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International Council for
the Exploration of the Sea/
ICES

C.M. 1989/F:17
Mariculture
Committee

R e p o r t
of the Working Group on Genetics, 1989
Dublin/Ireland, May 23-26, 1989

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* General Secretary
ICES, Palaegade 2-4,
DK-1261 Copenhagen K
Denmark

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(1) Introductory Remarks:

The joint NASCO-/ICES Working Groups meeting^{*} was recommended by the 1988th Statutory Meeting of ICES (see C.Res. 1988/3:1, see also C.Res. 1988/2:48a) and scheduled for May 23, 1989 at Dublin, Ireland. Progress and results of the joint meeting were already recorded in the NASCO-paper CNL (89) 19 which is attached to this report as appendix 4 (see pages 44ff). The recommendations were formulated in agreement with both participating working groups in fulfilling C.Res. 1988/3:1. Special attention should be paid to the summary and those recommendations which touch a particular aspect of common interest to both ICES-working groups. The latter is recorded in the document C.M.1989/F:15, edited by Carl. J. SINDERMANN, chairman of the Transfer-WG, and entitled "Assessment of effects of escapees on wild stocks (proposed ICES activities)". The contents were agreed by the signed rapporteur of this report. The text of this special recommendation is enclosed as appendix 3 (see p. 41). This procedure meets especially with C.Res. 1988/2:48a.

The following meeting of the WG on Genetics (Dublin, May 24-26, 1989) was planned on C.Res.1988/2:48b-d. The draft agenda (see appendix 1, p. 37) was mailed to the members of the WG on April 12, 1989, according to the updated list of members which was forwarded by Mrs. MOODY, ICES General Secretariat, on the base of January 25, 1989 (see appendix 2, p. 39). Unfortunately, of those 26 named just 6 showed up; three more sent brief statements on behalf of their countries (two were delayed and reached the rapporteur after the data of the Dublin meeting) and one member apologized for not coming. The remaining ones did not even give notice (see remarks to member list, appendix 2). Therefore, members concerned will be asked for their reasons of nonappearance. In case of no further interest in cooperating in the WG on Genetics the concerned ones will be requested to propose new delegates for their replacement who then may be elected or confirmed by ICES authorities.

* Working Group on Introductions and Transfers of Marine Organisms, Working Group on Genetics. In the following used abbreviations: Transfer-WG and WG on Genetics.

The agenda of the WG was treated within the two days of May 24 and 25 (instead of 2 1/2 days, see copy of circulated draft), so that the remaining time could be used by some members of the WG to participate in the morning meeting of the Transfer WG on May 26 (agreement between the chairmen). The reasons for this have to be seen in some 'overlapping' points of concern to both WGs, e. g. the ecological and genetic impact of salmon escapees on natural environments and wild populations, respectively (see remarks further above and appendix 3).

The meeting of the WG on Genetics ended at noon on May 26, 1989.

(2) Reports on genetics from the member countries (including papers not presented personally).

- Personal reports were given by the representatives of the following countries (in alphabetical order)

Canada (compiled by Richard L. Saunders, Dept. of Fisheries and Oceans, Aquaculture and Invertebrate Fisheries Division, Biological Station St. Andrews, Can.) annex 1

Federal Republic of Germany (reported by Wolfgang Villwock, Zoological Institute and Zoological Museum, University of Hamburg) annex 2

Norway (compiled by Knut E. Jørdstad & Gunnar Naevdal, Institute of Marine Research, Nordnes & Dept. of Fisheries Biology, University of Bergen, Nordnes) annex 3

Sweden (contribution by Håkan Jansson, Salmon Research Institute, Alvkärleby) annex 4

United Kingdom/England and Wales (report given by Colin Purdom, MAFF Fisheries Laboratory, Lowestoft, Suffolk) annex 5

U.K./Scotland (presentated by Alan Youngson, Dept. of Agriculture and Fisheries for Scotland, Marine Laboratory, Aberdeen) annex 6

- written contributions

Finland (compiled by Jarmo Koskiniemi, on behalf of WG member Marja Liisa Koljonen, Finnish Game and Fisheries Research Institute, Fisheries Division, Helsinki) annex 7

Poland (submitted by Krzysztof Goryczko, Inland Fisheries Institute, Salmonid Research Laboratory Rutki, Zukowo) annex 8

Portugal (submitted by Ana Maria Teia dos Santos, Instituto Nacional de Investigacao das Pescas, Centro de Investigacao Pesqueira de Aveiro, Lisbon) annex 9

- no comments from

Denmark

France

Iceland

Ireland

U.S.A.

2.1 Summary of reports listed above (see C.Res.1988/2:48b)

The 9 delivered contributions of member countries indicate the following different trends of genetic investigations:

2.1.1 Studies on population structures using morphological characters and classical genetical methods (by statistical means, crossbreeding and selection).

This make up of genetic investigations is still the most widely-held one, successfully applied wherever natural populations are in discussion as a whole or, Mendelian inheritance of certain characters was/is under investigation by crossbreeding and statistical evaluation. Results of this basic research are included in most of the listed contributions, mainly in the Canadian one* .

2.1.2 These still ongoing classical studies on morphological characters and measurements are increasingly supplemented by biochemical (e.g. enzyme-) markers, detected by electrophoretic techniques.

* see: TIEWS, K. (ed.), 1987: Selection, Hybridization and Genetic Engineering. Proc. World Symp. EIFAC/ICES, Bordeaux, France, June 27.-30., 1986, Vol. I & II.

'Genetic tagging' by controlling the inheritance mode of rare alleles may be a coming method (see diff. cod-populations in different parts of the Norwegian coast, annex 3). 'Blood group-discrimination', singularily started on cod in Norway, became a main field of genetic research in the Federal Republic of Germany (see annex 2) and seems to be an adequate supplementary path of research work which should be continued.

- 2.1.3 A third trend may be described as 'advanced genetechology'.
At least two subjects have to be distinguished,
- DNA-fingerprinting, and
- production of transgeneric ('transgenic') specimens.

While DNA-fingerprinting may offer (in future) a safe method to discriminate even between single individuals of the same species (or population), the production of transgeneric specimens (e.g. introduction of growth hormone DNA-sequences of a specific donor into an acceptor under investigation, both belonging to different genera of more or less relationship) aims to transfer the genetic code of wanted characters into a completely different species, without crossbreeding and selection - if the latter were applicable at all. Up to the present the success of this 'genetic manipulation' is not yet significant because no known and/or reliable research work has been done either on the expressivity of the 'transferred' characters or on their heridity. Investigations on these two subjects were started in some countries (Norway, Sweden, U.K., also Canada inserting genes in winter flounder to induce protection of antigene compounds in Atlantic salmon, see annex 1, 3, 4 and 5). It seems to be worth mentioned that nothing is recorded on the impact of transgenerically transformed specimens on their own native population and on natural environments!

Other, related technologies are less well developed than transgeneric manipulation (e.g. recombinant technology) but should be as

attentively followed as other kinds of genetic manipulation more especially, not at least because of their unknown consequences on the gene-pool of their own species and on natural environments.

2.1.4 The last component of genetic investigations is based on keywords as 'production of all-female (gynogenetic) offspring, all-male progeny and hyper-diploids (tetraploids, polyploids, etc.)'.

Methods to produce offspring of the above described characteristics are commonly used, namely in Norway, Poland, and the U.K. (see annexes 3, 5/6 and 8). These techniques are not synonymous with 'genetic engineering' because they depend mainly on non-genetic techniques. All-male progenies are produced by crossbreeding, taking advantage from reciprocally combined sexrealizing chromosomes (heterochromosomes) in different populations of the same species or of two nearly related ones. This process was developed for special aquacultural projects concerning cichlid fishes of the genus Tilapia ^{*}. As far as known this procedure has not been introduced to mariculture.

The production of hyper-diploids (e.g. triploids) was applied to aquacultured organisms for release in natural environments where an undesirable reproduction would be an actual or potential risk (applied to fin-fish as well as to shell-fish, mainly U.K., see annex 5, see also WG on Genetics report 1983/F:2, Lowestoft/U.K.).

* Main subject of joint German-Israeli cooperation project to the "Production of all-male Tilapia progeny". German counterpart: W. VILLWOCK. Further information available on request.

- 2.2 Developmental aspects in genetics of aquatic organisms which seem to be of particular significance for aquaculture and fisheries science (see C.Res.1988/2:48c).

The resolution should have better said " ... particular significance for aquaculture or fisheries science", because some of the most sophisticated and most recent developments in genetics are just on 'particular significance' to fisheries science and far off being applicable to aquaculture practices (see trends to pos. 2.1.3). Due to general understanding, only those developments in genetics of aquatic organisms may already have or may become 'particular significance' in the requested sense, these are:

- easily applicable to aquacultural practice, i.e. without fully equipped laboratories (e.g. Third World Countries), and
- safe in the course of their application to natural populations and environments.

According to the results, of the discussion with respect to this topic, the members of the WG on Genetics stated that all efforts of investigations concerning population structures should be supported, because still better knowledge than the existing one is of basic importance for the development of further strategies to improve aquaculture success. It was agreed in context to this statement that more, and more concrete, data on genetic variability should be recorded and kept available for intra- and interspecific comparisons for a still better understanding of general mechanisms of population dynamics. Computer databases should be considered as a most helpful instrument.

Of particular significance are genetic studies on tools for the discrimination of species, populations or even single specimens. Enzyme patterns, gene-tags, genetic fingerprints (including the analysis of mitochondrial DNA [mtDNA]) and bloodgroup-detection

(immune response in so-called crosstests) seem to be the most promising techniques for getting together missing information on a scientific level (e.g. for 'fisheries science'). The results have to be 'translated' into understandable advice for fishfarmers and aquaculturists (e.g. by means of specially prepared software: see remarks above).

2.3 Application of gene technology in aquaculture (C.Res.1988/2:48d).

As a consequence of the foregoing discussion, gene technology will not provide any direct applications to aquaculture in the sense that a certain fishfarmer may become personally enabled to apply 'gene hightec' to his farmed animals. This is mainly because of the absence of laboratory facilities, lack of responsibility for their careful use and of pre-knowledge of genetics. But even if all of those conditions would be met, the use of gene hightechnology in aquaculture by everybody would increase dramatically the risk of genetic and ecological impacts to nature. Even on the scientific level, new developments should be calculated against advances before their results become applied to aquaculture. Specifically, for the moment being it is impossible to estimate to what degree introduced genetic information will be incorporated into a given genome and, as a consequence of this, what the molecular interactions and results of this might be. This means that gene technology as used above (transfer of genetic information from one organism to another one) today is without any general applicability to commercial aquaculture; this does not exclude the possibility of its relevance to aquaculture in future. However, these and related technologies should remain under rigid scientific control and strong regulations.

(3) Recommendations

- 3.1 Since the subject of the joint NASCO-/ICES Working Groups meeting on May 23 seemed of general and pressing importance, the one-day

meeting was reviewed on the following day by the ICES Working Groups. Special emphasis was added to the actual or potential effects caused by cultured Salmon escapees on wild stocks and environments. The specific text of the concerned recommendation is recorded in the 'Report on joint meeting of the ICES Working Group on Introductions and Transfers of Marine Organisms, the ICES Working Group on Genetics, and NASCO representatives, Dublin, Ireland, May 23, 1989', ICES Code C.M. 1989/F:15, pp. 6-8 (Carl J. SINDERMANN, Chairman of the ICES WG on Introductions and Transfers of Marine Organisms, ed.). The text is attached to this report (see appendix 3). The genetic consequence of such escapees from mariculture should be the subject of major concern in the deliberations of the WG on Genetics.

- 3.2 Encourage and support methods to improve the knowledge of population dynamics to provide a better understanding of fluctuations and interactions between gene-pool and environment. Keep genetic variability high for future adaptability to changing environmental conditions (conservation of genetic resources).
- 3.3 Emphasize methods for developing genetic tools discriminating species, populations and specimens as well for advances in aquacultural practice as for conservation of genetic resources.
- 3.4 Genetic changes by artificial introduction of DNA-sequences (e.g. transgeneric manipulations and related techniques) should under strict regulations and should not be allowed to become applied to commercial aquaculture without rigid scientific supervision.
- 3.5 Do not release genetically changed organisms uncontrolled into natural habitats. Evaluate the risk before releasing and keep them under scientific control.
- 3.6 Carefully evaluate ecological demands of cultured or introduced species. Detailed studies should be made in advance on habitats to

which stocked forms are intended to be introduced in order to avoid competition or even extinction with/of endemic organisms. Introduced species should be kept in quarantine for an adequate time, depending on the species in question (see also: Recommendation no. 5 of Transfer WG, Report coded C.M. 1989/F:16, SINDERMANN, ed.).

