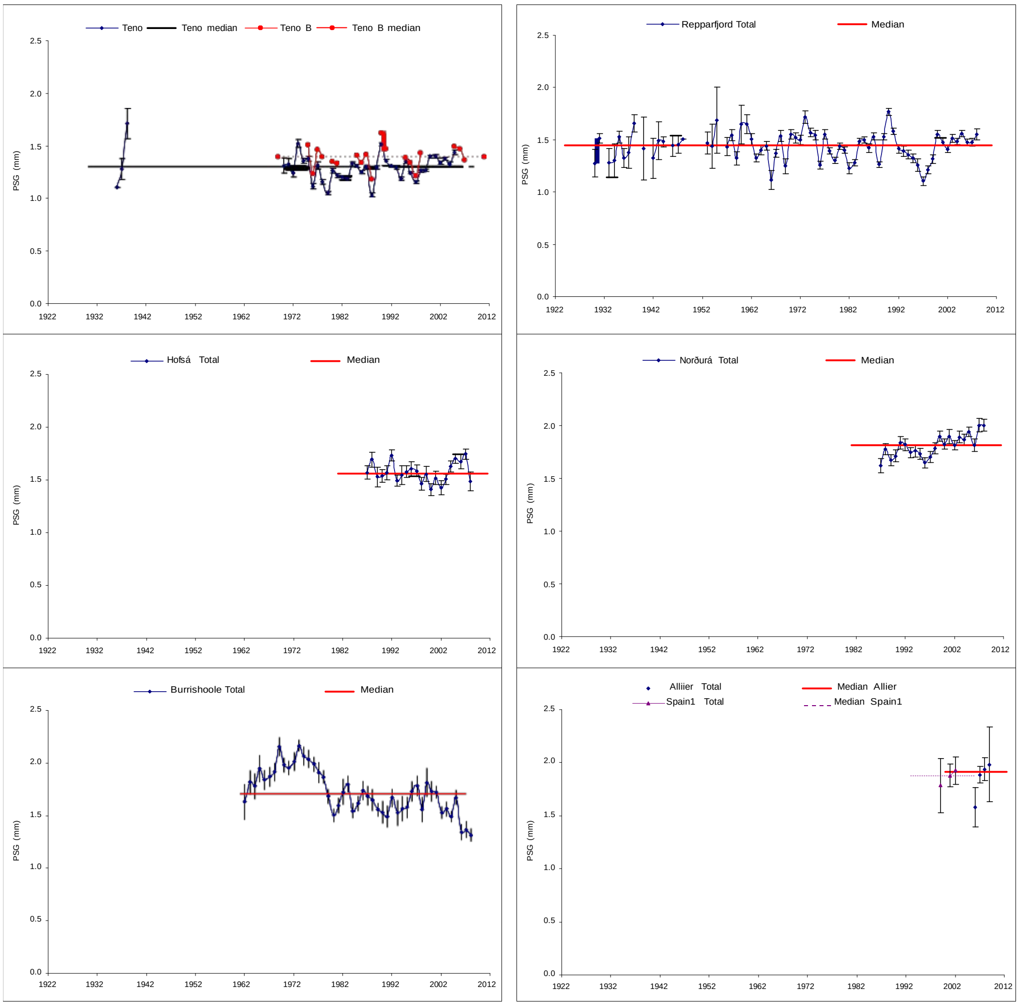


Figure 3.43: *Annual post-smolt growth (inter-circuli distance by smolt year) for selected rivers. Note: Temporal trends using post-smolt growth (PSG) or circuli count are similar, and only the results for PSG are shown for the purpose of the report.*

Annual growth indices (PSG and/or circuli count) generally correlated with SST (local spring or summer, or broadscale oceanic SST, annual or summer) while there were some correlations with specific months in the first year in the ocean for migrating post-smolts. Significant positive correlations were indicated between annual growth indices and Winter index of NAO for Repparfjord and Teno, but with negatively correlations indicated with the Burrishoole.

As suggested by Peyronnet et al. (2007, 2008) and Friedland et al. (2009), scale growth appears to be a proxy for survival/recruitment in this study. However, while consistent relationships were shown for the Burrishoole and Nordurá, it is less clear for the other rivers. The lack of temporal synchrony between these rivers, which are widely located geographically, may suggest very different post-smolt feeding areas which are influenced by different oceanic conditions and biological parameters. Growth is, however, clearly linked to oceanic conditions (either SST or NAO or both) for all rivers. Further investigation is also warranted to identify key periods and locations where these factors influence growth rates specifically as this could provide insights into how fish from different geographic origins are influenced by broader oceanic conditions.

Table 3.16: *Summary of Pearson correlations (uncorrected) for specific tests. Significant correlations (p< 0.05) in italic text, highly significant (p< 0.01) in* ***bold italic,*** *and very highly significant (p< 0.001) in* ***bold, italic and underline.***

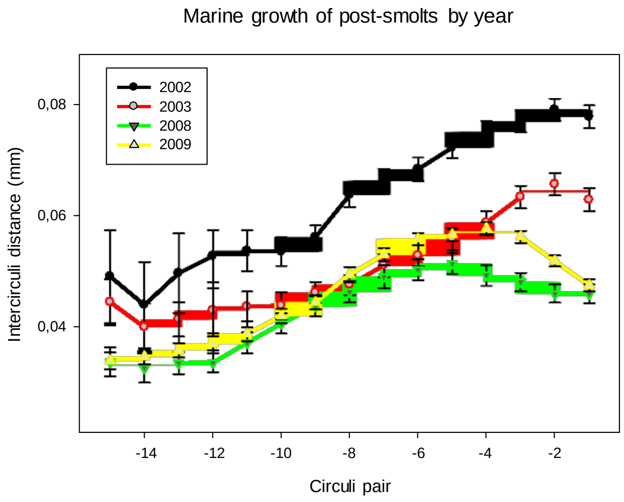
Test Name	Survival Index	PFA	Local Spring SST	Local Summer SST	Annual SST North Atlantic	Summer SST North Atlantic	Winter NAO
Mean Annual PSG							
Repparfjord			***0.408***	*0.247*			
Teno Hofsá			***0.554***	***0.484***	*0.384*		***0.484***
Nordurá							
Burrishoole	*0.445*	*-0.455*		*0.498*	***0.757***	*0.517*	
	0.415	***0.457***	***-0.449***	***-0.468***			*-0.37*
Mean Annual Circ Count							
Repparfjord							
Teno			***0.369***	*0.254*	***0.431***	*0.268*	***0.37***
Hofsá			***0.574***	***0.508***	***0.523***	*0.372*	***0.47***
Nordurá		*-0.486*	*0.423*		*0.526*	*0.474*	
Burrishoole	*0.443*	*-0.53*		*0.472*	***0.722***	***0.584***	
		0.459	***-0.388***	***-0.423***			***-0.385***

Table 3.17: *Summary of Pearson correlations (uncorrected) for specific tests using putative monthly growth indices in the first year at sea. Significant correlations (p< 0.05) in italic text, highly significant (p< 0.01) in* ***bold italic*** *and very highly significant (p< 0.001) in* ***bold, italic and underline.***

Monthly PSG	Survival Index Repparfjord	Survival Index Burrishoole	Local Summer SST Nordurá	Local Summer SST Burrishoole
May				*-0.3*
June			***0.598***	
July	*0.421*			
August				
September		***0.496***		
October	***0.489***	*0.413*		
November	*0.436*			
December	*0.415*			

Determination of growth indices from scale samples collected in expeditions
The objective of this sub-task was to study age and detailed growth patterns occurring between stocks of Atlantic salmon post-smolts from different parts of Europe, caught on their feeding grounds in the North-East Atlantic. This study includes twelve surveys with surface trawls, covering a large area of the North-East Atlantic, which were carried out in 2002, 2003, 2008 and 2009 to collect samples of Atlantic salmon post-smolts during their marine feeding migration. A total of 2,242 post-smolts were captured during these surveys. Smolt age and growth signatures were extracted from the scale samples using image processing. By this method, growth can now be estimated over short periods of time. During the summer period it was possible to estimate weekly growth rates. Inter-circuli distances were applied as a proxy variable of growth rate and the number of marine circuli as a proxy for the time spent at sea by the post-smolts. Since smolts from southern populations are younger, and leave their rivers earlier in spring than smolts from northern populations, it was possible to use smolt age and number of circuli to gauge the approximate geographical origin of the fish.

The predominating smolt age of post-smolts of wild origin was two years, followed by one and three years, and a few four years old fish. The average rate of circuli formation in the marine zone of scales was estimated to be 6.3 days per circulus. Both age structure and number of marine circuli in the scales suggest that the majority of the post-smolts caught belong to populations of southern European origin. Marine growth rates were found to vary among different areas and years, as growth rates were highest in 2002, followed by 2003 and 2009, and lowest in 2008 (Figure 3.44). Also, the first marine inter-circuli distances were narrowest in one year old smolts, successively increasing with smolt age, indicating that growth rates during the first period at sea were lowest for salmon of southernmost origin (Figure 3.45). Although only four years of data were available, the results suggest that in these years the annual variation in growth rate of post-smolts before July was controlled by food availability rather than sea temperature.



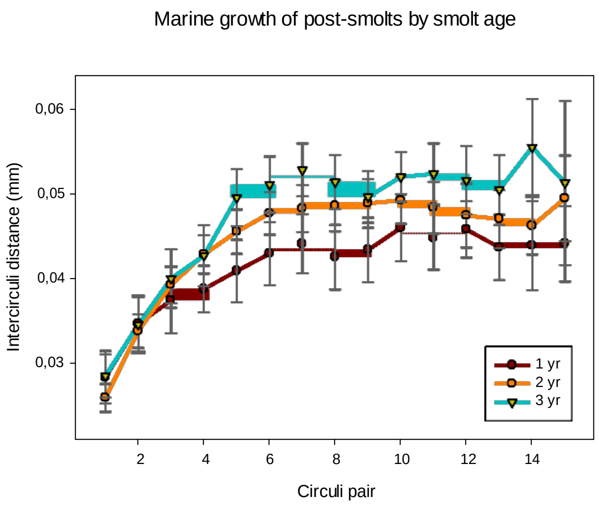


Figure 3.44, left: *Intercirculi distances (± 95 % conf. int.) in the marine zone of scales of post-smolts captured at the Vøring Plateau Area in 2002, 2003, 2008 and 2009. Distances are from the outer edge of the scales and towards the origin (from right to left).*

Figure 3.45, right: *Inter-circuli distances (± 95 % conf. int.) in the marine zone of scales of one-year-old, two-year-old and three-year-old post-smolts sampled in 2008, aligned from the end of the freshwater zone of the scale and toward the edge of the scale (from left to right). Circuli pair no. 1 is the distance between the last circulus laid down in fresh water and the first one in sea water.*

Feeding and food availability
The main objective of this Task was to study the diet of post-smolt salmon, relate it to the diet of co-occurring mackerel and herring and compare diet and feeding among years. To facilitate comparison of diet and feeding of post- smolts between good and bad growth years, we included post-smolt stomach data from 2002 and 2003 (Haugland et al. 2006). A total of 1634 stomachs of salmon, herring and mackerel sampled during the years 2008 and 2009 have been analysed in the laboratories of partner 1 and 15. All data are stored in the WGNAPES database maintained by partner 15. Stomach data from 2002 and 2003 were retrieved from the local database held by partner 1.

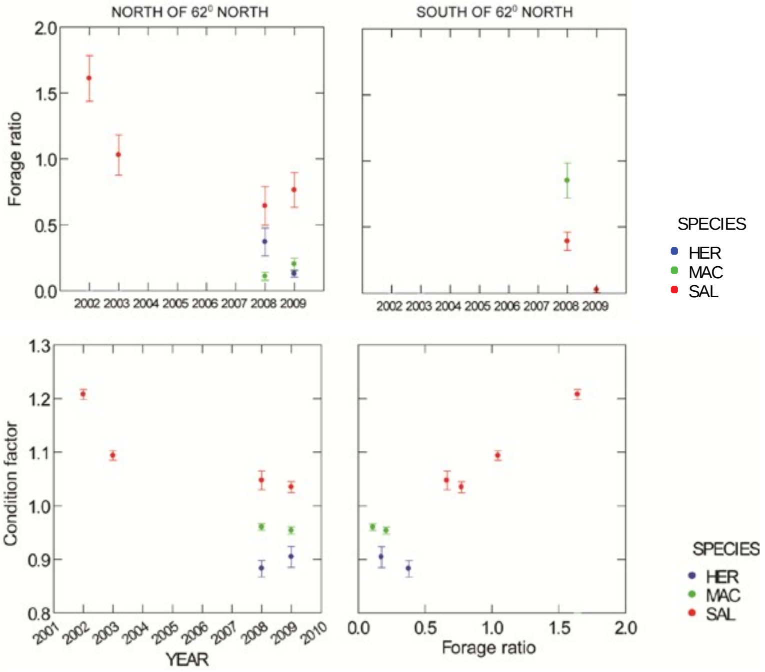


Figure 3.46: *Forage ratio and stomach content of salmon, herring and mackerel in 2002, 2003, 2008 and 2009, north and south of 62°N (upper panels). Condition factor of post-smolts vs. year and Forage ratio, north of 62°N (lower panels). Average and standard error of the mean.*

The diets of salmon, herring and mackerel differ although they feed in the same parts of the ocean. The main food of herring and mackerel is *Calanus finmarchicus*, and secondly *euphausids* and gastropods, respectively. The salmon's main food items are juvenile fish and amphipods of the genus *Themisto*. Salmon also show clear differences in diet among years from 2002-2009. In 2009, when *Themisto* and fish were less dominant in their diet, salmon post-smolts seemed to have a broader diet and were feeding more on small prey.

