REPORT OF THE WORKING GROUP ON THE APPLICATION OF GENETICS IN FISHERIES AND MARICULTURE

Faro, Portugal

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International Council for the Exploration of the Sea

Conseil International pour l'Exploration de la Mer

Palægade 2–4 DK–1261 Copenhagen K Denmark

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1 INTRODUCTION

Accordant with C.Res. 2:28 adopted at the 1995 Annual Science Conference in Aalborg, Denmark, the Working Group on the Application of Genetics in Fisheries and Mariculture (WGAGFM; Chairman J. Mork, Norway) met at the University of Algarve at Faro, Portugal, Feb. 19-23, 1996 to deal with its Terms of Reference (Appendix 2).

1.1 Attendance

There are currently 38 appointed members of the WGAGFM (Appendix 4). Eleven of these attended the 1996 WG meeting in Faro, Portugal (Appendix 3). Six members regretted by letter that they were absent for practical and/or economical reasons. Countries represented (number of persons in parenthesis) were Canada (1), Denmark (1), Finland (1), Iceland (2), Norway (2) , Portugal (1), Poland (1), Spain (1), and UK (1).

The sub-group format of the WGAGFM was reflected in the division of scientific tasks during the meeting, according to the following structure :

Qualitative genetics sub-group: **G. Dahle** (const. leader), L. Cancela, A.K. Danielsdottir, W. Davidson, M. M. Hansen, M.L. Koljonen, J.A. Sanchez.

Quantitative genetics sub-group: **J. Jonasson** (const. leader), K. Goryczko, A. Thompson.

1.2 Working form

Prior to the meeting, specific members were asked to prepare position papers related to specific issues in the Terms of Reference, and to chair the respective sessions. During the meeting, these position papers were first presented and discussed in plenary. Thereafter, each topic was discussed in its relevant sub-group, which then prepared an updated text for final plenary discussion and inclusion in the WG Report.

T. Thompson chaired 'Selective Fisheries', W. Davidson chaired 'Genetically Modified Organisms', J. Jonasson chaired 'Broodstock Manegement' (position paper prepared by Gerry Friars (Canada), the quantitative sub-group leader who unfortunately could not attend for economic reasons), M. M. Hansen chaired 'Good Stocking Practice', G. Dahle chaired an open scientific session, and J. Mork chaired 'Management Units/Genetic resources' (position paper partly prepared by Tom Cross, Ireland, the qualitative sub-group leader who too could not attend for economic reasons). The session chairmen were also responsible for leading the respective colloquia and for preparing the final report text from the session in question.

All members had been asked to collect national activity reports from their respective countries and bring with them (on diskette) to Faro. A preliminary report on national activities could thus be compiled during the meeting.

The Working Group decided that, like in 1994 and 1995, the preparation of the WG Report should mainly be done by the members present at the meeting.

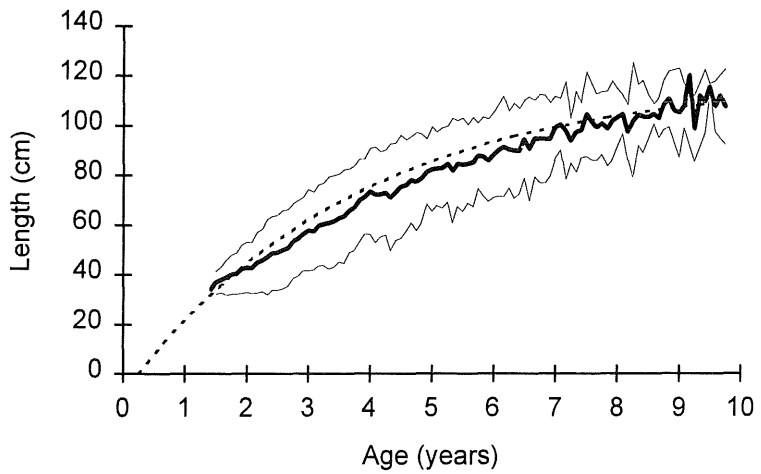
2 TERMS OF REFERENCE 1996 (CF. APPENDIX 1)

2.1a «Selective Fisheries»

In 1995, WGAGFM restricted its discussion on this topic to a principal level, recognizing that a more detailed treatment will require contribution from external expertise. It was agreed, however, that it was desirable to keep this important topic on the agenda for future work, with an aim to establish the necessary specialist contacts for expanding the list of recommendations. During fall 1995, contact was made with Dr. Kevin Stokes at MAFF (Lowestoft, UK) who responded very positively and suggested that a manuscript by him and Anthony Thompson, concerning modelling and simulations of possible genetic effects from a size-selecting fishery regime, was presented in Faro. The following section is based on that presentation and the discussions that followed it.

Selective fisheries
Natural populations have many different life history strategies made up of many traits. Examples of traits are spawning success, survival at hatching, growth rate at various stages throughout the life of the fish, age (size) at maturity, and migration patterns. Quantitative traits show phenotypic variation that has genetic and environmental components. An example of this is the variation in lengths-at-age in a fish species: a small amount of variation is due to the genetic component and a larger portion is due to the environmental effects such as food availability or temperature. There have been no rearing experiments to quantify the variance in length-at-age due to genetic (V_G) and environmental (V_E) effects on North Sea Cod. The phenotypic variance (V_P) in length at age was taken from MAFF Fisheries Statistics for fish aged from counting annual rings on otoliths sampled from port landings for the years 1980-1990. An estimate for heritability of growth rate in fish in aquaculture experiments is assumed to be 0.3 (range 0-0.6), and since $h^2 = V_G / V_P$ and $V_P = V_G + V_E$, it follows that $V_E = V_P(1 - h^2)$ and $V_G = V_P - V_E$. The mean length for a three year old cod, calculated from the monthly English Market Sampling Programme, is 60 cm with a phenotypic variance of 100 cm^2 (see Fig 2.1.1). Assuming a heritability of 0.3, the genotypic and environmental variances are calculated as 30 and 70 cm^2, respectively.

Figure 2.1.1. Growth of North Sea cod. Data are monthly means (thick line) and 95% confidence limits (thin line) from the English Market Sampling programme with ages determined from annual rings on otoliths. The dashed line is for the von Bertanlanffy growth curve determined by Daan (1974) where l_t=118.7(1-exp(-0.269(t-0.25))).



Breeding programmes in hatcheries use the genetic variability to predict the response to artificial selection for different traits in future generations. Ranching studies on Atlantic salmon in Iceland have produced heritability estimates ranging from 0-0.36 for mean body weight at different life history stages and for return rate of salmon returning after one year (grilse) 0.12 and for two sea-winter salmon of 0.04. The genetic correlation between various life-history traits was in general low. There was a low positive genetic correlation between growth rate and survival (and hence fitness), in that individuals with the genetic potential for faster growth had a higher return rate. The extent to which genetic control of a trait relates directly to survival, in the natural environment, is in need of more study. These are the first estimates made for salmon that have been released into the wild for 1-2 years, and therefore are more likely to apply to the wild situation of other fish species.

Simulation modelling is now underway to link quantitative genetics, fish biology, and fisheries exploitation, in a way that is consistent to all three disciplines. Fishing mortality is now high in the wild, often exceeding 70% mortality per year, and this can introduce significant size-related selection pressures. For example, trawl nets catch fish above a certain minimum size, whereas gillnets take only a narrow size range of fish usually towards their maximum lengths. There have been concerns that the increased mortality on larger individuals (where the large size will have both genetic and environmental components) will eventually result in the evolution of slow-growing late-maturing fish. The simulation studies, and the fact that growth rate is genetically linked to age at maturity, means that the evolution towards slow growing fish may not actually occur under length-dependent fishing mortality, as fast-growing fish produce many progeny as they are larger and mature earlier.

Recommendation 1: *WGAGFM recommends that there are further combined studies on relating quantitative genetics to the natural environment in conjunction with fisheries biology to understand the significance of correlated traits to the evolution of various traits, particularly growth rate. Continued consideration should be given to managing fisheries in a way that does not reduce the genetic diversity of fish populations.*

2.1b «Genetically Modified Organisms (GMOs)»

The application of biotechnologies, particularly in the areas of reproduction, growth, health, tolerance to physical factors, product quality, and nutrition has long term potential benefit for the aquaculture industry. Some of the "simpler" technologies, for example controlled breeding which is the basis for domestication and development of most of the agricultural plants and animals we know, has been practised for centuries. Controlled selection and mating regimes have also been applied to some species of fish (for example, carp) and in the last 20 years it has been the basis for the expansion of the aquaculture industry with salmonids, tilapia and catfish. Other technologies such as nutrition, endocrinology, hybridization, and chromosome manipulation have become familiar tools for the fish farmer and these have allowed great advances in how fish are produced. The latest trend in agricultural sciences involves a biotechnology that produces genetic modifications that do not, and could not, occur naturally. Advances in molecular biology make it possible (almost a routine procedure) to move genes between organisms. Moreover, novel gene constructs can be created such that the expression of genes is altered (for example, the tissue in which they are produced or the amount that is produced). Organisms that have had their genomes manipulated in this way are called transgenics.

The agricultural industry has embraced the use of transgenic plants to the extent that they are now in commercial production in Europe and North America. The use of transgenic animals has been more controversial. They are not being produced for food but are being used as "factories" for the production of human therapeutics such as blood clotting agents for haemophiliacs. Scientific

research is being carried out and transgenic fish are being produced in many labs throughout the world. A driving force in university labs is the use of zebrafish as a model system for studying development but other groups have put antifreeze genes into Atlantic salmon and growth hormone genes into a variety of species including carp and salmonids. The progress in the application of transgenic technology to fish aquaculture has been rapid. This is illustrated by the observation that outdoor performance tests of rapidly growing transgenic carp containing a rainbow trout growth hormone gene construct were being carried out within four years of the first published reports in 1985 on the successful production of transgenic fish with cloned genes. There can be no doubt that the technology is available for the production of transgenic fish, and it is probably only a question of time before they will be used in an aquacultural setting.

In 1994, the WGAGFM noted that transgenic fish (GMOs) were being produced but made no further comments. In 1995, the WGAGFM was asked by the Mariculture Committee to make comments on how ICES member countries should or could go about assessing a GMO release. WGAGFM did not have time to conduct an extensive discussion on GMOs at its meeting but it indicated that it was very interested in the "genetical" part of GMO questions and that it should be able to give advice on risk analysis of the spread of transgenes from GMOs to wild populations. There was, however, one major concern and that was the definition of a GMO that had been adopted by the WGITMO. This was the starting point of the discussions held at the 1996 WGAGFM meeting.

There are several definitions of what constitutes a GMO. The European Communities Directive no. 90/220/EEC dated April 23, 1990 defines a GMO as "an organism in which genetic material has been altered in a way that does not occur naturally by mating and/or by natural recombination". However, the ICES definition of a GMO in its Code of Practice is slightly different and describes it as "an organism in which the genetic material has been altered anthropogenically". The ICES' definition also notes that this includes such techniques as the isolation, characterisation and modification of genes and their introduction into living cells, as well as techniques for the production of living cells with new combinations of genetic material by the fusion of two or more cells. This is a very broad definition but one that the WGAGFM can accept.

The WGAGFM considers that the ICES' definition of a GMO does <u>not</u> include organisms that have been produced by controlled breeding procedures but it does include transgenic organisms and those whose chromosome set has been modified. For the sake of clarification, a transgenic organism is an organism bearing within its genome a copy or copies of novel genetic constructs produced through recombinant DNA technology. The important part of this definition is the phrase "novel genetic constructs produced by recombinant DNA technology". This definition of a transgenic would include organisms manipulated with their own genetic material (for example, the introduction of multiple copies of salmon growth hormone into salmon, or the use of the promoter for one carp gene to drive the expression of a different carp gene in carp). Similarly, an organism whose chromosome set has been manipulated refers to triploids, all female strains, all male strains, gynogens, and mitogens.

The WGAGFM recognises that there are many potential benefits and drawbacks for GMOs depending on the species, the origin of the transgenes, how the transgenics will be raised, and the final product used. However, WGAGFM did not feel that there was sufficient information available at present to be able to make specific recommendations for assessing the risk of potential releases of transgenics on the environment and on natural populations. The WGAGFM will keep a watching brief on the use of GMOs and in particular transgenics, in aquaculture. In this regard, the WGAGFM endorses the ICES Code of Practice as it applies to GMOs.

Recommendation 2: *WGAGFM recommends that member countries of ICES follow the ICES Code of Practice and notify ICES on an annual basis what licences have been granted for the genetic modification, importation, use or release of any GMO.*

Rationale: this would provide a data base and the information that the WGAGFM requires before it can make any further comments on GMOs and/or transgenics.

In its 1995 report, the WGAGFM suggested that a theme session on GMOs would be appropriate at a future Annual Science Conference. Given the rapid increase in the scientific research on GMOs, their use in agriculture, and their potential use in aquaculture, it seems appropriate to suggest this again.

Recommendation 3: *WGAGFM recommends that a theme session on "The use of genetically modified organisms (GMOs) in aquaculture" be part of the 1998 Annual Science Conference.*

Rationale: this time frame will allow ICES to receive information from its member countries for 1996 and 1997 regarding what activity is being carried out on GMOs. The WGAGFM will review this information and use it as part of its deliberations at the next working group meetings.

2.2 Management Units / Genetic Resources

The ability to identify and characterize populations in marine and anadromous finfish and shellfish species is important for several reasons. For fishery management it is mandatory because MSY (maximum sustainable yield) can best be achieved when managing at the population level. For population geneticists, who are expected to give advice on questions concerning the preservation of biodiversity and genetic reources, the genetic differences between populations may be as evolutionarily significant as the amount of genetic variability within populations. Both types of variability are included in the term 'genetic resources'.
If populations cannot be correctly identified and characterized, resource management and utilization will be suboptimal and genetic resources cannot be effectively preserved. Thus thorough knowledge of the actual population structure in exploited finfish and shellfish species is beneficial both for utilization and preservation.

Management units
To some extent, the interaction and understanding between fishery managers and population geneticists in these questions have been negatively affected by the lack of a common and distinct terminology. In particular, the content of the widely used term 'stock' may be very different for the two groups. While a fishery manager usually means 'management unit' which in its simplest form may be 'a group of fish exploited in a specific area or with a specific method' (Smith et al 1990), a population geneticists often would mean a population in the Mendelian interbreeding-group sense. The radical difference in the evolutionary time perspective between these two views is apparent, and clearly, the value of a 'stock' in a genetic resource context could thus be very different for the two professions.

WGAGFM will point to the importance of population geneticists using a scientifically correct and unambiguous terminology when giving recommendations to fishery management. Notably now when quantitative genetics gets increased attention, e.g. in studies of life history traits (see chapter 2.1a), it is important that efforts are made to secure that its terminology and principles are adequately explained and understood.

Despite the fact that both fishery management and the preservation of genetic resources suggest a resource utilization targeted at populations, the actual implementation of such management regimes have been a slow process. A number of factors have been identified which have created problems in the collection of the pertinent genetic knowledge, as well as in the implementation of the knowledge into practical resource management (see Carvalho & Pitcher 1994, Carvalho & Hauser 1994, Ferguson 1994, Ferguson et al 1995, Ryman et al 1995):

1. Factors may be of the socio-economic or political type, like tendencies of short-time optimitation of fishery output, or lack of regulation of the utilization of common resources in international zones ('the fish doesn't recognize national borders').

2. A second type of factors are practical, in that there may not be adequate data available for conclusions upon intraspecific genetic structure, or there may not be money available for collecting such data. In fact, only for a few species (notably some anadromous salmonids) is the stock structure currently well enough known that a population-level management can be implemented.

3. Other factors are formal, e.g. the lack of a common understanding of the terminology and the content of terms like 'stocks', 'populations' and 'genetic resources', or 'professional'. Even among scientists carrying out population genetic studies, there is need for discussions about criteria for 'populations' and 'genetic resources', about how well various marine 'stocks' meet such criteria, how well one is able to evaluate this with current metodology, and what is actually required in the way of biological and genetic information to do a realistic evaluation.

The WGAGFM meeting in 1996 discussed topics related to the two latter points.

Genetic resources

Basic population genetics theory infers that when a species is splitted into several populations between which there is some restriction to gene flow, differences in the frequencies of the alleles at polymorphic loci begin to develop. This genetic differentiation has several causes. First, different mutations may occur in different populations. Second, genetic drift (i.e., the stochastic variation in allelic frequencies between generations) can lead to an accumulation of differences. Third, natural selection can change allele frequencies in different directions due to different environments in the population habitats.

The balancing force for these differentiating forces (i.e., mutations, genetic drift and local adaptation) is the homogenizing effect of gene flow. For any level of the differentiating momentum, there is a level of gene flow which may cancel out its net effect. The strenght of the gene flow between populations is thus the restrictive factor which determines how much populations actually can differ from each other genetically. Therefore, estimates of the realized gene flow between tentative populations are so important in population genetic studies aimed at the identification and characterization of genetic resources.

Gene flow levels are usually estimated by studying the current distribution of alleles in the populations. It is very important to be aware that the underlying assumption for this procedure strictly demands that the 'genetic tags' used are selectively neutral. As pointed out in the 1994 WGAGFM report, absolute selective neutrality cannot be guaranteed for any of the genetic tags used hitherto in studies of marine finfish or shellfish species. This should be kept in mind when interpreting results from genetic studies. Recently, several new molecular techniques have been developed which can detect genetic variability at 'loci' with extremely high mutation rates (e.g., Variable Number of Tandem Repeats mini and microsatellites). These 'loci' are currently not

believed to be involved in any important cellular mechanism and have thus been tentatively regarded as selectively neutral. They are still, however, generally little studied and conclusions on this must await a closer examination. Particularly when dealing with cDNA tags, sequencing and comparing the sequences with all available databases should be a routine step before launching the markers for studies of intraspecific genetic structure.

Intraspecific genetic resources include:

1. Genetic variability between individuals within populations (the 'within' component).
2. Genetic variability between populations (the 'between' component)
    - a random variation component (due to genetic drift)
    - a directed local adaptation component (due to natural selection).