- 3.7 Document all relevant factors and informations of natural species as well as of cultured and/or manipulated strains to an international database, which has to be completed currently according to the scientific/genetic research progress and experiences from nature and aquaculture. This database should be held by the ICES General Secretariat.
- 3.8 In consequence to recommendations 3.1 - 3.6 codes of practice should be developed or reviewed with concern to genetically modified organisms, e.g. by extension of the ICES Code of Practice (see also: Recommendation no. 6e of Transfer WG, Report coded C.M. 1989/F:16, SINDERMANN, ed.). Retain severe and effective regulations against introduction of commercially valuable 'exotic' organisms from one European country to another after opening the EEC market borders in 1992. Take account of the fact, that the British Isles are today strongly protected by national rules, which should not be replaced by coming European ones, which might be less effective.
- 3.9 Next meeting of the ICES Working Group on Genetics is suggested to be held in summer 1990 at Tvärminne-Station, Finland (invitation by Koskiniemi on behalf of the WG-member Marja-Liisa Koljonen was sent to the rapporteur). Main subject should be a summing-up of genemarkers and their applicability to aquaculture with particular reference to evaluating the genetic consequences of escaped salmon from aquaculture on wild populations (see report pos. 2.1.2 and 2.1.3).

The proposed locality opens the reliable possibility that some scientists in the field of fish genetics from eastern European countries, especially those of the USSR, might participate and thereby add to our knowledge on what is going on in the field of interest in these countries.

The following meeting of the ICES WG on Genetics should possibly be arranged as a joint one, in connection with an "International Symposium on Biochemical Genetics and Taxonomy of Fish", announced by the Fisheries Society of the British Isles in collaboration with the School of Biology and Biochemistry, Queen's University of Belfast, Northern Ireland, Belfast July 22-26, 1991. The local head of the organization committee will be Andrew FERGUSON, one of the most experienced fish genetecist in the field of genetic fingerprints (see appendix 5).

The following pages include the annexes 1-9 (contribution of the member countries) and the appendices 1-5 as mentioned in the above report.

Hamburg, August 24., 1989



(Prof. Dr. W. Villwock)
Chairman
ICES-Working Group
of Genetics

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CANADIAN GENETICS STUDIES RELEVANT TO AQUACULTURE

Compiled by

Richard L. Saunders
Department of Fisheries and Oceans
Aquaculture and Invertebrate Fisheries Division
Biological Station
St. Andrews, N.B. E0G 2X0
Canada

Abstract

This document incorporates material solicited from individuals or groups in Canada conducting studies in genetics with particular reference to aquaculture. It updates information solicited for the last such report to the ICES Working Group on Genetics in June 1988. It is planned that this report be updated occasionally, incorporating any appropriate activities not mentioned this year and new studies planned or started between such updates.

Resume

Le document regroupe les renseignements demandés aux particuliers ou groupes canadiens menant des études sur la génétique dans le domaine de l'aquaculture. Le document met à jour les renseignements recueillis pour le rapport précédent ou groupe de travail sur la génétique du CIEM préparé en juin 1988. On prévoit mettre à jour le rapport de temps à autre en faisant état de toute activité connexe non mentionnée cette année ainsi que de toute nouvelle étude prévue ou entreprise entre la publication des mises à jour.

Aquaculture Section, Freshwater Institute, Department of Fisheries and Oceans, Winnipeg, Manitoba

M.H. Pabst, M. Giles, and B.G.E. de March

Growth of Arctic Charr

Genetic Studies relevant to aquaculture are conducted by the Aquaculture Section; studies are conducted primarily at the Rockwood Experimental Fish Hatchery. Since 1981 an emphasis has been placed on studies related to the culture of Arctic Charr. The growth performances of various strains of Arctic Charr is being tested under different rearing conditions. Six strains of Arctic Charr are maintained at the Rockwood facility. With the development of hatchery reared broodstock, an Arctic Charr selection program has been initiated. Studies to determine the genetics of early male sexual maturation, dwarf individuals and cold water fast growing individuals, have begun. Estimates of genotype-environment interactions have been made for rainbow trout and are being made for Arctic Charr.

Hemoglobin development in Arctic Charr

The ontogenetic development of the multiple hemoglobins of anadromous Arctic Charr from Nayuk Lake, N.W.T. has been established. Differences in the electrophoretic pattern of the hemoglobins present in the charr stocks from three widely separated areas have been identified. Preliminary analyses indicate that some of the differences are reflected in significant variations in certain biochemical characteristics of the hemoglobins (oxygen affinity and subunit interaction) and physiological capabilities of the intact fish (lethal oxygen levels and metabolic performance). A change in the frequency of one hemoglobin phenotype during intensive culture of Nayuk Lake Charr (anadromous strain) has also been identified although the significance of this change is not clear. Results of this program will be used in the development of Arctic Charr brood stock programs.

Genetic basis of growth and development in Labrador Arctic Charr

Factorial mating designs of full-sib families in which the parents were the first hatchery generation of Arctic Charr from the Fraser River, Labrador, were used to examine the genetic basis of growth parameters potentially important to aquaculture. Characters measured were: egg size, hatching success, weights at various ages, growth rates and condition at various weights, and some distributional properties of full-sib families reared together. Preliminary analysis shows genetic basis for most of the measured parameters, and that results can be repeated in different years. There is a complex structure of genetically correlated parameters in which the variation of larval sizes produced by each female and/or the founder variance of sizes of sibs reared in one tank may be an important factor.

Both the smallest fish with no obvious physical defects and the largest fish were selected from families in the first two experiments, and these will be used for future experiments examining the relative effectiveness of family vs. individual selection, and the importance of heterozygosity and inbreeding in selection programs.

Genetic basis of growth and development in Arctic Charr hybrids

The genetic basis of the same growth characteristics as described above were determined from repeated factorial mating sets each one of which consisted of 1 female from Nayuk Lake (N.W.T.) stock and one from Sunndalsora (Norway) stock each mated with one male from each stock (= 4 families per mating set). Genetics bases can be demonstrated for any of the measured characters. Previous experiments had established that the Nayuk Charr grew considerably faster than the Norwegian Charr, and this result was also evident here. Offspring from Nau. females x Nor. males grew faster than their pure strain half-sibs and also exhibited relatively little size variation, while offspring from Nor. females x Nau. males grew slower than either pure strain, and often exhibited large size variations and sometimes bimodal distributions. The complications due to the founder variance, lowered variances typically associated with heterozygosity, and also relating to the number of fish reared together, were more evident in these crosses.

A second experiment, performed with rearranged fish from the first, is designed to determine accurately the genetic basis of variance- and density-dependent growth in the four types of crosses.

Atlantic Salmon Federation, Salmon Genetics Research Program, St. Andrews, N.B.

G.W. Friars and J.K Bailey

Selection

Correlated responses to selection for fork length in grilse was reported in the ICES AnaCat Report, 1987. Responses have now been observed in the progeny to 70 weeks in sea water, approximately the stage at which selection was performed in the parents. Where the control and select line parents were 59.00 and 65.70 cm respectively, the corresponding progeny from these two groups were 66.65 and 68.49 cm in fork length. This results in a realized heritability of .27 and augers well for the improvement of growth rate in Atlantic salmon through selection.

UNIVERSITÄT HAMBURG

ZOOLOGISCHES INSTITUT
UND
ZOOLOGISCHES MUSEUM

Prof. Dr. W. Villwock
Zoologisches Institut und Zoologisches Museum
Martin-Luther-King-Platz 3, 2000 Hamburg 13

To
Joint NASCO-/ICES-
Working-Groups meeting,
Working Group on Genetics,
Dublin, May 23.-26., 1989.

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Behördennetz: 9.38. (" ") } Durchwahl

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Aktenzeichen (bei Antwort bitte angeben)

Datum May 22, 1989

rec.: Genetics on Fish, short report.

Genetic research work on fish is restricted to mainly 3 working-groups,

- (1) Prof. Dr. H.-J. Langholz,
Institut für Tierzucht und Haustiergenetik,
Universität Göttingen, Albrecht-Thaer-Weg 1,
D-3400 Göttingen

Known investigations are done on rainbow-trouts (strain genetics, growth efficiency) and on aquarium fish (Brachydanio rerio) (DNA-Transfer: No progress has been recorded since Trondheim-meeting, 1988).

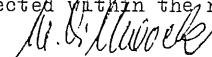
- (2) Dr. M. von Lukowicz, Director, Bayrische Landesanstalt für Fischerei, Weilheimer Str. 8a, D-8130 Starnberg (München).

Main subject are European carps (Cyprinus carpio). Investigation aims are improving growth rate, disease resistance and related questions, e.g. by feeding and crossbreeding experiments.

- (3) Prof. Dr. W. Villwock, Zoologisches Institut und Zoologisches Museum, Universität Hamburg, Martin-Luther-King-Pl. 3, D-2000 Hamburg 13.

Main subjects are European carps and different species of Tilapia (Cichlidae). Investigation aims are bloodgroup factors in teleostean fish for species and population discrimination. In carps the molecular structure of erythrocyte surfaces is in the center of interest, while in Tilapia the immune response has been investigated to get tools for distinguishing between different species (and populations). Results show that there are different blood-group factors existing and that the specifically arranged factors even allow statements on the relationship between tested species. As far as the results have been published, see attached publication list.

Further investigations' aim will be the development of a field test method for species discrimination for farmers and other aquaculturists on the base of crosstest techniques (compare father hood tests in human). Results are expected within the next two years.


(Prof. Dr. W. Villwock)

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- GROTH, V., L.RENWRANTZ, W.VILLWOCK, 1984b: Determination of different lectin-receptors on the surface of carp (Cyprinus carpio L.) erythrocytes. In: Research on aquaculture (H.Rosenthal and S.Sarig, eds.), European Mariculture Society, Bredene, Belgium, EMS Special Publication 8,168-76.
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ICES Working Group on
Genetics

Working Paper,
Dublin 22 - 24 May
1989

APPLICATION OF GENETIC METHODS IN
AQUACULTURE AND FISHERIES RESEARCH
IN NORWAY

An overview compiled

by

Knut E. Jørstad
Institute of Marine Research
P.O.Box 1870, 5024 Nordnes

and

Gunnar Nævdal
Department of Fisheries Biology
University of Bergen
P.O.Box 1839, Nordnes
N-5024 BERGEN

INTRODUCTION

Genetics methods have traditions back to around 1960 in Norwegian fisheries research when work on blood groups for population identification of cod was initiated by the Institute of Marine Research (Dag Møller). Population genetic studies on marine fish were extended by including electrophoresis of tissue enzymes and other proteins, and in later years also mitochondrial DNA studies have been applied.

Aquaculture (fish farming) started in the late 60-ties, and around 1970 work on quantitative genetics was initiated aiming on improvement of productive traits in farmed salmonids. This work has been continued since then, and also work on chromosome engineering has been started. In recent year, work on gene technology has been initiated with the prime target of being used for genetic improvement of farmed fish.

In the following overviews these topics are dealt with:

Identification of population units by using natural
gene markers

Genetic improvement of salmonids - classical quantitative genetics

Chromosome engineering

Gene technology

The present overview is an updated version of the overview worked out for the Working Group Meeting in 1988

STUDIES ON POPULATION STRUCTURES

At Biological Station, University of Trondheim (Jarle Mork), the following projects are carried out:

Population structure and evolution of various gadoid fish species studied by electrophoretic methods.

Studies on potential homing in marine fish (cod, plaice) by tagging/transplantation experiments.

Biochemical genetic identification of fish eggs.

A program for studies on species identification, species validity and intraspecies variation of redfishes (Genus Sebastes) is carried out jointly by the Institute of Marine Research and The Department of Fisheries Biology, University of Bergen.