Forage ratios north of 62°N decreased from 2002 to 2008 (Figure 3.46). Forage ratios in 2008 and 2009 do not seem to be different. Forage ratios of salmon are higher than for the other two species. Also the condition factor of salmon decreases from 2002 to 2009, and there was a positive relationship between forage ratio and the condition factor (Figure 3.46). It seems that the observed stomach content and the condition of the fish are related, although growth will be the result of the feeding pattern over the whole feeding season. Comparing forage ratios to the observations of growth of salmon (Figure 3.43), we see that there is a close relationship between the feeding of salmon and its growth. A possible implication of these results is that stomach content measured at a given time is representative for the feeding of salmon during its whole feeding season and can be used to study growth in relation to diet and feeding intensity. Similar to the salmon, condition factor and forage ratio of herring and mackerel do not differ much between 2008 and 2009.

References

Friedland, K. D., MacLean, J. C., Hansen, L. P., Peyronnet, A. J., Karlsson, L., Reddin, D. G., Ó Maoiléidigh, N., and McCarthy, J. L. 2009. The recruitment of Atlantic salmon in Europe. ICES Journal of Marine Science, 66: 289–304.

ICES. 2012. Report of the Working Group on North Atlantic Salmon (WGNAS), 22–31 March 2011, Copenhagen, Denmark. ICES 2011/ACOM:09. 45 pp.

Peyronnet, A., Friedland, K. D., Ó Maoileidigh, N., Manning, M., and Poole, W. R. 2007. Links between patterns of marine growth and survival of Atlantic salmon *Salmo salar*, L. Journal of Fish Biology, 71: 684-700.

Peyronnet, A., Friedland, K. D., Ó Maoileidigh, N. 2008. Different ocean and climate factors control the marine survival of wild and hatchery Atlantic salmon *Salmo salar* in the north-east Atlantic Oceans. Journal of Fish Biology, 73: 945-962.

Ó Maoiléidigh, N., Boylan, P., Crozier, W., Gargan, G., Kennedy, B., McGinnity, P., Marnell, F., de Eyto, E., Roche, W., Lawlor, I., Doherty, D., White, J., and O'Higgins, K. The Status of Irish Salmon Stocks in 2010, with Precautionary Catch Advice for 2011. Independent scientific report to Inland Fisheris Ireland, August. Department of Communications, Energy and Natural Resources, Ireland.

WP 5:
Merge and analyse genetic, biological and oceanographic data
Combined analysis of data

Map spatial distribution of specific stocks or populations

Within the SALSEA-Merge project information collected during the marine surveys (WP2), as well as information generated from WP3, WP4 and also WP5, are combined into a Geographical Information System (GIS), providing charts in a common geographical reference template. The advantage of having the data stored in a GIS format is that not only will the charts have a common geographical reference (similar projections, coasts, etc.) but the charts can also be overlaid.

The charts provided new information regarding the distribution and movement of the young salmon of specific stocks. Distribution of post-smolts from the three regions at assignment level 1, Iceland, North, and South, for months May, June and July/August visualized the northward movement of the Southern stocks (Figure 3.27-3.29). This stock followed the main pathways of the ocean currents from Ireland to northern Norwegian Sea. A striking example is the specific post-smolt stock from the river Allier (France) where a nearly continuous migration path can be drawn from the origin river to northern Norwegian Sea. The generated charts from the GIS are included in the PDF-Atlas (WP6) and is described in more detail in deliverable D5.1.

Analysis of the distribution patterns associated with biological and oceanographic data

The objective of this sub-task was to study relationships between the distribution of post-smolts with oceanographic and biological information that would support the development of the conceptual migration and ecological model. Marine surveys from 2008 and 2009 provided both biological and hydrographic data (WP2), and these data were analysed together with other information, such as SST data, to produce new associations between post-smolt behaviour and physical and biological parameters. The distribution of post-smolts were compared with a variety of different parameters, and the analysis are in detailed described in the report *D5.2 (Report on analyses of the relationships between distribution of post-smolts with physical and biological variables)*. In total there were 286 trawl stations in 2008-2009 and 1,727 post-smolts were caught. At all trawl stations the numbers of captured post-smolts were converted to number of post-smolts per trawl hour. In relation to the trawl stations 170 hydrographic stations were taken. The analysis showed that the captured post-smolts were mainly in water within 9-12 °C (Figure 3.47) and the observed distribution as function of ambient temperature had a normal distribution.

Similar analysis was done for the salinity, and most of the captured post-smolts were caught in water with salinity greater than 35 ‰. Thus post-smolts preferred Atlantic Water compared to Arctic or Coastal water. These temperature and salinity preferences were employed as swimming behaviour in the development of the migration model (Task 5.2).

The distribution of post-smolts were clearly linked to ocean currents as the majority of the post-smolts were caught in pathways of the northward flowing Atlantic Water, from the North East Atlantic to the northern Norwegian Sea. The speeds of the currents, obtained from the ocean model ROMS, showed that post-smolts are not randomly distributed within the migration route, but instead seek the locations where the currents are strongest. This was more revealed in Task 5.2.

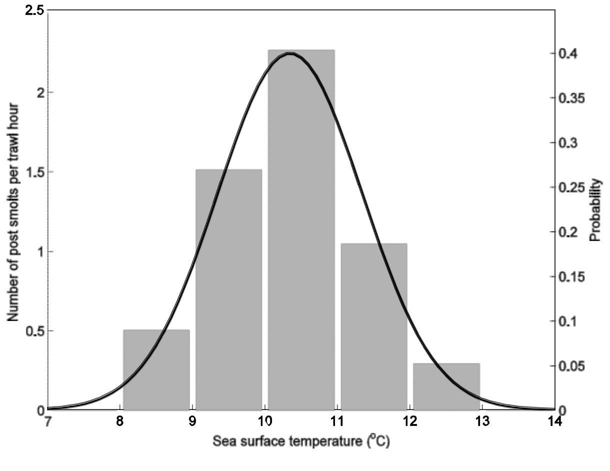


Figure 3.47: *Number of post-smolts caught per hour within different temperature ranges. The probability density function (thick line) is the normal distribution.*

The relationship between sea temperature at capture and growth rate during the last month before capture, was tested for post-smolts captured in the Norwegian Sea by using circuli spacings at the edge of scales of fish. In post-smolts, circuli are formed at a rate of one circulus each 6.3 days during the growth period (see WP4 for details). Hence, the sum of the five outermost spacings in the scales may be used as a proxy variable for growth in the last month before capture. In 2008, the growth rate increased with decreasing temperatures and increased with the latitude where the post-smolts were captured (Figure 3.48). This suggests that growth increased with latitude, indicating increased food availability to the north. Figure 3.49 also suggests that this was more pronounced in 2008 than 2009.

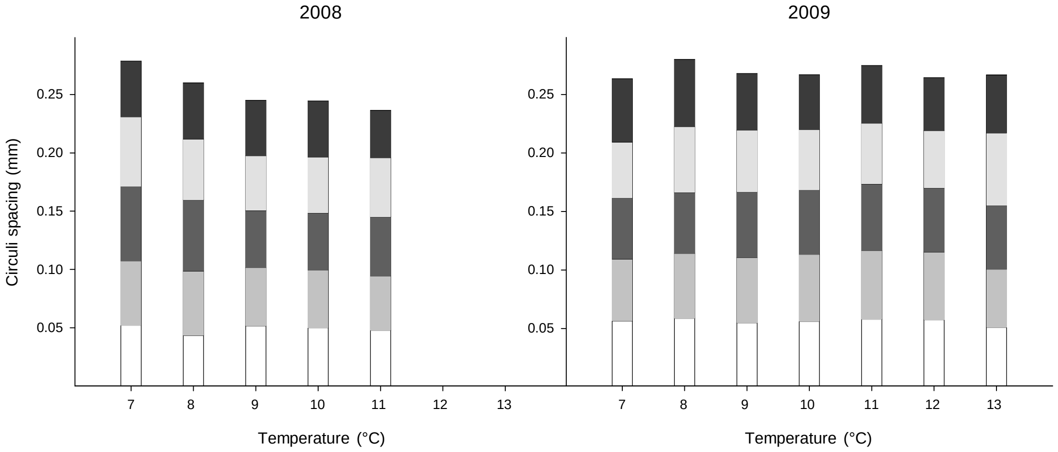


Figure 3.48: *Mean spacings (mm) between each of the five outermost circuli in scales of post-smolts collected at different sea temperatures in the Norwegian Sea in 2008 and 2009, with the spacing closest to the edge of the scale at the top of the bar.*

Development of a conceptual migration and ecological model for young salmon at sea

Integration of post-smolt data with oceanographic fields from the ROMS model

The objective of this task and sub-task was the development of a conceptual migration and ecological model for young salmon from different European stocks, which improved our understanding of key factors affecting their survival at sea. Advances in ecological modeling of Atlantic salmon has been hampered by a lack of knowledge on behavioral processes of the fish. To address this, oceanographic fields (such as ocean currents) from the three-dimensional Regional Ocean Modeling System (ROMS) ocean model were linked together with post-smolt distribution data acquired in previous WPs using a particle drift model. In addition, migration and swimming behavior identified from the other WPs together with other hypothesis on swimming behavior were tested with the particle tracking model. The main results from this task are divided into two parts: the first part addresses the modeling of the migration pattern of young salmon, while the second part address the conceptual ecological model that includes the different factors related to the distribution, mortality and growth of young salmon in the ocean. A more comprehensive report of the migration and the conceptual ecological model is given in deliverable *D5.3 Report describing a conceptual migration and ecological model*.

The migration model

To investigate and increase our understanding of salmon migration we used a 3D hydro-dynamical model (ROMS) that was forced with atmospheric data (sea surface air pressure, wind stress, etc.) from ERA40 to produce oceanographic fields (currents, temperature and salinity). The model domain covered the North-East Atlantic, Nordic seas, North Sea, Barents Sea, Kara Sea and partly the Arctic, and had a spatial resolution of 4 km. Daily averages of oceanographic fields were stored on disk for use in the offline particle drift model for transport of particles (i.e. post-smolts) from the release locations.

The migration speed of post-smolts is a sum of drift with the ocean currents and active swimming. Based on captured post-smolts and distribution of historical catches a likely migration path for the post-smolts was assumed (Figure 49), and along the defined migration path the migration speed was calculated from recaptured tagged fish. Within the band, the averaged and maximum velocity was calculated from the surface velocity component of the ocean model. This relates to two possible scenarios: either a randomly distributed location of post-smolts within the band or that the post-smolts are always found where the current is strongest (i.e. the core of the current).

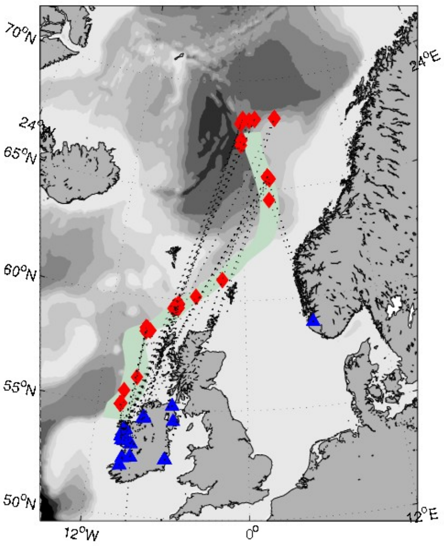


Figure 3.49, left: *Release and captured locations of tagged fish. The main defined migration route based on highest trawl catch rates is indicated as a green band.*

The total migration speed was generally greater than the speed of the surface current. The assumption that the post-smolts do not merely drift passively with the ocean currents, but also have an active swimming component was therefore reasonable. The active swimming component, which is the difference between the total migration speed and the surface velocity, is in many cases similar to the speed of the current. By including body length the swimming speed as function of body length was calculated. The maximum active swimming speed is approximately 1.5 body length per second and the highest speed were associated with the longer migrations (Figure 3.50). Since near river migrations may be affected by less directed swimming before strong currents are entered and long-distance migrations were of primary interest in this study a swimming speed of 1.5 body length per second was used in the migration model.