Ad. 1. Genetic variation at the individual level is the result of mutations accumulated over a large evolutionary time scale. The number of alleles determines the number of possible genotypes, which is the raw material for differentiation and evolution in general. A high level of individual genetic varibility is considered evolutionarily beneficial for a species.

Ad. 2. Genetic differences between populations can result from genetic drift, from natural selection, or from a combination of those two effects.

Genetic drift

Genetic drift is the random fluctuation of allele frequencies between generations. The amount of fluctuation depends on the effective population size (larger fluctuations in small populations). Without the countering effect of immigration and mutation, genetic drift would sooner or later lead to the extinction of allelic polymorphisms (fixation for one of the alleles) in any natural population. Thus, in a structure with few, and numerically small populations, genetic drift will have mainly negative effects on the genetic resources (the 'zoological garden' effect).

On the other hand; if there are numerous populations with a restricted gene flow between them, genetic drift can be a very effective way of preserving the total genetic variability in the species through the fixation of different alleles in different populations (Altukhov 1990). This kind of genetic resource may not be very common among marine finfish and shellfish species, in which populations typically are very large. Also, in some areas the available evolutionary time since population establishments would in fact be too short for statistically detectable differentiation by genetic drift to be expected in very large populations (e.g., a few thousand generations since the last glaciation for species in the North Atlantic; Ferguson 1995). In some anadromous salmonid species, however, population sizes are rather restricted and genetic drift may there be an important cause for observed differences both between populations and between generations within populations.

At loci with extremely high mutations rates (e.g., some of the newly developed DNA markers), allele frequency differences that are detectable in reasonably sized samples can develop in much shorter periods of time, even if gene flow is substantial. This increases the chances to identify finfish and shellfish groups at a more trivial stage of evolutionary differentiation, and may thus meet certain demands in practical 'stock' management. However, chances that such groups are simply temporal, evolutionarily insignificant aggregations of individuals also increase. Hence, as discrimination tools get more and more sensitive, the need for criteria to decide when such groups deserve status as 'genetic resources' also becomes more acute.

Local adaptations

The basis for milieu adaptation (and thus for evolution in the Darwinian sense) is that many structural and regulatory loci are not selectively neutral. Various genotypes at such loci have different fitnesses which, under a selection pressure, can change the allelic composition of the population over time.

The factors which determine the efficiency of a natural selection regime is well known from quantitative genetics and can be summarized as follows:

Factors which speed up local adaptation processes:

1. Large population size (less disturbing effect of genetic drift).
2. High amount of genetic variability in the population (cf Fisher's fundamental theorem).
3. High selection intensity.
4. Long term stability (many generations) in the environmental factors that causes selection.
5. Restricted immigration of non-selected individuals.
6. High selection coefficients.
7. Few loci behind the selected trait.

Local adaptations are regarded as especially valuable genetic resources because they increase the evolutionary potential of species by tayloring populations to inhabit a variety of specific environments. As indicated by points 1-7 above, local adaptation is hampered if population sizes are very small. It is well known that genetic drift generally disturbes the selection process. In fact, in very small effective population sizes, the disturbance by genetic drift will make all genotypes appear as if selectively neutral (e.g., Hartl & Clark 1989, p. 351). Furthermore, genetic drift inevitably reduces local genetic variability which in turn reduces adaptivity (according to Fisher's Fundamental Theorem of Natural Selection (Fisher 1930), the rate of genetic change due to selection is directly proportional to the amount of genetic variability for the trait under selection).

In conclusion genetic drift, which under certain very specific circumstances mentioned above (i.e., a large number of small populations with restricted gene flow between them) can be beneficial for the preservation of the overall amount of allelic variability in a species (Wright 1951, Kimura 1968), has no local adaptional value for additive traits *per se*. On the contrary, its effects will on average be negative for the development and persistence of local adaptations. WGAGFM sees it as important to stress this point because it emphasizes the risk of genetic losses when antropogenic impact acts to reduce the sizes of natural populations.

It follows that when looking for genetic resources in the form of genetic adaptations in nature, chances for finding them are greatest when dealing with large and old populations with limited immigration, and environmental selection factors which has been relatively constant for an evolutionarily substantial period of time. It also follows that the preservation of existing genetic resources in the form of local adaptations must include meaures to avoid serious bottlenecks in population size.

Most marine finfish and shellfish species are often characterized by very large subpopulation sizes which fullfill the first of the seven criteria mentioned above. Also, most marine species studied so far have shown fairly high levels of genetic variability (point 2 above). In the areas most intensively studied genetically in finfish and shellfish (i.e., the North Atlantic), environmental factors (point 4) have been fairly stable for some 10.000 years (since last glaciation). This may equal some 1000-10000 generations depending on species. Considering the often extremely large individual numbers in marine populations, this is much too short a period for equilibria to have developed between, e.g.,

selection and immigration. Nevertheless, substantial allelic change may have taken place in local subpopulations, especially for traits that are affected by few polymorphic loci. However, we currently know very little about points 3,5,6 and 7 listed above, and will have problems even making qualified guesses about the 'adaptational genetic resource' value of most marine finfish and shellfish subpopulations today.

This information gap is partly due to the *modus operandi* of current population genetic studies. In general, qualitative population genetics is primarily concerned with allelic variation at single loci, and has no effective means to identify and screen loci responsible for variation in quantitative traits. In order to establish the pertinent knowledge thus, methodology from quantitative genetics (see section 2.1a about studies of life history traits) must be employed, as argued for also in the WGWGFM reports of 1994 and 1995.

A large array of statistical measures and computer software are currently in use for estimating similarities and differences between subpopulations. It is important to be aware that the various measures may have widely different statistical properties and areas of use. Especially after the launching of many new molecular techniques is it mandatory that users are educated in the background, properties, underlying assumptions and limitations of the techniques as well as of the mathematical/statistical procedures and measures before drawing conclusions from data sets.

Recommendation 4: *WGAGFM will again stress the importance of using a combined qualitative/quatitative genetics approach to the identification and management of marine genetic resources, and in particular that theory as well as recent results from quantitative genetics should be a part of the discussion on population structure and differentiation in marine species, as suggested also on other grounds by WGAGFM in its reports in 1994 and 1995. We will also point to the importance that samples for studies of genetic structure and local adaptations also contain biological information (i.e., individual size, age, sex, maturity stage etc).*

Recommendation 5: *WGAGFM feels that its meeting in 1997 should be a suitable opportunity for the WG to discuss the merits so far of the many new molecular techniques developed and implemented in population genetic studies in the last decade. It would also be useful to discuss and evaluate the variety of computer software packages now available for population genetic analysis, in order to come up with recommendations for tools that are suitable for specific types of problems.*

References

Altukhov, Y.P. (ed.) 1990. Population genetics. Diversity and Stability. Harwood Academic Publishers GmbH. 352 p.

Carvalho, G.R. & Hauser, L. 1994. Molecular genetics and the stock concept in fisheries. *Reviews in Fish Biology & Fisheries, 4,* 326-350.

Carvalho, G.R. & Pitcher, T.J. (eds) 1994. Molecular genetics in fisheries. *Reviews in Fish Biology & Fisheries, 4,* 269-399.

Ferguson, A. 1994. Molecular genetics in fisheries: current and future perspectives. *Reviews in Fish Biology & Fisheries, 4,* 379-383.

Ferguson, A., Taggart, J.P., Prodohl, P.A., McMeel, O., Thompson, C., Stone, C., McGinnity, P. & Hynes, R.A. 1995. The application of molecular markers to the study and conservation of fish populations, with special reference to Salmo. *J. Fish. Biol. 47,* (Supplement A), 103-126.

Fisher, R.A. 1930. The genetical theory of natural selection. Clarendon Press, Oxford.

Hartl, D.L. & Clark, A.G. 1989. Principles of population genetics. Sinauer Associates, Inc. Sunderland, Massachusetts.

Kimura 1968. Genetic variability maintained in a finite population due to mutational production of neutral and nearly neutral isoalleles. *Genet. Res. 11*, 247-269.
Ryman, N., Utter, F.M. & Laikre, L. 1995. Protection of intraspecific biodiversity of exploited fishes. *Reviews in Fish Biology & Fisheries, 5*, 417-446.
Smith, P.J., Francis, R.I.C.C.,& McVeagh, M. 1990. Loss of genetic diversity due to fishing pressure. *Fish. Res. 10*, 309-316.
Wright, S. 1951. The genetic structure of populations. *Ann. Eugen. 15*, 323-354.

2.3a Broodstock Management

Introduction
The realisation of genetic gains, through controlled selection and mating regimes, was highlighted in the 1994 and 1995 WGAGFM reports. The early evidence indicates that the tremendous genetic advances, accrued in terrestrial agriculture, are similarly possible in fish. The application of breeding programs in fish requires detailed considerations of broodstock management.

The role of genetic principles in fish encompasses both wild and domesticated stocks. Aquaculture now supplies more than 20 percent of the fish consumed in the world and helps to alleviate pressure on wild stocks. Nevertheless, overfishing has seriously affected many wild populations (e.g. Adams, 1995). Hence, management of shrinking gene pools becomes important--in parallel with the application of breeding practices in aquacultural stocks.

The sampling of wild stocks to establish domestic broodstocks requires great care. Due to possible damage to the maintenance of certain stocks, small wild populations should not be used in the procurement of gene pools for aquaculture and sea ranching. The application of breeding principles for stocking is considered in a separate WGAGFM report and is another area that involves both wild and domestic stocks. Fish that escape from aquaculture may exchange genes with wild populations. Hence, the well being of natural and cultured populations needs to be considered simultaneously.

The purpose of broodstock management can be divided into three categories.

1) Controlled breeding with known pedigrees. At the beginning of the controlled breeding, an establishment of a gene pool from the wild requires attention with respect to the traits desired in a domesticated population of a species. The amount of genetic variance, affecting the required traits among and within subsets of the available population(s), needs to be considered in order to allow gains from selection. For example, knowledge related to a wild stock's growth rate, age at maturity, disease resistance, adaptability to culture, etc. will help in the initial choice. Appropriate sampling from wild populations allows informed choices that can both reduce the amount of selection required and lead to faster genetic gains under domestication.

The effective number of parents is of concern in both the establishment of and the subsequent conduct of a breeding program. The larger the effective number of parents, the smaller the increase in inbreeding that is realised each generation. Low levels of inbreeding within a population are required to preserve genetic variation and promote maximum gains from selection in an interbreeding population (Jui and Friars, 1974). In commercial breeding programs involving fish, this is usually done by keeping track of pedigrees in the population and deliberately avoiding the mating of siblings. Computer software used in controlled breeding programs can keep track of inbreeding coefficient for each individual in each generation.

Crossing stocks that have never interbred, because of spatial or temporal separation, may lead to genetic disequilibrium. The incomplete mixing of genes from the different primary stocks allows the loss of genes that could benefit subsequent rounds of selection. Random mating within such crosses, for one or more generations prior to selection, will be necessary to yield maximum genetic gains.

The ultimate goal of a breeding program in aquaculture is to meet market demands at minimum cost. The array of traits, that could be incorporated into a multiple objective selection program, can become too wide to allow appreciable gains in individual traits. In conjunction with genetic considerations, non-genetic influences, such as feeding regimes, disease control and husbandry, all require improvement in order to boost the efficiency of production. The enhancement of growth rate, through adequate diets and optimal levels of feeding, or the alleviation of disease, through vaccination and enhanced environmental management, can greatly complement the gains realised through selection.

The dispersement of improved stock from a breeding nucleus requires attention from the standpoint of rewarding the developer. The development of legal agreements, possibly coupled with genetic markers, may be necessary in this context. Also, the distribution of stock requires attention to the concerns raised in conjunction with escapees from aquaculture.

2) Short term broodstock management for stocking hatchery and wild populations with unknown pedigrees (random mating) without conservation oobjectives.
Earlier suggestions have indicated that a minimum of 50 individuals should be used each generations as broodstock. New evidence show that the number should be higher or 150-300 individuals to allow for minimum changes in allele frequencies.

3) Broodstock management for long term conservation purposes. These projects each need at least 500 individuals per generation to conserve allele frequencies and rare alleles. This can be achieved by maintaining, each generation, a live broodstock with at least 500 random matings of different age classes similar in proportion to the natural population. A long term conservation program can also be achieved by cryopreservation of sperm for later use in restocking if the natural population is in any way threatened by extinction.

Recommendation 6: *WGAGFM recommends that the principles and protocols outlined above (section 2.3) are followed in the establishment and management of broodstocks of marine finfish and shellfish.*

References
Adams, S., 1995. Genetic studies may provide keys to Gulf of Maine fisheries problems. In: T. Corey, Editor, Nor'Easter 7, No. 1:21-23, Univ. of Rhode Island, Narragansett, R1, USA, 02882-1197.
Jui, P.Y. and G.W. Friars, 1974. Two way selection on pupal wieght with different degrees of inbreeding in *Tribolium castaneum. Can. Jour. Genet. Cytol. 16*:765-775.

2.3b Good Stocking Practice

Background
The working group discussed the subject of "good stocking practices" and how to develop guidelines for this. There is a rich body of literature on the subject, describing basic principles for ameliorating harmful genetic effects of stocking activity. These principles include recommendations for effective numbers of parent fish used for producing stocking material and the preferred use of stocking material of local origin instead of exogenous hatchery fish etc. (e.g., Hindar et al., 1991; Waples, 1991; Cowx, 1994). Also, in several countries guidelines have been developed that describe these principles in a popular form to people and authorities responsible for the stocking. However, even though this point has been raised repeatedly in the literature (Waples, 1991; Cowx, 1994), the members of the working group feel that the purpose and objectives of stocking activity still are much too often vaguely or incorrectly defined:

Stocking is seen as a universal method for counteracting declines in population sizes and, furthermore, stocking programmes are often regarded as conservation programmes. In principle, however, any stocking programme will inevitably affect the genetic integrity and composition of the stocked population, even if all recommendations for "good stocking practices" have been followed. Therefore, for conservation purposes stocking should only be considered as a last resort.

Objectives of stocking
Stocking may be inevitable in some conservation programmes in order to avoid the possibility that very small and endangered populations or species die out or are genetically detoriated for purely demographic reasons. In such cases stocking programmes should only be operating on a short time scale and should not be considered a permanent solution to the problem. Also, stocking may be useful for restoring populations at localities where the original populations have gone extinct. However, most stocking programmes are aimed at increasing the sizes of the populations available to fisheries (recreative or commercial). The decision of implementing a stocking programme must therefore be based on balancing the possible socioeconomical benefits with the genetic distinctness and "value" represented by the stocked populations. Good stocking practices can be useful for slowing down genetic changes in stocked populations, but they cannot ensure that such changes do not occur in the long run.

The working group recommends that the objectives of stocking programmes are clearly defined and that alternative measures for elevating population sizes, for instance restoration of spawning grounds and regulation of fisheries, are considered before stocking is undertaken. In particular, it is important to determine if there is at all a need for elevating population sizes, and, if this is the case, to identify the causes for the decline of numbers of individuals in the populations

A description of the steps in the decision making is given by Cowx (1994).

References
Cowx, I.G. (1994). Stocking strategies. *Fish. Manage. Ecol. 1*: 15-30.
Hindar, K., Ryman, N. and Utter, F.M. 1991. Genetic effects of cultured fish on natural

fish populations. *Can. J. Fish. Aquat. Sci. 48*: 945-957.
Waples, R.S. (1991). Genetic interactions between hatchery and wild salmonids: lessons from the Pacific Northwest. *Can. J. Fish. Aquat. Sci. 48* (Suppl. 1): 124-133.

2.4 National activity reports / international cooperation

Information about relevant activities going on in the various countries is important for triggering international cooperation. WGAGFM therefore sees the importance of including an annually updated protocol of relevant activities in the different countries in the annual Reports. The protocol this year (Appendix 1) has been substantially increased compared to 1994 and 1995.

The WGAGFM meetings have proved to be a suitable forum for informal discussions among the members which has proven fruitful for international cooperation. Since the 1994 meeting several cooperation projects have been discussed within the Working Group, of which some now has emerged as joint EU-projects. Practical agreements for the exchange of samples between WGAGFM members and laboratories have also increased and works satisfactorily.

2.5 The joint NASCO/ICES Symposium in Bath, UK, 17-22nd April 1977

In a letter of Feb. 8, 1996 to WGAGFM, one of the convenors of the Bath Symposium (Alan Youngson, Scotland) asked for advice on

1) the likely thrust of the submissions that would be received on genetic aspects, and
2) how the WGAGFM would like to see the genetic issues treated.

The discussion in the Working Group considered projects that the members were aware of and which were relevant to the Bath Symposium. This discussion ended up with a list of topics that are treated in ongoing projects in the ICES member countries:

* Estimates of gene flow and fitness coefficients in farmed - wild fish interactions.
* Estimates of realised straying rates from ranching.
* Estimates of heritability (h^2) of life history traits.
* Estimates of effective population sizes (N_e) of wild populations.
* Life history traits in stocking (enhancement of stocking practice).
* Migration (behaviour) differences between farmed and wild fish.
* Genetic variation in disease resistance.
* Mixed stock fisheries of wild and enhanced stocks.

In 1997, eight years will have passed since the international symposium on interactions between farmed and wild salmon (in Loen, Norway). WGAGFM will point out that important issues treated at that symposium (e.g., the development and implementation of sterilisation techniques, the utilization of modelling and simulation studies in interactions) may not have got sufficient attention in the years after. It is recommended that the convenors plan the Bath Symposium with a view that 'forgotten' issues defined as particularly important in former symposia get adequate room on the agenda.

3 WORKING GROUP BUSINESS

3.1 Comments on Working Group function

WGAGFM is improving on its working form, and benefited at the Faro WG meeting from the implementation of its own 1995 suggestions regarding pre-made position papers, distribution of specific tasks, and session chairing. At the same time, however, the ambitions have increased. Thus, having 4 days at disposition at the annual WG meeting showed to be a necessity in order to deal with the 1996 Terms of Reference.

There is still room for improvements in the administration of the group activities. One significant improvement would be that all appointed members supply the Chairman with their telephone, fax and E-mail numbers. Distributing such a list would ease the contact between members, and simplify and hasten all administrative functions in connection with the WG meeting and preparation of the annual Report. Such information is currently available for only about half of the Working Group. Experience shows that communication by ordinary mail is not efficient enough with 38 members distributed on both sides of the Atlantic.