The same institutions are cooperating on studies of genetic composition of natural and stocked cod populations, and their actual and potential interaction in several stocking areas in different part of the Norwegian coast. A central part of these investigations is the plans for use of genetically tagged offspring from a broodstock homozygotous for a rare PGI-allele.

In a cooperative project between the same institutions, a morphological genetic marker in trout (fine spottet) has been identified. This morph will be used for studies on genetic interactions between farmed and wild stocks of salmonids. The heredity of the fine spottet morph has been revealed by crossing experiments.

At the latter institute genetic studies on cod and herring stocks have been continued, including analyses of all new yearclasses as well as the spawning population of Arctic cod. The last mentioned work is mainly focused on yearclass variation and identification of subpopulations by using protein electrophoresis and restriction fragment analysis of mtDNA.

The Department of Biology at the University of Oslo, investigations on the population structure of Iceland scallops are carried out. Similar studies on different invertebrates (i.e. Arctic krill, Noble caryfish, blue mussels etc.) have been carried out for many years.

A large scale study on genetic structure of Atlantic salmon in Norway have been initiated at Norwegian Institute for Nature Research in Trondheim. Presently, about 6000 samples from 70 different river have been collected, and the aim is to present a base-line genetic data on natural populations.

QUANTITATIVE GENETICS

A large scale program for genetic improvement of salmonid have been

started by the fish farmers organizations (Fiskeoppdretternes Selslag and Norske Fiskeoppdretteres Forening, Trondheim). The breeding program is carried out at the breeding station at Kyrksæterøra about 100 km south of Trondheim. The improved fish material is transferred to the fish farming industry via multiplying stations in each county.

Institute of Aquaculture Research (AKVAFORSK), under the Agriculture Research Council, carries out quantitative genetic studies on salmonids at the research stations at Sunndalsøra and Averøya (both located in the county of Møre og Romsdal) and at the Agricultural University of Norway, (NLH) Ås. The following projects give an overview of the activity:

Selection for genetic improvement in cooperation with NFA, Kyrksæterøra, is carried out continuously on growth rate, age at maturity and survival. Genetic parameter of "new" productive traits are also estimated.

Additive as well as non-additive genetic variations are found to contribute to the variation of traits connected to fish quality (fat in flesh, intestine fat, flesh colour, belly thickness etc.) in rainbow trout. Such studies are started also for Atlantic salmon. Datatomography was found to be of considerable help in the registrations of body composition in fish.

Immunological factors which may be connected to genetically determined disease resistance are identified and tested for genetic variation and covariation with productive traits and actual resistance. Also the connection between "stress" and immuneresponse is studied. These studies are carried out in cooperation with Department of Animal Breeding, NLH and Department of Microbiology and Immunology, Veterinarian University of Norway.

A project for studying the ironbinding proteins (transferrins) and their effect on disease resistance has been started. In vitro-tests on fish pathogens will be carried out, and also cell lines and model fish will be used for studies on gene regulations.

At Division Aquaculture, Institute of Marine Research, Bergen, research on quantitative genetics on Atlantic salmon are continued. A study on the performance of sibgroups placed at different commercial fish farms along the Norwegian coast is ended. Similar studies are now carried out in different fish farms within an restricted area. These studies are closely connected to studies on environmental impact by fish farming and field studies on fish health. Genetic/environmental interactions were indicated in these studies.

In cooperation with Department of Biotechnology, University of Bergen, studies on genetic variation in immune response have been undertaken.

Studies on growth rate variation connected to genetic variation in trypsin-like isozymes in Atlantic salmon are carried out at the Aquaculture Station, Matredal (Institute of Marine Research).

CHROMOSOME ENGINEERING

Studies on the combination of triploidy and gynogenesis are carried out at Institute of Aquaculture Research, N-6600 Sunndalsøra, with the aim of producing sterile all-female rainbow trout and Atlantic salmon.

GENE TECHNOLOGY

Isolation of genes coding for growth hormones, prolactine, insuline or disease resistance have been undertaken by several laboratories with the double aim of basic studies of such mechanisms and of transferring "valuable" genes between and within species. Both Atlantic salmon and modell fish (zebrafish) are used for such investigations.

Another aspect of these investigations have been constructions of "genome libraries" and studies on homeobox-genes of salmon.

The laboratories engaged in gene technology studies on fish in Norway are listed below:

Laboratory for Biotechnology, University of Bergen
P.O. Box 3152, Arstad, N-5029 BERGEN

Marine Genetics
c/o Laboratory for Biotechnology (address above)

Zoological Laboratory, University of Bergen
Allegt. 41, N-5007 BERGEN

Department of Biochemistry, University of Bergen
Arstadveien 19, N-5009 BERGEN

Department of Microbiology and Plant Physiology
University of Bergen, Allegt. 70, N-5007 BERGEN

Department of Biotechnology, Norwegian Technical University
N-7034 TRONDHEIM

Department of Genetics and Biotechnical Disease Control
Norwegian Veterinarian University
P.O. Box 8146 Dep., N-0033 OSLO 1

Department of Physiology
(same address)

Institute for Aquaculture Research, Agricultural University
P.O. Box 32, N-1432 Ås-NLH

Norwegian Fisheries High School, University of Tromsø
P.O. Box 3083, Guleng, N-9000 TROMSØ

Department of Medical Biochemistry
P.O. Box 1112, Blindern, N-0317 OSLO 3

Norsk Hydro, Research Center, N-3901 PORSGRUNN

Laboratory for Microbial Gene Technology
Agricultural University, P.O.Box 37, N-1432 Ås-NLH

Reports on applied genetics in aquaculture and fisheries.

ICES Working Group on Genetics, Dublin 1989

Håkan Jansson, Salmon Research Institute, S-810 70 Älvkarleby, SWEDEN

This is a compilation of reports and manuscripts on applied genetics in Sweden from 1986. It includes the application of electrophoresis to management problems as well as guidelines for breeding methodology. The papers are mainly addressed to fish managers and therefore written in Swedish with an English abstract or summary.

Nyman L. 1986. Avelsmetodik för fiskevården. (A breeding methodology for fisheries management.) Information från Sötvattenslaboratoriet 2/86.

Nyman L. & Norman L. 1987. Genetiska aspekter på odling av lax och havsöring för utplantering: Riktlinjer för avelsmetodik och fiskevård. (Genetic aspects on culture of Atlantic salmon and sea trout for stocking: Guidelines for breeding methodology and management.) LFI Meddelande 1987:4.

Hammar J. & Filipsson O. 1988. Rödingen i Stora Rensjön: Ett genbanks- och naturreservatobjekt. (The Arctic charr in lake Stora Rensjön: A primary gene bank for conservation in a natural reserve.) Information från Sötvattenslaboratoriet 13/88.

Nyman L. & Norman L. 1988. Genetiska effekter av åldersspridning vid fiskutsättning. (Genetic effects of age distribution when stocking fish.) LFI Meddelande 1988:2.

Jansson H., Rüetschi E., Alfjorden A. & Öst T. (manuscript) Genetisk variation hos lax i Götaälvsområdet. (Genetic variation in Atlantic salmon stocks from the Göta älv drainage system in Sweden.)

Jansson H., Höggren M., Johlander A. & Johansson R. (manuscript) Genetisk undersökning av lax från Viskan och Ätran. (A genetic study of Atlantic salmon from the Swedish rivers Viskan and Ätran.)

Developments in genetics of aquatic organisms in Sweden.

ICES Working Group on Genetics, Dublin 1989

Håkan Jansson, Salmon Research Institute, S-810 70 Älvkarleby, SWEDEN

The developments and ongoing research in Sweden can be divided in two major parts: (1) Artificial breeding and selection of salmonid species, and (2) the application of molecular methods to study population structure and genetic effects of breeding.

The artificial breeding and selection program is a joint project between Dept. of Aquaculture, Swedish University of Agricultural Science, and Kålarne Research Station, Institute of Freshwater Research. The work is concentrated on two species, rainbow trout and Arctic charr, and includes strain crosses to study heterosis effects.

The application of isozyme electrophoresis to study population structure and genetic effects of breeding is in rapid progress. A number of species are currently under investigation: Atlantic salmon (Salmon Research Institute, and Institute of Freshwater Research), brown trout (Salmon Research Institute, and Institute of Freshwater Research), Arctic charr (Institute of Freshwater Research), European grayling (Dept. of Genetics, Uppsala University), vendace (Dept. of Genetics, Uppsala University, and Dept. of Limnology, Lund University), and crayfish (Dept. of Genetics, Uppsala University, and Dept. of Limnology, Uppsala University).

A new technique, "DNA fingerprint", will be applied on specific problems concerning small populations of salmonids. If the technique is successful in identifying closely related individuals it will be possible to reduce inbreeding when managing valuable populations of landlocked Atlantic salmon and brown trout. (Institute of Freshwater Research, and Dept. of Genetics, Uppsala University)

Applications of gene technology in aquaculture.

ICES Working Group on Genetics, Dublin 1989

Håkan Jansson, Salmon Research Institute, S-810 70 Älvkarleby, SWEDEN

If gene technology is defined as manipulation of the genome by introduction of novel genes there is no research in Sweden at the moment.

ICES GENETICS WORKING GROUP 1989: DUBLIN

Report from England and Wales

- 1) Work on sex-ratio control in salmonids is now largely completed as techniques have been widely adopted in the fish farming industry.
- 2) Induced triploidy in salmonids is also applied in industry although not so widely as is the sex ratio technology. Government research in this area is now very greatly reduced.
- 3) Production of homozygous gynogenetic diploid rainbow trout is being attempted again. Past experience has been that homozygous individuals fail to survive to one year of age. Current work suggests that survival may be better this year.
- 4) The most active genetics work is on salmon population genetics and comprises studies of protein polymorphisms within alkaline and oligotrophic environments. Work on mitochondrial DNA is conducted in association with Buckingham University, and so far several "genotypes" have been identified using 4-5-base cutters.
- 5) The production of transgenic trout is under study at Southampton University, using mammalian and salmonid growth hormone sequences. Incorporation has been achieved, but no work has been done yet on inheritance and expression.
- 6) A small programme at Conwy (MAFF) attempts to assess sex-control mechanisms in Dover sole using gynogenesis via halibut sperm egg activation.
- 7) A small project at Lowestoft (MAFF) seeks to assess the extent of inbreeding depression in an experimental fish (*Lebistes*) and the existence of Y-linked obligate heterozygosity.
- 8) Induced triploidy in Manila clam is being assessed at Conwy for production of clams in good condition and for use in environments where undesirable reproduction is a risk.

C E Purdom
24 May 1989

DEPARTMENT OF AGRICULTURE AND FISHERIES FOR SCOTLAND

Genetics Research Completed or in Hand

1. A study of the spatial distribution of allele frequency variation in wild Scottish salmon and its temporal stability, initially over three hatch-years.
2. A study of the genetic constitution of farmed strains of salmon in Scotland, comparing allele frequencies in strains with their wild source populations.
3. A study of the adaptive significance of variation at the Me-2 locus. Allele frequencies show clinal variation with latitude and temperature and within river variation with temperature. Juvenile growth and age at adult maturity are partially dependent on Me-2 genotype. Allele frequencies at the Me-2 locus in farmed strains differ in a directionally consistent manner from the frequency in their wild source populations.
4. Estimation of gene flow within and between Scottish rivers.
5. Assessment of the continent of origin of salmon in the commercial fishery conducted at West Greenland, using protein variation.
6. A study of the reproductive success of precociously mature parr in natural spawning, using protein variation and DNA finger printing.

7. A study of the effectiveness of the stocking programme carried out in Spanish rivers using ova imported from Northern Europe. Allele frequencies at the Me-2 locus in imported fish differ from those in the progeny of indigenous spawners.

8. A study of hybridisation rates between brown trout and salmon using protein variation. Establishing sexual condition and parentage in hybrid adults using protein and mtDNA techniques.

9. The development of methods for the routine analysis of mtDNA rflps in salmon. The identification of regional differences in the presence or representation of mtDNA polymorphisms.