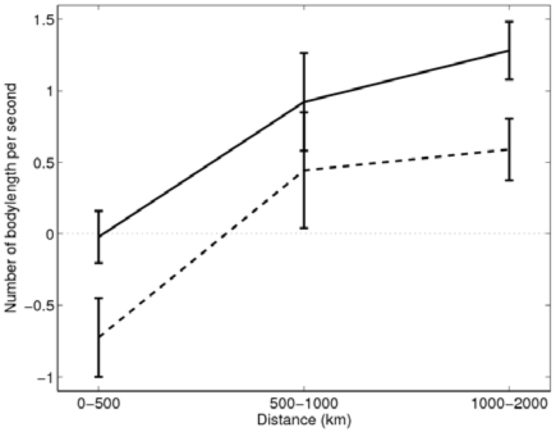
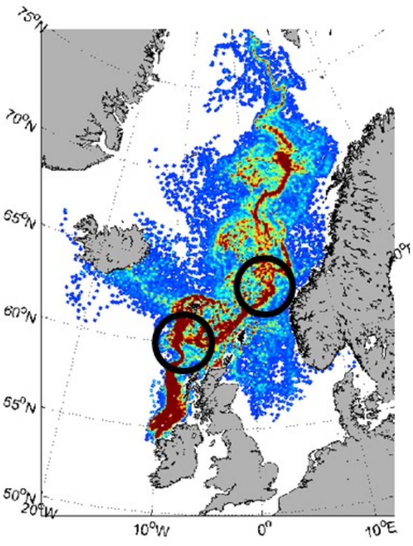


Figure 3.50, right: *Active swimming speed of the migrating post-smolts as function of body length per second. Solid line indicates mean current along the defined path while dash line indicates maximum velocity.*

Based on post-smolt catches the increase in body length after the post-smolts enter the sea, was estimated to 0.6% per day. This figure was included in the migration model. Two key regions of post-smolt origin were defined to simulate a southern stock and a northern stock: West of Ireland (56N, 9.5W) and southwest of Norway (58N,5E). At these two locations 2,000 particles were released, distributed over 3 weeks, centered on 1st May and 15th May for southern and northern stocks, respectively. The simulations were done over four months, i.e.to end of August.

The concentration plot (Figure 3.51 and 3.52) clearly shows the migration route for the southern stock; the post-smolts migrate northward, some through the Faroe-Shetland Channel and some around the Faroese, to the northern Norwegian Sea. Some particles even go westward to Iceland. Two important key regions are found where the migration direction may alter between the years because of shifts in the surface currents due to wind changes. The southern key region influence the rate of particles flowing into the Faroe-Shetland Channel compared to a more westward and northern route. A migration simulation for year 2002 resulted in no westward migrated particles at this key region. Almost all particles were instead forced through the Faroe-Shetland Channel and northward along the Norwegian continental shelf edge (the inner branch of the Norwegian Atlantic Current). This was a result of more southwesterly winds in 2002 compared to 2008.



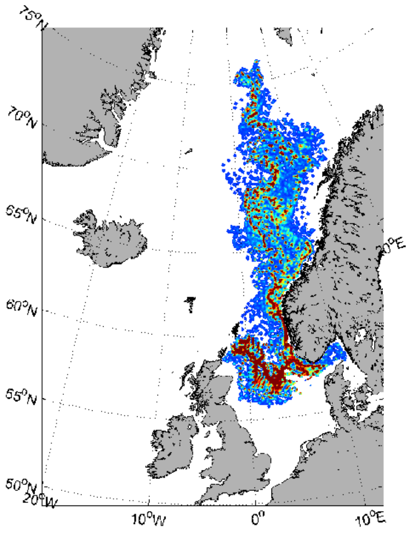


Figure 3.51, left: *Simulated post-smolt trajectories to end of August 2008 (20 April – 31 August) and concentration plots (red colours indicate more than 5 particles) for southern stocks. The black circles indicate key areas where important shifts in migration direction may occur.*

Figure 3.52, right: *As figure 3.51 for northern stocks.*

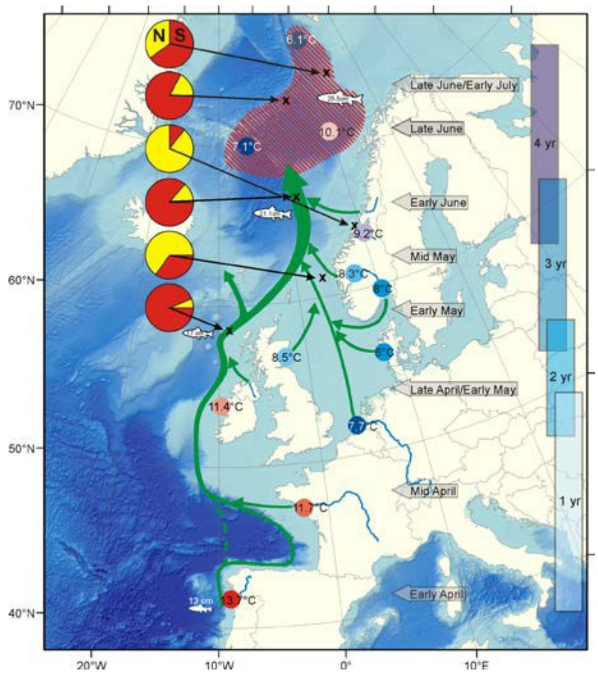


Figure 3.53: *Schematic migration routes for European salmon stocks and the ambient temperatures at the start of the sea migrations and at the feeding area. Body length, migration dates, smolt ages and ratios between distribution of southern and northern stocks are also indicated.*

The other (northern) key area defines either a coastal near-shore route (the inner branch of the Norwegian Atlantic Current) as observed in 2002, or a more northward offshore route (the outer branch of the Norwegian Atlantic Current), as observed in 2008. However, including a salinity preference of higher salinity in the swimming behavior changed the migration pattern. Because of the low salinity surface layer over the Norwegian shelf the high salinity preference swimming behavior forced the post-smolts to the northward offshore branch instead of the near coastal branch. This demonstrated how the salinity distribution affects the migration routes.

The particles from the northern stock (West of Norway) migrated mainly northwards and would overlap with the southern stock when reaching the feeding area (northern Norwegian Sea). The alteration of suitable migratory pathways, as observed from the migration model, has been suggested as a factor in the survival of post-smolts. Migratory species are known to change routes in association with changing currents, temperature and salinity distributions. The results from this task clearly indicate that the migratory pathways of European post-smolts may alter in a similar manner. The migration routes for different stocks are shown schematically in Figure 3.53, together with ambient temperatures, timing of migration, smolt age, and ratio between southern and northern stock groups.

The conceptual ecological model

There are many factors known to affect salmon at sea, and within the SALSEA-Merge project these factors were identified and described. Based on these factors a conceptual ecological model was developed, which includes the key regulatory factors. A schematic view of this model is shown in Figure 3.54. The most important regulatory factors are: growth, predation, and fisheries. However, there are also synergistic effects, specific stocks and distribution dependence, and climate variability and changes affecting these factors.

A brief summary and gaps of the main factors in the ecological model are given below. A more comprehensive description of the conceptual ecological model is given in the in the deliverable *D5.3 Report describing a conceptual migration and ecological model*.

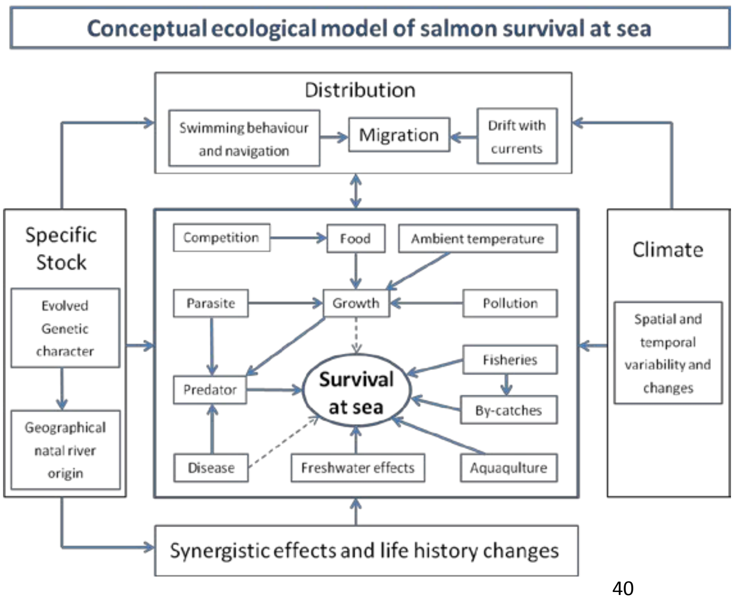


Figure 3.54: *The SALSEA-Merge conceptual ecological model of salmon survival at sea.*

Brief summary and gaps of the main factors:

<u>*Growth:*</u>

Most post-smolts captured in the Northeast Atlantic belonged to the southern component of the Atlantic salmon stocks, and within this group growth rates decreased from north to south, suggesting highest mortality during this life stage in the southernmost populations. Forage ratio was positively related to both condition and growth of post-smolts, showing the importance of good feeding conditions to growth and probably survival. It is still not known how feeding is related to food supply. Different adult fish populations, which are widely located geographically, may have very different post-smolt feeding areas, which are influenced by different oceanic conditions and biological parameters. In contrast to the more northern populations, post-smolt growth declined substantially during the most recent years in the Irish population, which is of concern.

Predator:

The information on distribution of salmon stocks at sea and growth of post-smolts resulting from SALSEA-Merge will be of importance in assessing the areas where spatial and temporal overlap with important predator species may occur. The gaps in knowledge relate mainly to the magnitude of predation on salmon by marine mammals. However, the necessity of sacrificing the predator species in order to quantify the number of salmon eaten, makes this issue a difficult one to solve, unless non-lethal sampling methods can be developed for future research.

Fisheries:

The novel information on the distribution of young salmon from different regions resulting from this study may significantly improve the potential for avoiding interception from the pelagic fisheries, e.g. by enabling recommendations for closed areas, closed times, depth regulations of trawl fisheries, etc. during the transition of post-smolts through the main fishery areas. The largest gap in knowledge regarding interception of salmon in other fisheries relates to the level of mortality of those individuals who pass through commercial fishing gear without being captured (non-catch fishing mortality). Addressing this issue was beyond the scope of SALSEA-Merge and can be studied through scientifically controlled fishing experiments with commercial gear types.

Specific stock:

Considered collectively, the existing evidence provides compelling support for the existence of biologically important variation in migration patterns among regional stock groups and individual river stocks, most likely driven by a combination of geography, evolutionary history, or contemporary oceanographic conditions. In turn, this makes it is difficult to envisage that such variation is not a factor in the nature and extent of marine mortality. The genetic work carried out demonstrates the clear potential for using genetic markers of region/river of origin, such as GRAASP, to develop an extensive detailed picture of the migratory differences among regional stock groups and individual river stocks. The preliminary study carried out demonstrates this potential and provides compelling evidence of differences at the regional stock group level. However, the limited spatial and temporal scope of the samples precludes the development of a complete and detailed picture of these differences.

Synergistic effects and life history changes:

It has been demonstrated in the SALSEA-Merge project that the GRAASP tool can identify fish captured at sea with respect to their region or river of origin with great accuracy. Future studies will increase in intensity and coverage of marine sampling e.g. plans to genotype archive material from Faroese and West Greenland and to undertake new studies of areas of the Atlantic not previously surveyed e.g. the Barents Sea, the Irminger Sea and the North Sea. These studies represent the best opportunity to determine for specific river population components when and where life history types diverge in the ocean. An unequivocal demonstration of ocean distribution diverged phenotypes would provide an excellent opportunity to make the link between feeding areas with temporal trajectories in regional abundance of, for example, sea age of maturity and run time phenotypes. The advantage of using the feeding areas is that such areas can be defined oceanographically, while their exact boundaries vary from season to season and from year to year. This proffers some possibility for managers to improve stock size predictive capacity and to recognize and respond to ecosystem (regime) changes as they occur.

Distribution:

Migration routes may alter on time scales like days, weeks or between years because of changes in the ocean currents and winds. Several key regions are identified where such shifts in migration may occur resulting in varying post-smolts distributions. Different stock groups are affected differently because some migration routes may be more influenced by variable physical conditions than others.

Climate:

Climate variability affects the migration routes through changes in the ocean currents and different stock groups are differently affected. A warmer climate affects the survival of the post-smolts through several processes. The post-smolts may migrate a longer distance to stay in the preferred temperature range, but also an earlier smolt migration date may alter the present life cycle. There are still large uncertainties in how the future global climate change will affect the regional climate and the ocean currents; factors that are important for the survival of salmon post-smolts.

Potential impact and main dissemination activities

WP 6:

Dissemination of Project Output

A comprehensive overview of the dissemination activities undertaken to date is found in the document 'Dissemination SALSEA-Merge' found on http://www.nasco.int/sas/salseamerge documents.htm. This includes scientific publications, publications in the popular media, radio, television and preparations for a movie on the survival of salmon at sea. The publication list arising from SALSEA Merge is constantly increasing and it is planned to submit several key publications following completion of this report. A complete overview of coverage covering the period 2008 to 2011, is not available but a Google search for 'SALSEA-Merge' returned 1,820 pages in early January 2012.

As committed to in the DoW, an ICES/NASCO Salmon Summit was held in La Rochelle, France, in October 2011. This scientific conference included 35 presentations and 15 posters and was attended by some 130 participants. The presentations, abstracts and Chairman's reports from the summit are to be found on the NASCO website - http://www.nasco.int/sas/salmonsummit.htm. The material presented was selected from all four of NASCO SALSEA programs including a comprehensive contribution from SALSEA-Merge. The material presented covered the life of salmon in both the Atlantic and the Pacific oceans.

SALSEA-Merge was the focus of the Ocean Silver Conference which was organised by the Atlantic Salmon Trust and took place in mid-December 2011, in Fishmongers Hall in London. The objective of this dialogue meeting was to outline the implications of the SALSEA Merge results for those involved with wild Atlantic salmon management and to engage in a full and detailed dialogue with a wide range of stakeholders. Over 200 participants attended the one-day meeting and feedback has been exceptionally positive. The conference was covered by the media, both in the UK and in Ireland. The material presented at the Ocean Silver Conference is available on the Atlantic salmon trust website (www.atlanticsalmontrust.org).