3.2 Comments on travel funds for WG members

Lack of travel funds continues to be a major obstacle for members to attend the annual WG meeting. In Faro, the scientific work of WGAGFM was affected by the absence of several outstanding scientists, not least its two subgroup leaders (from Canada and Ireland) who could not attend due to lack of travel funds. WGAGFM has previously noted this problem, in the 1994 as well as in the 1995 WG Report. At the 1995 WG Meeting, WGAGFM agreed upon the contents of a letter on this problem. The letter was sent to the General Secretary, with copies to Chairmen of the Consultative Committee, ACME, ACFM, and the Mariculture Committee. An initiative from the General Secretary towards specific national delegates early in 1996 seemed to solve some, but not all, problems. WGAGFM recommends that ICES member countries follow up their appointment of members to the Working Groups with some responsibility that travel funds are made available.

3.3. Suggestions for WG Terms of Reference and meetings in 1997

The attendance at the 1995 WG meeting in Faro was better than in the two previous years, indicating that mid-February is an adequate period of time. A discussion on possible dates for the 1997 meeting concluded that week 8 was most suitable. Possible meeting places were discussed, but it was decided to await a conclusion on this until some candidate institutions had been contacted. This process led up to the acceptance of a kind invitation from the Director of the Sea Fisheries Institute in Gdynia, Poland (Prof. Zygmunt Polanski) to arrange the 1997 WG meeting there. Dr. Roman Wenne and Ms. Ewa Wlodarsczyk will be in charge of the preparations for the meeting.

Concerning Terms of Reference for 1997, WGAGFM recommends that:

The Working group on the Application of Genetics in Fisheries and Mariculture (Chairman: Prof. J. Mork, Norway) will meet at the Sea Fisheries Institute in Gdynia, Poland, from 17 to 21 February 1997, to:

a - continue the review of population genetic topics in fisheries and mariculture, including the questions of selective fisheries and GMOs (Genetically Modified Organisms), with emphasis on a combination of qualitative and quantitative genetics,

b - review the new molecular techniques recently developed and implemented in population genetic studies, with a view to evaluate their merits so far in studies of marine finfish and shellfish,

c - review and evaluate the variety of computer software packages now available for population genetic analysis, in order to come up with recommendations for tools that are suitable for different types of problems,

d - prepare updated protocols of fishery and mariculture genetic research in the member countries, and identify scopes for enhanced international cooperation.

Justifications:

The issue of selective fisheries is a very important one which deserves broad attention in fisheries biology. The complexity of the problem suggests that it should be attacked on a broader front in ICES, e.g. as a joint approach by geneticists, fishery statisticians and modellers. In 1996, WGAGFM initiated a cooperation between geneticists and modellers which proved very fruitful for both parts and which clearly must be continued. WGAGFM therefore wants to keep this topic on its agenda also in 1997, with a view to create the basis for a broader approach to the problem.

Finfish and shellfish farming are rapidly increasing in ICES countries. An extremely rapid development in molecular biology suggests that it may only be a matter of time before the industry wants to start production based on Genetically Modified Organisms (GMOs). On this background, biologists, including geneticists, have expressed serious concerns about unwanted effects that GMOs may have on natural populations and ecosystems. WGAGFM has recommended a theme session devoted to this issue at the 1998 ASC, and wants to monitor the development in this field by keeping GMO as an agenda topic also at its 1997 meeting.

In the last decade, a wide variety of molecular techniques have made it possible to develop new DNA markers for use in studies of genetic population structure. Many of these markers are assumed to have a higher 'sensitivity' compared to traditional markers (e.g., isozymes), which is explained by much higher mutation rates and/or tentative selective neutrality. However, results from various studies using such markers have not been univocal. WGAGFM feels that there is now need for a review of their merits relative to each other and to traditional methodology.

The analysis of complex genetic data has undergone a silent revolution with the development of powerful computers and software for advanced data analysis and simulation studies. For the educated user these tools are invaluable. However, their use require thorough knowledge at to their potentials and limitations, to the underlying assumptions, and to the type of problems the tools are supposed to treat. It is not easy for newcomers to navigate in this complicity, and WGAGFM feels there is a need for a review of the flora of software in order to evaluate their relative potentials and merits as well as to make recommendations as to which tools should be applied to specific types of problems.

APPENDIX 1

NATIONAL ACTIVITY REPORTS

Studies reported in standard format

BELGIUM

Study 1
LABORATORY/RESEARCHER: Filip Volckaert, Katholieke Universiteit Leuven, Zoological Institute, Naamsestraat 59, B-3000 Leuven, Belgium. Univ. Wurtzburg (D), Univ. Padova (I), Insituto de Acuicultua de Torre de la Sal (ES) and Sepia Conseil (F).
SPECIES: European eel (*Anguilla anguilla* L.) ans sea bass (*Dicentrarchus labrax*)
PROJECT FUNDING: EU-AIR2-CT93-1543
OBJECTIVE: The isolation of sex-specific molecular markers in European eel and sea bass.
DESIGN: First, molecular markers are isolated in model species with known sex determining systems and then the same methods are applied to eel and bass.
METHODOLOGY: Various techniques to isolate sex-specific DNA sequences such as subtractive hybridization, RAPD, microsatellite DNA fingerprinting, SOX and Smcy genes, FISH hybridization, Southern blotting and selective breeding.
STATUS: Ph.D. thesis in progress; project funding till December 1996.
COMMENTS: Several publications in preparation.

Study 2
LABORATORY/RESEARCHER: F. Volckaert, Zoological Institute, Katholieke Universiteit Leuven, Leuven, Belgium. Agricultural University Wageningen (NL), University College Cork (IE).
SPECIES: European eel *Anguilla anguilla* L.
PROJECT FUNDING: EU fellowship and university grants.
OBJECTIVE: To characterise the population genetics of European eel.
DESIGN: Comparative study of 5 glass eel populations along the European continental shelf. Study of the genetic structure of this catadromous and semelparous species.
METHODOLOGY: DNA microsatellites, mitochondrial DNA and allozymes.
STATUS: Ph.D. project in progress.
COMMENTS: Project is open ended and has room for cooperation with physical oceanographers/modellers; one paper published, several publications in progress.

Study 3
LABORATORY/RESEARCHER: Thierry Backeljau, Royal Belgian Institute of Natural Sciences, Vautierstraat 29, B-1000 Brussels, Belgium and Hans de Wolf, University of Antwerp (RUCA), Groenenborgerlaan 171, B-2020 Antwerp, Belgium. Joint program with the University of the Azores (P), University of Leeds (UK) and University College of Galway (IE).
SPECIES: Littorinidae (periwinkles), particularly *Littorina striata*
PROJECT FUNDING: EU MAST-III, IWT (Belgium) and National Fund for Scientific Research (Belgium).

OBJECTIVE: Integrating population genetic and morphological variation over the entire geographical range of the species; separating genetic and phenotypic elements in shell polymorhisms and determining their biological significance in order to investigate what factors/mechanisms are responsible for the macro- and microgeographic maintenance of shell polymorphisms in the presence of extensive gene flow (i.e. selection vs. phenotypic plasticity).

DESIGN: The whole geographic range of *L. Striata* (Macronesian archipelagio: Azores, Madeira, Canary Islands, Cape Verde) has been intensively sampled (several thousands individuals analysed for morphometric and genetic variation). Field transplant experiments are in progress.

METHODOLOGY: Electrophoresis of allozymes and radular myoglobins, RAPD, microsatellite DNA markers, Single Strand Conformation Polymorphisms, morphometrics of shell features.
STATUS: Ph.D. project in progress; programme in progress in MAST-III; undergraduate thesis.
COMMENTS: To publications are in preparation.

Study 4
LABORATORY/RESEARCHER: Thierry Backeljau, Royal Belgian Institute of Natural Sciences, Vautierstraat 29, B-1000 Brussels, Belgium, in collaboration with the University of the Azores (P).
SPECIES: *Tapes decussatus* and *T. philippinarum* (Mollusca, Bivalvia)
PROJECT FUNDING: EU-STRIDE, National Fund for Scientific Research (Belgium), and Royal Belgium Institute of Natural Sciences.
OBJECTIVE: Genetic characterisation of *T. decussatus* in the Azores as a highly isolated, pure stock of the species (founder effects, genetic differentiation, conservation and exploitation issues); investigating relationships and possible genetic interaction between *T. decussatus* and *T. Philippinarum.*
DESIGN: Temporal sampling of *T. decussatus* an Faja de Santo Cristo (island of Sao Jorge in the Azores). Additional sampling of the species and *T. philippinarum* along the European coasts.
METHODOLOGY: Allozyme electrophoresis; in the future possibly RAPD, Single Strand Conformation Polymorphisms and microsatellites.
STATUS: Undergraduate thesis
COMMENTS: A first publication in progress.

CANADA

Study 1
LABORATORY/RESEARCHER: Salmon Genetics Research Program, Atlantic Salmon Federation, St. Andrews, New Brunswick, Canada EOG 2XO. G. Friars, J. Bailey and F. O'Flynn.
SPECIES: Atlantic salmon (*Salmo salar*).
PROJECT FUNDING: Atlantic Canada Opportunities Agency, Canadian Institute of Biotechnology, Department of Fisheries and Oceans, National Research Council, New Brunswick Department of Fisheries and Aquaculture, New Brunswick Salmon Growers Association.
OBJECTIVE: To establish four Atlantic salmon strains for aquaculture.
DESIGN: Growth and developmental traits are monitored in both fresh and sea water for each year class of each strain. Selection is carried out when the fish have spent 18 months in sea water and the broodstock population is reduced from approximately 5000 to 800. Spawning takes place the following year with a population of approximately 400 fish.

METHODOLOGY: Selection is based on an index to increase percent 1+ smolts, percent non-grilse, market length and resistance to bacterial kidney disease. In one of the strains, selection was based on truncated mass selection for market length.
STATUS: Ongoing.
COMMENTS: Substantial genetic gains of significant economic value to salmon farmers have been made.

Study 2
LABORATORY/RESEARCHER: Salmon Genetics Research Program, Atlantic Salmon Federation, St. Andrews, New Brunswick, Canada EOG 2XO. G. Friars, J. Bailey and F. O'Flynn. University of New Brunswick. T. Benfey and A. McGeachy
SPECIES: Atlantic salmon (*Salmo salar*).
PROJECT FUNDING: Atlantic Canada Opportunities Agency, Canadian Institute of Biotechnology, Department of Fisheries and Oceans, National Research Council, New Brunswick Department of Fisheries and Aquaculture, New Brunswick Salmon Growers Association.
OBJECTIVE: To compare the aquacultural performance of diploid and triploid Atlantic salmon.
DESIGN: Mixed-sex triploid groups of Atlantic salmon were made in all SGRP aquaculture strains. All-female triploid groups were made in two SGRP strains and have all-female diploid contemporaries. Growth and survival is being monitored in both fresh and sea water.
METHODOLOGY: A 2.7 litre pressure vessel was used to produce triploid salmon. Fertilization with mono-milt produced all-female groups. At the parr stage blood samples were taken to test the ploidy level of the fish by flow cytometry.
STATUS: Ongoing.

Study 3
LABORATORY/RESEARCHER: Salmon Genetics Research Program, Atlantic Salmon Federation, St. Andrews, New Brunswick, Canada EOG 2XO. G. Friars, J. Bailey and F. O'Flynn. Research & Productivity Council. S. Griffiths.
SPECIES: Atlantic salmon (*Salmo salar*).
PROJECT FUNDING: Atlantic Canada Opportunities Agency, Canadian Institute of Biotechnology, Department of Fisheries and Oceans, National Research Council, New Brunswick Department of Fisheries and Aquaculture, New Brunswick Salmon Growers Association.
OBJECTIVE: To investigate genetic variation in resistance to Bacterial Kidney Disease (BKD).
DESIGN: Samples of parr and smolt from three SGRP strains were challenged with Renibacterium salmonimum.
METHODOLOGY: Heritability values were estimated, based on full-sib families, for survival and time to death.
STATUS: Ongoing.
COMMENTS: The information obtained from this study was used to include resistance to BKD as an index trait in the selection of broodstock.

Study 4
LABORATORY/RESEARCHER: University of Saskatchewan. P. H. Krone.
SPECIES: Zebrafish (*Danio rerio*).
PROJECT FUNDING: NSERC.
OBJECTIVE:
1. Elucidate role which heat shock proteins play during normal developmental events and in the protection of embryos from environmental stress.

2. Elucidate mechanism responsible for regulation of heat shock protein synthesis during embryonic development.

DESIGN: Isolation of cDNA and genomic clones encoding zebrafish heat shock proteins and subsequent characterization of their patterns of stage- and tissue-specific expression during normal development and during exposure to heat shock and other environmental stresses. Expression data is then used as a basis for the design of microinjection experiments in which wild-type heat shock proteins and those altered through site-specific mutagenesis are expressed in embryos. Cultured cells are being used as an in vitro model to examine the role of these proteins.
METHODOLOGY: Isolation and characterization of cDNA and genomic clones encoding zebrafish heat shock proteins. Northern blot and in situ hybridization analyses, microinjection, tissue culture and transfection.
STATUS: Ongoing.

Study 5
LABORATORY/RESEARCHER: Institute of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, B.C. V5A 1S6. B. P. Brandhorst, G. Corley-Smith and J. Chinten Lim.
SPECIES: *Danio rerio* (zebrafish).
PROJECT FUNDING: NSERC
OBJECTIVE: The production of diploid androgenetic fish and their use as a genetic tool.
DESIGN: The female genome is eliminated by X-ray irradiation, and the first cleavage is inhibited by heat shock. Polymorphic DNA markers are used to assess transmission from the female and male parents.
METHODOLOGY:
STATUS: Numerous diploid androgenotes have been produced with a success rate of 1-2%. These have a normal appearance and have been bred. A manuscript has been submitted. Haploid androgenotes have been produced with an efficiency of up 30-50%. This should allow their use in haploid genetic mutational screens, and production of a male meiotic cross-over map in collaboration with J. Postlethwait (U. Oregon) is planned. Currently, the focus is on improving the efficiency of production of androgenotes and assessing the sex of androgenotes and their progeny, which may be informative about sex determination, another interest of the laboratory.
COMMENTS: The extensive DNA marker data provides compelling evidence for the production of androgenotes with little or no leakage of maternal genes. The methods may be adaptable to other fish.

Study 6
LABORATORY/RESEARCHER: Institute of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, B.C. V5A 1S6. B. P. Brandhorst, G. Corley-Smith and J. Chinten Lim.
SPECIES: *Oncorhynchus nerka* (sockeye salmon).
PROJECT FUNDING: None at present.
OBJECTIVE: Development of a method for the rapid identification of stock specific DNA markers.
DESIGN: Random amplified polymorphic DNA (RAPD) analysis using fluorescent primers is being applied to bulked DNA samples of spawning sockeye salmon from adjacent and distant geographic regions, in an effort to establish the efficacy of a method for quickly identifying stock specific markers. Sequence analysis of distinctive amplification products, if any, should result in the production of highly specific PCR primers allowing for rapid DNA typing on small amounts of material.
METHODOLOGY: RAPD analysis using fluorescent primers and an ABI automated DNA sequencer, running GeneScan software.

STATUS: The sensitivity and reliability of RAPD analysis is considerably improved with the use of fluorescent primers and high resolution polyacrylamide gel electrophoresis. Application to identification of stock specific DNA markers is just beginning.
COMMENTS: This is a proof of concept project, not part of a planned long term program.

Study 7
LABORATORY/RESEARCHER: Departments of Clinical Biochemistry and Biochemistry, University of Toronto. C. L. Hew.
SPECIES: Winter flounder (*Pleuronectes americanus*), ocean pout (*Macrozoarces americanus*).
PROJECT FUNDING: Medical Research Council of Canada.
OBJECTIVE: To investigate the molecular mechanisms controlling the seasonal and hormonal regulated synthesis of fish antifreeze proteins, and to explore the use of antifreeze protein genes in conferring freeze resistance to other fish species.
DESIGN: used. These include gene cloning, promoter analysis in tissue culture cells, characterization of transcription factors, and the development of transgenic fish.
METHODOLOGY:
STATUS: We have demonstrated that the winter flounder contains both extracellular and intracellular AFPs. These have raised further questions on the structure and function, regulation and evolution of AFPs (Gong et al., 1996, Skin antifreeze protein genes of the winter flounder, Pleuronectes americanus, encode distinct and active polypeptides without the secretory signal sequences. J. Biol. Chem. In Press).

Study 8
LABORATORY/RESEARCHER: Departments of Clinical Biochemistry and Biochemistry, University of Toronto. C. L. Hew.
SPECIES: Chinook salmon (*Oncorhynchus tschawytscha*), rainbow trout (*Oncorhynchus mykiss).*
PROJECT FUNDING: Medical Research Council of Canada.
OBJECTIVE: Using salmon as a model, we are studying the molecular events controlling fish reproduction. The genetic mechanism(s) for gonadotropin gene expression is examined.
DESIGN: The cis-acting and transcription factors important in gonadotropin gene expression are characterized by a wide variety of biochemical and molecular biological techniques.
METHODOLOGY: Gene cloning, promoter analysis, characterization of transcription factors, etc.
STATUS: We have demonstrated for the first time in the gonadotropin gene that both steroidogenic factor and estrogen receptor act in synergism for the gonadotrope-specific expression of the salmon gonadotropin IIß subunit gene (Le Drean et al., 1996, Steroidogenic factor 1 and estradiol receptor act in synergism to regulate the expression of the salmon gonadotropin IIß subunit gene. Mol. Endocrinol. In Press).

Study 9
LABORATORY/RESEARCHER: Departments of Clinical Biochemistry and Biochemistry, University of Toronto. C. L. Hew.
SPECIES: Atlantic salmon (*Salmo salar*).
PROJECT FUNDING: Natural Sciences and Engineering Research Council of Canada.
OBJECTIVE: The objective is the development of transgenic salmon beneficial to aquaculture. these include: (i) the transfer of antifreeze protein gene (AFP) for freeze resistance; (ii) the transfer of growth hormone gene (GH) for growth enhancement; and (iii) the transfer of lysozyme gene (LYZ) for disease resistance.