Current genetic studies on fishes in Finland
Compiled by Jarmo Koskiniemi on behalf of Working
Group member Marja-Liisa Koljonen

I) Finnish Game and Fisheries Research Institute, Fisheries
Division, P.O. Box 202, SF-00151 Helsinki, Finland
(Marja-Liisa Koljonen, Jarmo Koskiniemi, Irma Kallio-Nyberg)

Population genetic studies:

Work continues on the survey of genetic population structure
on the basis of enzyme genetic variation for breeding and
management purposes. The main topics are:

- 1) Temporal monitoring of allele frequencies in Atlantic
salmon in the Bothnian Bay.
- 2) The survey of genetic variation of brown trout stocks.
Both natural and cultured stocks are included.
On the basis of genetical analyses, some proposals for
the conservation and managing of the stocks have been
made (Koljonen, 1989b).
- 3) Genetic differentiation between some Finnish
populations of the Baltic herring (Clupea harengus),
in co-operation with the University of Kuopio.
Both enzyme genetic polymorphism and mtDNA RFLP
are monitored.

Gynogenesis:

Studies on gynogenesis in rainbow trout were started in
1988, and the work continues.

II) University of Joensuu, Department of Biology, P.O. Box
111, SF-80101 Joensuu, Finland.
(Jukka Vuorinen)

Work on population genetics of coregonids (whitefish,
vendase) and Atlantic salmon continues. Recently,
results on the genetic divergence of anadromous and
non-anadromous Atlantic salmon in the River Namsen,

Norway, have been published (Vuorinen, 1989).

III) University of Kuopio, Department of Physiology,
P.O. Box 6, SF-70211 Kuopio, Finland
(M. Hakumäki, K. Partti-Pellinen)

Work continues on stock identification on the basis of mitochondrial DNA RFLP. The species included in these studies are Atlantic salmon, whitefish, vendace, grayling, char and Baltic herring.

List of publications of Finnish fish genetists from recent years:

Falkowski, S., Luczynski, M. and Vuorinen, J. 1987. Embryonic development in hybrids of whitefish (Coregonus lavaretus L.) and peled (C. peled Gmelin). International Symposium on Biology and Management of Coregonids 1987, Joensuu, Finland. Abstract 1p.

Heinonen, M. 1987. Suur-Saimaan siikojen taksonomia ja geneettinen muuntelu. (Taxonomy and genetic variation of whitefish in Lake Saimaa.) RKTL kalantutkimusosasto, Monistettuja julkaisuja No 59. Helsinki 1987. 88 p. (in Finnish).

Heinonen, M. 1988. Taxonomy and genetic variation of whitefish (Coregonus spp.) in Lake Saimaa. Finnish Fish. Res. 9:00-00 (in press).

Ikonen, E., Jutila, E., Koljonen, M-L., Pruuki, V. ja Romakkaniemi A. 1986. Tornionjoen vesistön meritaimenkantojen tila, geneettiset erot ja viljelytarpeet. (The state, genetic differences and needs for breeding of the sea trout stocks from the River Tornionjoki.) RKTL kalantutkimusosasto, Monistettuja julkaisuja No 57. Helsinki 1986. 103 pp.

Juntunen, K. 1987. Kromosomimääritys apuna siikojen taksonomisten ongelmien ratkaisemisessa. (Chromosome analyses used to solve problems in coregonid taxonomy.) RKTL kalantutkimusosasto, Monistettuja julkaisuja No 64. Helsinki 1987. 77 pp (in Finnish).

Koljonen, M-L. ja Sarjamo, H. 1987. Paatsjoen vesistön taimenkantojen geneettinen tutkimus. (Genetic study on the brown trout stocks in the Paatsjoki riversystem) Suomen Kalastuslehti 8/87 (94): 428-423. (in Finnish).

Koskiniemi, J. 1987. Harjuskantojen perinnöllisten erojen selvitys. (A survey of genetic differences between grayling stocks.) Suomen Kalastuslehti 8/87 (94): 424-427, (in Finnish)

Kuusela, J., Partti-Pellinen, K., Oja, E. and Hakumäki, M. Image analyses of DNA restriction fragments from paper prints and X-ray film using microcomputers (submitted for publication).

Manninen, J.K., Palva, T.K., Olkkonen, H., Räsänen, T. Hakumäki, M. 1985. Laboratory computer aided digitizing system based on high resolution optical reflective sensor. Proc of the 14th International Conference on Medical and Biological Engineering and 7th International Conference on Medical Physics, Espoo, Finland 7:23 (abstract).

Palva, T. K. Ph.D.thesis. 1986. Cytogenetic and mitochondrial DNA analyses of four salmonid fish species. Publications of the University of Kuopio. Natural Sciences. Original Reports 6/1986, 139 p.

Palva, T.K., Partti, K., Perosvuo, M. Palva E.T., Hakumäki, M. 1987. Analyses of mitochondrial DNA from whitefish, Coregonus muksun (Pallas) by using restriction endonuclease digestion. Proceedings of the Scandinavian Physiological Society Meeting in Copenhagen 15.-16.11.1986. Acta Physiol Scand 129: 3. (abstract)

Partti-Pellinen, K., Hakumäki, M. and Tuunainen, P. 1988. Restriction analysis of mitochondrial DNA of some coregonid stocks in Finland. Finnish Fish. Res. 9:00-00 (in press).

Kallio, I. and Koljonen, M-L. 1986. Management of the salmon stock in the Tornionjoki River. Mini-Symposium on population genetics in regard to fisheries and mariculture, ICES 74th Statutory Meeting, Copenhagen, C.M.1986 Mini-Symposium No 10. 9 p.

Kallio-Nyberg, I. and Koljonen, M-L. 1988. A stock registry of the Finnish whitefish. Finnish Fish. Res. 9:00-00 (in press)

Kallio, I. and Pruuki, V. 1987. The diversity and seasonal spawning of salmon (Salmo salar L.) in the River Tornionjoki. Proc. World Symp. on Selection, Hybridization, and Genetic Engineering in Aquaculture, Bordeaux 27-30 May, 1986. Vol.1. Heeneman Verlagsgesellschaft mbH, Berlin 1987. p 166-176.

Kallio-Nyberg, I. and Pruuki, V. 1988. Dynamics of age-size composition in the spawning population of salmon (Salmo salar) in the Tornionjoki River. Symposium on Baltic Sea Fishery Resources. Rostock, German Democratic Republic, 29 February-3 Marc 1988. ICES 1988 Bal/No. 58. 15 pp.

Koljonen, M-L. 1986. The enzyme gene variation of ten Finnish rainbow trout strains and the relation between growth rate and mean heterozygosity. Aquaculture 57: 253-260.

Koljonen, M-L. 1989a. Electrophoretically detectable genetic variation in natural and hatchery stocks of Atlantic salmon in Finland. Hereditas 110:23-35.

Koljonen, M-L. 1989b. Uudenmaan meritaimenkantojen geneettinen tutkimus. (Genetic study on the sea trout stocks in Uusimaa, southern Finland.) Suomen kalastuslehti 3/1989:128-131. (in Finnish).

Koljonen, M-L., Koskiniemi, J. and Pasanen, P. 1988. Electrophoretic markers for the whitefish species pair Coregonus palasi and Coregonus peled. Aquaculture 74:217-226.

Palva, T. K. and Palva, E. T. 1985. Rapid isolation of animal mitochondrial DNA by alkaline extraction. FEBS Lett 192: 267-270.

Piironen, J. and Vuorinen, J. 1986. Cultivation practices of the Finnish landlocked salmon (Salmo salar m. sebago Girard). Mini-Symposium on Population genetics in regard to fisheries and mariculture, ICES 74th Statutory Meeting, Copenhagen, 15 p.

Vuorinen, J. 1985. Genetically distinct sympatric populations of vendace, Coregonus albula. Third International Congress of Systematic and Evolutionary Biology, Brighton, England. Abstracts, 201.

Vuorinen, J., Champigneulle, A., Dabrowski, K., Eckman, R. and Rösch, R. 1986. Electrophoretic variation in central European coregonid populations. Arc. Hydrobiol. Beih. Ergebn. Limnol. 22: 291-298.

Vuorinen, J. and Kuusipalo, L. 1986. Electrophoretic variation in six rainbow trout strains. Aquaculture 57: 337. (abstract).

Vuorinen, J. 1987. Muikkukantojen geneettiset erot ja niiden merkitys kantojen hoidossa (Abstract: Genetic differences of vendace (Coregonus albula) stocks and their management implications). Publications of the University of Kuopio. Natural Sciences. Statistics and Reviews. 1/1987. p. 5-17.

Vuorinen, J. 1987. Enzyme genes as interspecific hybridization probes in Coregoninae fishes. International symposium on Biology and Management of Coregonids, Joensuu August 1987. Abstract 1 p.

Vuorinen, J. 1988. Enzyme genes as interspecific hybridization probes in Coregoninae fishes. Finnish Fisheries Research, 9 (in print).

Vuorinen, J. and Berg, O.K. 1989. Genetic divergence of anadromous and non-anadromous Atlantic salmon (Salmo salar) in the River Namsen, Norway. Can. J. Fish. Aquat. Sci. 46: 406-409.

RUTKI FEBRUARY 1989-02-20

Professor W.P. Wilkins
Chairman of ICES W.G. on Genetics
National University of Ireland
Dep. of Zoology
Galway, Ireland.

Poland report on the activities in 1988.

1. The family selection based on 5 strains of spring spawning rainbow trout at Inland Fisheries Institute Salmonid Research Laboratory was commenced.

Present part of this programme has two purposes - firstly to build up the outbred broodstock characterized by fairly high genetic variability and secondly to check up if any heterosis effect can be observed between tested strains.

2. Sex control in rainbow trout.

Prooved functional phenotypic males / XX genotype / were distributed to several fish farms for the whole female market fish production.

3. Polyploidization.

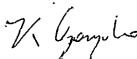
3.1. The experiment aimed to compare " normal ", whole female and sterile / triploidized females / rainbow trout was continued / second season /.

3.2. Effects of polyploidization on survival and growth rate of hybrids among brook, sea and rainbow trout involving reciprocal crosses were tested during the first year

of experimental fish life.

4. Gynogenesis.

The experiments aimed to improve the methods of sperm sterilization / UV radiation / for artificial gynogenesis were continued.



Krzysztof Goryczko

Inland Fisheries Institute Salmonid

Research Laboratory Rutki

83-330 Żukowo Poland.

copy to Prof. H. Rosenthal Chairman Mariculture Committee.



MINISTÉRIO DA AGRICULTURA E PESCAS
SECRETARIA DE ESTADO DAS PESCAS

INSTITUTO NACIONAL DE INVESTIGAÇÃO DAS PESCAS

CENTRO DE INVESTIGAÇÃO PESQUEIRA DE AVEIRO

Prof.Dr.W.Villwock
Chairman of the ICES-Working Group of
Genetics
Martin-Luther-King-Platz 3
2000 Hamburg 13

Sua referência:	Sua comunicação de:	Nossa referência	Data
		102/89	89/05/20

ASSUNTO

- 5 JUN. 89 - 2018

Dear Colleague,

Unfortunately, I can't be present to the Working-Group meeting next May 23-27. I hope it will be successful.

The Projects on Genetics that are carried out in Portugal and their responsables are:

- "Genetic divergence degree analysis in Chondrostoma (Cyprinidae) populations from Portuguese basins"

- M.M. Coelho (University Lisboa)

- "Cytogenetic of primary fishes (Cyprinidae and Cobitidae Families) and peripheral fishes (Gobiidae Family) from Iberian Peninsula"

- M.J. Collares-Pereira (University Lisboa)

- "Comparative study of the genetic duplication rates of the Iberian Cyprinidae"

- M.M. Coelho (University Lisboa)

Na resposta deve indicar o número e as referências constantes deste documento

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MINISTÉRIO DA AGRICULTURA E PESCAS
SECRETARIA DE ESTADO DAS PESCAS

INSTITUTO NACIONAL DE INVESTIGAÇÃO DAS PESCAS

CENTRO DE INVESTIGAÇÃO PESQUEIRA DE AVEIRO

Pag. 2

Ref.: 102../.89.....

N.º

Data: 89/05/20.....

-"Electrophoretic studies in *Nephrops norvegicus* L."

-A.M.T.Santos (National Institut of Fisheries Research)

Yours sincerely,

Ana Maria Teia dos Santos
(Ana Maria Teia dos Santos)

Prof. Dr. W. Villwock

Zoologisches Institut und Zoologisches Museum
Martin-Luther-King-Platz 3, 2000 Hamburg 13

ZOOLOGISCHES INSTITUT
UND
ZOOLOGISCHES MUSEUM

Fernsprecher: (040) 41 23 - 3873 }
Behördenexz.: 9.38. (" ") } Durchwahl

Telex-Nr.: 2 14 732 unihhd.