A major article was published in early December 2011 in the ***Trout and Salmon*** angling magazine, detailing the outcome of the La Rochelle salmon summit and the implications of the research for those involved in angling. As a result of this publication there was heightened interest in the Ocean Silver Conference which was organised by the Atlantic Salmon Trust and took place in mid-December 2011, in London. The objective of this dialogue meeting was to outline the implications of the SALSEA Merge results for those involved with wild Atlantic salmon management and to engage in a full and detailed dialogue with a wide range of stakeholders. Over 200 participants attended the one-day meeting and feedback has been exceptionally positive. The conference was covered by the media, both in the UK and in Ireland. The material presented at the Ocean Silver Conference is available on the Atlantic salmon trust website (www.atlanticsalmontrust.org).

Work is on-going on the ***Atlantic Salmon – Lost at Sea*** movie. It is hoped to complete filming at sea and in Europe by the end of 2012. This film is unique in that it will, for the first time, focus on the life of the marine of Atlantic salmon, based on groundbreaking salmon research carried out during SALSEA Merge. In combination with the ecosystem based research which is on- going in the North Atlantic, the film will also highlight the methods developed and the results emerging from SALSEA-Merge. The search for sponsorship is ongoing and for those interested in supporting the initiative the contact details to the producer are listed below. This initiative has the greatest potential of all the dissemination activities to reach the general public and to graphically outline

the insights gained through SALSEA Merge into the oceanic life and role of the salmon in the pelagic ecosystem of the North Atlantic. Further details on the movie can be obtained from (http://www.atlanticsalmonlostatsea.net/). There is also a Facebook page, Atlantic Salmon – Lost at Sea!, which is continuously updated..

Exploitation of results

As previously outlined SALSEA-Merge has delivered innovation in the areas of genetic stock identification techniques, new genetic marker development, fine scale estimates of growth, the use of novel high seas pelagic trawling technology and estimates of food and feeding patterns. In addition it has provided for the first time, fine scale migration and distribution models, merging hydrography, oceanographic, genetic and ecological data.
The toolbox developed during the course of the programme has direct implications for the future scientific study of salmon stocks as well as the management of stocks throughout the North-East Atlantic. The wealth of biological, genetic and modeling data contained in the in the SALSEA PGNAPES database has direct relevance to the day to day management of Atlantic salmon stocks in the North East Atlantic. Once the SALSEA Merge program is completed it would

be prudent that funding is made available to ensure the long-term integrity and expansion of this important database.

Genetic Assignment

Genetic profiles are now available in for some 26, 813 individuals from 467 locations, in 284 rivers across Europe. The ability to identify stocks from individual rivers or individual regions will be of direct and immense practical value to the river manager. Many of the questions that managers deal with on a day-to-day basis are confused by the lack of detail in relation to the number of populations contained either within a large river system or within a coastal region. Decisions in relation to commercial exploitation of fish, sport fisheries exploitation and the overall impact of planned developments in salmon catchments will be greatly improved by the availability of a genetic assignment methodology. Harvest decisions will become clearer as a result of the techniques developed in SALSEA-Merge and in the case of the remaining commercial fisheries for wild salmon, assessments of stock composition will facilitate, for the first time, the management of discrete stocks. Using the profiles developed in SALSEA-Merge, studies are underway to assess the relative contribution of Norwegian, Russian and Finnish stocks to the large Norwegian salmon mixed stock fishery in Finmark. These studies are part Kolartic Programme (http://www.fylkesmannen.no/hoved.aspx?m=67246) and may well directly contribute to the development of an international agreement at the forthcoming NASCO meeting, in June 2012.

Work is also underway to undertake an international research programme relating to the West Greenland subsistence salmon fishery. Using the panels of genetic markers arising from SALSEA-Merge, this study will assess the current and historic components of the commercial salmon catch in West Greenland and to assign the fish taken to river or region of origin in Europe and North America. This will lead to a much greater level of sophistication in managing the remaining subsistence fishery and will also improve greatly the protection of the remaining weak stocks feeding along the West Greenland coast.

The genetic techniques developed within SALSEA-Merge have also shown their ability to separate wild stocks from feral farmed stocks caught at sea. This ability to quickly separate out the two forms of salmon will add greatly to the manager's ability to assess the overall impact of fish farm escapes on ocean feeding grounds and also estimate the levels of returning adults of farmed origin entering wild salmon rivers and their impacts on wild spawning stocks. In the context of large juvenile pen rearing facilities in freshwater lakes, the new genetic assignment tools will facilitate an assessment of the level of impact of leakage/escapes from these net pens into the neighbouring freshwater systems.

Migration and Distribution Models

The development of migration and distribution models in SALSEA-Merge has greatly expanded our understanding of the pattern of migration of individual stocks and regional complexes of salmon at sea. The concept of a migration corridor, covering the complete migration route of salmon from their spawning grounds to the most northerly point in their feeding migration and return to homewaters, has major implications for the definition of scientific areas of conservation (SAC’s). It may well lead to an extended definition of an SAC for migratory species, spanning both fresh and salt water and extending from the river mouth, out to the furthest most point in the migration route of the adult salmon.

A major issue highlighted at the La Rochelle salmon summit was the question of by-catch and the potential impacts on salmon post-smolts of the large pelagic fisheries for species such as herring and mackerel, which take place in international waters in the North Atlantic. It is clear from the work of SALSEA-Merge that both salmon and other pelagic species share feeding areas of the North Atlantic. The migration and distribution maps may facilitate a more rational management of these areas. This could result in closure of key migration routes to commercial fishing during specific time periods in spring and early summer or the use of refined fishing gears, which would fish below critical zones in which the post-smolts are located. Actions such as these could contribute greatly to improvements in the survival of juvenile Atlantic salmon during their early months at sea.

Growth at Sea

SALSEA-Merge have clearly shown that growth at sea is determined by changes in the temperature regime in the surface layers of the North-East Atlantic. During periods when sea surface temperatures (SSTs) rise, the overall survival of the post-smolts drops whereas in situations where the temperature decreases there is an increase in terms of the overall survival of post-smolts in the North East-Atlantic. The detailed maps resulting from SALSEA-Merge will facilitate ongoing monitoring of conditions in specific areas of the ocean and may lead in the future to predictive growth and survival models. Given our new knowledge in relation to the location of specific regional stock complexes over time and the possibility of future river specific data, the inclusion of post-smolt salmon surveys in pelagic monitoring programs at sea could, in the future, lead to real time forecasting of stock abundance of returning adult salmon.

The novel scale reading techniques, which can assess weekly growth rates of smolts at sea, will be immensely valuable in the future monitoring of conditions at sea and how the effects of temperature, food availability, predation and climate impacts are integrated into the overall growth profile of post-smolts at sea.

Database

The publically available SALSEA PGNAPES database integrates all of the data collected and analysed during the course of the SALSEA-Merge programme. During the course of the studies , additional data were also collected on marine plankton, parasites, lipids and isotopes, etc, the analysis of which lay outside the scope of the current program. However once analysed, the results from these samples can, through the database, be directly integrated with the existing SALSEA-Merge data. In addition this database will serve as an integrated repository for Atlantic salmon data, potentially covering both Europe and North America, for many years to come.

Implications for other Marine fisheries

The multidisciplinary approach taken in SALSEA-Merge may have direct application for studies relating to other marine fish species. The concept of assignment and assignment to a population level, if it could be achieved for other pelagic species such as herring and mackerel, would be invaluable in the future management of these stocks. Equally the integrated approach taken in SALSEA-Merge has demonstrated the value of clearly focused cooperative international research programs. The lessons learned and the success achieved within SALSEA-Merge, may in the future encourage other similar programs.

Project website and relevant contact details

The project webpage is found at http://www.nasco.int/sas/salseamerge.htm and all reports on deliveries and the Final report at http://www.nasco.int/sas/salseamerge_documents.htm.

Publication consortium members
The publication consortium members list of SALSEA-Merge is found at http://www.nasco.int/sas/salseamergeconsort.htm. People in this list has contributed to the total results of SALSEA-Merge to such a degree that their name is on publications marked with 'The SALSEA-Merge consortium' in the author list.

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4.2 Use and dissemination of foreground

Section A

Dissemination measures

A comprehensive overview of the dissemination activities undertaken to date is found in the document 'Dissemination SALSEA-Merge' found on http://www.nasco.int/sas/salseamerge documents.htm. This includes scientific publications, publications in the popular media, radio, television and preparations for a movie on the survival of salmon at sea. Below follow a systematic overview of the main dissemination activities so far.

Publications

So far 16 publications has been accepted or submitted for international publication. The publication list arising from SALSEA Merge is constantly increasing and it is planned to submit several key publications following completion of this report. A significant number, probably close to 10 papers, will be published this coming year.

Conferences and speeches

So far the results of SALSEA-Merge have been presented in two large conferences and a large number of smaller conferences and meetings. Approximately 90 presentations have been made by SALSEA-Merge scientists on various SALSEA-Merge subjects during the course of the project. In addition SALSEA-Merge has been referred to in a large number of related talks. A large mixed audience of scientists, anglers, NGO's, Politicians, river owners, river managers and journalists have attended these talks.

The first major conference where SALSEA-Merge was presented was the ICES/NASCO Salmon Summit in La Rochelle, France, in October 2011. This scientific conference included 35 presentations and 15 posters and was attended by some 130 participants. The presentations, abstracts and Chairman's reports from the summit are to be found on the NASCO website - http://www.nasco.int/sas/salmonsummit.htm. The material presented was selected from all four of NASCO SALSEA programs including a comprehensive contribution from SALSEA-Merge composed of 8 speeches and 7 posters. The presentations covered the life of salmon in both the Atlantic and the Pacific oceans.

The second large conference was the Ocean Silver Conference which was organised by the Atlantic Salmon Trust and took place in mid-December 2011, in Fishmongers Hall in London. The objective of this dialogue meeting was to outline the implications of the SALSEA Merge results for those involved with wild Atlantic salmon management and to engage in a full and detailed dialogue with a wide range of stakeholders. Over 200 participants attended the one-day meeting and feedback has been exceptionally positive. The conference was covered by the media, both in the UK and in Ireland. The material presented at the Ocean Silver Conference is available on the Atlantic salmon trust website (www.atlanticsalmontrust.org). As a result of the conference invitations have been received, through the Atlantic Salmon Trust, for a number of additional talks to be given at venues throughout the UK over the coming months.

Internet page

The SALSEA-Merge homepage is found at http://www.nasco.int/sas/salseamerge.htm. All public documents are found at http://www.nasco.int/sas/salseamerge documents.htm.

Media/Internet

A complete overview of coverage over the project period, 2008 to 2011, is not available but a search for **SALSEA-Merge** on Google returned some 1800 pages in January 2012. Many of these are articles on SALSEA-Merge in papers, web sites and the popular media etc.

A major article was published in early December 2011 in the ***Trout and Salmon*** angling magazine, detailing the outcome of the La Rochelle salmon summit and the implications of the research for those involved in angling. As a result of this publication there was heightened interest in the Ocean Silver Conference which was organised by the Atlantic Salmon Trust and took place in mid-December 2011, in London. The objective of this dialogue meeting was to outline the implications of the SALSEA Merge results for those involved with wild Atlantic salmon management and to engage in a full and detailed dialogue with a wide range of stakeholders. Over 200 participants attended the one-day meeting and feedback has been exceptionally positive. The conference was covered by the media, both in the UK and in Ireland. The material presented at the Ocean Silver Conference is available on the Atlantic salmon trust website (www.atlanticsalmontrust.org).

Film production

Work is on-going on the ***Atlantic Salmon – Lost at Sea*** movie. It is hoped to complete filming at sea and in Europe by the end of 2012. This film is unique in that it will, for the first time, focus on marine life of the Atlantic salmon, based on groundbreaking salmon research carried out during SALSEA Merge. In combination with the ecosystem based research, which is ongoing in the North Atlantic, the film will also highlight the methods developed and the results emerging from SALSEA-Merge. The search for sponsorship is ongoing and for those interested in supporting the initiative the contact details to the producer are listed below. This initiative has the greatest potential of all the dissemination activities to reach the general public and to graphically outline the insights gained through SALSEA Merge into the oceanic life and role of the salmon in the pelagic ecosystem of the North Atlantic. Further details on the movie can be obtained from (http://www.atlanticsalmonlostatsea.net/). There is also a Facebook page, ***Atlantic Salmon – Lost at Sea!*** which is continuously updated on activities related to the production of the film.

Paths of Silver – An Atlas of Atlantic Salmon Migrations

Based on the maps in this report, a selection of unique images collected over the course of the study, and a range of additional material available through the SALSEA Merge partners, it is planned to produce a coffee table type atlas of the salmon's migrations in both marine and freshwater. Through one of the SALSEA Merge partners, the Atlantic Salmon Trust (www.atlanticsalmontrust.org), work has been on-going on planning the Atlas for the past twelve months. A fundraising brochure has been compiled by the publisher, Medlar Press (www.medlarpress.com) and following discussions in the autumn of last year, the Atlantic Salmon Federation in Canada (www.asf.ca) have expressed a great interest in supporting the project. The Atlas will present to the general public, in an enjoyable and accessible manner, the migrations of the Atlantic salmon. The emphasis will be on the original knowledge regarding ocean migration patterns acquired through the SALSEA Merge programme. The production of the Atlas is being run as a separate project and will be financed through sponsorship. Partners include: the Atlantic Salmon Trust, Institute of Marine Research Bergen, and the scientists and technicians from SALSEA Merge responsible for the compilation of the marine migration maps and the collection of images and relevant biological data. The success of the fundraising initiative will determine the publication date but it is hoped to have the Atlas available by the autumn of 2013. The Atlas project will complement the movie *Atlantic Salmon - Lost at Sea* described earlier in this report (www.atlanticsalmonlostatsea.net).