DESIGN: These genes (AFP, GH, LYZ) were injected separately into salmon eggs by gene transfer. The inheritance and expression of the transgene is being studied.
METHODOLOGY:
STATUS: Positive transgenic fish have been accomplished for AFP and GH gene transfer. GH transgenic fish grow 5 to 10 times faster than the control and the inheritance of transgenes to F2 generation is established (See Gong and Hew (1995), Transgenic fish in aquaculture and developmental biology. Current Topics in Developmental Biology, vol. 30, pp. 177-214).

Study 10
LABORATORY/RESEARCHER: Departments of Clinical Biochemistry and Biochemistry, University of Toronto. C. L. Hew.
SPECIES: Chinook salmon (*Oncorhynchus tschawytscha*) and zebrafish (*Danio rerio*).
FUNDING: Natural Sciences and Engineering Research Council of Canada
OBJECTIVE: To investigate the structure, function and regulation of Isl-1 and related gene family in the neuroendocrine cell and motor neuron development.
DESIGNS: Isl-1, Isl-2 and Isl-3 are LIM domain homeodomain transcription factors. They are detected in brain, pituitary and other organs. However, the role of these proteins is unclear. Biochemical, molecular biological and cell biology techniques are used to examine the role of these proteins.
METHODOLOGY: In situ hybridization, DNA binding assay and others.
STATUS: The genes are cloned and their ontogeny established. In situ hybridization indicates that the transcripts of all three genes are localized in subsets of neurons in the brain and spinal cord (Gong et al., 1995. Presence of isl-1-related LIM domain homeobox genes in teleost and their similar patterns of expression in brain and spinal cord. J. Biol. Chem. 270. 3335-3345).

Study 11
LABORATORY/RESEARCHER: Magaguadavic Watershed Management Association, General Delivery, St. George, New Brunswick, Canada E0G 2Y0 and Marine Gene Probe Laboratory, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4J7. J. Carr, G. Hammond, A.J.D. Ambali and J. Anderson.
SPECIES: Atlantic salmon (*Salmo salar*)
PROJECT FUNDING: Magaguadavic Watershed Management Association, Atlantic Salmon Federation, Canada\N.B. Coop. Agreement on Rec. Fisheries, N.B. Salmon Growers Association, N.B. Depart. of Fisheries and Aquaculture, Depart. of Fisheries and Oceans, N.B. Salmon Council.
OBJECTIVE: To establish if genetic introgression is occurring between wild and aquaculture escapees in the Magaguadavic River, New Brunswick.
DESIGN: Scale and blood samples were collected from wild salmon of the Magaguadavic River, N.B., and from aquaculture salmon that escaped from the N.B. industry. Samples included wild salmon scales collected from 1975-77, wild salmon scale and blood samples from 1992-94, and scales from aquaculture escapees from 1994. The 1975-77 samples represented the original Magaguadavic River strain before the development of the N.B. salmon aquaculture industry in 1979.
METHODOLOGY: Population polymorphisms at four microsatelite loci (Omy 27,38,105, and Ssa 4) were examined in Atlantic salmon from 7 year-classes by extracting DNA from scale and blood samples.
STATUS: The wild 1970's strain was genetically distinct from the wild 1990's strain. The 1994 escapees were genetically distinct from both year classes of wild salmon, but were closer to the 1990's strain of wild salmon.

Study 12
LABORATORY/RESEARCHER: University of New Brunswick. T.J. Benfey.
SPECIES: Various salmonids (incl. Brook trout, Arctic charr, Atlantic salmon and rainbow trout).
PROJECT FUNDING: Natural Sciences and Engineering Research Council of Canada, Canada Department of Fisheries and Oceans, New Brunswick salmon Growers Association, Canada/New Brunswick Subsidiary Agreement on Industrial Innovation and Technology Development, University of New Brunswick, Atlantic Veterinary College (University of Prince Edward Island).
OBJECTIVE: To examine the basic physiology and behaviour of triploid salmonids.
DESIGN: Experimental assessment of physiological and behavioural characteristics under controlled laboratory conditions.
METHODOLOGY: Currently concentrating in the following areas: (1) respiratory physiology - haematology, oxygen consumption rate, opercular pumping and swimming efficiency, and aerobic capacity; (2) competitive abilities - feeding hierarchies and growth rates for triploids cohabitating at different densities with diploids; (3) ovarian development - histological examination of ovarian development in triploids beyond the normal age of reproduction; (4) thermal optima - development and growth at various temperatures, acute and chronic tolerance of high temperatures; and (5) stress response - endocrinological and haematological responses to stress.
STATUS: Ongoing.
COMMENTS: There is growing pressure from various sources for Canadian fish farmers to use triploid fish, in order to prevent spawning in the wild of any escaping farmed fish. Optimal rearing conditions for triploids, based on a better understanding of their basic biology, must be determined before advocating their widespread use in commercial culture.

Study 13
LABORATORY/RESEARCHER: Memorial University of Newfoundland. T.J. Benfey and W.S. Davidson.
SPECIES: Arctic charr and brook trout.
PROJECT FUNDING: Natural Sciences and Engineering Research Council of Canada.
OBJECTIVE: To develop a method to distinguish normal XY males from sex-reversed XX males.
DESIGN: Screening a library of primers for any that show differences in DNA fragment sizes after PCR amplification.
METHODOLOGY: RAPD technique - randomly amplified polymorphic DNA based on screening a library of oligonucleotide primers (each 10 base pair long) on DNA purified from male and female Arctic charr and brook trout.
STATUS: Ongoing.
COMMENTS: The RAPD technique has been used successfully to determine the sex of birds and plants.

Study 14
LABORATORY/RESEARCHER: Dept. of Biochemistry, Memorial University, St. John's, Newfoundland, C. M^{c}Gowan & W. Davidson.
SPECIES: Brown trout and Atlantic salmon.
PROJECT FUNDING: NSERC/DFO.
OBJECTIVE: Genome mapping of *Salmo* species.
DESIGN: Hybrid families have been produced and segregation of alleles at different loci is being examined.
METHODOLOGY: Genetic markers being examined include: RAPD, microsatellites, expressed sequence tags (cDNA's).
STATUS: Four linkage groups have been identified to date for brown trout. This is an on-going project.

Study 15
LABORATORY/RESEARCHER: Daniel's Harbour Arctic Char Hatchery, G. Wilton, and Dept. of Biochemistry, Memorial University, St. John's, Newfoundland, W. Davidson.
SPECIES: Arctic char.
PROJECT FUNDING: Private.
OBJECTIVE: Broodstock development and gene mapping in char.
DESIGN: Families have been bred and reared separately and together for selection of quantitative traits.
METHODOLOGY: Measures of growth rates will be compared within and between families and there will be correlated with a group of more than 50 microsatellites for marker selection purposes.
STATUS: Started November 1995.

Study 16
LABORATORY/RESEARCHER: Dept. of Biology, Memorial University. S. Carr. Dept. of Biochemistry, Memorial University. W. Davidson. Department of Fisheries and Oceans, St. John's, Newfoundland. R. Bowering.
SPECIES: Greenland halibut (turbot).
PROJECT FUNDING: CCFI.
OBJECTIVE: Population structure of Greenland halibut in the North Atlantic.
DESIGN: 40 turbot from 7 sampling sites across the North Atlantic were examined for genetic variation within and between samples.
METHODOLOGY: Sequence analysis of a 400 bp region of the cytochrome b mitochondrial DNA was examined.
STATUS: Completed January 1996. No evidence for genetic substructuring of turbot in the North Atlantic from as far apart as Norway and the Gulf of St. Lawrence.

Study 17
LABORATORY/RESEARCHER: Dept. of Biology, Memorial University, St. John's, Newfoundland. S. Carr.
SPECIES: Atlantic cod.
PROJECT FUNDING: NSERC.
OBJECTIVE: Population structure of Atlantic cod.
DESIGN: many samples of cod from all over the North Atlantic have bred examined for evidence of population structuring.
METHODOLOGY: Mitochondrial DNA and microsatellites.
STATUS: On-going project.

Study 18
LABORATORY/RESEARCHER: Simon Fraser University, Dept. of Biological Sciences, Burnaby, B.C., Canada V5A 1S6. B. McKeown and D. Otto.
SPECIES: Arctic charr.
PROJECT FUNDING: IRAP funded.
OBJECTIVE: Masculinization for aquaculture.
DESIGN/: Hormone treatments for all-male populations.
METHODOLOGY: Hormone treatments.
STATUS: Results are now known for various hormones, dosages, treatment times and number of treatments.

Study 19
LABORATORY/RESEARCHER: Simon Fraser University, Dept. of Biological Sciences, Burnaby, B.C., Canada V5A 1S6. B. McKeown and J. Panno.
SPECIES: Rainbow trout.
PROJECT FUNDING: NSERC funded.
OBJECTIVE: To characterize the myc oncogene and study controls of expression.
DESIGN: Gene cloning and investigations of *in vitro* controls of expression.
METHODOLOGY: Gene cloning.
STATUS: Ongoing.
COMMENTS: The myc gene has been pulled and sequenced and a number of expression controls identified.

Study 20
LABORATORY/RESEARCHER: Simon Fraser University, Dept. of Biological Sciences, Burnaby, B.C., Canada V5A 1S6. B. McKeown and S. Tang.
SPECIES: Rainbow trout.
PROJECT FUNDING: NSERC funded.
OBJECTIVE: To characterized the SPARC (secreted protein acidic and rich in cystine) and PLP (proteolipid protein) genes.
DESIGN: Gene cloning and controls of expression.
METHODOLOGY: Gene cloning.
STATUS: Ongoing.
COMMENTS: This genes have been identified and sequenced. Expression in various tissues and conditions have been found.

Study 21
LABORATORY/RESEARCHER: Simon Fraser University, Dept. of Biological Sciences, Burnaby, B.C., Canada V5A 1S6. B. McKeown and K. Poon.
SPECIES: Rainbow trout.
PROJECT FUNDING: NSERC funded.
OBJECTIVE: To characterize the ras oncogene.
DESIGN: Gene cloning and controls of expression.
METHODOLOGY: Gene cloning.
STATUS: Ongoing.
COMMENTS: This gene has been isolated and sequenced. Work is now continuing on controls of expression.

Study 22
LABORATORY/RESEARCHER: Simon Fraser University, Dept. of Biological Sciences, Burnaby, B.C., Canada V5A 1S6. B. McKeown and K. Poon.
SPECIES: Rainbow trout.
PROJECT FUNDING: NSERC funded.
OBJECTIVE: To identify the growth hormone receptor gene.
DESIGN: Gene cloning.
METHODOLOGY: Gene cloning.
STATUS: Ongoing.
COMMENTS: We are presently in the process of trying to clone this gene.

Study 23

LABORATORY/RESEARCHER: R. M^{c}Gowan.

SPECIES: *Danio rerio.*

PROJECT FUNDING: NSERC.

OBJECTIVE: (1) To identify whether genome imprinting exists in the zebrafish and to then exploit the unique attributes of these fish to investigate the molecular details of that process.
(2) To investigate the role of methylation and the DNA methyltransferase gene in zebrafish development.

DESIGN: Breeding of transgenetic zebrafish to non-transgenic mates and track the methylation and expression of the transgene after inheritance of the locus from either males or females. Look at methylation status of a variety of loci during early developmental stages of the zebrafish in order to produce a developmental profile of methylation changes. Isolation of homologue of the DNA methyltransferase gene from zebrafish in order to investigate its role in early developmental decision making processes.

METHODOLOGY: Variety of molecular techniques. Methylation is assayed with the use of methylation-sensitive restriction enzymes and Southern blotting techniques. The isolation of genes is accomplished by using already cloned sequences from other species to identify homologous sequences in zebrafish cDNA libraries.

STATUS: Ongoing.

COMMENTS: We have been able to establish that a parent-of-origin-effect is evident in these fish at the level of a transgene locus. We are now attempting to evaluate endogenous loci. The methylation analyses are fairly preliminary but results are very promising.

Study 24

LABORATORY/RESEARCHER: Animal and Poultry Science, University of Guelph. M^{c}Millan and M^{c}Kay

SPECIES: Salmonids

PROJECT FUNDING:

OBJECTIVE: Genetic improvement of commercial stocks of salmonids in the province. (1) Comparison of growth, mortality, maturation rates and reproductive traits among four strains of spring-spawned rainbow trout and two management groups (1991 year class). (2) Comparison of early growth, maturation and mortality in crosses of three of four strains from (1) (1994 year class). (3) Initiation of additional crosses of three of the four strains in (1) (95/96 year class). (4) Development of computer models to compare inbreeding and rates of genetic progress under different genetic improvement strategies.

DESIGN: Characterisation of four pure strains and crosses between 95/96 year classes.

METHODOLOGY: Measurements of growth, mortality, maturation rates and reproductive traits. Development of computer models

STATUS: Ongoing.

Study 25

LABORATORY/RESEARCHER: Stocks Assessment and Genetics Unit, Ontario Ministry of Natural Resources, P.O. Box 5000, Maple, ON L6A 1S9. P.E. Ihssen, G.Wm. Martin.

SPECIES: Atlantic salmon, aurora trout, brook trout, brown trout, Chinook salmon, trout, lake whitefish.

PROJECT FUNDING: Ontario Ministry of Natural Resources (OMNR).

OBJECTIVE: Monitoring of OMNR hatchery stocks for maintenance of genetic variability.

DESIGN: Successive year classes of hatchery-reared fish of the above species are monitored for approximately 50 allozyme loci. In cases where the phenotypes of the original parents were

determined, comparison is made with succeeding year classes to determine if there has been a loss of genetic variability. In the case of Atlantic salmon, Chinook salmon and lake whitefish, gametes are collected from wild fish. For all other species, gametes are collected from hatchery brood stock.
METHODOLOGY: Starch gel and cellulose acetate electrophoresis of cathodal and general muscle protein and 23 allozyme systems.
STATUS: Ongoing.

Study 26
LABORATORY/RESEARCHER: Stocks Assessment and Genetics Unit, Ontario Ministry of Natural Resources, P.O. Box 5000, Maple, ON L6A 1S9 and M^{c}Master University. W. Stott, P.E. Ihssen and B. White.
SPECIES: Lake trout (*Salvelinus namaycush*)
PROJECT FUNDING: OMNR and NSERC grants and Internship program through MBS.
OBJECTIVE: Stock differentiation in Lake trout and its application to fisheries management.
DESIGN: Lake trout from six lakes with different stocking histories are sampled and analysed with different DNA markers and estimates of their effective population size compared.
METHODOLOGY: RFLP's of mtDNA, RAPD and microsatellite DNA.
STATUS: Ongoing to end in December 1996.

Study 27
LABORATORY/RESEARCHER: B. Desrosiers and J.-M. Sevigny*, Centre Oceanographique de Rimouski, Departement d'Oceanographie, Universite du Quebec á Rimouski, Quevec, Canada G5l 3A1. *Department of Fisheries and Oceans, Maurice Lamontagne Institute, Mont-Joli (Qc), Canada G5H 3Z4.
SPECIES: Redfish (Sebastes spp.)
PROJECT FUNDING: Department of Fisheries and Oceans.
OBJECTIVE: Yo detect molecular markers to distinguish the different species of redfish in the Gulf of St. Lawrence.
DESIGN: Refish are classified according to the criteria described below to determine the congruence among the 3 different approaches.
METHODOLOGY: rDNA, allozymes, morphology.
STATUS: Three year project that will end in 1996.

DENMARK

STUDY 1
LABORATORY/RESEARCHER: National Institute of Animal Sciences. L.-E. Holm.
SPECIES: Rainbow Trout.
PROJECT FUNDING: In house / Agricultural Science Research Council.
OBJECTIVE: Development and use of genetic markers to be used for identification of hatchery strains and for markers of commercially important traits.
DESIGN: Screening of rainbow trout from a number of Danish hatchery strains.
METHODOLOGY: Microsatellites.
STATUS: Ongoing.

STUDY 2
LABORATORY/RESEARCHER: Dept. of Ecology and Genetics, University of Aarhus. E. E. Nielsen.
SPECIES: Atlantic salmon, brown trout.
PROJECT FUNDING: In house / Danish Institute for Fisheries Research, Dept. of Inland Fisheries.
OBJECTIVE: Estimation of effective population sizes in natural salmon and trout populations from observed temporal changes in allele/haplotype frequencies. Studies of long-term temporal changes in allele frequencies in Atlantic salmon populations and estimation of genetic relationships among Danish salmon populations which are now extinct.
DESIGN: Selected populations are sampled at certain time intervals and screened using relevant techniques. Data from populations in the 1930's -1950's have been obtained by amplifying microsatellites from old scale samples.
METHODOLOGY: Microsatellites.
STATUS: Ongoing.

STUDY 3
LABORATORY/RESEARCHER: Danish Institute for Fisheries Research, Dept. of Inland Fisheries, Silkeborg. M. M. Hansen.
SPECIES: Brown trout.
PROJECT FUNDING: In house.
OBJECTIVE: Estimation of genetic variability and differentiation in and among Danish brown trout populations and hatchery strains.
DESIGN: Sampling of trout from various localities.
METHODOLOGY: Microsatellites.
STATUS: Ongoing.

STUDY 4
LABORATORY/RESEARCHER: Danish Institute for Fisheries Research, Dept. of Inland Fisheries, Silkeborg. M. M. Hansen.
SPECIES: Brown trout.
PROJECT FUNDING: In house.
OBJECTIVE: Estimation of the impact of stocking activity (using non-native hatchery trout) on natural brown trout populations.
DESIGN: Controlled stocking experiments in two rivers with traps. Hatchery trout are stocked into wild populations. Reproductive performance and interbreeding between stocked and wild trout is monitored, using genetic markers. The development in the stocked populations will be followed through more generations.
METHODOLOGY: Microsatellites.
STATUS: Ongoing.