To
the members
of ICES-working group on genetics

Datum und Zeichen Ihres Schreibens

Aktenzeichen (bei Antwort bitte angeben)

Datum April 12, 1989

Second Circular

- (1) Thanks to everybody who made proposals and/or recommendations for our Dublin-meeting.
- (2) Tentative program according to ICES-recommendations 1988 (including the above mentioned personal proposals)

- May 23: Joint NASCO/ICES meeting on the "Genetic threats to wild salmon posed by salmon aquaculture" (see enclosed program).
- May 24:
 - 08.45 a) Retrospective to joint meeting NASCO/ICES with special contributions by single members of ICES working group. Evaluation of genetic and other impacts on natural populations by deliberate or inadvertent release of cultured fish (in general).
 - 10.40 Coffee
 - 11.00 b) Reports on genetics from the member countries*. Discussion on monitoring the trends they indicate in applying genetic methods in aquaculture and fisheries.
 - 12.30 Lunch
 - 14.00 Continuation of position b) and recommendations to member countries and/or ICES.
 - 17.00 Conclusion.
- May 25:
 - 08.45 c) Developments in genetics of aquatic organisms and identification of those aspects which seem to be of particular significance for aquaculture and fisheries science: Contributions of working group members*.
 - 10.40 Coffee.
 - 11.00 Discussion and recommendations to pos. c)
 - 12.30 Lunch

tentative program (continued)

- May 25:
14.00 d) Applications of gene technology in aquaculture: Contributions of working group members*.
- 15.45 Tea
- 16.00 Discussion and recommendations to member countries and/or ICES.
- 17.30 Conclusion
- May 26: Final meeting and discussion on the future of the working group (aspects to be followed, next meeting a.o.).
- 08.45
- 10.00 End.

* working group members who are unable to join the joint NASCO/ ICES meeting are kindly asked to deliver short papers documenting the requested aspects in the view of the member country concerned. Participants should contribute short statements on the basis of an about one-page written contribution, the latter will be used for later summing-up report to ICES by the sender/ chairman of the group. Written contributions without oral presentation should be delivered to the sender's address not later than May 20. Thank you.

Hotel accomodations: delivered to everybody's own decision and activity. Please follow the recommendation-list which was mailed to each member directly by the organizing committee.

Best regards


(Wolfgang Willwock)

List of Members/ Working Group on Genetics
(explanations see p. 40, below)

appendix 2/ pp. 39-40

25.01.1989 - GEN/ALL

- o Ms G. Andorsdottir
Fiskirannsóknarstofan
Debessartrøð
FR-100 Torshavn
Faroe Islands
Denmark
- o M S. Bougrier
IFREMER
12, rue des Résistants
56100 La Trinité-sur-Mer
France
- o M Chevassus
INRA
Dép. d'Hydrobiologie
CNRS Domaine de Vilevert
78350 Jouy en Josas
France
- o Dr J. Clayton
Dept. of Fisheries & Oceans
Freshwater Institute
501 University Crescent
Winnipeg, Manitoba R3T 2N6
Canada
- o Mr M. Lima Dias
INIP
Avenida de Brasilia
1400 Lisbon
Portugal
- o Mr L. Dickie
Dept. of Fisheries & Oceans
Bedford Inst. of Oceanogr.
P.O. Box 1006
Dartmouth, NS B2Y 4A2
Canada
- n Mr Goryczko
Inland Fisheries Institute
River Fisheries Laboratory
5, Bytowska Street
80-328 Gdansk-Oliva
Poland
- o M Guyomard
INRA
Dép. d'Hydrobiologie
CNRS Domaine de Vilevert
78350 Jouy en Josas
France
- o Prof. E.A. Huisman
Agricultural University
Zodiac Building
P.O. Box 338
6700 AH Wageningen
Netherlands
- + Mr J. Jansson
Salmon Research Institute
810-70 Älvkarleby
Sweden
- + Mr K. Jørstad
Institute of Marine Research
P.O. Box 1870/72, Nordnes
5024 Bergen
Norway
- (n) Ms M.L. Koljonen
Finnish Game and Fisheries
Research Institute
P.O. Box 202
00151 Helsinki
Finland
- o Dr (Ms) A. Longwell
Milford Laboratory
NEFC/NMFS
212 Rogers Avenue
Milford, CT 06460
USA
- o Mr G. Nøvdal (substituted by Jørstad)
Institute of Marine Research
P.O. Box 1870/72, Nordnes
5024 Bergen
Norway

- o Dr G. Newkirk
Dept. of Biology
Dalhousie University
Halifax, N.S. B3J 3J5
Canada
- o Dr L. Nyman (substituted by Jansson)
Institute of Freshwater
Research
Drottningholm
Sweden
- o Dr D. Powers
Johns Hopkins University
Chesapeake Bay Inst.
4800 Atwell Road
Shady Side MD 20867
USA
- + Dr C. Purdom
Fisheries Laboratory
Lowestoft NR33 OHT
Suffolk
United Kingdom
- n Ms A.M.T. Santos
INIP
Avenida de Brasilia
1400 Lisbon
Portugal
- + Mr R. Saunders
Dept. of Fisheries & Oceans
Biological Station
St Andrews, N.B. EOG 2XO
Canada
- o Dr J.M. Sévigny
Dept of Fisheries & Oceans
Inst. Maurice-Lamontagne
850, route de la Mer
PO Box 5000
Mont-Joli, Quebec G5H 3Z4
Canada
- o Mr V. Thorsteinsson
Marine Research Institute
P.O. Box 1390
Skulagata 4
121 Reykjavik
Iceland
- + Prof. W. Villwock
Zoologisches Inst.
Martin-Luther-King Platz
2000 Hamburg 13
Federal Republic of Germany
- o Prof. N.P. Wilkins (excused)
National University of
Ireland
University College
Galway
Ireland
- o Dr J. Worms
Dept. of Fisheries & Oceans
P.O. Box 5030
Moncton, N.B. E1C 9B6
Canada
- + Mr A.F. Youngson
Marine Laboratory
P.O.Box 101
Victoria Road
Aberdeen AB9 8DB
United Kingdom

explanations: + present
o absent
n notice (letter)
(n) notice (letter by non-member in behalf of a member)

Since the subject of Genetic Threats to Wild Salmon Stocks seemed of pressing importance, the one-day meeting was reviewed on the following day by the ICES Working Groups, particularly with a view toward further ICES involvement. Results of the Working Group discussions, in the form of a summary and recommendations are presented in the next section.

ASSESSMENT OF EFFECTS OF ESCAPEES ON WILD STOCKS
(PROPOSED ICES ACTIVITIES)

The Working Group on Introductions and Transfers of Marine Organisms and the Working Group on Genetics reviewed the results of the joint NASCO/ICES meeting and the NASCO paper CNL (89) 19, (Report of Dublin Meeting on Genetic threats to Wild Stocks). The information presented was considered to be insufficient to evaluate the degree of risk (if any) of adverse effects of cultured Atlantic salmon which have escaped from cultivation on wild Atlantic salmon stocks. However, the large number of escapees observed in the spawning populations in Norwegian rivers gives cause for grave concern that the potential exists for serious effects on the productivity of wild stocks.

The Working Groups concluded that a conservative approach should be followed in development of the Atlantic salmon aquaculture industry until the risk of adverse effects on wild Atlantic salmon stocks has been evaluated. The development of broodstocks from stocks of local origin should be encouraged. The Working Groups noted that there is insufficient genetic, ecological and behavioral research presently being undertaken to evaluate the effects of escapees on wild Atlantic salmon populations. This research is urgently required. Since the magnitude of this research necessitates international cooperation, ICES should encourage and possibly coordinate its implementation.

The Working Groups then recommended that:

(1) studies on ecological and behavioral interactions of wild and cultured salmon be continued and expanded, and that

(2) a study group be formed, under the Chairmanship of Mr. Alan Youngson of Aberdeen, Scotland, to:

(a) review, consolidate, and report on the current status of techniques to detect genetic changes in Atlantic salmon stocks due to interbreeding of wild and cultured populations; and

(b) provide the experimental design for a research program to evaluate the possible effects of escapees of Atlantic salmon on wild stocks.

(The research should include genetic consequences, and ecological and behavioral interactions, as well as selection of appropriate locations for the research. The cost and duration should also be estimated.)

The study group should report to both the Genetics Working Group and the Working Group on Introductions and Transfers of Marine Organisms. It should consist of experts in the fields of genetics, ecology, behavior and population dynamics. These experts could be members of the above ICES Working Groups, or the North Atlantic Salmon Working Group, or other experts recommended by the Chairman of the Study Group in consultation with ICES delegates.

The Study Group should hold a meeting to coincide with the meeting of the ICES Working Group on North Atlantic Salmon in March of 1990 to enable the members of that Working Group to participate in the discussions of the Study Group.

The report of the Study Group should be made available by the May 1990 meetings of the Introductions and Transfers and the Genetics Working Groups.

It was apparent to all participants that the subject of the meeting was of serious concern, especially to Norway and Scotland, but that factual information was minimal. Of the countries represented at the joint meeting, Norway seems to be taking a substantial lead in research on the subject, as would be logical in view of its large aquaculture production of salmon. Encouragement of national research and possible cooperative international studies could be effected through continuing joint ICES/NASCO involvement. To that end, another joint ICES/NASCO meeting on the topic should be held in 1991.



appendix 4/ pp.44-69

CNL8919

COUNCIL

PAPER CNL(89)19

**REPORT OF DUBLIN MEETING ON GENETIC THREATS
TO WILD STOCKS FROM SALMON AQUACULTURE**



RES23.046

DRAFT

JOINT NASCO/ICES MEETING ON THE
"GENETIC THREATS TO WILD SALMON POSED BY SALMON AQUACULTURE"

THE DEPARTMENT OF THE MARINE, LEESON LANE, DUBLIN 2
ON TUESDAY 23 MAY 1989

PROGRAMME

- 08.45 Registration
- 09.15 Opening Remarks - Dr Alan Youngson (Chairman)
- 09.20 Introduction - Dr Malcolm Windsor (Secretary of NASCO)
- X 09.30 *"To what extent are farmed and wild salmon genetically distinct?"*
Dr Tom Cross, University of Cork, Ireland
- 10.05 *"Do breeding studies suggest that there are differences in performance related traits between farmed and wild fish and their crosses?"*
Dr John Bailey, Atlantic Salmon Federation, Canada
- 10.40 Coffee
- 11.00 *"Is the stage of life at which fish are released or escape a determinant of their subsequent performance?"* Dr Lars Hansen, NINA, Norway
- X 11.35 *"Can the features likely to limit the crossing of wild fish and fish of farmed origin be identified?"* Dr Alan Youngson, DAFS, Scotland
- 12.10 *"Is aquaculture likely to affect the genetic integrity of wild populations?"*
Dr Eric Verspoor, DAFS, Scotland
- 12.45 Lunch
- 14.00 General Discussion on the genetic threats to wild stocks. Formulation of Research and other needs and possible international collaboration.
- 16.00 Tea
- 16.15 Consideration of recommendations
- 17.00 Conclusion
- 18.30 Reception at the invitation of NASCO

CNL(89)19
REPORT OF THE DUBLIN MEETING ON GENETIC
THREATS TO WILD STOCKS FROM SALMON AQUACULTURE

1. At its Fifth Annual Meeting the Council requested the Secretary, in consultation with the General Secretary of ICES, to convene a one-day meeting during the first half of 1989 to assemble what information was available on genetic threats to wild stocks.
2. In accordance with this decision a joint NASCO/ICES meeting was held at the Department of the Marine, Dublin on 23 May. The meeting was well attended by salmon geneticists, biologists and managers from throughout the North Atlantic countries and the report of this meeting is appended to this paper as Attachment 1.
3. The meeting consisted of five formal papers which were presented in the morning session and which served as a basis for an afternoon discussion session. The papers addressed the following questions:
 - To what extent are farmed and wild salmon genetically distinct?
 - Are difference in performance related traits likely to exist between farmed and wild fish and their crosses?
 - Is the stage of life at which fish are released or escape a determinant of their subsequent performance?
 - Can the factors likely to limit the crossing of wild fish and fish of farmed origin be identified?
 - Is aquaculture likely to affect the genetic integrity of wild populations?
4. A number of views on the impacts of farmed fish on the wild stocks was expressed. These ranged from no impact (or even benefits) to serious impacts. The only evidence presented, however, suggested that adverse effects were possible. There was general agreement that there were considerable gaps in our knowledge, and on the need for the necessary experimentation to assess the genetic impact. Such experimentation would be facilitated by the development of techniques to identify individual fish through genetic markers. The urgent need to support such research was recognised.
5. The meeting agreed a number of basic questions including:
 - what are natural straying rates?
 - where do escapees go?
 - to what extent are fish of farmed origin represented among spawners?
 - do wild and farmed fish interbreed?
 - do wild fish and fish of farmed origin interact ecologically?