Section B

Exploitable foreground

As previously outlined SALSEA-Merge has delivered innovation in the areas of genetic stock identification techniques, new genetic marker development, fine scale estimates of growth, the use of novel high seas pelagic trawling technology and estimates of food and feeding patterns. In addition it has provided for the first time, fine scale migration and distribution models, merging hydrography, oceanographic, genetic and ecological data.

The toolbox developed during the course of the programme has direct implications for the future scientific study of salmon stocks as well as the management of stocks throughout the North-East Atlantic. The wealth of biological, genetic and modeling data contained in the in the SALSEA PGNAPES database has direct relevance to the day to day management of Atlantic salmon stocks in the North East Atlantic. Once the SALSEA Merge program is completed it would be prudent that funding is made available to ensure the long-term integrity and expansion of this important database.

Genetic Assignment

Genetic profiles are now available in for some 26, 813 individuals from 467 locations, in 284 rivers across Europe. The ability to identify stocks from individual rivers or individual regions will be of direct and immense practical value to the river manager. Many of the questions that managers deal with on a day-to-day basis are confused by the lack of detail in relation to the number of populations contained either within a large river system or within a coastal region. Decisions in relation to commercial exploitation of fish, sport fisheries exploitation and the overall impact of planned developments in salmon catchments will be greatly improved by the availability of a genetic assignment methodology. Harvest decisions will become clearer as a result of the techniques developed in SALSEA-Merge and in the case of the remaining commercial fisheries for wild salmon, assessments of stock composition will facilitate, for the first time, the management of discrete stocks. Using the profiles developed in SALSEA-Merge, studies are underway to assess the relative contribution of Norwegian, Russian and Finnish stocks to the large Norwegian salmon mixed stock fishery in

Finmark. These studies are part Kolartic Programme (http://www.fylkesmannen.no/hoved.aspx?m=67246) and may well directly contribute to the development of an international agreement at the forthcoming NASCO meeting, in June2012.

Work is also underway to undertake an international research programme relating to the West Greenland subsistence salmon fishery. Using the panels of genetic markers arising from SALSEA-Merge, this study will assess the current and historic components of the commercial salmon catch in West Greenland and to assign the fish taken to river or region of origin in Europe and North America. This will lead to a much greater level of sophistication in managing the remaining subsistence fishery and will also improve greatly the protection of the remaining weak stocks feeding along the West Greenland coast.

The genetic techniques developed within SALSEA-Merge have also shown their ability to separate wild stocks from feral farmed stocks caught at sea. This ability to quickly separate out the two forms of salmon will add greatly to the manager's ability to assess the overall impact of fish farm escapes on ocean feeding grounds and also estimate the levels of returning adults of farmed origin entering wild salmon rivers and their impacts on wild spawning stocks. In the context of large juvenile pen rearing facilities in freshwater lakes, the new genetic assignment tools will facilitate an assessment of the level of impact of leakage/escapes from these net pens into the neighbouring freshwater systems.

Migration and Distribution Models

The development of migration and distribution models in SALSEA-Merge has greatly expanded our understanding of the pattern of migration of individual stocks and regional complexes of salmon at sea. The concept of a migration corridor, covering the complete migration route of salmon from their spawning grounds to the most northerly point in their feeding migration and return to homewaters, has major implications for the definition of scientific areas of conservation (SAC’s). It may well lead to an extended definition of an SAC for migratory species, spanning both fresh and salt water and extending from the river mouth, out to the furthest most point in the migration route of the adult salmon.
A major issue highlighted at the La Rochelle salmon summit was the question of by-catch and the potential impacts on salmon post-smolts of the large pelagic fisheries for species such as herring and mackerel, which take place in international waters in the North Atlantic. It is clear from the work of SALSEA-Merge that both salmon and other pelagic species share feeding areas of the North Atlantic. The migration and distribution maps may facilitate a more rational management of these areas. This could result in closure of key migration routes to commercial fishing during specific time periods in spring and early summer or the use of refined fishing gears, which would fish below critical zones in which the post-smolts are located. Actions such as these could contribute greatly to improvements in the survival of juvenile Atlantic salmon during their early months at sea.

SALSEA-Merge in the future management of salmon stocks

SALSEA-Merge has clearly shown that growth at sea is determined by changes in the temperature regime in the surface layers of the North-East Atlantic. During periods when sea surface temperatures (SSTs) rise, the overall survival of the post-smolts drops whereas in situations where the temperature decreases there is an increase in terms of the overall survival of post-smolts in the North East-Atlantic. If a salmon is caught anywhere in the Atlantic Ocean it is now possible to quickly assess its continent of origin and in the case of European salmon, to identify the fish back, with remarkable accuracy, to its region or indeed in some cases, it's river of origin. The scientific connection has now been made between the salmon's oceanic feeding grounds and the remote freshwater streams of its birth. For the first time we can now directly link survival of these fish at sea with the prevailing ecological characteristics of specific migration pathways and feeding zones in the ocean.

It is now clear that, in the future, management of the wild salmon resource will involve not alone a knowledge of adult returns to freshwater and an estimate of spawning stock, but equally a knowledge and understanding of the ecology of the oceans in which the salmon grow to adulthood and mature. The outcomes from SALSEA-Merge also point towards the potential of a predictive salmon management methodology which will base its predictions on a thorough knowledge and understanding of the salmon's oceanic feeding areas. It also points towards a new management regime which will, in equal parts, base its predictions on knowledge and understanding of the fish’s life, both in fresh water and in salt water.

Database

The publically available SALSEA PGNAPES database integrates all of the data collected and analysed during the course of the SALSEA-Merge programme. During the course of the studies, additional data were also collected on marine plankton, parasites, lipids and isotopes, etc, the analysis of which lay outside the scope of the current program. However once analysed, the results from these samples can, through the database,be directly integrated with the existing SALSEA-Merge data. In addition this database will serve as an integrated repository for Atlantic salmon data, potentially covering both Europe and North America, for many years to come.

PUBLICATIONS:

TEMPLATE A1: LIST OF SCIENTIFIC (PEER REVIEWED) PUBLICATIONS, STARTING WITH THE MOST IMPORTANT ONES										
No.	Title	Main author	Title of the periodical or the series	Number, date or frequency	Publisher	Place of publication	Year of publication	Relevant pages	Permanent identifiers[2] (if available)	Is/Will open access[3] provided to this publication?
1	Microsatellites reveal clear genetic boundaries among Atlantic salmon (Salmo salar) populations from the Barents and White Seas, northwest Russia.	A. Tonteri et al.	Canadian Journal of Fisheries and Aquatic Sciences	66:	NRC Research Press	Canada	2009	717-735.		No
2	Beyond MHC: signals of elevated selection pressure in Atlantic salmon (Salmo salar) immune relevant loci.	A. Tonteri et al.	Molecular Ecology	19	Wiley-Blackwell	UK	2010	1273-1282		No
3	Novel set of multiplex asseys (SalPrint15) for efficient analysis of 15 microsatellite loci of contemporary samples of the Atlantic salmon (Salmo salar).	K.Ólafsson et al.	Molecular Ecology Resources	10	Wiley-Blackwell	Molecular Ecology Resources	2010	533-537	DOI: 10.1111/j.1755-0998.2009.02781.x	Yes

4	Anasakid larvae in Atlantic Salmon (Salmo salar L.) grilse and post-smolts: molecular identification and histopathology	T. Murphy et al.	The Journal of Parasitology	96 (1)	American Society of Parasitologists	USA	2010	77-82	DOI: 10.1645/GE-2194.1	Yes
5	Synchrony in marine growth among Atlantic salmon (Salmo salar) populations	A. J. Jensen et al.	Canadian Journal of Fisheries and Aquatic Sciences	68	NRC Research Press	Canada	2011	444-457	Doi:10.1139/F10-156	No
6	Detection and mapping of mtDNA SNPs in Atlantic salmon using high throughput DNA sequencing	O.Fridjonsson et al.	BMC Genomics	12	Biomedcentral	Online	2011	179	DOI: 10.1186/1471-2164-12-179	Yes
7	Regional and temporal variation in marine growth of Atlantic salmon (Salmo salar, L.) from North-East Atlantic populations – links to marine survival and oceanographic conditions	N. Ó Maoiléidigh et al.	ICES Journal of Marine Science	Manuscript	Oxford Journals	UK	Submitted /2012			No
8	Smolt age and fine scale marine growth of Atlantic salmon post-smolts in the Northeast Atlantic	A. J. Jensen et al.	ICES Journal of Marine Science	Manuscript	Oxford Journals	UK	Submitted /2012			No

9	The diet of Atlantic salmon post-smolts during their first feeding season in Northeast Atlantic	W. Melle et al.	ICES Journal of Marine Science	Manuscript	Oxford Journals	UK	Submitted /2012			No
10	The SALSEA Programme – Unravelling the Life of the Atlantic Salmon at Sea	K. Whelan et al.	ICES Journal of Marine Science	Manuscript	Oxford Journals	UK	Submitted /2012			No
11	Extending understanding of marine migration, ecology and mortality of Atlantic salmon post-smolts using oceanographic modeling, recaptured tagged salmon and SALSEA-GRAASP	K. A. Mork et al.	ICES Journal of Marine Science	Manuscript	Oxford Journals	UK	Submitted /2012			No
12	Analysis of historical tagging data from the salmon fisheries at the Faroe Islands	J. A.Jacobsen et al.	ICES Journal of Marine Science	Manuscript	Oxford Journals	UK	Submitted /2012			No
13	Regional mtDNA SNP differentiation in European Atlantic salmon (Salmo salar): an assessment of potential utility for	E. Verspoor et al.	ICES Journal of Marine Science	Monthly	Oxford Journals	UK	Submitted /2012			No

	determination of natal-origin									
14	Marine distribution of regional Atlantic salmon post-smolt stocks in the NE Atlantic ascertained by microsatellite DNA based assignment.	J. Gilbey et al.	ICES Journal of Marine Science	Monthly	Oxford Journals	UK	Submitted /2012			No
15	The SALSEA-Merge GRAASP database – a resource for the assignment of natal origin of Atlantic salmon from Eastern Atlantic rivers	J. Gilbey et al.	Molecular Ecology Resources	Monthly	Wiley	UK	Submitted/2012			No
16	Microsatellite standardization and genotyping error in a large multi-partner research programme for conservation of Atlantic salmon (Salmo salar L.).	J. S. Ellis					(in prep)			

ORAL PRESENTATIONS:

TEMPLATE A2: LIST OF DISSEMINATION ACTIVITIES

No.	Type of activities[4]	Main leader	Title	Date	Place	Type of audience[1]	Size of audience	Countries addressed
1	Presentation	S.M.Einarsson S.Gudjonsson	The use of DST tags to map oceanic routes and habitat of salmon in the sea	February 2007	Annual meeting of the agricultural society in Iceland	Scientific Community,	100	Iceland
2	Presentation	K. Whelan	The Salsea Merge Programme	March 2007	Memorial University, Newfoundland, Canada	Scientific Community, Civil Society	30	Canada
3	Presentation	S. Gudjonsson S.M.Einarsson	Research on salmon in the sea by DST tags.	June 2007	Annual meeting of the Icelandic farmers fisheries association	Civil Society	100	Iceland
4	Presentation	K. Whelan	The SALSEA Programme 2008 to 2011	October 2007	Management - 2007 Annual Study Course, Bunclody, Ireland	Scientific Community, Civil Society	100	UK and Ireland
5	Presentation	N .Ó Maoiléidigh	Marine Migration of Atlantic Salmon - What do we know and why do we need SALSEA?	20th February 2008	Ulster Anglers Federation Toomebridge, Co. Antrim, N. Ireland	Civil Society	50	UK and Ireland
6	Presentation	C. Primmer	Clear genetic boundaries among Atlantic salmon populations from the Barents and White Seas	February 2008	International symposium: Population Structuring of Atlantic salmon: from within rivers to between continents, Paris, France	Scientific Community	50	International
7	Presentation	M. Holm	The SALSEA Project	March 2008	The Scientific Advisory Group on Norwegian Salmon, Bergen, Norway	Scientific Community	10	Norway
8	Presentation	S. Guðjónsson and G.	The decline of multi sea winter salmon stocks in Icelandic	27 March 2008.	Hótel Loftleiðum, Reykjavík	Scientific Community	50	Iceland