STUDY 5
LABORATORY/RESEARCHER: Danish Institute for Fisheries Research, Dept. of Inland Fisheries, Silkeborg. M. M. Hansen.
SPECIES: *Coregonus lavaretus, C. oxyrhynchus, C. albula.*
PROJECT FUNDING: In house.
OBJECTIVE: Estimation of genetic variability, differentiation, and gene flow among populations.
DESIGN: Screening of samples from both geographically distinct populations and from populations spawning in different rivers with outlets in the same fjord.
METHODOLOGY: Microsatellites, mtDNA ampFLP's.

STATUS: Ongoing.

STUDY 6
LABORATORY/RESEARCHER: University of Aarhus. E. E. Nielsen, P. Grønkjær, and V. Loeschcke. Danish Institute for Fisheries Research, Dept. of Inland Fisheries, Silkeborg. M. M. Hansen. Several collaborators from the Danish Institute for Fisheries Research and Dept. of Marine Fisheries, Copenhagen.
SPECIES: Cod.
PROJECT FUNDING: The Danish Ministry of Agriculture and Fisheries.
OBJECTIVE: Studies of the genetic population structure of cod in the South-eastern part of Kattegat, the Danish Belt Sea and in the Baltic Sea area. Estimation of the possible drift of juvenile cod into the Baltic Sea and the contribution of Belt Sea cod to the fishery in the Baltic Sea area.
DESIGN: Sampling of cod larvae and adult spawners from various localities.
METHODOLOGY: Microsatellites.
STATUS: Starting 1996.

ESTONIA

Study 1
LABORATORY/RESEARCHER: T. Paaver, Dept. of Fish Farming, Institute of Animal Husbandry, Estonian Agricultural University, Tartu
SPECIES: Sea trout, Atlantic salmon.
PROJECT FUNDING: In house.
OBJECTIVE: To follow the genetic stability of the wild and stocked populations of salmonids in Estonian coastal rivers and estimate the genetic differences between them.
DESIGN: The relatively occasional samples from test fishings and hatcheries are monitored for genetic variability of proteins.
METHODOLOGY: Allozymes, (6 polymorphic enzymes for brown trout, 3 polymorphic enzymes for Atlantic salmon), egg yolk proteins.
STATUS: Ongoing.

Study 2
LABORATORY/RESEARCHER: R. Gross & T. Paaver. Dept. of Fish Farming, Inst. of Animal Husbandry, Estonian Agricultural University, 1 Kreutzwaldi St., EE2400 Tartu, Estonia. Co-operation with J. Nilsson, Dept. of Aquaculture, Swedish University of Agricultural Sciences.
SPECIES: Atlantic salmon
PROJECT FUNDING: Estonian Fisheries Foundation
OBJECTIVE: To examine the genetic structure in native and introduced salmon populations/stocks in Estonia
DESIGN: Samples are collected from juvenile salmon from five rivers and two hatcheries.
METHODOLOGY: Allozymes, and PCR-amplified DNA markers (microsatellites, growth hormine genes, mtDNA genes).
STATUS: Ongoing one-year project (1996).

FINLAND

Study 1
LABORATORY/RESEARCHER: Finnish Game and Fisheries Research. M.-L. Koljonen. Institute, Helsinki.
SPECIES: Atlantic salmon.
PROJECT FUNDING: In house.
OBJEKTIVE: Estimate stock composition of salmon catches, possibly proportion of wild stocks in the catches.
METHODOLOGY: Genetic stock identification, allozymes.
STATUS: Ongoing.

Study 2
LABORATORY/RESEARCHER: Finnish Game and Fisheries Research Institute. L. Siitonen. Helsinki and Acricultural Recearch Center, Department of Animal Breeding, Jokioinen.
SPECIES: Rainbow trout.
PROJECT FUNDING: In house.
OBJEKTIVE: Develope rainbow trout stocks with better growth rate.
METHODOLOGY: Selective breeding.
STATUS: Ongoing.

Study 3
LABORATORY/RESEARCHER: Agricultural Recearch Centre, Institute of Animal Production, Section of Animal Breeding, Jokioinen. K. Elo.
SPECIES: Coregonids, Atlantic salmon and brown trout.
PROJECT FUNDING: In house.
OBJEKTIVE: Species identification, detection of interspecific hybrids, phylogenetic analysis and genomic variation in Salmonids.
METHODOLOGY: Allozymes and RAPD.
STATUS: Laboratory analysis are completed. End 1996.

Study 4
LABORATORY/RESEARCHER: University of Joensuu, Department of Biology. J. Vuorinen.
SPECIES: Coregonids.
PROJECT FUNDING: In house.
OBJEKTIVE: Evolution and taxonomy of Holarctic Coregonids.
DESIGN: Mapping of gene frequencies.
METHODOLOGY: Enzyme electrophoresis.
STATUS: Ongoing.

Study 5
LABORATORY/RESEARCHER: H. Molsa, T. Pitkanen, M. Reinisalo, A. Krasnov, University of Kuopio, Dept. of Applied Zoology and Veterinary Medicine.
SPECIES: Rainbow trout.
PROJECT FUNDING: Ministry of Agriculture and Forestry, Ministry of Interior Affairs, Academy of Finland, and in house.
OBJEKTIVE: Enhanced growth and metabilosm of rainbow trout via gene transfer technology.
DESIGN: Microinjections and integration assays, gene expression
METHODOLOGY: Microinjections, mRNA, RT-PCR.
STATUS: Ongoing.

ICELAND

Study 1

LABORATORY/RESEARCHER: Holar Agricultural College, IS-550 Saudarkrokur. E. Svavarsson.
SPECIES: Arctic charr.
PROJECT FUNDING: The National Research Council and the Agricultural Productivity Fund in Iceland.
OBJECTIVES: To determine genetic parameters, i.e. heritability and genetic correlations of economically important traits of Arctic charr in Aquaculture. The results will be utilized in a national breeding program of Arctic charr.
DESIGN AND METODOLOGY: Data are collected from charr in the first 2 or 3 year classes of the Arctic charr breeding program. Each year class is made up of 100 - 120 full sib families, with two or three families pr. sire. The families are reared for two and a half year from hatching. Data are collected on growth, sexual maturity at different life stages, flesh coloration and possibly fat content of fish. Data are analyzed after standard methods in animal breeding.
STATUS: The project started in 1993 and is planned for four years. Preliminary results for the first year class have been published in Iceland. A revised project plan has been sent to the Research Council for the years 1996 - 1998. Continued work according to the revised plan will depend on funding.
COMMENTS: The project is in cooperation between The Agricultural school at Hólar in North Iceland, that is in charge of the actual breeding program for Arctic charr, The Institute of Freshwater Fisheries and The Agricultural Research Institute. The breeding program is funded by the Agricultural Productivity Fund in Iceland.

Study 2

LABORATORY/RESEARCHER: Marine Research Institute, c/o Biotechnology House, IceTech, Reykjavík. A. K. Daníelsdóttir. Collaboration with J. Mork (University of Trondheim, Norway), T. Cross (University College Cork, Ireland), Godfrey M. Hewitt and Ciro Rico (University of East Anglia, U.K.) and R. S. Millner and M. Nicholson (Directorate of Fisheries Research, MAFF, U.K.).
SPECIES: Cod, hake, blue whiting and poor cod.
PROJECT FUNDING: MRI and EU FAIR.
OBJECTIVE: Eluciating cod stock structure in Icelandic waters and calibration of different molecular markers for use in discrimination and management of cod, blue whiting, hake and poor cod.
METHODOLOGY: Heamoglobins, allozymes and anonymous cDNA RFLP.
STATUS: Four year project. Cod sampling has started, analysis of samples will start 1ST April 1996.

Study 3

LABORATORY/RESEARCHER: Marine Research Institute, c/o Biotechnology House, IceTech, Reykjavík. A. K. Daníelsdóttir.
SPECIES: Redfish (*Sebastes mentella*).
PROJECT FUNDING: MRI, The National Research Council of Iceland and various trawlers.
OBJECTIVE: Study the genetic population structure of oceanic and deep-sea *S. mentella* in Irminger sea and Icelandic waters.
DESIGN: Redfish samples from different locations southwest of Iceland and the Irminger Sea.
METHODOLOGY: Allozymes, heamoglobins and anonymous cDNA RFLP.
STATUS: Three to four year project. Redfish sampling and analyses started summer 1995.

COMMENTS: The project is in collaboration with T. Johansen and G. Nævdal (University of Bergen, Norway).

Study 4
LABORATORY/RESEARCHER: Institute of Freshwater Fisheries, c/o Biotechnology House, IceTech, Reykjavík. A.K. Daníelsdóttir and S. Guðjónsson.
PROJECT FUNDING: In house and the Icelandic Science fund.
OBJECTIVE: Genetic variation in wild populations of brown trout (Landlocked and Anandromous) in Iceland.
DESIGN: Mapping of gene frequencies.
METHODOLOGY: Allozymes.
STATUS: Samples from 13 locations have been analysed and the study is ongoing.

Study 5
LABORATORY/RESEARCHER: University of Iceland, Department of Biology, Reykjavik. E. Árnason.
SPECIES: Cod, salmon, brown trout, Arctic charr.
PROJECT FUNDING: In house and the Icelandic Science fund.
OBJECTIVE: Genetic population structure and species variation.
DESIGN: Mapping of gene frequencies and seqeunce variation.
METHODOLOGY: RFLP of mtDNA and mtDNA cytochrome b sequencing.
STATUS: Ongoing.

Study 6
LABORATORY/RESEARCHER: University of Iceland. S. Sigurdardóttir and J. Svavarsson.
SPECIES: Marine isopods (Crustacea).
PROJECT FUNDING: The Icelandic Science fund.
OBJECTIVE: To establish phylogenetic tree for marine isopods and to study the relationship between Arctic and North Atlantic isopod fauna.
DESIGN: Samples have been collected from the deep and shallow North Atlantic.
METHODOLOGY: Nuclear DNA.
STATUS: Started in 1992.

Study 7
LABORATORY/RESEARCHER: Institute for Fisheries and Aquaculture Research, Stofnfiskur Ltd., private fishfarmers. J. Jónasson.
SPECIES: Atlantic salmon.
PROJECT FUNDING: Icelandic government, private.
OBJECTIVE: Use selective breeding to improve economically important traits in salmon ranching, like return rate and body weight.
DESIGN: Produce 100 families a year for selection.
STATUS: Started in 1987, ongoing.

Study 8
LABORATORY/RESEARCHER: Institute for Fisheries and Aquaculture Research, Stofnfiskur ltd., private fishfarmers. J. Jónasson.
SPECIES: Atlantic salmon.
PROJECT FUNDING: Icelandic government, private.
OBJECTIVE: Use selective breeding to improve economically important traits in rearing of salmon in landbased units and net pens.

DESIGN: Produce 100-200 families a year for selection.
STATUS: Started in 1991, ongoing.

Study 9
LABORATORY/RESEARCHER: Institute for Fisheries and Aquaculture Research, Stofnfiskur ltd., private fishfarmers. J. Jónasson.
SPECIES: Atlantic salmon.
PROJECT FUNDING: Icelandic Research Council.
OBJECTIVE: Establish rearing methods by using geothermal heat and light regimes to accelerate growth and age at maturity to shorten the generation interval to increase response to selection.
DESIGN: Produce 100-150 families a year.
STATUS: Started in 1993-1996.

Study 10
LABORATORY/RESEARCHER: Institute for Fisheries and Aquaculture Research, Stofnfiskur Ltd., private fishfarmers. J. Jónasson.
SPECIES: Atlantic salmon.
PROJECT FUNDING: Icelandic Research Council.
OBJECTIVE: Salmon quality. Estimate heritabilities for fat content and genetic correlation between fat content and other life history traits in salmon farming.
METHODOLOGY: Use Tory-fish fat meter to measure fat content.
DESIGN: Produce 100-150 families a year.
STATUS: Started in 1995-1997.

IRELAND

Study 1
LABORATORY/RESEARCHER: T. Cross, L. Bourke, J.Coughlan, Aquaculture Development Centre, Zoology Department, University College, Cork, and one Irish
(Salmon Research Agency), two UK and two Spanish groups.
SPECIES: Altantic salmon, Salmo salar.
PROJECT FUNDING: EC AIR1.CT92.0719
OBJECTIVE: To quantify genetic variability in wild Atlantic samon populations throughout the European range.
DESIGN: Parr samples have been collected from 14 European rivers from Russia to Spain, with one Canadian sample being included.
METHODOLOGY: Allozymes, minisatellite DNA SLPs, mt DNA, MHC genes.
STATUS: Three-year project finishing in January 1996.

Study 2
LABORATORY/RESEARCHER: T. Cross, R. FitzGerald, J. Coughlan,P. Galvin, Aquaculture Development Centre, Zoology Department, University College, Cork.
SPECIES: Turbot, Scophthalmus maximus.
PROJECT FUNDING: Irish Marine Operational Programme.
OBJECTIVE: To compare genetic variability in wild and farmed turbot.
DESIGN: Samples of wild fish have been taken off the Irish coast. Two common farmed strains are being sampled.
METHODOLOGY: Microsatellite DNA.
STATUS: Two year project which began in November 1995.

Study 3
LABORATORY/RESEARCHER: T. Cross, E. Daeman, Aquaculture Development Centre, Zoology Department, University College, Cork, plus F. Volkaert, Katholike University of Leuven.
SPECIES: Eel, Anguilla anguilla.
PROJECT FUNDING: EC HCM.
OBJECTIVE: To investigate population structure of eels in Europe.
DESIGN: Samples of elvers have been received from Italy, Ireland and Sweden.
METHODOLOGY: Microsatellite and mt DNA.
STATUS: One year study which began in April 1995.

Study 4
LABORATORY/RESEARCHER: T. Cross, P. Galvin, University College, Cork, with two UK groups.
SPECIES: Whiting, Merlangius merlangus
PROJECT FUNDING: EC FAR MA-3.781.
OBJECTIVE: To detect DNA markers for use in stock discrimination.
DESIGN: Samples taken from the southern and northern North Sea, Baltic, Norwegian coast, Celtic Sea, Iceland, Black Sea and Irish Sea are being investigated
for differences at two hypervariable PCRable minisatellite loci.
METHODOLOGY: PCRable minisatellite DNA loci.
STATUS: Three-and-a-half year project to be completed in March 1996.
COMMENTS: Ongoing work. Interspecies applicability of probes will be tested (those already developed work well for cod and haddock and show variability).

Study 5
LABORATORY/ RESEARCHER: P. McGinnity, Salmon Research Agency of with one Irish, two UK and two Spanish partners.
SPECIES: Atlantic Salmon
FUNDING: EU AIR 1 3003 92 719
OBJECTIVE: To study the genetic impact of introduced non native salmon on natural populations.
DESIGN: (a) Simulation of a farm escape to a natural stream contained high specification fine screened trap, individual fish identified to using DNA minisatellites. (b) A study of temporal changes, a consequence farm escapes, in the genetic composition of juvenile salmon from selected rivers in North-West Ireland.
METHODOLOGY: Establishment of experimental population, hatchery trap and field monitoring, sampling, minisatelliteDNA and Mitochondrial (QUB), Allozymes
(UCC).
STATUS: Three year project to be completed January 1996.

Study 6
LABORATORY/ RESEARCHER: P. McGinnity, Salmon Research Agency of Ireland
SPECIES: Atlantic salmon
FUNDING: Atlantic Salmon Trust, Salmon Research Agency of Ireland.
OBJECTIVE: To study the adaptive significance of genotypic variation at Malic Enzyme Locus MEP-2*.
DESIGN: Establishment of hatchery population, observation population study 1, monitoring of a number of West of Ireland populations, relate MEP-2* genotype and performance.
METHODOLOGY: Allozyme analysis
STATUS: Four year part-time project to be completed June 1996.

Study 7
LABORATORY/ RESEARCHER: P. McGinnity, Salmon Research Agency of reland
SPECIES: Atlantic salmon
FUNDING: Salmon Research Agency of Ireland.
OBJECTIVE: To determine the genetic impact of Ocean Ranch Atlantic salmon on natural populations.
DESIGN: Two scenario's are being studied where (a) the ocean ranch population has originated from the recipient wild population and (b) where there is no relationship between the ocean ranch population and the recipient population.
METHODOLOGY: Allozyme analysis
STATUS: Ongoing study.

Study 8
LABORATORY/ RESEARCHER: Russell Poole, Salmon Research Agency of Ireland with one Norwegian and two UK partners.
SPECIES: Atlantic salmon, anadromous and resident brown trout.
FUNDING: AIR3 PL94 2484
OBJECTIVE: The goal of the research project is to quantify and understand the effects of hybridisation between Atlantic salmon and brown trout, particularly as it relates to escapes from aquaculture.
DESIGN: Quantify interspecific hybridisation and introgression in unspoiled and genetically compromised rivers
METHODOLOGY: Application of mini-satellite and mitochondrial DNA identification techniques.
STATUS: Two year project to be completed 1996.

Study 9
LABORATORY/ RESEARCHER: Deidre Cotter, Salmon Research Agency of Ireland with one Irish (N. Wilkins, UCG), two Scottish and one Norwegian partner.
SPECIES: Atlantic salmon.
FUNDING: AIR3 CT 94 2216.
OBJECTIVE: A comprehensive evaluation of the use of sterile triploid Atlantic salmon in reducing the interaction between wild and farm stocks.
DESIGN: Characterisation of the performance of triploids in culture
METHODOLOGY: Setting up experimental population, control population, ocean ranching, rearing experiments, tagging, simulation of escapes from seacages.
STATUS: Four year programme to be completed October 1998.