In addition the need to develop improved methods of identifying farmed fish in the wild was recognised.

6. In these circumstances where large numbers of farmed fish are occurring in the habitat of wild salmon and their impact is unknown, the meeting recognised the need for caution. The development of gene banks and of internationally agreed Codes of Practice or recommendations was agreed. Such codes or recommendations could include the following elements:
- cage security
 - the use of sterile fish
 - tagging of farmed fish and adequate reporting of escapes
 - zones free of aquaculture
 - emergency netting of severe escapes of farmed fish where legislation permits
 - encouragement for the use of local stocks for farming purposes
 - measures to maintain the vigour of existing natural stocks
 - adoption of Codes of Practice for reducing genetic threats and the impacts of introductions and transfers in general.
 - introduction and permanent scientific control of gene banks including sperm preservation as well as wild stock preservation.
7. The Council might like to consider if and how the development of genetic markers and research on impacts might be stimulated. The Council might wish to take note of the recommendation on the practical steps which might be taken in the meantime (such as the development of Codes of Practice or series of recommendations, and gene banks) as covered in other papers on these subjects CNL(89)21 and CNL(89)23.

Secretary
Edinburgh
26 May 1989

ATTACHMENT 1

JOINT NASCO/ICES MEETING ON

"THE GENETIC THREATS TO WILD SALMON POSED BY SALMON AQUACULTURE"
THE DEPARTMENT OF THE MARINE, LEESON LANE, DUBLIN 2
TUESDAY 23 MAY 1989

1. OPENING REMARKS

- 1.1 The Chairman Dr Alan Youngson opened the meeting, thanked the Irish Government for the arrangements which had been made for the meeting and welcomed all delegates.

2. INTRODUCTION

- 2.1 The Secretary of NASCO, Dr Malcolm Windsor, introduced the meeting by outlining the involvement of NASCO in the debate concerning the interactions of salmon aquaculture and the wild stocks (Annex 1).

3. PRESENTATION OF PAPERS

- 3.1 Dr Tom Cross of the University of Cork, Ireland, presented a paper entitled "To what extent are farmed and wild salmon genetically distinct?" (Annex 2).
- 3.2 Dr John Bailey of the Atlantic Salmon Federation, Canada, presented a paper entitled "Are differences in performance related traits likely to exist between farmed and wild fish and their crosses?" (Annex 3).
- 3.3 Mr Lars Hansen, of the Norwegian Institute for Nature Research, Norway, presented a paper entitled "Is the stage of life at which fish are released or escape a determinant of their subsequent performance?" (Annex 4).
- 3.4 Dr Alan Youngson of the Department of Agriculture and Fisheries for Scotland, presented a paper entitled "Can the factors likely to limit the crossing of wild fish and fish of farmed origin be identified?" (Annex 5).
- 3.5 Dr Eric Verspoor of the Department of Agriculture and Fisheries for Scotland, presented a paper entitled "Is aquaculture likely to affect the genetic integrity of wild populations?" (Annex 6).

4. GENERAL DISCUSSION ON THE GENETIC THREATS TO WILD STOCKS.

- 4.1 A list of objectives for possible future research was presented by the Chairman and discussed by the meeting. These objectives were:
1. To define genetic units in wild fish assessing gene flow between units.
 2. To monitor strains in culture identifying genetic changes entrained by culture itself.

3. To find the means by which introgression of genetic material from farmed fish to wild fish may be studied in the field.
 4. To determine the nature of any behavioural or physiological constraints to introgression.
 5. To describe the dynamics of introgressed genetic material in wild populations.
 6. To monitor the genetic condition of wild and domestic stocks and their performance and productivity.
 7. To understand the genetic basis of performance.
- 4.2 The need to establish priorities for these issues was recognised. Some of these studies might be pursued with existing expertise and facilities. Others would be facilitated by accelerated development of emerging techniques.
- 4.3 The development of techniques for the analysis of variation in nuclear DNA was described by Dr Ferguson of Queens University, Belfast. Such markers would be very useful in establishing natural gene flow and in structuring experimental studies using neutral genetic tags. The technique is expensive to develop but once suitable probes have been developed it is quicker and screening costs are therefore lower than for mitochondrial DNA analysis. The development of these techniques might enable a biological impact experiment to be set up.
- 4.4 Present electrophoretic studies being conducted in Scotland, Ireland, England and Wales and Norway were described. In Norway 25% of fish ascending rivers were escapees from fish farms but there is not enough knowledge to predict what the genetic impact of these fish will be. A review of the literature was presented which suggested that some adverse effects were possible. However, in order to make better predictions experiments needed to be devised involving the use of genetic markers. One proposal was that a controlled experiment could be carried out in a monitored salmon stream by manipulation with a farmed stock.
- 4.5 The attention of delegates was drawn to a number of forthcoming meetings concerning the interactions between aquaculture and wild stocks. These include a meeting in Ireland in September 1989, a meeting in Norway in April or May 1990, a one day meeting of the World Aquaculture Society in Halifax, Nova Scotia in July 1990 and a meeting in Nanaimo, British Columbia in September 1990. It was agreed that there might also be a need for a further joint NASCO/ICES meeting on this subject in 1991.

5. CONSIDERATION OF RECOMMENDATIONS.

- 5.1 A range of views was expressed by the delegates concerning the genetic threats to the wild stocks posed by salmon aquaculture. These ranged from those who felt that there was unlikely to be any impact (or might even be benefits) to those who felt that there were potentially serious impacts.

- 5.2 The only evidence presented, however, suggested that some adverse effects were possible. There was general agreement that there were considerable gaps in our knowledge regarding the genetic impact of reared fish on wild stocks. There was also general agreement on the need for, and difficulty associated with, the necessary experimentation required to assess the genetic impact. The development of techniques for the analysis of variation in nuclear DNA would help to solve many of these and other open questions, including introgression, as a basic part of genetic impact and the meeting therefore urgently recommended that development work in this field should be supported.
- 5.3 The meeting agreed a number of basic questions which need to be answered in order to assess the genetic impact of farmed salmon on wild stocks. These were
- what are natural straying rates?
 - where do escapees go?
 - to what extent are fish of farmed origin represented among spawners?
 - do wild fish and farmed fish interbreed?
 - do wild fish and fish of farmed origin interact ecologically?

A number of these questions may be answered by applying or improving current methods. Some of these questions have been addressed by research presently being undertaken in Norway. Similar studies should be conducted in other countries. In addition the need to develop improved methods of identifying farmed fish in the wild was recognised.

- 5.4 The meeting approved the list of objectives presented by the Chairman as guidelines for future work (Paragraph 4.1). Much of this research was likely to be of a long term nature. The meeting recognised that in the absence of knowledge on impacts there is a need for caution in the meantime and endorsed a number of practical measures such as the development of gene banks and the development of Codes of Practice or Recommendations to minimise possible impacts. Such Codes or Recommendations might include the following elements:
- cage security
 - the use of sterile fish
 - tagging of farmed fish and adequate reporting of escapes
 - zones free of aquaculture
 - emergency netting of severe escapes of farmed fish where legislation permits
 - encouragement for the use of local stocks for farming purposes
 - measures to maintain the vigour of existing natural stocks
 - adoption of Codes of Practice for reducing genetic threats and the impacts of introductions and transfers in general.
 - introduction and permanent scientific control of gene banks including sperm preservation as well as wild stock preservation.

Dublin
24 May 1989

INTRODUCTION

by

Malcolm Windsor

Secretary

North Atlantic Salmon Conservation Organization

11 Rutland Square, Edinburgh EH1 2AS

Over the last 15 or 20 years we have seen the rise of a completely new industry - salmon farming. It did not exist in its present form before 1965. The growth of this industry has been so spectacular that we may have already reached the stage where there are more salmon in the sea in cages than there are in the wild. While there is much to admire in this new industry, and it may exert some protective influence on the wild stocks, at least economically, concerns have been expressed about the possible threats this industry poses to the wild stocks. There are a number of potential interactions between aquaculture and the wild stocks including interactions with the aquatic environment, interactions relating to diseases and parasites and, what we are here to discuss today, genetic interactions. We know that farmed salmon now occur in considerable numbers in the wild and these numbers are likely to increase if industry growth projections are accurate. However, little attention has been given to the question of the effects these fish have on the wild stocks. NASCO Council took the view that, as the international body charged with the conservation, restoration, enhancement and rational management of the salmon, we should try to assess the situation. To this end, at its Fifth Annual Meeting the Council recognised the serious nature of some of the threats posed by the aquaculture industry and agreed on a number of steps. These included the possibility of developing an internationally agreed Code of Practice to minimise the impacts on wild stocks, a review of the benefits of gene banks, a request to ICES for information available on the environmental threats, a review of legislation relating to introductions and transfers and, of course, convening this meeting to assess the genetic threats.

I think the basic question we need to address is "Are we now placing at risk 10,000 years of genetic selection and diversity, and if so is this a cause for concern?". I suspect that we shall find various points of view expressed in this room today.

TO WHAT EXTENT ARE FARMED AND WILD SALMON GENETICALLY DISTINCT?

by
Tom F Cross
Department of Zoology, University College, Cork, Ireland

Most studies comparing the genetic composition of reared strains and wild populations of Atlantic salmon (*Salmo salar*) have utilised enzyme electrophoresis. The method is briefly described and ways of calculating genetic composition (as gene frequencies at polymorphic loci) and extent of genetic variability (as mean heterozygosity) are demonstrated. Results of electrophoretic surveys, from Sweden, Norway, Finland, Ireland and Canada are summarised and other studies, as yet unpublished or in the planning stage, are mentioned. Published results fall into two categories: (i) where reared strains (and sometimes different year-classes of the same strain) are compared directly with the wild populations from which they were derived; and (ii) where a number of reared strains are compared with wild populations from the same general area, but not with their ancestral populations. The first category demonstrates that statistically significant differences in gene frequencies usually occur between reared strains and their wild progenitors. Furthermore, significant differences in allele frequency may occur between various year classes of a particular strain. Both categories show that some reared strains have lower genetic variability (measured as mean heterozygosity) than wild populations. One aspect of this loss of variability is that rare alleles present in the wild ancestral population may be lost in a reared strain.

Mitochondrial (mt) DNA analysis has also been applied to the comparison of reared strains and wild populations of Atlantic salmon. The methodology is described and it is noted that mt DNA, because it is haploid and inherited maternally, is more sensitive to factors which reduce genetic variability, than the nuclear DNA which is assayed indirectly by enzyme electrophoresis. One published investigation of Atlantic salmon from Sweden showed a profound reduction in variability in reared strains compared with wild populations.

It is argued that genetic differences between reared strains and neighbouring wild populations can be due to the origin and/or breeding regime of the reared salmon. If a reared strain originates from another geographic race than local wild populations, then genetic differences are likely to be very large. Three major races, detected electrophoretically, occur in Atlantic salmon. These occupy rivers: (1) in countries surrounding the Baltic; (2) in western Europe and Iceland; and (3) in eastern North America. Inter-racial transfers are not recommended, since for example, differences in disease occurrence or susceptibility have been demonstrated between races. Within races, significant allele frequency differences occur between nearly all wild populations assayed. Thus reared strains are likely to differ genetically from all wild populations except their ancestral population. There have been suggestions by managers and conservationists that reared strains should not be moved between countries. The present evidence from population genetics to support such a ban is ambiguous, with a positive relationship between genetic difference and geographic distance being reported in a few cases and not in most. In this context, it is noted, that the Scottish and Irish salmon farming industries rely heavily on strains of Norwegian origin. In the short term, it

would be difficult to replace these with native strains since the imported strains have been selected for fast growth and late maturity over several generations.