		Gudbergsson	rivers.					
9	Presentation	S. Guðjónsson	Where does the salmon stay in the sea? New research Methods.	31 March 2008.	The agricultural university of Iceland	Scientific Community	25	Iceland
10	Presentation	M. Holm	The SALSEA Project	April 2008.	ICES , Working Group on north Atlantic salmon (WGNAS) Galway, Ireland,	Scientific community	25	International
11	Presentation	N .Ó Maoiléidigh	Salsea Merge - Post smolts surveys in 2008	April 2008	ICES Working Group on North Atlantic Salmon.Galway, Ireland.	Scientific Community	24	International
12	Presentation	V. Wennevik	“SALSEA-Merge Genetic studies”.	April 2008.	ICES , Working Group on North Atlantic salmon (WGNAS) Galway, Ireland	Scientific Community	25	International
13	Presentation	S. M. Einarsson	The ecology of salmon in the sea. The Salsea merge research project.	8 May 2008.	Annual meeting og the Institute of Freshwater Fisheries.	Scientific Community Civil Society	75	Iceland
14	Presentation	V. Wennevik	“Genetics and development of the SALSEA program”.	May 2008.	Directorate of Nature Management, Trondheim, Norway	Policy Makers	35	Norway
15	Presentation	J. C. Holst	SALSEA scientific coordination	May 2008	Salsea Kick off meeting Sligo, Ireland	Scientific Community	30	International
16	Presentation	K. A. Mork	WP 5 - Merge and analyse genetic, biological and oceanographic data	May 2008	Sligo, Ireland	Scientific community	60	International
17	Presentation	M. Holm	Salmon at Sea and the EU-SALSEA Project	02.June 2008	Board Meeting of ”The KLV” (Centre for salmon and water habitats), Namsos, Norway	Industry, Civil Society, Policy Makers	50	Norway
18	Presentation	J. C. Holst	The SALSEA project	June 2008.	NASCO annual meeting Gijon, Spain	Scientific Community	20	International

19	Presentation	N .Ó Maoiléidigh	Post smolt surveys in 2008 – SALSEA Merge	June 2008.	National Salmon Commission Killybegs.Ireland	Scientific Community	20	Ireland
20	Presentation	J. C. Holst	SALSEA- Salmon at Sea	July 2008	Given on fishing vessel Eros for crew and scientists	Civil Society, Scientific Community	20	Norway
21	Presentation	N .Ó Maoiléidigh	Salsea Merge - Post smolts surveys in 2008	July 2008	Board of the Marine Institute Oranmore, Galway	Industry, Civil Society, Policy Makers	12	Ireland
22	Presentation / Exhibition	K. Whelan and E. Babatunde	The Salsea Merge Programme	9 – 11 Sep 2008	European Commission's stand in Oceanology International 2008 Prague	Scientific Community, Civil Society	N/A	International
23	Presentation	J. C. Holst	Management of wild salmon at sea – SALSEA	September 2008	Given for Chinese fisheries delegation IMR, Bergen	Scientific Community	5	Norway, China
24	Presentation	M. Holm	“We Won Gold”, The SALSEA Project	October 16, 2008	Pelagic Research Section, IMR, Bergen, Norway	Scientific Community	25	Norway
25	Presentation	M. Holm	The EU SALSEA Project	10 December 2008	The Weekly Science Lecture of IMR, Bergen, Norway	Scientific Community ,Policy Makers	45	Norway
26	Presentation	M. Holm	SALSEA Work Package 2, Status report	16 December 2008	SALSEA Steering Committee Meeting, Edinburgh, UK	Scientific Community	10	International
27	Presentation	C. Primmer	Evolutionary genetic approaches for the management and conservation of exploited Atlantic salmon populations’	December 2008	University of Aarhus, Denmark	Scientific Community	30	Denmark
28	Presentation	K. Whelan	The Salsea Merge Programme	2008, 2009, 2010, 2011	NASCO Annual Meetings	Scientific Community, Civil Society	150	North Atlantic wide – North America to Russia
29	Presentation	K. A. Mork	SALSEA-Merge - WP5	March 2009	Bergen	Scientific Community	60	International

30	Presentation	M. Holm	SALSEA Work Package 2 and Norwegian Cruise report 2008,Status report	05 March 2009	SALSEA General Assembly , Bergen, Norway	Scientific Community	100	International
31	Presentation	J. A. Jacobsen	Faroes Cruise Report 2008	05 March 2009	SALSEA General Assembly , Bergen, Norway	Scientific Community	100	International
32	Presentation	W .Melle	Plankton analyses, preliminary data from Norwegian cruises	05 March 2009	SALSEA General Assembly , Bergen, Norway	Scientific Community	100	International
33	Presentation	N .Ó Maoiléidigh	Irish Cruise report 2008	05 March 2009	SALSEA General Assembly , Bergen, Norway	Scientific Community	100	International
34	Presentation	N .Ó Maoiléidigh	Salsea Merge - Post smolts surveys in 2008 and 2009	April 2009	ICES Working Group on North Atlantic Salmon Copenhagen, Denmark.	Scientific Community	24	International
35	Presentation	E. Verspoor	Fish, Chips and DNA	30 April 2009	Symposium. Freshwater Fisheries Forum: Edinburgh, UK	Scientific Community, Policy makers, Civil society, Industry and Media	120	UK
36	Presentation	J. C. Holst	Ecology of salmon in the Norwegian Sea	June 2009	Given to crew and scientists on RV Celtic Explorer ,Ireland	Scientific Community	15	Ireland
37	Presentation	J. C. Holst	SALSEA. The salmon at sea programme	June 2009	Meeting on sea lice problems in Norway. Øystese, Norway	Scientific Community	40	Norway
38	Presentation	S. Gujonsson	The status of multi sea winter salmon in Iceland	June 2009	Annual meeting of the Federation of Icelandic river owners	Civil Society	75	Iceland
39	Presentation	K. Whelan	The Salmon at Sea (Salsea) Programme	July 2009	Ballina Salmon Festival. Ireland	Civil Society	80	Ireland
40	Presentation	N .Ó Maoiléidigh	Irish Cruise report 2009	24 August 2009	Wrap up meeting of 2009 Expeditions, IMR, Bergen, Norway	Scientific Community	10	Norway, Faroes, Ireland

41	Presentation	J. A. Jacobsen	2009 Faroes Cruise Report	24 August 2009	Wrap up meeting of 2009 Expeditions, IMR, Bergen, Norway	Scientific Community	10	Norway, Faroes, Ireland
42	Presentation	M. Holm	Norwegian Cruise report 2009	24 August 2009	Wrap up meeting of 2009 Expeditions, .IMR, Bergen, Norway	Scientific community	10	Norway, Faroes, Ireland
43	Presentation	J. A. Jacobsen	PGNAPES SALSE database: biological data storage from sampling at sea	26 August 2009	Wrap up meeting of 2009 Expeditions, IMR, Bergen, Norway	Scientific Community	10	Norway, Faroes, Ireland
44	Presentation	P. McGinnity	Observations from National (Ireland) Atlantic salmon Genetic Stock Identification Project & SALSEA-Merge Project. Genetics Workshop,	October 2009	Celtic Sea Trout Inter-reg group Bangor, Wales	Scientific Community	100	Ireland, UK
45	Presentation	K. Whelan	"Salmon: The Climate Change Forecasters"	9th October 2009	Royal Irish Academy Dublin, Ireland	Scientific Community, Civil Society	150	Ireland
46	Presentation	E. Verspoor	The Atlantic Salmon: Genetics and Marine Migration	10 November 2009	Symposium: Salmon at Sea: Edinburgh, UK	Scientific Community, Policy makers, Civil society, Industry and Media	80	UK, Ireland
47	Presentation	V. Wennevik	”Salmon at Sea”	November 2009	Board Meeting of ”The KLV” (Centre for salmon and water habitats), Oslo, Norway	Scientific Community, Industry, Civil Society, Policy Makers	50	Norway
48	Presentation	K. Whelan	The Salsea Merge Programme	Jan 2010	Trim Anglers, Ireland	Civil Society	80	Ireland
49	Presentation	K. A. Mork	SALSEA-Merge - WP5	January 2010	London	Scientific Community	8	International
50	Presentation	N .Ó Maoiléidigh	International assessment and status of MSW stocks from ICES/NASCO with a description of the salmon at sea,	30th January 2010	Annual General Meeting of Salmon Watch Ireland Limerick, Ireland.	Civil Society	30	Ireland

			distributions and likely migration routes from the SALSEA Merge EU project.					
51	Presentation	J. C. Holst	SALSEA-Merge. Present living condition for salmon at sea	February 2010.	Norwegian parliament. Oslo, Norway	Policy makers, Civil Society	20	Norway
52	Presentation	K. Thomas	SALSEA-Merge – collation of ecological data	February 2010	Beaufort Fish Population Genetics Mini-symposium Mayo, Ireland	Scientific Community	50	Ireland, UK
53	Presentation	N .Ó Maoiléidigh	Results from Coded Wire Tag Recovery Programme in Ireland Beaufort Fish Population Genetics Mini-Symposium	February 2010	Young Scientists Newport, Co. mayo	Scientific Community	60	Irl, France, UK, Holland
54	Presentation	J .Coughlan	nSNPs for stock discrimination Beaufort	February 2010	Young Scientists Newport, Co. Mayo	Scientific Community	60	Ireland, UK,
55	Presentation/ Exibition	J. A. Jacobsen	Powerpoint presentation of the Salsea-Merge project in "Vitan á skák" / ”Research made public”	15-20 February 2010	SMS Shopping Mall, Tórshavn, Faroes	Civil Society	300+	Faroes
56	Presentation	E. Verspoor	Genetics: the hidden dimension	27 February 2010	Symposium: Salmon Management:: Ayr, UK	Scientific Community, Policy makers, Civil society, Industry	45	UK
57	Presentation	N .Ó Maoiléidigh	Salsea project Update to ICES Working Group on North Atlantic Salmon	March 2010	ICES WGNAS members Copenhagen	Scientific Community	22	International
58	Presentation	K. Thomas	PGNAPES - on standardisation of trawls and data using ICES PGNAPES format:	May 2010	CELTIC SEA TROUT project Newport, Co. Mayo	Scientific Community	15	Irl, UK
59	Presentation	E. Verspoor	FASMOP: Fish and Chips	21 May 2010	Private Presentation	Industry, Charity	6	UK
60	Presentation	E. Verspoor	Focusing Atlantic Salmon Management on Populations(FASMOP): workshop summary	12 August 2010	Workshop: FASMOP, Perth, UK	Scientific Community, Policy makers, Civil society, Industry	45	UK

61	Presentation	J .Coughlan	The use of nuclear SNP loci for determining stock structure and for GSI in Atlantic salmon	6-7 October 2010	SALSEA-Merge General Assembly Dublin, Ireland	Scientific Community	50	International
62	Presentation	K. A. Mork	WP 5 - Merge and analyse genetic, biological and oceanographic data	6-7 October 2010	SALSEA-Merge General Assembly Dublin, Ireland	Scientific Community	60	International
63	Presentation	J. A. Jacobsen	PGNAPES SALSEA database: Biological data storage. WP 5 - Merge and analyse genetic, biological and oceanographic data	6-7 October 2010	SALSEA-Merge General Assembly Dublin, Ireland	Scientific Community	60	International
64	Presentation	K. Ólafsson	Population structure of Icelandic salmon stocks	26 November 2010	Meeting on value of genetic resources in agriculture.	Scientific Community	30	Iceland
65	Presentation	K. Whelan	The Salsea Merge Programme	3 Dec 2010	Kerry Federation of Anglers, Ireland	Civil Society	80	Ireland
66	Presentation	K. A. Mork	New results from the Migration/Ecological model	January 2011	Bergen	Scientific Community	8	International
67	Presentation	A. J. Jensen	Scale reading within SALSEA-Merge	18 January 2011	Workshop on Age Determination of Salmon (WKADS)Galway, Ireland	Scientific Community	30	International
68	Presentation	P. Fiske	Scale reading within NINA	18 January 2011	Workshop on Age Determination of Salmon (WKADS)Galway, Ireland	Scientific Community	30	International
69	Presentation	N .Ó Maoiléidigh	Data Analyses: Between rivers, across years, others, methods	19 January 2011	Workshop on Age Determination of Salmon (WKADS)Galway, Ireland	Scientific Community	30	International
70	Presentation	C. Primmer	Linking population genetics and conservation biology: some examples in salmonid fishes	March 2011	Karlstad Universiy, Sweden	Scientific Community	20	Sweden