Study 10
LABORATORY/RESEARCHER: Dr. L. Byrnes, Department of Zoology, U.C.D.
SPECIES: Atlantic salmon
PROJECT FUNDING: Forbairt Scientific Research Programme
OBJECTIVE: To analyse gene structure and regulation of expression of transferrin during smoltification.
DESIGN: Transferrin gene has been cloned. Regulation of expression will be examined at both the molecular level and in vivo during smoltification.
METHODOLOGY:The following standard molecular biology techniques are being employed: DNA cloning and sequencing, preparation of salmon liver nuclear extracts, DNase I footprinting, electrophoretic mobility shift assays, Northern blots, PCR
STATUS: Project duration: October '94 until September '96

Study 11
LABORATORY/RESEARCHER: Dr. Richard Powell, Recombinant DNA Group, Department of Microbiology, University College, Galway.
SPECIES: Atlantic salmon, Salmo salar.
PROJECT FUNDING: No dedicated funding in 1995.
OBJECTIVE: Description of microsatellite repetitive elements in the genome of Atlantic salmon.
STATUS: Research involves the isolation and description of repetitive microsatellite DNA sequences in the genome of Atlantic salmon. The goals are to define molecular tools to aid the study of the genetic diversity of natural salmon stocks, to define
quantitative traits in commercial brood stocks, and to develop a genetic map of the salmon genome. To date, over 100 microsatellite sequences have been identified.
20 PCR assays have been described from these microsatellite sequences. These sequences are being added to European and Canadian initiatives to microsatelliute-based genome maps for Atlantic salmon and rainbow trout.

Study 12
LABORATORY/RESEARCHER: Dr. Richard Powell, Recombinant DNA Group, Department of Microbiology, University College, Galway.
SPECIES: Pacific oyster, Crassostrea gigas
PROJECT FUNDING: EU FAIR Programme
OBJECTIVE: Development of a molecular karyotype system for Pacific oyster.
STATUS: Research involves the construction of large-insert genomic DNA libraries of Pacific oyster using E. coli cosmid and P1 vectors. Clones with inserts of oyster DNA ranging from 10 kb to 100 kb in length will be chosen and using in fluorescent in situ hybridisations on oyster chromosomes. The aim is to define clones that mark specific chromosome pairs and develop a chromosomal karyotype system based on such molecular markers. cosmid and P1 vectors. Clones with inserts of oyster DNA ranging from 10 kb to 100 kb in length will be chosen and using in fluorescent in situ hybridisations on oyster chromosomes. The aim is to define clones that mark specific chromosome pairs and develop a chromosomal karyotype system based on such
molecular markers.

Study 13
LABORATORY/RESEARCHER: Dr. Richard Powell, Recombinant DNA Group, Department of Microbiology, University College, Galway.
SPECIES: Aeromonas salmonicida, Yersinia ruckerii, Vibrio vulnificus, IPN virus, salmon, trout, eel.
PROJECT FUNDING: EU AIR Programme.
OBJECTIVE: Molecular Detection Systems for Bacterial and Viral Pathogens of Cultured Fish Species.
STATUS: Research involves the description of DNA probe and ELISA diagnostic tests for the fish pathogens, Aeromonas salmonicida, Yersinia ruckerii, IPN Virus and
Vibrio vulnificus which detrimentally effect the commercial culture of salmon, trout and eel with significant financial loss. To date, DNA probe and ELISA tests have been developed for these pathogens.Of more significance, these tests have been designed and have been shown to have the ability to detect low levels of these pathogens in the environment of fish farms. The goal is to show these molecular-based detection systems can act as early-warning devices for fish farm management.

Study 14
LABORATORY/RESEARCHER: Dr. Richard Powell, Recombinant DNA Group, Department of Microbiology, University College, Galway.
SPECIES: Aeromonas salmonicida (atypical strains).
FUNDING: EU AIR Programme
OBJECTIVE: Improved identification and taxonomic analysis of atypical isolates of the fish pathogen Aeromonas salmonicida.
STATUS: Research is underway on a genetic, biochemical and immunological analysis of new isolates of 'atypical' Aeromonas salmonicida presently being isolated from a large range of diseased sea- and fresh-water fish species. The objectives are (i) to develop definitive diagnostic procedures for the identification of this bacterial group, and (ii) to quantify the detrimental effect of this group on native fish resources. Genetic techniques include 16S rRNA sequence analysis, ribotyping, RAPD and PFGE analysis.

Study 15
LABORATORY/RESEARCHER: National Diagnostics Centre, Bioresearch Ireland, Galway / Terry Smith Title:Biological containment of transgenic fish and risk assessment of interspecies gene transfer.
SPECIES: Salmon (Galway), Trout (Rennes), tilapia (Southampton), Zebrafish
(Oslo and Southampton)
FUNDING: EU Biotech programme (130,000ECU)
Duration: 2 years (Dec. 94-Dec 96; Continuation
applied for)
OBJECTIVE: The use of transgenesis to render fish sterile and to evaluate the
effectiveness of the induced sterility.
Design: Antisense and ribozyme technology is being used to inhibit the synthesis
of gonadotropin releasing hormone (GnRH). This is expected to render fish sterile as has been shown previously in the mouse. Injections of GnRH will be used to return some fish to fertility and provide brood stocks. As part of the studies further insights into fish reporoductive physiology will be achieved. Reporter genes will be co-injected into fish to monitor transgenesis and possible gene flow. Ultimately the aim would be to introduce sterility in conjunction with a valuable trait (e.g. disease
resistance).
METHODOLOGY: The Galway group is involved in the isolation of strong all tissue expressing promoters from salmon which will be used to drive expression of antisense GnRH and reporter genes.
Status: The current situation is that antisense and reporter gene expression constructs have been made and are being tested in vitro and being microinjected into fish for in vivo analysis.

Study 16
LABORATORY/RESEARCHER:.NDC / Frank Gannon and Terry Smith
Title: Identification of genes involved in early fish development
SPECIES: Salmon (Galway), Trout and Medaka (INRA, Paris), Medaka (Wurzburg), Sea Bass (Malaga)
FUNDING: EU Biotech programme (210,000ECU): 3 years (Sept.. 94 - Sept. 96)
OBJECTIVE: Isolate and characterise genes involved in early development of fish species.
DESIGN: Differential cloning, differential display RT-PCR and homology cloning
being used to identify, isolate and characterise fish genes whose expression is up or down-regulated during early embryo development.

METHODOLOGY: The Galway group is involved in the isolation of genes using the above methods in salmon using RNA collected at different stages post-fertilisation
STATUS: A number of genes have been isolated and are currently being characterised. Further genes will be identified and characterised

Study 17
LABORATORY/RESEARCHER: NDC / Frank Gannon
SPECIES: Salmon (Galway) Mammalian (others)
FUNDING: EU Biotech programme (210,000ECU): 3 years (Sept. 94 - sept. 96)
OBJECTIVE: Isolation and characterisation of the genes encloding liver-enriched transcription factors HNF 1 and HNF 3 from salmon. Analysis of regulatory regions and control of expression during development
DESIGN: cDNA library screening to isolate cDNA sequences and genomic library
screening to isolate genomic clones and promoter regions.
METHODOLOGY: The Galway group is involved in the isolation and characterisation of genes and promoters including sequence analysis, DNA /protein binding studies.
STATUS: Ongoing studies on HNF 3 gene and HNF 1 promoter

Study 18
LABORATORY/RESEARCHER: NDC/ Terry Smith
SPECIES: Salmon (Galway), Trout and Medaka (INRA, Paris), Medaka (Wurzburg)
FUNDING: EU FAIR programme (210,000ECU)
DURATION: 3 years (Jan. 96-Dec 98)
OBJECTIVE: Identification of genes involved in fish immunity. Generation of molecular markers to predict fish immunity and use identified genes to protect fish from pathogen infection.
DESIGN: a) Cloning of cellular and humoral factors involved in immune response using a variety of approaches.
b) Isolation and culture of fish cells involved in immune response.
c) Combination of a) and b) above to establish funtional relationship. Transfer of genes identified into fish.
METHODOLOGY: The Galway group is involved in the isolation of genes whose expression is up or down-regulated as a result of infection. Differential cloning and differential display RT-PCR will be used to identify such genes.
STATUS: Project work just underway

NORWAY

Study 1
LABORATORY/RESEARCHER: Department of Aquaculture, Institute of Marine Research (IMR), Bergen. G. Dahle.
SPECIES: Atlantic halibut.
PROJECT FUNDING: Norwegian Research Council.
OBJECTIVE: Produce genetic markers in the aquaculture species halibut.
DESIGN: Recover parts of the halibut genom cloned into vectors in *E. coli*, and produce microsatellite primers based on sequencing data. Optimize the PCR condition for every possible primer sets, and test the Heritability of each primer set.
METHODOLOGY: Cloning, sequencing and extensive testing of possible microsatellite primers.
STATUS: Three year project started in 1996.

Study 2
LABORATORY/RESEARCHER: Department of Aquaculture, Institute of Marine Research (IMR), Bergen/G. Dahle.
SPECIES: Cod (*Gadus morhua*).
PROJECT FUNDING: Norwegian Research Council.
OBJECTIVE: Study the mini- and microsatellite loci variation in historic material.
DESIGN: Otolithes have been sampled and stored for many decades at IMR. These old otolithes are being used to analyse the genetic composition of historic samples of cod with mini- and microsatellite primers.
METHODOLOGY: Mini- and microsatellite analysis.
STATUS: Two year project started in 1996.

Study 3
LABORATORY/RESEARCHER: Institute of Marine Research (IMR), Bergen, Ø. Skaala.
SPECIES: Atlantic salmon (*Salmo salar L.*).
PROJECT FUNDING: The Norwegian Research Council.
OBJECTIVE: (1) To study the genetic implications of transgenic fish by using genetically marked multigeneration cultivated salmon as a model organism. (2) To quantify gene flow from the model species to wild salmon populations. (3) To estimate growth and survival of different genotypes (wild, introduced and heterozygotes). (4) To investigate the extent of genetic introgression from the model organism to sympatric salmonid species, i.e. brown trout (*Salmo trutta* L.).
DESIGN: Release of genetically marked multigeneration farmed salmon in a river with salmon and trout stocks.
METHODOLOGY: Allozymes and minisatellite DNA.
STATUS: Genetically marked smolt produced and released in 1994. Allozyme and DNA baseline data on wild and released stocks done. Fry will be sampled and screened in 1996 and 1997.
COMMENTS: The study does not include transgenic fish , but employ multigeneration farmed salmon as a model to investigate impacts from transgenic fish potentially used in fish farming in the future.

Study 4
LABORATORY/RESEARCHER: Institute of Marine Research (IMR), Bergen, Ø. Skaala.
SPECIES: Atlantic salmon.
PROJECT FUNDING: The Directorate for nature management.
OBJECTIVE: Studies of temporal stability of gene frequencies in R. Vosso salmon.
DESIGN: Screening of naturally spawned year classes between 1983 and 1996, and farmed salmon.
METHODOLOGY: Starch gel electrophoresis with emphasis on the MEP-2* locus, where the fast allele is close to fixation in the major brood stock of farmed salmon.
STATUS: Baseline samples of wild Vosso salmon and farmed salmon analysed.
COMMENTS: Collaborative work with Dr. K. Hindar at NINA.

Study 5
LABORATORY/RESEARCHER: Institute of Marine Research (IMR), Bergen, Ø. Skaala.
SPECIES: Brown trout (*Salmo trutta*).
PROJECT FUNDING: Norwegian electricity industry.
OBJECTIVE: Quantify the contribution of wild and stocked populations to trout fisheries in L. Tinnsjøen.
DESIGN: Genetic screening of wild and released stocks.
METHODOLOGY: Starch gel electrophoresis, statistics by Pella.
STATUS: All stocks screened, statistical testing initiated.

COMMENTS: Collaborative work with Prof. J. Heggenes, Institute of Biology and Nature conservation, Ås Agricultural University.

Study 6
LABORATORY/RESEARCHER: Institute of Marine Research (IMR), Bergen, Ø. Skaala.
SPECIES: Atlantic salmon and brown trout.
PROJECT FUNDING: The Norwegian Sea ranching program (PUSH).
OBJECTIVE: Investigate gene flow from sea ranched salmon to wild stock, and species hybridization.
DESIGN: Genetically marked smolt released from a small stream with salmon and sea trout. Genetic screening of various year classes done.
METHODOLOGY: Allozymes.
STATUS: Several year classes screened. Fry will be collected and screened in 1996.

Study 7
LABORATORY/RESEARCHER: Department of Fisheries and Marine Biology/University of Bergen (DFMB), G. Nævdal.
SPECIES: Sandeels (*Ammodytidae*).
PROJECT FUNDING: The Norwegian Research Council/University of Bergen
OBJECTIVE: Study the genetic variation between morphological similar species, and the population structure within the most abundant species of sandeels.
DESIGN: Samples from localities from the North Sea, Iceland and Scotland, the Faeroe Islands and Denmark are being analysed.
METHODOLOGY: Gel electrophoresis and isoelectric focusing (allozymes).
STATUS: Three year project started in January 1995.
COMMENTS: Cooperation has been established with several fisheries research institutes around the North Sea and Iceland.

Study 8
LABORATORY/RESEARCHER: Department of Fisheries and Marine Biology/University of Bergen (DFMB), G. Nævdal, in collaboration with Institute of Marine Research (IMR) Bergen, and Møreforskning, Ålesund.
SPECIES: Redfish, Genus *Sebastes*.
PROJECT FUNDING: The Norwegian Research Council, IMR and the University of Bergen.
OBJECTIVE: Study the genetic variation between morphologically similar species, and the population structure within the species.
DESIGN: Extensive sampling has taken place throughout the distribution areas of the redfish species, except from Canadian waters. In later years sampling has been concentrated on the western areas in collaboration with Møreforskning.
METHODOLOGY: Gel electrophoresis and isoelectric focusing (allozymes).
STATUS: Studies on haemoglobins and allozymes by electrophoresis and isoelectric focusing have been going on since 1987; the last years with main emphasize on Icelandic and Greenland waters. From 1995 DNA-analyses have been included with the main emphasize of studying the oceanic and deep sea *S. mentella*. A "new" three year project started in January 1995.
COMMENTS: The project has revealed a relative simple species and population structure for redfish species in the eastern North Atlantic, while the picture seems very complicated in Greenland waters, and very little is known about the structure west of the Davis Strait.

Study 9
LABORATORY/RESEARCHER: Department of Fisheries and Marine Biology/University of Bergen (DFMB), G. Nævdal, in collaboration with Institute of Marine Research (IMR) Bergen, and Møreforskning, Ålesund.
SPECIES: Ling, blue ling and tusk.
PROJECT FUNDING: The Norwegian Research Council and the Nordic Council.
OBJECTIVE: Study the population structure of the mentioned species as part of a larger project for studies on the biological resources of these species.
DESIGN: Samples from localities around Greenland and Iceland, the northern North Sea, the Shetland area and the Norwegian coast have so far been analysed.
METHODOLOGY: Gel electrophoresis and isoelectric focusing (allozymes and haemoglobins).
STATUS: A three year project (1993-1995) which is now being reported.
COMMENTS: The project has revealed rather little genetic variation within these species, especially in ling. Haemoglobin variations are found in tusk and blue ling. No significant variation between samples are found in the northeast Atlantic, but the hemoglobin type distributions of the two samples from the northwest Atlantic deviated significantly. (Why do different species behave so different with respect to degree of genetic variation?).

Study 10
LABORATORY/RESEARCHER: Department of Fisheries and Marine Biology/University of Bergen (DFMB), G. Nævdal.
SPECIES: Herring, *Clupea harengus.*
PROJECT FUNDING: The Norwegian Research Council.
OBJECTIVE: To describe the esterase and hemoglobin variation in herring and to reveal the genetic and ontogenetic background control mechanisms.
DESIGN: A series of samples of herring distributed on potential population and different life stages are being analysed.
METHODOLOGY: Isoelectric focusing.
STATUS: The project is started in winter 1996, and will last for one year.
COMMENTS: It has been known for long that the heamoglobins of herring are changing during the fish's ontogeny. However, preliminary studies using isoelectric focusing also have indicated genetic variations. Likewise, isoelectric focusing of blood esterase indicates variations in different loci. Hopefully, the study will give a "yes" or "no" answer on the question about the usefulness of these variation for further utilization in population studies.

Study 11
LABORATORY/RESEARCHER: Department of Fisheries and Marine Biology/University of Bergen (DUMB), G. Nævdal
SPECIES: Northern shrimps, *Pandalus borealis.*
PROJECT FUNDING: No special funding (student thesis).
OBJECTIVES: To reveal, describe and utilize genetic variation in northern shrimps.
DESIGN: An extensive material have been collected in coastal and offshore waters northwest of Iceland and in the Denmark Strait. The samples have been analysed by standard starch gel electrophoresis.
STATUS: Frequency distributions of three polymorphic systems are being used to study the structure of shrimps in the mentioned areas. The thesis is now in the process of being ready for evaluation.
COMMENTS: The results are very encouraging with respect to further use of allozymes in studies of shrimp population structure.

Study 12
LABORATORY/RESEARCHER: Department of Fisheries and Marine Biology/University of Bergen (DFMB), G. Nævdal.
SPECIES: Roughead grenadier, *Macrourus berglax.*
PROJECT FUNDING: No special funding (student thesis).
OBJECTIVES: To reveal, describe and utilize genetic variation in the grenadier. **DESIGN:** Material has been collected in areas between Iceland and Greenland
and in the Norwegian Sea. The analyses so far have revealed several polymorphic systems.
STATUS: The results are encouraging so far, and the project is anticipated to be finished in 1996.
COMMENTS: The analyses are carried out by a foreign student which also has to take several courses in different disciplines to be accepted as a graduate student at the University of Bergen.

*In addition smaller projects on halibut, Greenland halibut and turbot (genetics/physiology interactions) are being carried out or are planned. Project outside the ICES area is not mentioned here. Should they?

Study 13
LABORATORY RESEARCHER: The Norwegian College of Fishery Science, University of Tromsø, S. E. Fevolden; in collaboration with Norwegian Institute of Fisheries and Aquaculture (NIFA), Tromsø.
SPECIES: Deep water shrimp, *Pandalus borealis.*
PROJECT FUNDING: The Norwegian Research Council.
OBJECTIVES: To study the population structure of deep water shrimp in the Barents Sea and fjords of Northern Norway.
DESIGN: Shrimps are sampled north (Spitsbergen), east and west in the Barents Sea plus in various fjords in Northern Norway.
METHODOLOGY: Allozyme variation plus RAPDs (NIFA).
STATUS: Three years project starting in 1995.