The other factor discussed which acts on genetic composition is breeding regime. Two aspects are of importance here: the number of adults used as broodstock and artificial selection. The use of inadequate numbers of parents (less than 50 of each sex equally represented) leads to a type of inbreeding which results in a loss of genetic variability and changes in gene frequencies at polymorphic loci. This form of inbreeding is progressive in each generation where small numbers of parents have been used. It can be halted by increasing parental number but not reversed except by outcrossing with suitable stock. Many authors have reported such inbreeding in Atlantic salmon and in other salmonid species.

The importance of changes in gene frequencies is not known. If a particular suite of gene frequencies is adaptive or marks adaptation to a certain river, then any change in genetic composition will reduce fitness. (In this context, it is noted that polymorphic gene frequencies of wild populations seem relatively constant over time.) It has been reported that various year classes of the same strain can have significantly different gene frequencies. If such frequency differences are indicative of fitness variations, then cohorts could vary in performance.

Such inbreeding can also result in reductions in variability. Some authors have shown in other salmonid species that such reductions can lead to a decline in overall performance. A reduction in variability can also lead to the loss of rare alleles at polymorphic loci. A loss of this type is permanent (unless outbreeding occurs) and reduces the adaptive potential of a strain. All of the sources of change listed above are potentially alterable. Directional selection as discussed below is less so.

Directional selection for fast growth and late maturity is widely applied in producing smolts for the farming industry. A typical selection programme, while improving the targeted traits, can lead to reduction in heterozygosity and to changes in gene frequencies at other polymorphic loci. It is noted that such a reduction in variability has been prevented in some reported cases by strain crossing, which artificially boosts variability before commencing selection. Such a practice, while suitable for producing smolts for captive rearing, may actually reduce the fitness of these fish in the wild.

In conclusion, it is noted that many more reared strains need to be assayed electrophoretically. It is also noted that reared fish may not only enter the wild through escapes from sea farms. Freshwater rearing facilities and enhancement and ranching programmes are also potential problem areas.

**ARE DIFFERENCES IN PERFORMANCE RELATED TRAITS LIKELY TO EXIST
BETWEEN FARMED AND WILD FISH AND THEIR CROSSES?**

by
John K Bailey
Atlantic Salmon Federation, Canada

To my knowledge, there have been no studies where marked, domestic salmon have been willfully released from aquaculture sites. However, there have been several studies, with brook trout (*Salvelinus fontinalis*) and wild rainbow trout (*Salmo gairdneri*) in natural and semi-natural environments that bear directly on this question. Although their results were not consistent, the above trials indicated that performance differences exist between domestic and wild trout and their hybrids. Similar differences should be anticipated between domestic and wild Atlantic salmon.

In Atlantic salmon, differences in performance have been found among wild stocks grown in a common environment, released from the same sea ranching facility, grown in cages, and stocked into the same stream for enhancement purposes. Similar results have been found among domestic strains reared in the same environment and within the same strain reared in different environments. In total, the above examples lead to one general conclusion. Quantitative genetic differences exist among salmon populations, whether they are wild or domestic, and genotype-environment interactions can be expected when stocks or strains are transferred from one environment to another. The question of real concern to salmon managers is whether escaped aquaculture fish are likely to have detrimental genetic effects on indigenous, wild salmon populations.

The homing habitat of Atlantic salmon has led to the differentiation of a large number of relatively discrete stocks that are generally assumed to be locally adaptive. However, it is inappropriate to think that all stock characteristics are necessarily adaptive. Examples exist that suggest some traits may result from a relaxation of selection pressure. Similarly, with respect to fitness, it is naive to suspect that there could only be one successful life history strategy for a given set of environmental conditions. In addition to the pressures of natural selection, gene pools can also be altered by mutation, migration and genetic drift. The latter three forces occur at random and are not predictable. Chance is also a genetic isolating mechanism.

In order to realise a genetic effect in a wild stock, its gene pool, and therefore, gene frequencies, must be permanently altered. However, because selection, mutation, migration and drift act in concert, at all times, the gene frequencies of wild stocks must be considered as dynamic and not static. Similarly, environments are also dynamic. A detrimental effect is more likely to be the result of too rapid change.

Where stable stocks exist in pristine habitats, the relative importance of these forces much achieve some form of equilibrium and remain balanced over protracted time intervals. Throughout their natural range, many salmon stocks are not stable. This may be symptomatic of an environment that is changing faster than new checks and balances can be re-established and natural selection cannot keep pace with the rate of environmental change.

Aquaculture has the potential to further upset this balance by making it possible for a significant increase in the immigration of domestic stocks into the wild. To have a genetic impact, the escapees' alleles and allele frequencies must differ from wild stocks and they must either add their genes to the gene pool or cause the loss of indigenous genes. A genetic impact can result from either introgression or displacement.

The introgression of new alleles from aquaculture escapees may provide additional raw material for natural selection. Escapees can be expected to increase the genetic variability within stocks at the expense of genetic variation between stocks. This may prove to be a benefit in rapidly changing habitats. With respect to fitness, there can be three possible effects. Fitness can remain unchanged, it may decrease or it may increase.

Few will argue that a decrease in natural fitness is not detrimental. However, if the alleles of the "initial gene packet" are not destroyed, this is unlikely. If the alleles contributed by escapees confer a selection disadvantage, the directional nature of natural selection will attempt to redefine the "historically established" gene frequencies. If they are neutral, allele frequencies may change, but fitness and stock characteristics should remain similar to that of the wild stocks. Should the novel alleles confer a selection advantage, fitness may actually increase. The nature and direction of such changes are only speculative.

The "historically established" gene and allele frequencies of proven fitness, cannot be re-established, if alleles from the "initial gene packet" are lost. Natural selection must then begin a new experiment to determine alternative successful combinations. Thus, displacement has the potential to be much more disruptive than introgression.

Among other animals, there are few examples where domestic strains both escape and successfully breed with wild stocks. The majority of domestic animals are unable to survive in the wild or compete successfully for wild mates. In the examples that do exist, there has been a broad range of responses. These include examples of minimal impact in the case of domestic dog (*Canis familiaris*) and coyote (*Canis latrans*) hybrids, successful introgression of domestic genes into a wild pig (*Sus scrofa*) stock, and the virtually complete displacement of European by African honeybees (different sub-species of *Apis mellifera*).

The second example, that of domestic and wild pigs may be of particular relevance in a discussion of the possible genetic effects of escaped salmon. Salmon, like pigs, are noted for their plasticity. They have adapted to inhabit a wide range of environmental conditions, both among stocks and within the same stock in different years. Perhaps the greatest effect of domestication is the simple relaxation of a variety of natural selection pressures which also may vary with environmental conditions.

In domestic environments, alleles that were adaptive in the wild may be unnecessary and therefore have a neutral effect, in terms of fitness. If broodstocks are large enough to minimize inbreeding and drift, null alleles can be maintained in the gene pool for many domestic generations. Should these fish escape they may be capable of a rapid return to the feral state.

While it is uncertain whether all of the conditions necessary to make a genetic impact even exist, it is prudent to assume that some changes will occur. The magnitude of

any potential genetic impact will be influenced by the genetic differences between the populations involved. The long term consequences of changing the gene frequencies in wild stocks are unknown.

Nevertheless, in the absence of definitive evidence, the conservation of genetic diversity among stocks is a desirable objective. Preventing the escape of farmed fish is the only sure method of avoiding a genetic impact in wild stocks and husbandry techniques can be expected to improve in this respect. Practices designed to reduce the risk of detrimental genetic impacts should be encouraged.

Some will undoubtedly contend that any change is detrimental and should be prevented, at all costs. Such an inflexible stance is somewhat utopian and perhaps unrealistic. Evidence from other species suggests that, in the rare instances of hybridization between domestic strains and wild stocks, the long term genetic effects are usually of little consequence with respect to either fitness or behaviour. Both the gene pools and environments of wild stocks are dynamic and natural selection will continue to operate on any new gene pool.

**IS THE STAGE AT WHICH FISH ARE RELEASED OR ESCAPE A
DETERMINANT OF THEIR SUBSEQUENT PERFORMANCE?**

by

Lars P Hansen

Norwegian Institute for Nature Research, Tungasletta 2,
7004 Trondheim, Norway

The development in farming and ocean ranching of Atlantic salmon has led to an increased proportion of reared fish in nature. Salmon may escape from fish farms at all life stages, while ranched fish are mainly released at smolt stage. The life stage at which fish are released or escape determines the future migration pattern and survival of the salmon. This paper reviews this, with particular reference to Norwegian conditions.

Fish that are released or escape at smolt stage from a river, return with high precision to that system when mature, independent of stock origin (eg Carlin 1969). If smolts are released in the estuary, the straying rate will increase (Carlin 1955, Eriksson et al, 1981). If salmon escape at smolt stage from a marine locality, the adults will tend to return to the area from which they escaped (Sutterlin et al, 1982, Hansen et al, 1989a). These fish are not imprinted to (or have learned) the "home stream" and would therefore have no motivation to enter freshwater before they of physiological reasons have to (Jonsson et al, 1989, Lund & Hansen in prep.), but they will enter rivers and streams in the area to spawn. This lack of motivation might also result in a lower proportion of escaped fish among the spawners far upstream than in the lower part of the stream. When salmon are released or escape at postsmolt or adult stage, they seem to stray to rivers farther away from the site of release when mature (Hansen et al 1987, Hansen & Jonsson in prep). The reason for this could be that salmon are not able to imprint to cues used in homing throughout the whole year and/or at all life stages.

There are many factors determining the survival of salmon in nature. In particular, released salmon and escapees from fish farms have to pass through a number of "bottlenecks" before they are ready to spread their genes. To survive in the sea, the salmon must be physiologically and behaviourally fit for a life in sea water. Size, age and state of maturity of the salmon, and the time and site of release or escape are important factors determining the future fate of these fish.

Experimental releases of reared Atlantic salmon show that there is a seasonal variation in survival (Hansen & Jonsson 1989). Survival is much higher for those fish escaping at smolt stage in the spring than those escaping the following summer and autumn. However, survival will also improve with increased body size which will reduce the predation. Previous male maturity will reduce the number of migrating smolts (Hansen et al, 1989b), and therefore contribute in reducing the overall survival of a smolt group (Lundqvist et al, 1988).

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**CAN THE FACTORS LIKELY TO LIMIT THE CROSSING OF
WILD FISH AND FISH OF FARMED ORIGIN BE IDENTIFIED?**

by
Alan F Youngson
DAFS Marine Laboratory, Victoria Road, Aberdeen

When both native Atlantic salmon (*Salmo salar*) and fish which have escaped or been released from culture are present in a single drainage system they may not cross freely at spawning. Two categories of restraint can be envisaged. One category will limit contact through differences in the distribution of the two types of fish in the spatial framework of the catchment. The other category will restrain the interaction of fish of both types through behavioral or physiological incompatibility, even when they are present together in the same reaches of stream.

While native fish will disperse throughout a drainage system, escapes or releases may be confined to particular parts of the system. Lack of homing stimulus in opportunist entrants may impair migratory drive. Low motor capacity in recent escapes from culture may reduce migratory vigour. Both effects may be expected to confine farmed fish to the lower parts of catchments. When indigenous and non-native fish are present together, crossing may be limited by behavioral differences between the groups. The density dependent mortalities to which groups of wild fish are exposed are greatly reduced in culture. This may also result in lowered overall levels of aggression. The performance of cultured fish generally may be impaired because of this. In particular, many cultured males may not compete effectively with wild males in pairing with wild females.

In addition, both large and small adult males of the salmonid *Oncorhynchus kisutch* are more effective in competitive spawning than those of intermediate size. Gross (1985) considered this to result from disruptive selection for size at maturity. Cultured *S. salar* males may be disadvantaged in this way since they are often smaller than wild males at adulthood. Crossing will be reduced if farmed males spawn less with wild females than either large, dominant wild adults or sneaking wild parr (Hutchings and Myers, 1988).