71	Presentation	E. Verspoor	An Update on the EU SALSEA-Merge Programme	4-6 May 2011	ICES Working Group on the Application of Genetics in Fisheries and Mariculture: Bangor, United Kingdom	Scientific Community	35	International
72	Presentation	K. Whelan	The Salsea Merge Programme	21 May 2011	Salmon Watch Ireland	Civil Society	30	Ireland
73	Presentation	S. Gudjonsson	The origin of salmon in the mackerel fishery within the Icelandic fishery limit.	11 June 2011	Annual meeting of the Federation of Icelandic river owners	Civil Society	75	Iceland
74	Presentation	K. Whelan	The Salmon at Sea (Salsea) Programme	August 2011	Miramichi Salmon Association, Canada	Scientific Community, Civil Society	20	Canada
75	Presentation	J. A. Jacobsen	Analysis of historical tagging data from the salmon fisheries at West Greenland and the Faroe Islands	11 October 2011	Symposium. Salmon at Sea: La Rochelle, France	Scientific Community, Policy makers, Civil society, Industry and Media	150	International
76	Presentation	K. A. Mork	Extending understanding of marine migration, ecology and mortality of Atlantic salmon post-smolts using oceanographic modeling, recaptured tagged salmon and SALSEA-GRAASP	11 October 2011	Symposium. Salmon at Sea: La Rochelle, France	Scientific Community, Policy makers, Civil society, Industry and Media	150	International
77	Presentation	N .Ó Maoiléidigh	Regional and temporal variation in marine growth of Atlantic salmon (Salmo salar, L.) from North-East Atlantic populations – links to marine survival and oceanographic conditions	12 October 2011	Symposium. Salmon at Sea: La Rochelle, France	Scientific Community, Policy makers, Civil society, Industry and Media	150	International
78	Presentation	W. Melle	The diet of Atlantic salmon post-smolts during their first feeding season in Northeast Atlantic	12 October 2011	Symposium. Salmon at Sea: La Rochelle, France	Scientific Community, Policy makers, Civil society, Industry and Media	150	International
79	Presentation	J. Gilbey	Marine distribution of regional Atlantic salmon post-smolt stocks in the NE Atlantic ascertained by	12 October 2011	Symposium. Salmon at Sea: La Rochelle, France	Scientific Community, Policy makers, Civil society, Industry and	150	International

			microsatellite DNA based assignment.			Media		
80	Presentation	E. Verspoor	GRAASP: a genetic tool for advancing understanding of the marine ecology of Atlantic salmon Salmo salar in the Eastern Atlantic Ocean	12 October 2011	Symposium. Salmon at Sea: La Rochelle, France	Scientific Community, Policy makers, Civil society, Industry and Media	150	International
81	Presentation	P. McGinnity	Minimising the impact of climate change on Atlantic salmon populations in freshwater: applying knowledge of evolutionary processes. Salmon at Sea	13 October 2011	Symposium. Salmon at Sea: La Rochelle, France	Scientific Community, Policy makers, Civil society, Industry and Media	150	International
82	Presentation	E. Verspoor	Salmon Conservation: the big picture and the hidden dimension	22 October 2011	Symposium: Eden Rivers Trust, Carlisle, UK	Scientific Community, Policy makers, Civil society, Industry and Media	60	UK
83	Presentation	M. Holm	The salmon's place in the ecology of the pelagic zone	13 December 2011	Conference: Ocean Silver, the Atlantic salmon's ocean odyssey: implications for fishery managers Fishmongers' Hall London Bridge, London, UK	Scientific Community, Policy makers, Civil society, Industry and Media	200	Europe
84	Presentation	P. McGinnity	Management of discrete populations – new perspectives and new challenges	13 December 2011	Conference: Ocean Silver, the Atlantic salmon's ocean odyssey: implications for fishery managers Fishmongers' Hall London Bridge, London, UK	Scientific Community, Policy makers, Civil society, Industry and Media	200	Europe

85	Presentation	E.Verspoor	Separating out the stocks – a lot done, more to do	13 December 2011	Conference: Ocean Silver, the Atlantic salmon's ocean odyssey: implications for fishery managers Fishmongers' Hall London Bridge, London, UK	Scientific Community, Policy makers, Civil society, Industry and Media	200	Europe
86	Presentation	K. A. Mork	The dynamics of salmon at sea – understanding their distribution in time and space	13 December 2011	Conference: Ocean Silver, the Atlantic salmon's ocean odyssey: implications for fishery managers Fishmongers' Hall London Bridge, London, UK	Scientific Community, Policy makers, Civil society, Industry and Media	200	Europe
87	Presentation	A.J Jensen	New approaches to scale reading - a biological treasure trove	13 December 2011	Conference: Ocean Silver, the Atlantic salmon's ocean odyssey: implications for fishery managers Fishmongers' Hall London Bridge, London, UK	Scientific Community, Policy makers, Civil society, Industry and Media	200	Europe
88	Presentation	Niall O'Maoileidigh	Trends in marine survival of salmon – has the tide turned?	13 December 2011	Conference: Ocean Silver, the Atlantic salmon's ocean odyssey: implications for fishery managers Fishmongers' Hall London Bridge, London, UK	Scientific Community, Policy makers, Civil society, Industry and Media	200	Europe

89	Presentation	Philip McGinnity, Tom Cross & Jamie Coughlan	Management of discrete populations: new perspectives and new challenges Applying genetic methods to resolve difficult management questions.	13 December 2011	Conference: Ocean Silver, the Atlantic salmon's ocean odyssey: implications for fishery managers Fishmongers' Hall London Bridge, London, UK	Scientific Community, Policy makers, Civil society, Industry and Media	200	Europe

WORKSHOPS:

TEMPLATE A2: LIST OF DISSEMINATION ACTIVITIES								
NO.	Type of activities[2]	Main leader	Title	Date	Place	Type of audience[3]	Size of audience	Countries addressed
1	Workshop	A. J. Jensen	Workshop on Digital Scale reading Methodology	8-10 September 2008	Trondheim, Norway	Scientific Community	15	Ireland, Finland, Iceland, UK, Norway, USA
2	Workshop	P. McGinnity	WP1 – Workshop on genetic assignment workshop	29-30 March 2010	Cork, Ireland	Scientific community	5	Ireland, UK, Norway

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[2] A drop down list allows choosing the dissemination activity: publications, conferences, workshops, web, press releases, flyers, articles published in the popular press, videos, media briefings, presentations, exhibitions, thesis, interviews, films, TV clips, posters, Other.

[3] A drop down list allows choosing the type of public: Scientific Community (higher education, Research), Industry, Civil Society, Policy makers, Medias ('multiple choices' is possible.

3	Workshop	K. A. Mork	WP5 Working Group meeting	8-9 April 2010	Bergen, Norway	Scientific community	12	Norway, Ireland, Scotland
4	Workshop	K. A. Mork	SALSEA-Merge WP5 Working Group meeting	11-15 April 2011	Bergen, Norway	Scientific community	25	Norway, Ireland, France, Scotland, Iceland
5	Workshop	A. J. Jensen	SALSEA –Merge: WP4 Workshop on post-smolt growth and feeding	27-28 April 2010	Bergen, Norway	Scientific Community	9	Faroe Island, Ireland, Norway
6	Workshop	A. J. Jensen	WP4 – Workshop on post-smolt growth	22-23 June 2010	Reykjavik, Iceland	Scientific Community	12	Ireland, Finland, Iceland, Norway
7	Workshop	K. A. Mork	Workshop: WP 5a –migration behaviour – , WP 5b – Salmon in the pelagic ecosystem, WP 5c – defining a detailed work programme for WP5	October 2010	Dublin, Ireland	Scientific Community	60	International
8	Workshop	K. A. Mork	WP5 Working Group meeting	4 February 2011	Bergen, Norway	Scientific Community	11	Norway, Ireland, Scotland
9	Workshop	P. Mc Ginnity	WP1 – Workshop on baseline delineation and structure	8-10 February 2011	Geilo, Norway	Scientific Community	9	Ireland, UK, Norway
10	Conference	L. P. Hansen, D. Reddin, M. Windsor	Salmon at sea: Scientific advances and their implications for management	11-13 October 2011	Symposium. Salmon at Sea: La Rochelle, France	Scientific Community, Policy makers, Civil society, Industry and Media	150	International

REPORTS:

TEMPLATE A2: LIST OF DISSEMINATION ACTIVITIES

No.	Type of activities[4]	Main leader	Title	Date	Place	Type of audience[4]	Size of audience	Countries addressed
1	Report	K. Whelan	Marine Survival of Atlantic Salmon	February 2007	IFM Conference Proceedings	Scientific Community Industry, Civil Society,	N/A	International
2	Cruise Report	N. Ó Maoiléidigh	Salmon at Sea: Merging Genetics and Ecology to Resolve Stock-specific Migration and Distribution patterns. Irish Research Cruise Report 2008	May 2008	NASCO http://www.nasco.int/sas/	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	International
3	Cruise Report	J. A. Jacobsen	Research on salmon post-smolts north of the Faroes in July 2008, SALSEA-Merge cruise # 2 .	July 2008	NASCO http://www.nasco.int/sas/	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	International
4	Cruise Report	M. Holm	Ecosystem Survey & Whale Observations in Southeast Greenland Sea and Northern Norwegian Sea Part 2, 26 July – 09 August, 2008. Cruise Report	August 2008	NASCO http://www.nasco.int/sas/	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	International
5	Cruise Report	K. Thomas	SALSEA-Merge: Irish Research Survey Report, 2009.	July 2009	NASCO http://www.nasco.int/sas/	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	International
6	Cruise Report	J. A. Jacobsen	Research on salmon post-smolts north of cruise # 2 the Faroes in July 2009, SALSEA-Merge	July 2009	NASCO http://www.nasco.int/sas/	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	International

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7	Cruise Report	L. Nøttestad	Cruise report from the coordinated ecosystem survey and SALSEA salmon	August 2009	NASCO http://www.nasco.int/sas/	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	International
8	Report	P. McGinnity, and E. Verspoor	Update and insights from the EU project SALSEA-Merge on establishment of a large-scale genetic database for assigning individual to population origin.	2009	ICES WGAGFM REPORT 2009	Scientific Community	N/A	International
9	Report	K. Whelan	SALSEA Merge programme	2008 - 2011	NASCO http://www.nasco.int/sas/	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	International
10	Report	Anon	Detective work in the sea– Investigating Depleting Salmon Stocks	November 2010	www.projectsmagazine.eu.com	Scientific Community Industry, Civil Society,	N/A	International
11	Report	E. Verspoor	Pursuing the establishment of a meta-database cataloguing molecular data in the field of fish and shellfish population	2010	ICES WGAGFM REPORT 2010	Scientific Community	N/A	International
12	Report	K. Whelan	Implications of Climate Change for Salmon and other Anadromous Species	2011	IFM Conference Proceedings	Scientific Community Industry, Civil Society,	N/A	International

MEDIA:

TEMPLATE A2: LIST OF DISSEMINATION ACTIVITIES

No.	Type of activities[4]	Main leader	Title	Date	Place	Type of audience[5]	Size of audience	Countries addressed
1		K. Whelan	Why are salmon dying at sea?	May 2008	FishfsrmingXpert	Industry, Civil Society, Policy makers, Medias	N/A	Ireland
2	Media	M. Holm	Salmon at Sea and planned activities at SALSEA cruises in 2008,	May 2008.	Adressavisen, newspaper Trondheim, Norway	Scientific Community Industry, Civil Society, Policy makers, Medias	20 000 subscribers	Norway
3	Internet media	K.Whelan	DNA analysis may explain salmon sea deaths	May 2008	Yahoo!	Internet	N/A	UK&Ireland
4	Media	M. Holm	"The Endangered Salmon, the Secret of the Sea" : Salmon at Sea and planned activities at SALSEA cruises in 2008	June 2008	Bergens Tidende, Newspaper Bergen, Norway	Scientific Community Industry, Civil Society, Policy makers, Medias	30 000 subscribers	Norway
5	Internet media	K. Whelan	Searching for reasons for the salmon shortage	September, 2008	IRISHTIMES.com	Civil Society, Policy makers, Medias	N/A	Ireland
6	Web	J. A. Jacobsen	The SALSE-MERGE project / "Laksaverkætlanin SALSEA-Merge"	June 2008	http://www.hav.fo/index.php?option=com_content&view=article&id=59&Itemid=113#Altjóða (www.hav.fo)	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	Faroes
7	Media	M. Holm	The Salmon Marine Habitat: still enigmatic	November 2008.	Kystmagasinet , " The West Coast Magazine", Bergen, Norway	Scientific Community Industry, Civil	N/A	Norway

						Society, Policy makers, Medias		
8	Media	D. Evans	Mystery at Sea	February 2009	The Irish Times	Civil Society, Policy makers, Medias	N/A	Ireland
9	Media	M. Holm	Results from 2008 SALSEA cruises and planned activities in 2009	February 2009	Bergens Tidende, Newspaper Bergen, Norway	Civil Society, Policy makers, Medias	30 000 subscribers	Norway
10	Medfia	K. Whelan	EU funds to halt decline of salmon in Mayo rivers	August 2009	Western People	Civil Society, Policy makers, Medias	N/A	Ireland
11	Media	J.C.Holst	Hvor blir laksen av (Presentation of SALSEA- merge)	March, 2009	Altaposten.no	Civil Society	N/A	Norway
12	Media	J.C.Holst	Hva skjer med villaksen (Presentation of SALSEA- merge)	March, 2009	Forskning.no	Scientific Community, Civil Society, Policy makers, Medias	N/A	Norway
13	Media	J.C.Holst	Silda tek maten frå laksen	August, 2009	Bergens Tidende, Bergen	Civil Society	Around 30 000 subscribers	Norway
14	Media	K. Whelan	Salsea Merge Updates	2008 - 2011	RTE Radio, Ireland	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	Ireland
15	Media	K. Whelan	Salsea Merge Updates	2008 - 2011	Irish times Newspaper, Ireland	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	Ireland
16	Media	C. Primmer	Teno salmon: their home address is in their genes	July 2011	Yle Yksi Radio	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	Finland

17	Media	K. Whelan	Salsea Merge Updates	2011	BBC Radio, Scotland	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	UK
18	Media	S. Gudjonsson	“Use genetic to reveal new knowledge on salmon at sea”	11 July 2011	Fréttablaðið Newspaper, Iceland http://vefblod.visir.is/index.php?netpaper=1684 http://vefblod.visir.is/index.php?s=5205&p=115267	Scientific Community Industry, Civil Society, Policy makers, Medias	103.000 Free subscribtions	Iceland
19	Media	Atlantic Salmon Trust (AST)	Finding Out What's Happening With Salmon at Sea	August 2011	Anglingnews.net	Civil Society,	N/A	Great Britiain
20	Media	P. Martin	Le saumon sauvage est en danger	October 2011	Le Sud Ouest	Industry, Civil Society, Policy makers, Medias	N/A	France
21	Media	J.J.Arene	Pourquoi lea Saumons meurent en mer?	October 2011	www.Info Magazine.com Edition Allier	Industry, Civil Society, Policy makers, Medias	N/A	France
22	Media	T. Andrews	AST at Salmon Summit	October 2011	Anglingnews.net	Industry, Civil Society, Policy makers,	N/A	Great Britain
23	Media	K.Whelan	Atlantic Salmon Trust conference	December 2011	Fishing Magic	Industry, Civil Society, Policy makers,	N/A	Great Britain
24	Media	K. Whelan	Salmon at Sea	December 2011	Trout and Salmon Magazine - Bauer Media, Peterborough, UK (www.bauermedia.com)	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	International

25	Film	In Production	“Lost at Sea” Marine mortality of Atlantic salmon.	In Production	http://www.atlanticsalmonlostatsea.net/index.htm	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	International
26	Media	T. Andrews	Salmon Fisheries Study	January 2012	The Irish Times	Scientific Community Industry, Civil Society, Policy makers, Medias	N/A	Ireland

A search for SALSEA-Merge on Google returns about 1800 pages, many of these are articles on SALSEA-Merge in papers, web sites etc.