Study 14
LABORATORY RESEARCHER: The Norwegian College of Fishery Science, University of Tromsø, S. E. Fevolden (Norwegian partner in a joint EU-project coordinated by Institute of Freshwater Ecology, The Windermere Laboratory).
SPECIES: Rainbow trout, *Oncorhynchus mykiss.*
PROJECT FUNDING: EU.
OBJECTIVES: To establish a protocol for the selective breeding of finfish for increased tolerance to stress and to assess whether stress tolerance is at an advantage under aquaculture conditions in terms of growth, disease resistance and reproductive performance.
DESIGN: The heritability, or genetic components of stress-related traits will be determined in progenies groups from parents selected among 50 families being tested for stress tolerance. The performance of each progeny group (growth, adaptability and disease resistance)will be assessed.
METHODOLOGY: The selection scheme will be based on stress response of individuals within families. The selection traits are post-stress plasma cortisol levels and post-stress lysozyme levels.
STATUS: Four year project starting in 1996.

Study 15
LABORATORY/RESEARCHER: K. Hindar, Norwegian Institute for Nature Research (NINA).
SPECIES: Atlantic salmon.
PROJECT FUNDING: Directorate for Nature Management, Norway and NINA.

OBJECTIVE: Establish baseline information about the population genetic structure of Atlantic salmon in Norway.
DESIGN: Samples from all over Norway to analyse spatial and temporal variation in gene frequencies.
METHODOLOGY: Allozymes.
STATUS: Ten-year project to be completed 1996.

Study 16
LABORATORY/RESEARCHER: K. Hindar, NINA in collaboration with two UK and one Irish group.
SPECIES: Atlantic salmon and brown trout.
PROJECT FUNDING: EU AIR3 94 2484.
OBJECTIVE: Quantify and understand hybridisation between Atlantic salmon and brown trout, especially in the light of an increasing tendency of escaped farmed salmon to hybridise with trout.
DESIGN: Index samples from Ireland, Scotland and Norway including undisturbed and «genetically polluted» rivers; behavioural studies of spawning; estimates of fitness components in artificially produced hybrids.
METHODOLOGY: Genetic markers (allozymes, nuclear and mitochondrial DNA); feeding history markers (natural and synthetic pigments); constructed spawning arenas; rearing and release studies.
STATUS: 27 month study to be completed December 1996.

Study 17
LABORATORY/RESEARCHER: I. Fleming, B. Jonsson, K. Hindar, NINA.
SPECIES: Atlantic salmon.
PROJECT FUNDING: Research Council of Norway.
OBJECTIVE: Quantify reproductive success of farmed and sea ranched fish relative to wild fish.
DESIGN: Behavioural-ecological analysis of reproduction in artificial spawning arenas; release of genetically marked wild and farmed fish into a river.
METHODOLOGY: Video recording and direct observation of spawning; ecological and genetic analysis of spawners and their offspring.
STATUS: Seven-year project to be completed December 1996.

Study 18
LABORATORY/RESEARCHER: I.B. Mjølnerød and K. Hindar; University of Oslo, NINA and U.H. Refseth and K.S. Jakobsen.
SPECIES: Atlantic salmon.
PROJECT FUNDING: Research Council of Norway.
OBJECTIVE: Analyse genetic variation detected by allozymes and nuclear DNA markers.
DESIGN: Compare levels of genetic variation in two wild and one farmed population.
METHODOLOGY: Allozymes; multi-locus and single-locus minisatellites.
STATUS: Three-year project to be completed 1996.

Study 19
LABORATORY/RESEARCHER: Univ. of Trondheim, Biological Station, J. Mork.
SPECIES: Indifferent.
PROJECT FUNDING: Institutional.
OBJECTIVE: General, interactive PC simulation program for, e.g., prediction and analysis of genetic effects of interaction between cultured and wild populations.

DESIGN: Simultaneous handling of combined genetic effects from random genetic drift, gene flow (model-independent), and selection (additive effects) at multiple loci on a genetically pre-characterized set of populations. Any number of generations can be run.
METHODOLOGY: Theoretical population genetics, mathematical modelling, computer, Monte Carlo simulations.
STATUS: Functional version in use at several sites.

Study 20
LABORATORY/RESEARCHER: Univ. of Trondheim, Biological Station, J. Mork. and M. Giæver.
SPECIES: Blue whiting (Micromesistius poutassou)
PROJECT FUNDING: The Norwegian Research Council, grant NF 108 093/110.
OBJECTIVE: To enlighten the genetic population structure in the blue whiting, with special emphasis on the north-eastern parts of its distribution range (the Norwegian Sea and the Barents Sea).
DESIGN: Genotyping of a large number of individuals from a tight sampling net in the relevant areas, during and outside the spawning season.
METHODOLOGY: Allozymes and DNA markers.
STATUS: Two year project started in 1995.
COMMENTS: Allozyme allele frequencies in a previous study indicated a separate stock in the north-east part of the blue whiting distribution area.

Study 21
LABORATORY/RESEARCHER: Univ. of Trondheim, Biological Station, J. Mork.
SPECIES: Cod (Gadus morhua).
PROJECT FUNDING: Institutional.
OBJECTIVE: Study of the long term stability of haemoglobin and allozyme allele frequencies in a local population of cod, and test for correlations between genotype and growth/survival.
DESIGN: Bi-annual sampling (research vessel) of about 200 specimens from a local cod population with no commercial exploitation.
METHODOLOGY: Collection of biological data (length, age, sex etc), and genotyping for polymorphic haemoglobins and tissue enzymes.
STATUS: Haemoglobin analysis started in 1974 and is ongoing; allozymes from 1980 and ongoing.
COMMENTS: DNA mini- and microsatellites included from 1996.

Study 22
LABORATORY/RESEARCHER: J. Mork, Biological Station, University of Trondheim. Collaboration with T. Cross and P. Galvin (University College, Cork, Ireland), G. Carvalho and C. Turan (University of Wales, Swansea, U.K.), and J.E. Eliassen (The Norwegian Institute of Fisheries and Aquaculture, Tromsø, Norway).
SPECIES: Cod, haddock, whiting, saithe, blue whiting, Norway pout, capelin, herring.
PROJECT FUNDING: The Norwegian Research Council & The Directorate for Nature Management
OBJECTIVE: Baseline studies of genetic population structures in Norwegian coastal waters
DESIGN: Collection of ~100 specimens from each Norwegian fjord from the Kola peninsula to Aalesund, storing tissue samples at -84 °C, and analysing them using allozymes and various others techniques when such become available. Sample collection during intensive research vessel cruises along the Norwegan coast 6-7 weeks each year 1992-1994.
METHODOLOGY: Allozymes, haemoglobins, DNA mini- and micro-satellites.
STATUS: Haddock, cod and blue whiting allozyme analyses are a jour (>3000 specimens each). DNA minisatellite analyses ongoing for whiting and (as pilot studies) some other species.

COMMENTS: The genetic studies are coordinated with biological studies on the same material by The Norwegian Institute of Fisheries and Aquaculture, Tromsø, in its Coastal Resource Program. All specimens are biologically characterized (sex, length, age etc). Tissue samples can be made available for researchers with interesting projects.

POLAND

Study 1

LABORATORY/RESEARCHER: Inland Fisheries Institute; Salmonid Research Laboratory Rutki, Institute of Freshwater Ecology and Inland Fisheries Berlin and Warsaw University of Agriculture. K. Goryczko, S. Dobosz, K. Kohlmann, A. Zynczynski.
SPECIES: Rainbow trout.
PROJECT FUNDING: Committee of Scientific Research (CSR) and Institutional.
OBJECTIVE: To improve the breeding value of rainbow trout.
DESIGN: Family selection from outbred broodstock the 100 F_1 families were started in 1991. In 1994 from the 10 selected families the 100 F_2 families were produced and reared during 1995. Growth and mortality were monitored.
METHODOLOGY: Each family reared separately until the end of the first season, then the fish is tagged (PIT tags), amount of families culled (60), fish reared in one pond until sexual maturity.
STATUS: The second year of F_2 cycle.

Study 2

LABORATORY/RESEARCHER: IFI; Salmonid Research Laboratory Rutki,
K. Goryczko, S. Dobosz, H. Kuzminski.
SPECIES: Sea trout.
PROJECT FUNDING: Institutional.
OBJECTIVE: Vistula sea trout gene bank.
DESIGN: Freshwater broodstock produced from representative group of river ascending sea trout.
METHODOLOGY: A sample of 50g of fertilised eggs from each wild female spawned were taken, incubated and reared at SRL. A random samples of 1991 and 1993 year generations presmolts were PIT tagged (1200 and 600 fish respectively). Smoltification, growth and age at first maturity are monitored.
STATUS: Fourth and second year life. Elder fish second spawn.
COMMENTS: Project aimed at protection of genetic diversity in a valuable strain maintained by stocking.

Study 3

LABORATORY/RESEARCHER: IFI; Salmonid Research Laboratory Rutki. K. Goryczko, S. Dobosz, H. Kuzminski. University of Agriculture and Technology, Olsztyn, Dept. of Basic Fishery Sciences. M. Kuczynski.
SPECIES: Whitefish.
PROJECT FUNDING: CSR grant no ZO22/S3/94/01.
OBJECTIVE: Enhancement of endangered stock of Baltic whitefish.
DESIGN: Freshwater broodstock produced from eggs obtained during 3 consecutive years from wild spawners.
METHODOLOGY: Using the trout farming methods the stocking material (summer fingerlings) and brood fish were produced. The biochemical genetic study of farmed whitefish were realised.
STATUS: Second spawning season of farmed fish; 4 million eggs were obtained, 100 000 fry and 80 000 summer fingerlings (from the first spawn) were stocked.

COMMENTS: Farmed broodstock enabled enhancement and reintroduction projects realisation without curtailing of wild broodstock.

Study 4
LABORATORY/RESEARCHER: Inland Fisheries Institute, Olsztyn. M. Zolkiewicz.
SPECIES: Rainbow trout.
PROJECT FUNDING: Institutional.
OBJECTIVE: Genetic monitoring of rainbow trout hatchery stocks to detect changes and take measures preventing unwanted inbred.
DESIGN: Farmed stocks through Poland were sampled and analysed for genetic variation.
METHODOLOGY: Allozymes.
STATUS: To be repeated periodically.

Study 5
LABORATORY/RESEARCHER: Olsztyn University of Agriculture and Technology; Department of Basic Fisheries Sciences, Fischereiforschungsstelle des Landes Baden-Wurttemberg, Muhlesch University of Joensuu; Department of Biology. M. Kuczynski, R. Rosh, J. Vuorinen, P. Brzuzan.
SPECIES: Whitefish.
PROJECT FUNDING: CSR grant no.5/5477/91/02.
OBJECTIVE: Biochemical genetic study of sympatric Lake Constance whitefish populations.
DESIGN: Two populations were sampled to find out the genetic source of meristic and biological differences.
METHODOLOGY: Biometric and biochemical analysis.
STATUS: Project completed.
COMMENTS: Additional research should be carried to provide more information on the genetic status of Lake Constance whitefish.

UNITED KINGDOM

Study 1
LABORATORY/RESEARCHER: SOAFD Marine and Freshwater Fisheries Laboratories, E. Verspoor and collaborators
SPECIES: Atlantic salmon
PROJECT FUNDING: SOAFD and EC AIR1-CT92-0719
OBJECTIVE: to assess whether the documented interbreeding of farm Atlantic salmon, which ascended the River Polla in 1989 and 1990, with the wild stock has resulted in genetic changes to the juvenile populations in the river.
DESIGN: Samples of juvenile Atlantic salmon from two year classes were collected from the lower, middle and upper reaches of the river pre-spawning of farm fish in 1989. The genetic composition of these fish will be compared with post spawning juvenile samples from the same locations taken in 1991 and differences related to the genetic make-up of adult farm Atlantic salmon ascending the river.
METHODOLOGY: Allozymes, RFL analysis of PCR amplified mtDNA, mini- and micro-satellite analysis of nuclear DNA, PCR amplification of structural gene nDNA.
STATUS: Currently underway and due for completion in 1995.
COMMENTS: This represents an opportunistic study.

Study 2
LABORATORY/RESEARCHER: SOAFD Marine and Freshwater Fisheries Laboratories, E. Verspoor and collaborators
SPECIES: Atlantic salmon
PROJECT FUNDING: SOAFD and EC AIR1-CT92-0719
OBJECTIVE: to assess whether genetic differences among stocks are relevant to their biological performance during the juvenile freshwater phase in the wild in ways that relevant to their fitness.
DESIGN: Simultaneously spawned eggs of different regional stocks and their hybrids have been planted out within 48 hrs of fertilization in artificial redds using a random stratified planting strategy in a small experimental river where natural spawning is precluded. Performance parameters such as egg mortality, hatching and emergence timing, developmental state, maturation, growth and smoltification will be compared among groups.
METHODOLOGY: Stock groups will be genetically marked using RFLP's PCR amplified mtDNA and single locus minisatellite fingerprinting.
STATUS: Currently underway and due for completion in 1996.
COMMENTS: This represents an experimental study.

Study 3
LABORATORY/RESEARCHER: SOAFD Marine and Freshwater Laboratories, A. Youngson, J. Webb
SPECIES: Atlantic salmon
PROJECT FUNDING: SOAFD and Atlantic Salmon Trust
OBJECTIVE: to determine the frequency of farm escapes among Atlantic salmon in the coastal Atlantic salmon fisheries in Scotland.
DESIGN: regular sampling of Atlantic salmon taken by four representative coastal net fisheries off Scotland.
METHODOLOGY: Identification of farm fish on basis of body morphology and scale analysis.
STATUS: Started in 1992 and ongoing.
COMMENTS: This represents an opportunistic study.

Study 4
LABORATORY/RESEARCHER: SOAFD Marine and Freshwater Laboratories, E. Verspoor
SPECIES: Atlantic salmon
PROJECT FUNDING: SOAFD
OBJECTIVE: To determine the nature and extent of population structuring of Atlantic salmon in Scotland within and among rivers so as to assess the impact of farm escapes on natural structure.
DESIGN: geographic sampling of within and among river genetic variation and statistical analysis of differentiation.
METHODOLOGY: Allozymes, mtDNA, mathematical modelling.
STATUS: Started in 1989 and ongoing.

Study 5
LABORATORY/RESEARCHER: G. R. Carvalho & C. Turan; Marine & Fisheries Genetics Laboratory, School of Biological Sciences, University of Wales, Swansea, Singleton Park, Swansea SA2 8PP, UK
SPECIES: Atlantic herring Clupea harengus
PROJECT FUNDING: Overseas postgraduate studentship (Turkey) + in-house funding
OBJECTIVE: To develop novel molecular markers for stock discrimination in herring.
DESIGN: Examine molecular markers in widely-separated populations of herring from the North Sea (Esp. Norwegian fjords), Baltic and Canadian waters using novel approaches (Polymerase chain

reaction (PCR)- based analysis of the mitochondrial and nuclear DNA genome). Data will be compared with other approaches (allozymes, morphometrics, otoliths, meristics) and published work.
METHODOLOGY: PCR-based analysis of DNA, allozymes, morphometrics (truss) and meristics.
STATUS: April 1994 - April 1997
COMMENTS: The study will form the substance for a PhD thesis and is part of an on-going programme of research on the genetic management of capture fisheries (past studies include Adriatic clupeids).

Study 6
LABORATORY/RESEARCHER: G. R. Carvahlo; Marine & Fisheries Genetics Laboratory, School of Biological Sciences, University of Wales, Swansea, Singleton Park, Swansea SA2 8PP, UK
SPECIES: Squid (*Illex argentinus*)
PROJECT FUNDING: In-house funding (application pending)
OBJECTIVE: To examine stock structure and species identity in South atlantic *Illex* populations.
DESIGN: To examine genetic differentiation among putative stocks (seasonal spawning groups) and possible cryptic species.
METHODOLOGY: To develop novel DNA markers for use in stock structure analysis, and to integrate molecular genetic approach with morphological and meristic analysis. Possible new species description.
STATUS: 1994 and on-going (initial samples collected and awaiting analysis.)
COMMENTS: The project involves collaborative efforts with the Falkland Islands Fisheries, Dr Paul Rodhouse (British Antarctic Survey) and Dr C. Nigmatullin (AtlantNIRO, Russia).

Study 7
LABORATORY/RESEARCHER: A. R. Child MAFF, Directorate of Fisheries Research, Fisheries Laboratory, Benarth Road, Conwy, Gwynedd, LL32 8UB.
SPECIES: Pacific oyster (*Crassostrea gigas*).
PROJECT FUNDING: MAFF in-house.
OBJECTIVE: Genetic variation in commercial populations of *C. gigas*.
DESIGN: Examine genetic variation in commercial and natural spat of *C. gigas*.
METHODOLOGY: Allozyme variation.
STATUS: On-going.
COMMENTS: Paper in preparation, A R Child, P Papageorgiou & A R Beaumont. Identification of Pacific oysters (*Crassostrea gigas*) of possible French origin in natural spat in the British Isles.

Study 8
LABORATORY/RESEARCHER: A. R. Child, MAFF, Directorate of Fisheries Research, Fisheries Laboratory, Benarth Road, Conwy, Gwynedd, LL32 8UB.
SPECIES: King scallop (*Pecten maximus*).
PROJECT FUNDING: MAFF in-house.
OBJECTIVE: Genetic variation in geographic stocks of scallop.
DESIGN: Examine variation in mtDNA.
METHODOLOGY: PCR of mtDNA fragments. Restriction enzyme analysis.
STATUS: Complete 1996.

Study 9
LABORATORY/RESEARCHER: Dr D O F Skibinski, School of Biological Sciences, University of Wales Swansea, Singleton Park, Swansea, SA2 8PP.

SPECIES: Mussels (*Mytilus*).
PROJECT FUNDING: NERC.
OBJECTIVE: To analyse growth and gene flow in mussel populations.
DESIGN: Allozyme, nuclear DNA and mitochondrial DNA analysis of diverse populations and species.
METHODOLOGY: As above.
STATUS: On-going.

Study 10
LABORATORY/RESEARCHER: Dr D O F Skibinski, School of Biological Sciences, University of Wales Swansea, Singleton Park, Swansea, SA2 8PP.
SPECIES: Aquatic animals.
PROJECT FUNDING: NERC.
OBJECTIVE: To analyse causes of genetic diversity in aquatic animals.
DESIGN: Use of allozyme database.
METHODOLOGY: Statistical and simulation analyses of database.
STATUS: On-going.