Under other circumstances, normally dominant wild males may be prevented from crossing with smaller cultured females by their large size. Female choice of spawning site is in part determined by body size. The lesser flows and water depths likely to be particularly favoured for spawning by small cultured females may preclude the attendance of larger wild males. Cultured males may be reciprocally favoured because of their size-match with cultured females.

Any restraints to the crossing of wild and farmed fish which depend on alterations in the behaviour or physiology of cultured fish caused by the culture environment itself will only act in the first generation of escape or release. Even in this group, the strength with which the restraints may act will be dependent on the stage of life at which release has occurred. Early releases will revert most fully to the condition of wild fish.

However, physiological incompatibility based on genetic differences may limit crossing to an extent which is independent of stage of release. Heggberget (1989) described wide variation in the date of peak spawning in different rivers in Norway. Heggberget hypothesised that the differences were adaptive and a response to differences in over-winter temperature. Spawning early in streams where winter temperatures are low and later where temperatures are higher may result in the matching of the duration of egg incubation to optimum hatching date.

Spawning date may be determined by environmental cues which differ between streams before or as spawning takes place. However, to be of adaptive value in the context of Heggberget's hypothesis, any such cues must be predictive of over-winter temperatures. It seems unlikely that cues of consistent predictive value exist, at least in temperate regions of Scotland, where the same wide range of peak spawning dates exists. In Scotland, as in Norway, peak spawning date also appears correlated with over-winter temperatures but in many rivers peak spawning takes place in the transitional period when winter temperatures are becoming established. Peak spawning date is relatively fixed at single sites but the time at which water temperatures fall to winter levels is often weather dependent rather than seasonal. As a consequence, in single Scottish rivers, fish may spawn in different years at about the same date but over a relatively wide part of the normal temperature range.

The differences in spawning date identified by Heggberget probably therefore result from stock specific selection for spawning date itself. If the differences are genetic they may limit the crossing of escapes or releases from culture with native fish, through asynchronous sexual maturation.

Most of the factors listed above as possible limits on the crossing of wild and farmed fish of the single species *S. salar* might also be considered to be among those limiting the intergeneric crossing of brown trout (*S. trutta*) and Atlantic salmon. Yet such crossing can be demonstrated to occur. Salmon-trout hybrids can be identified electrophoretically particularly where trout have been introduced into the salmon's range (Verspoor, 1988) or where distribution of one or other species is patchy (Garcia de Leaniz and Verspoor, 1989). Since hybridisation between these species is occasionally quite common, it seems unlikely that any of the factors which may limit the intraspecific crossing of native and introduced salmon will prove to be of major or consistent significance.

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IS AQUACULTURE LIKELY TO AFFECT THE GENETIC INTEGRITY OF WILD POPULATIONS?

by

Eric Verspoor

DAFS Marine Laboratory, Victoria Road, Aberdeen

Farmed Atlantic salmon ascending into a river with an existing wild population of salmon may potentially cause a genetic impact through ecological or reproductive interactions. Ecological interactions could cause a reduction in the numbers of wild fish in subsequent generations increasing genetic drift and reducing genetic variability. Ecological interaction could also cause selective pressures on wild populations to change and so change their genetic make-up. Whether a change occurs will be dependent on the specific nature of the interaction and the circumstances in which it occurs. In contrast, interbreeding will always have a genetic impact. However, its significance will be highly dependent on the degree of adaptively relevant genetic differentiation existing between the farmed and wild stocks involved.

A number of ecological interactions can be envisaged which might give rise to genetic change in the wild stock. The first is the introduction of a disease vector to which the farm but not the wild stock is resistant. Here the wild population would be reduced in size, at least short term and possibly for a large number of generations, until the vector disappears or the population evolves resistance. The second is interference with reproduction. For example, farmed fish may breed later and superimpose their redds on those of wild fish, or they may compete with wild fish for a limited amount of suitable spawning sites. This might both reduce numbers of wild fish the next generation as well as select for changes in spawning timing. Such specific changes may be immediately adaptive but also disruptive of the overall coadaptive nature of the existing gene complex. This could lead to a lower productivity in the longer term until selective pressures restore an optimal genetic make-up. Ecological interactions will also occur between the offspring of farm fish and those of wild fish. For example, with respect to territories and food. Unfortunately, few studies are available to shed light on the actual and potential extent to which ecological interactions might be adverse.

The impact of interbreeding between wild and farm salmon will be to introduce into the wild population genetic types which would normally be infrequent or absent. As the genetic make-up of wild populations will have been moulded by natural selection to provide the mix of genetic types which is optimal for long-term survival and maximum productivity, the new genetic types will on average be expected to be less well adapted. If so, then the productivity of the population will decrease until selection can restore an optimal genetic constitution for the population. This may take many generations. The degree of decrease in productivity and the time taken to restore it will depend on the extent to which the farm stock differs genetically. The genetic change caused by interbreeding may also result in short-term, or even permanent changes to the character of the wild population affected. Studies which have been carried out on interbreeding between salmonid stocks suggest that hybrids between native and hatchery fish will often do less well than native fish in the wild, for example, with regard to juvenile survival and probability of returning as an adult to the natal river to spawn.

Concern for adverse impacts of escaped farm salmon on wild salmon populations is justified based on our understanding of population genetics and on the evidence currently available. How concerned we should be is unclear but undoubtedly the extent of any impact will be highly dependent on the numbers of farm salmon relative to wild salmon involved in the interactions which occur.

LIST OF PARTICIPANTS AT JOINT NASCO/ICES MEETING ON THE
'GENETIC THREATS TO WILD SALMON POSED BY SALMON AQUACULTURE'

BAILEY, John
Atlantic Salmon Federation
Box 429
St. Andrews, N.B.
CANADA EOG 2XO

BERNTSSON, Karl - Erik
Fishery Board of Sweden
Box 2565
Goteborg
SWEDEN

BROWNE, John
Fisheries Research Centre
Abbotstown, Castleknock,
Dublin 15
IRELAND

CROSS, Tom
University College Cork
Zoology Department
Cork
IRELAND

CUTTING, Richard E.
Dept. of Fisheries & Oceans
P.O. Box 550 Stn "M"
Halifax N.S.
CANADA

DOYLE, Jacqueline
Fisheries Research Centre
Abbotstown, Castleknock,
Dublin 15
IRELAND

DYBERN, Bernt I.
National Fisheries Board of Sweden
Institute of Marine Research
Box 4, 45300 Lysekil
SWEDEN

FERGUSON, Andrew
Queen's University
Dept. of Biology
David Keir Building
Belfast BT7 1NN
NORTHERN IRELAND

GAUSEN, Dagfinn
Directorate for Nature Management
Tungasletta 2
7004 Trondheim
NORWAY

GRIZEL, Henri
IFREMER
B.P. 133
17390 La Tremblade
FRANCE

HANSEN, Lars P.
Norwegian Institute for Nature Research
Tungasletta 2
7004 Trondheim
NORWAY

HARACHE, Yves
IFREMER
BP 70 Centre de Brest
29263 Plouzane
FRANCE

HINDAR, Kjetil
NINA
Tungasletta 2
N 7004 Trondheim
NORWAY

HUTCHINSON, Peter
NASCO
11 Rutland Square
Edinburgh EH1 2AS
SCOTLAND

ISAKSSON, Arni
Institute of Freshwater Fish
P.O. Box 5252
Reykjavik 125
ICELAND

JACOBSEN, Vogg H.
Danish Institute for Fisheries and Marine Research
Charlottenlund Castle
DK-2920 Charlottenlund
DENMARK

x JANSSON, Hakan WGen. (instead of L. Nyman).
Salmon Research Institute
S-81070 Alvkarleby
SWEDEN

x JORSTAD, Kuut, E. WGen. (instead of G. Naevdal)
Institute Marine Research
Bergen,
P.O. Box 1870
502Y - Nordnes
Bergen
NORWAY

MC ARDLE, John
Fisheries Research Centre
Abbotstown, Castleknock,
Dublin 15
IRELAND

MAC KENZIE, D.J.
Atlantic Salmon Trust
Moulin
Pitlochry, Perthshire
SCOTLAND

MUNRO, Alan L.S.
Dept of Agriculture & Fisheries for Scotland
Marine Laboratory,
P.O. Box 101,
Victoria Road,
Aberdeen,
SCOTLAND

MORK, Jarle
Biol. St./University of Trondheim
Bynesvesen 46
N-7018 Trondheim
NORWAY

PIGGINS, D.J.
Salmon Research Trust
Newport
Co. Mayo
IRELAND

PORTER, Rex
Dept. of Fisheries & Oceans
P.O. Box 5667
St. John's Nfld
CANADA AIC 1X1

x SAUNDERS, Richard L. WGen.
Dept of Fisheries & Oceans
Biological Station
St. Andrews, N.B. EOG 2XO
CANADA

SINDERMANN, Carl
National Marine Fisheries Station
Oxford Lab
Oxford MD
USA

THORPE, John
DAFS
Freshwater Fisheries Laboratory
Pitlochry
SCOTLAND PH16 5LB

TWOMEY, Eileen
Fisheries Research Centre
Abbotstown, Castleknock
Dublin 15
IRELAND

UTTING, Susan
MAFF
Fisheries Laboratory
Benarth Road
Conwy Gwynedd, Wales
UNITED KINGDOM

VERSPoor, Erik
DAFS Marine Lab.
Victoria Road
P.O. Box 101
Aberdeen
SCOTLAND

x VILLWOCK, Wolfgang WGen.
University of Hamburg
D-2000 Hamburg 13
FEDERAL REPUBLIC OF GERMANY

WALLENTINUS, Inger
University of Goteborg
Carl Skoffsbergs gata 22
S-Y1319 Goteborg
SWEDEN

WINDSOR, Malcolm
NASCO
11 Rutland Sq.
Edinburgh
SCOTLAND

WHELAN, Ken
Central Fisheries Board
Balnagowan
Mobhi Boreen
Glasnevin
Dublin 9
IRELAND

x YOUNGSON, Alan WGen.
DAFS
Marine Laboratory
Aberdeen
UNITED KINGDOM

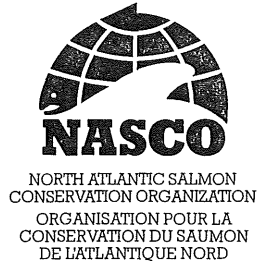
x PURDOM, Colin WGen.
Fisheries Laboratory
Lowestoft NR33 OHT
Suffolk
UNITED KINGDOM

NASCO 11 Rutland Square Edinburgh EH1 2AS Scotland UK
Telephone: 031-228 2551 Telex: 94011321 NASC G Fax: 031-228 4384

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1 June 1989

Dr Wolfgang Villwock
University of Hamburg
D-2000 Hamburg 13
Federal Republic of Germany



Dear Dr Villwock.

JOINT NASCO/ICES MEETING

It was good to meet you in Dublin and I hope that the rest of your Working Group meeting went well. Thank you for the comments on the paper, we were able to include most of these in the final version as sent to NASCO Council. I attach a copy.

We were very pleased that the genetics working group participated in this meeting and I look forward to further contact.

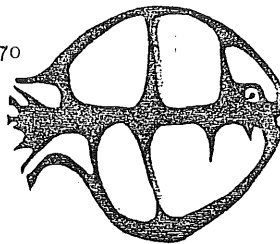
Yours sincerely

Malcolm Windsor

Malcolm Windsor
Secretary

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A DATE FOR YOUR DIARY

THE FISHERIES SOCIETY OF THE BRITISH ISLES

in collaboration with

The School of Biology and Biochemistry, Queen's University of Belfast
announce an International Symposium on

BIOCHEMICAL GENETICS AND TAXONOMY OF FISH

at

QUEEN'S UNIVERSITY, BELFAST, NORTHERN IRELAND

22 - 26 JULY 1991

The symposium will review the application of isozyme, mitochondrial DNA, nuclear DNA and RNA markers to the study of family, population and species level problems in natural and artificial stocks of fish. Selected papers based on contributions to the symposium will be published in a special issue of the Journal of Fish Biology.

For further information or to offer suggestions please contact:

Dr Andrew Ferguson
Division of Environmental and Evolutionary Biology
School of Biology & Biochemistry
David Keir Building
Queen's University
Belfast BT9 5AG
Northern Ireland, UK

Tel: 44 (0)232 661111 x. 4150

Fax: 44 (0)232 247395