4.3 Report on societal implications

Replies to the following questions will assist the Commission to obtain statistics and indicators on societal and socio-economic issues addressed by projects. The questions are arranged in a number of key themes. As well as producing certain statistics, the replies will also help identify those projects that have shown a real engagement with wider societal issues, and thereby identify interesting approaches to these issues and best practices. The replies for individual projects will not be made public.

A General Information *(completed automatically when **Grant Agreement number** is entered.*

Grant Agreement Number:	212529
Title of Project:	SALSEA-Merge
Name and Title of Coordinator:	Jens Christian Holst, Dr. Senior scientist.

B Ethics

1. Did your project undergo an Ethics Review (and/or Screening)? • If Yes: have you described the progress of compliance with the relevant Ethics Review/Screening Requirements in the frame of the periodic/final project reports? Special Reminder: the progress of compliance with the Ethics Review/Screening Requirements should be described in the Period/Final Project Reports under the Section 3.2.2 *'Work Progress and Achievements'*	***0Yes xNo***
2. Please indicate whether your project involved any of the following issues (tick box) :	***YES***
RESEARCH ON HUMANS	
• Did the project involve children?	
• Did the project involve patients?	
• Did the project involve persons not able to give consent?	
• Did the project involve adult healthy volunteers?	
• Did the project involve Human genetic material?	
• Did the project involve Human biological samples?	
• Did the project involve Human data collection?	
RESEARCH ON HUMAN EMBRYO/FOETUS	
• Did the project involve Human Embryos?	
• Did the project involve Human Foetal Tissue / Cells?	
• Did the project involve Human Embryonic Stem Cells (hESCs)?	
• Did the project on human Embryonic Stem Cells involve cells in culture?	
• Did the project on human Embryonic Stem Cells involve the derivation of cells from Embryos?	
PRIVACY	
• Did the project involve processing of genetic information or personal data (eg. health, sexual lifestyle, ethnicity, political opinion, religious or philosophical conviction)?	
• Did the project involve tracking the location or observation of people?	
RESEARCH ON ANIMALS	
• Did the project involve research on animals?	
• Were those animals transgenic small laboratory animals?	

- Were those animals transgenic farm animals?	
- Were those animals cloned farm animals?	
- Were those animals non-human primates?	
RESEARCH INVOLVING DEVELOPING COUNTRIES	
- Did the project involve the use of local resources (genetic, animal, plant etc)?	
- Was the project of benefit to local community (capacity building, access to healthcare, education etc)?	
DUAL USE	
- Research having direct military use	0 Yes X No
- Research having the potential for terrorist abuse	0 Yes X No

C Workforce Statistics

3. Workforce statistics for the project: Please indicate in the table below the number of people who worked on the project (on a headcount basis).

Type of Position	Number of Women	Number of Men
Scientific Coordinator		1
Work package leaders	2	5
Experienced researchers (i.e. PhD holders)	6	33
PhD Students		
Other	21	17

4. How many additional researchers (in companies and universities) were recruited specifically for this project?	3
Of which, indicate the number of men:	1

D Gender Aspects

5. Did you carry out specific Gender Equality Actions under the project?	x ○	Yes No

6. Which of the following actions did you carry out and how effective were they?

		Not at all effective				Very effective
☐	Design and implement an equal opportunity policy	○	○	○	○	○
X	Set targets to achieve a gender balance in the workforce	○	X	○	○	○
☐	Organise conferences and workshops on gender	○	○	○	○	○
☐	Actions to improve work-life balance	○	○	○	○	○
○	Other:					

7. Was there a gender dimension associated with the research content – i.e. wherever people were the focus of the research as, for example, consumers, users, patients or in trials, was the issue of gender considered and addressed?

○ Yes- please specify

X No

E Synergies with Science Education

8. Did your project involve working with students and/or school pupils (e.g. open days, participation in science festivals and events, prizes/competitions or joint projects)?

X Yes- please specify

Open day for school classes on Celtic Explorer on Salsea-Merge launch in Killibegs (Ireland). +Follow the Fleet – Marine Institute Ireland, Internet page.

○ No

9. Did the project generate any science education material (e.g. kits, websites, explanatory booklets, DVDs)?

○ Yes- please specify

x No

F Interdisciplinarity

10. Which disciplines (see list below) are involved in your project?

X Main discipline[1]: 1.5

X Associated discipline[1]: 1.4

X Associated discipline[1]:1.1

G Engaging with Civil society and policy makers

11a Did your project engage with societal actors beyond the research community? *(if 'No', go to Question 14)*	X ○	Yes YES

11b If yes, did you engage with citizens (citizens' panels / juries) or organised civil society (NGOs, patients' groups etc.)?

○ No

○ Yes- in determining what research should be performed

X Yes - in implementing the research

X Yes, in communicating /disseminating / using the results of the project

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[1] Insert number from list below (Frascati Manual).

11c In doing so, did your project involve actors whose role is mainly to organise the dialogue with citizens and organised civil society (e.g. professional mediator; communication company, science museums)?	X ○	Yes No

12. Did you engage with government / public bodies or policy makers (including international organisations)

○ No
X Yes- in framing the research agenda
X Yes - in implementing the research agenda
X Yes, in communicating /disseminating / using the results of the project

13a Will the project generate outputs (expertise or scientific advice) which could be used by policy makers?

X Yes – as a **primary** objective (please indicate areas below- multiple answers possible)
X Yes – as a **secondary** objective (please indicate areas below - multiple answer possible)
○ No

13b If Yes, in which fields?

Agriculture (fish farming)
Audiovisual and Media
Budget
Competition
Consumers
Culture
Customs
Development Economic and Monetary Affairs
Education, Training, Youth
Employment and Social Affairs

Energy
Enlargement
Enterprise
Environment
External Relations
External Trade
Fisheries and Maritime Affairs
Food Safety
Foreign and Security Policy
Fraud
Humanitarian aid

Human rights
Information Society
Institutional affairs
Internal Market
Justice, freedom and security
Public Health
Regional Policy
Research and Innovation
Space
Taxation
Transport

13c If Yes, at which level?

- X Local / regional levels
- X National level
- X European level
- X International level

H Use and dissemination

14. How many Articles were published/accepted for publication in peer-reviewed journals?	**16**
To how many of these is open access[2] provided?	**2**
How many of these are published in open access journals?	**2**
How many of these are published in open repositories?	**0**
To how many of these is open access not provided?	**-**
Please check all applicable reasons for not providing open access:	
☐ publisher's licensing agreement would not permit publishing in a repository ☐ no suitable repository available ☐ no suitable open access journal available X no funds available to publish in an open access journal ☐ lack of time and resources ☐ lack of information on open access ☐ other[3]: ……………	

15. How many new patent applications ('priority filings') have been made? *("Technologically unique": multiple applications for the same invention in different jurisdictions should be counted as just one application of grant).*	**0**

16. Indicate how many of the following Intellectual Property Rights were applied for (give number in each box).	Trademark	**0**
	Registered design	**0**
	Other	**0**

17. How many spin-off companies were created / are planned as a direct result of the project?	**0**
Indicate the approximate number of additional jobs in these companies:	**0**

18. Please indicate whether your project has a potential impact on employment, in comparison with the situation before your project:

X Increase in employment, or	☐ In small & medium-sized enterprises
☐ Safeguard employment, or	☐ In large companies
☐ Decrease in employment,	☐ None of the above / not relevant to the project
☐ Difficult to estimate / not possible to quantify	

19. For your project partnership please estimate the employment effect resulting directly from your participation in Full Time Equivalent (*FTE = one person working fulltime for a year*) jobs:	*Indicate figure:* 35

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[2] Open Access is defined as free of charge access for anyone via Internet.

[3] For instance: classification for security project.

Difficult to estimate / not possible to quantify	

I Media and Communication to the general public

20. As part of the project, were any of the beneficiaries professionals in communication or media relations?

○ Yes X No

21. As part of the project, have any beneficiaries received professional media / communication training / advice to improve communication with the general public?

○ Yes X No

22 Which of the following have been used to communicate information about your project to the general public, or have resulted from your project?

X Press Release
X Media briefing
X TV coverage / report
X Radio coverage / report
X Brochures /posters / flyers
X DVD /Film /Multimedia
X Coverage in specialist press
X Coverage in general (non-specialist) press
X Coverage in national press
X Coverage in international press
X Website for the general public / internet
X Event targeting general public (festival, conference, exhibition, science café)

23 In which languages are the information products for the general public produced?

☐ Language of the coordinator
☐ Other language(s)
X English

Question F-10: Classification of Scientific Disciplines according to the Frascati Manual 2002 (Proposed Standard Practice for Surveys on Research and Experimental Development, OECD 2002):

FIELDS OF SCIENCE AND TECHNOLOGY

1. NATURAL SCIENCES
1.1 Mathematics and computer sciences [mathematics and other allied fields: computer sciences and other allied subjects (software development only; hardware development should be classified in the engineering fields)]
1.2 Physical sciences (astronomy and space sciences, physics and other allied subjects)
1.3 Chemical sciences (chemistry, other allied subjects)
1.4 Earth and related environmental sciences (geology, geophysics, mineralogy, physical geography and other geosciences, meteorology and other atmospheric sciences including climatic research, oceanography, vulcanology, palaeoecology, other allied sciences)
1.5 Biological sciences (biology, botany, bacteriology, microbiology, zoology, entomology, genetics, biochemistry, biophysics, other allied sciences, excluding clinical and veterinary sciences)

2 ENGINEERING AND TECHNOLOGY
2.1 Civil engineering (architecture engineering, building science and engineering, construction engineering, municipal and structural engineering and other allied subjects)
2.2 Electrical engineering, electronics [electrical engineering, electronics, communication engineering and systems, computer engineering (hardware only) and other allied subjects]
2.3. Other engineering sciences (such as chemical, aeronautical and space, mechanical, metallurgical and materials engineering, and their specialised subdivisions; forest products; applied sciences such as

geodesy, industrial chemistry, etc.; the science and technology of food production; specialised technologies of interdisciplinary fields, e.g. systems analysis, metallurgy, mining, textile technology and other applied subjects)

3. MEDICAL SCIENCES

3.1 Basic medicine (anatomy, cytology, physiology, genetics, pharmacy, pharmacology, toxicology, immunology and immunohaematology, clinical chemistry, clinical microbiology, pathology)

3.2 Clinical medicine (anaesthesiology, paediatrics, obstetrics and gynaecology, internal medicine, surgery, dentistry, neurology, psychiatry, radiology, therapeutics, otorhinolaryngology, ophthalmology)

3.3 Health sciences (public health services, social medicine, hygiene, nursing, epidemiology)

4. AGRICULTURAL SCIENCES

4.1 Agriculture, forestry, fisheries and allied sciences (agronomy, animal husbandry, fisheries, forestry, horticulture, other allied subjects)

4.2 Veterinary medicine

5. SOCIAL SCIENCES

5.1 Psychology

5.2 Economics

5.3 Educational sciences (education and training and other allied subjects)

5.4 Other social sciences [anthropology (social and cultural) and ethnology, demography, geography (human, economic and social), town and country planning, management, law, linguistics, political sciences, sociology, organisation and methods, miscellaneous social sciences and interdisciplinary , methodological and historical S1T activities relating to subjects in this group. Physical anthropology, physical geography and psychophysiology should normally be classified with the natural sciences].

6. HUMANITIES

6.1 History (history, prehistory and history, together with auxiliary historical disciplines such as archaeology, numismatics, palaeography, genealogy, etc.)

6.2 Languages and literature (ancient and modern)

6.3 Other humanities [philosophy (including the history of science and technology) arts, history of art, art criticism, painting, sculpture, musicology, dramatic art excluding artistic "research" of any kind, religion, theology, other fields and subjects pertaining to the humanities, methodological, historical and other S1T activities relating to the subjects in this group]