Study 11
LABORATORY/RESEARCHER: Dr D O F Skibinski, School of Biological Sciences, University of Wales Swansea, Singleton Park, Swansea, SA2 8PP.
SPECIES: Tilapia.
PROJECT FUNDING: ODA.
OBJECTIVE: To produce improved strains for aquaculture in Africa and the Far East.
DESIGN: Selective breeding and chromosome manipulation.
METHODOLOGY: DNA and transgenic technology.
STATUS: On-going.

SPAIN

Study 1
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Science, University of Vigo. A. Sanjuan López.
SPECIES: *Cephalopod.*
PROJECT FUNDING: AMB94-0371. CICYT.
PROJECT TITLE: Genetic variation in *cephalopod* species of commercial importance by mean of mtDNA sequence and allozyme polymorphism.

Study 2
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Biology, University of Granada. M. Ruiz Rejón.
SPECIES: *Sparidae.*
PROJECT FUNDING: PB92-0964. DGICYT.
PROJECT TITLE: Study of phylogenetic relationships between *Sparidae* species using ribosomal and satellite DNA analysis.

Study 3
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Sciences, University of Málaga. M. C. Alvarez Herrero.

PROJECT FUNDING: BIO93-1461-CE. CICYT.
PROJECT TITLE: Identification of genes involved in early development of fish.

Study 4
LABORATORY/RESEARCHER: Instituto de Acuicultura de Torre de Sal. IARS, CSIC. S. Zanuy Doste.
PROJECT FUNDING: AGF94-1321-CE. CICYT.
PROJECT TITLE: Development of genetic DNA markers for sex determination in farmed fish.

Study 5
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Medicine, University of Oviedo. E. García Vázquez.
SPECIES: Atlantic salmon.
PROJECT FUNDING: AIR1-CT-92-0719. UE.
PROJECT TITLE: An assessment of the genetic consequences of deliberate or inadvertent introduction of non-native Atlantic salmon into natural populations.

Study 6
LABORATORY/RESEARCHER: Department of Genetics. Faculty of Medicine. University of Oviedo. E. García Vázquez.
SPECIES: Atlantic salmon and brown trout.
PROJECT FUNDING: DGICYT.
PROJECT TITLE: Contribution of precocious mature Atlantic salmon male to hybridization with brown trout.

Study 7
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Medicine, University of Oviedo. J. A. Sánchez Prado.
SPECIES: Atlantic salmon and brown trout.
PROJECT FUNDING: AQ-2.493. UE.
PROJECT TITLE: Selective breeding and genetic management through genome marking and inbred clones.

Study 8
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Medicine, University of Oviedo. J. A. Sánchez Prado.
SPECIES: Atlantic salmon.
PROJECT FUNDING: PB-92-0992. DGICYT.
PROJECT TITLE: Development of molecular genetic markers to identify natural populations of Atlantic salmon.

Study 9
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Medicine, University of Oviedo. J. A. Sánchez Prado.
SPECIES: Turbot.
PROJECT FUNDING: PB-94-1348. DGICYT.
PROJECT TITLE: Use of chromosome manipulation and molecular technique s in genetic improvement of turbot.

Study 10
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Medicine, University of Oviedo. J. A. Sánchez Prado.
SPECIES: Brown trout and Atlantic salmon.
PROJECT FUNDING: Institutional and regional funds of Navarra, Guipúzcoa and León Governments.
PROJECT TITLE: Genetics studies of brown trout and/or Atlantic salmon restocking programs in rivers of Navarra, Guipúzcoa and León.

Study 11
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Medicine, University of Oviedo. J. A. Sánchez Prado.
SPECIES: Brown trout, rainbow trout, Atlantic salmon, Pacific salmon.
PROJECT FUNDING: ICI (Spain), FONDEF PI-10 (Chile).
PROJECT TITLE: Genetic analysis of Chilean salmonid species.

Study 12
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Veterinaria, University of Santiago de Compostela, Campus de Lugo. L. Sánchez Piñón.
SPECIES: Brown trout.
PROJECT FUNDING: PB-93-0648. DGICYT.
PROJECT TITLE: Chromosomal distribution of DNA tandem repeats in salmonids.

Study 13
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Veterinaria, University of Santiago de Compostela, Campus de Lugo. L. Sánchez Piñón.
SPECIES: Eel.
PROJECT FUNDING: XUGA-26109B95. Xunta de Galicia.
PROJECT TITLE: Molecular analysis and chromosomal location of satellite sequences in eel species.

Study 14
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Veterinaria, University of Santiago de Compostela, Campus de Lugo. P. Martínez Portela.
SPECIES: Brown trout.
PROJECT FUNDING: XUGA 26201A94. Xunta de Galicia.
PROJECT TITLE: Polymorphism of ribosomal genes of brown trout.

Study 15
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Veterinaria, University of Santiago de Compostela, Campus de Lugo. P. Martínez Portela.
SPECIES: Turbot.
PROJECT FUNDING: MAR95-1855. CICYT.
PROJECT TITLE: Use of chromosomal techniques and genetic diversity analysis in the improvement of turbot.

Study 16
LABORATORY/RESEARCHER: Department of Genetics, Faculty of Veterinaria, University of Santiago de Compostela, Campus de Lugo. L. Sánchez Piñón and P. Martínez Portela.
SPECIES: Brown trout.

PROJECT FUNDING: SC95/005. INIA.
PROJECT TITLE: Ecological and genetic variation in brown trout.

SWEDEN

Study 1
LABORATORY/RESEARCHER: H. Jansson, Salmon Research Institute.
SPECIES: Atlantic salmon.
PROJECT FUNDING: The Swedish National Board of Fisheries.
OBJECTIVE: To study genetic variation among Atlantic salmon populations at the Swedish west coast.
DESIGN: Samples of salmon from twelve rivers will be analysed for spatial and temporal genetic variation.
METHODOLOGY: Allozymes.
STATUS: Three year project started in 1994.

Study 2
LABORATORY/RESEARCHER: H. Jansson, Salmon Research Institute.
SPECIES: Atlantic salmon and brown trout.
PROJECT FUNDING: The Swedish National Board of Fisheries and power companies.
OBJECTIVE: Genetic monitoring of hatchery stocks to detect possible genetic changes.
DESIGN: The hatchery stocks used for the Swedish compensatory program are sampled and analysed for genetic variation at regular intervals.
METHODOLOGY: Allozymes.
STATUS: Long term study.

Study 3
LABORATORY/RESEARCHER: J. Dannewitz, Department of Genetics, Uppsala University and H. Jansson, Salmon Research Institute.
SPECIES: Atlantic salmon and brown trout.
PROJECT FUNDING: Internal funds.
OBJECTIVE: To study the extent of hybridization between Atlantic salmon and brown trout in Sweden.
DESIGN: Spatial and temporal variation in hybrid frequencies are examined. The maternal species of the hybrids is determined.
METHODOLOGY: Allozymes and mitochondrial DNA.
STATUS: Long term study.

Study 4
LABORATORY/RESEARCHER: Dept. of Aquaculture, Swedish University of Agricultural Sciences, Umeå. J. Nilsson and M. Schmitz. Cooperation with R. Gross, Estonian Institute of Veterinary Sciences and Animal Breeding, Tartu, Estonia.
SPECIES: Brown trout (anadromous and non-anadromous)
PROJECT FUNDING: Institutional and regional funds.
OBJECTIVE: To find new DNA markers in trout and to use these markers in studies of population genetic structure and in studies of population mixing.
DESIGN: A number of European sea trout and brown trout populations are screened for variation at DNA level. Microgeographic population genetic structure is studied in River Ammerån, N. Sweden.

Effects of introducing migratory trout in a stationary trout population is studied in Låktabacken Creek, N. Sweden.
METHODOLOGY: Variation in single copy genes, microsatellites.
STATUS: Project started in 1994, will go on to 1997.

Study 5
LABORATORY/RESEARCHER: Dept. of Animal Ecology, University of Lund, T. von Schantz, and The Wallenberg Laboratory, University of Lund, B. Widergren.
SPECIES: Atlantic salmon
PROJECT FUNDING: The Swedish Council for Forestry and Agricultural Research, and The Swedish Environmental Protection Agency.
OBJECTIVE: To study the genetic variation in MCH and Cytochrome P450s in different salmon populations to see whether variation at these loci affects disease resistance and the ability to process different persistent organochlorine pollutants.
DESIGN: DNA from three different populations is analysed for typing of genotypes and haplotypes.
METHODOLOGY: RFLP analyses, DNA sequencing, and DGGE analyses. **STATUS:** The project started in summer 1993. New funding was applied for in January 1995.

Studies reported in non-standard format

Fisheries and Oceans Canada
4160 Marine Drive, West Vancouver, B.C., Canada
(Reported by R. Devlin)

1) Production of transgenic salmon with enhanced growth and altered reproductive capability using "all-salmon" gene constructs.

2) Characterization of Y-chromosomal DNA probes from salmon for use in monosex all-female culture

3) Development of DNA-based diagnostics for several Microsporean and Myxosporean parasites to assist with management of infection in sea-farm facilities.

4) Examination of the potential for hybridization between Atlantic and Pacific salmon with regard to the possible reproductive interaction between escaped farmed Atlantic salmon and wild Pacific salmon stocks.

5) Development of a RAPD linkage map for Chinook salmon.

6) Development of a sensitive PCR-based assay for CYPIA1 gene expression to evaluate the biological effects of xenobiotic exposure.

APPENDIX 2

TERMS OF REFERENCE 1995 (C. Res. 1995, 2:28).

The **Working Group on the Application of Genetics in Fisheries and Mariculture** (Chairman: Prof. J. Mork, Norway) will meet in Faro, Portugal, from 19-23 February 1996 to:

a) continue the review of knowledge of basic population genetic topics in fisheries and mariculture, including the questions of selective fisheries and GMOs (Genetically Modified Organisms) with emphasis on a combination of qualitative and quantitative genetics;

b) review the contents of the terms «Genetic Resources» and «Management Units» with a view to establishing adequate working definitions, suitable criteria, and methods for identification and characterisation of such entities;

c) review the question of Genetic Brood Stock Management with a view to create protocols and recommendations for genetically adequate regimes;

d) prepare updated protocols of fishery and mariculture genetic research in the member countries, and identify scope for enhanced international cooperation;

e) consider potential contributions to the 1997 ICES/NASCO Symposium on the «Interactions between Salmon Culture and Wild Stocks of Atlantic Salmon: The Scientific and Management Issues».

APPENDIX 3

ATTENDANTS AT THE WGAGFM MEETING FEB. 19-23, 1996 IN FARO, PORTUGAL.

Name	Address	Telephone	FAX	E-mail
Jarle Mork (Chairman)	Norwegian University of Science and Technology, Biological Station, Bynesveien 46, N-7018 Trondheim, NORWAY	47-73-591589	47-73-591597	jarle.mork@ vm.unit.no
Leonor Cancela (in part repr. by M. Castro)	Universidade do Algarve, UCTRA, Campus de Gambelas 8000 Faro, PORTUGAL	351-89-800971	351-89-818353	lcancela@mozart. si.ualg.pt
Geir Dahle	Institute of Marine Research P.O. Box 1870 Nordnes N-5024 Bergen, NORWAY	47-55-238305	47-55-238333	geird@ imr.no
Anna Kristin Danielsdóttir	Marine Research Institute, c/o Biotechnology House, Keldnaholt, IS-112 Reykjavik, ICELAND	354-5877000	354-5877409	andan@ iti.is
Willie Davidson	Memorial University of Newfoundland, St. Johns, Nfld A1B 3X5, CANADA	1-709-7374468	1-709-7372422	willied@ morgan.ucs.mun.ca
Krzysztof Goryczko	Inland Fisheries Institute, River Fisheries Laboratory, 5 Bytowska Street 80-328 Gdansk-Oliva, POLAND	48-58-818426	48-58-818427	
Michael Møller Hansen	Inland Fisheries Laboratory Vejlsøvej 39 8600 Silkeborg, DENMARK	45-89-213145	45-89-213150	mmh@ dfu.min.dk
Jonas Jonasson	Institute of Freshwater Fisheries Vagnhøfdi 7, IS-112 Reykjavik, ICELAND	354-5676400	354-5676420	jonasson@ rhi.hi.is
Marja-Liisa Koljonen	Finnish Game and Fisheries Research Institute, Fisheries Division. P.O. Box 202, 00151 Helsinki, FINLAND	358-0-22881225	358-0-631513	mlkoljon@ helsinki.rktl.fi
Jose Antonio Sanchez	Universidad de Oviedo, Dpto de Biologia Funcional, Area de Genetica. Julian Claveria s/n 33071 Oviedo, SPAIN	34-8-5103889	34-8-5103534	jafsp@ dwarf1.quimica.uni ovi.es
Anthony B. Thompson	Fisheries Laboratory, Lowestoft NR33 OHT, Suffolk, UK	44-1502-524229	44-1502-524511	a.b.thompson@ dfr.maff.gov.uk

APPENDIX 4

WGAGFM MEMBER LIST

(27. APRIL 1996)

Ms G. Andorsdottir
Fiskirannsoknarstovan
P.O. Box 3051, Noatun
FR-110 Torshavn
Faroe Islands
Denmark

Dr. M.F. Borges
IPIMAR
Avenida de Brasil
1400 Lisbon
Portugal

Dr. L. Cancela
Universidado do Algarve, UCTRA
Campus de Gambelas
8000 Faro
Portugal

Dr. M. Castro
Universidado do Algarve, UCTRA
Campus de Gambelas
8000 Faro
Portugal

Mr A.R. Child
MAFF Fisheries Lab.
Benarth Road
Conway Gwynedd LL32 8UB
United Kingdom

Dr T. Cross
Zoology Department
University College Cork
Cork
Ireland

Mr G. Dahle
Institute of Marine Research
P.O. Box 1870 Nordnes
5024 Bergen
Norway

Dr. A.K. Danielsdottir
Marine Research Institute
P.O. Box 1390
Skulagata 4
121 Reykjavik
Iceland

Dr G. Friars
Atlantic Salmon Federation
Box 429
St Andrews, EOG 2XO
Canada

M A. Gerard
IFREMER, B.P. 133
17390 La Tremblade
France

Mr B. Gjerde
Akvaforsk
P.O. Box 5010
1432 Ås
Norway

Mr K. Goryczko
Inland Fisheries Institute
River Fisheries Laboratory
5, Bytowska Street
80-328 Gdansk-Oliva
Poland

M R. Guyomard
INRA
Lab. de Genetique des Poissons
78350 Jouy-en-Josas
France

Mr M.M. Hansen
Institut for Ferskvandsfiskeri
og Fiskepleie
Lysbrogade 52
8600 Silkeborg
Denmark

Mr H. Jansson
Salmon Research Institute
810 70 Elvkarleby
Sweden

Mr J. Jonasson
Institute of Freshwater
Fisheries
Vagnhøfdi 7
112 Reykjavik
Iceland

Dr. E. Kenchington
Dept. of Fisheries & Oceans
P.O. Box 550
Halifax, N.S. B3J 2S7
Canada

Dr. H. Kincaid
National Fisheries
R&D Laboratory
R.D.4, P.O. Box 63
Wellsboro, PA 16901
USA

Ms M.L. Koljonen
Finnish Game and Fisheries
Research Institute
Fisheries Division
P.O. Box 202
00151 Helsinki
Finland

Dr. A. Moore
Fisheries Laboratory
Lowestoft NR33 OHT
Suffolk
United Kingdom

Prof. J. Mork
University of Trondheim
Biological Station
Bynesveien 46
7018 Trondheim
Norway

Dr. T. Paaver
Estonian Fisheries Institute
Str. Lai 32
EE0001 Tallinn
Estonia

Mr. V. Pepper
Dept. of Fisheries & Oceans
P.O. Box 5667
St. John's, Nfld A1C 5X1
Canada

Dr. U. Piatowski
Institut fur Meereskunde
an der Universitet Kiel
Dusternbrooker Weg 20
24105 Kiel
Germany

Prof. H. Rosenthal
Institut fur Meereskunde
an der Universitat Kiel
Dosternbrooker Weg 20
24105 Kiel
Germany

Dr J.A. Sanchez
Dpto de Biologia Funcional
Area de Gen,tica
Julian Claveria s/n
33071 Oviedo
Spain

Ms L. Sanchez
Area de Genetica
Dpto de Biologia Animal
Universidad de Santiago
27002 Lugo
Spain

Ms A.M.T. Santos
IPIMAR
Avenida de Brasilia
1400 Lisbon
Portugal

Dr J.M. Sevigny
Dept of Fisheries & Oceans
Institut Maurice-Lamontagne
850, route de la Mer, C.P. 1000
Mont-Joli, Quebec G5H 3Z4
Canada

Dr. T.K. Stokes
Fisheries Laboratory
Lowestoft NR33 OHT
Suffolk
United Kingdom

Dr. A.B. Thompson
Fisheries Laboratory
Lowestoft NR33 OHT
Suffolk
United Kingdom

Mr V. Thorsteinsson
Marine Research Institute
P.O. Box 1390
Skulagata 4
121 Reykjavik
Iceland

Mr. J. Trautner
Institute fur Hydrobiologie und
Fischereiwissenschaft
Olbersweg 24
22767 Hamburg
Germany

Dr E. Verspoor
Marine Laboratory
P.O. Box 101
Victoria Road
Aberdeen AB9 8DB
United Kingdom

Dr R. Waples
Northwest Fisheries Science Center
NMFS/NOAA
2725 Montlake Blvd East
Seattle, WA 98112-2097
USA

Dr. B. Ward
CSIRO Division of Fisheries
P.O. Box 120
Cleveland QLD 4163
Australia

Dr. C. Woodley
Southeast Fisheries Center
NMFS/NOAA
P.O. Box 12607
Charleston, SC 29422-2607
USA

Mr A.F. Youngson
Marine Laboratory
P.O. Box 101, Victoria Road
Aberdeen AB9 8DB
United Kingdom.