



Genetic Diversity in Commercially Exploited Fish Species

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Interim Report

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Genetic Diversity in Commercially Exploited Fish Species

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Introduction

This document was produced during a three-day seminar and workshop on the genetic diversity of commercially exploited fish species in Nordic waters held at Hólar College, Iceland. The aim of the seminar was to discuss current knowledge regarding the effects of commercial fishing activities on the genetic diversity of wild, marine species of fish in Nordic waters, and to provide recommendations for necessary actions to minimize further loss of such diversity. This document expresses the joint view of the selected expert scientists invited to the meeting (Appendix 1), and the content concerns fish populations exploited in Nordic waters.

During the first day of the meeting short presentations were given by some of the participants. The abstracts of these presentations are provided in Appendix 2 and the full workshop program in Appendix 3. Topics for working groups during workshop sections, and the initial questions outlined for the discussions are provided in Appendix 4.

The project was led by Dr. Teija Aho, Swedish National Board of Fisheries, Institute of Coastal Research, Öregrund, Sweden, and this report was edited by Dr. Linda Laikre, Department of Zoology, Division of Population Genetics, Stockholm University, Sweden.

Terminology

Genetic diversity (synonymous with *genetic variability*, *intraspecific (bio)diversity* and *biological diversity on the gene level*) represents the existence of variants (alleles) of individual genes resulting from alterations of the DNA sequence. The alleles of a particular gene may occur in different frequencies in different groups of interbreeding individuals (populations) and the genetic variation of a particular species is therefore distributed both within populations (expressed as different allele combinations between individuals) and between populations (differences in occurrence and frequency between populations).

We interpret the *precautionary principle* to imply that lack of scientific information on potentially adverse effects on genetic diversity should not be used as a reason to prevent or postpone measures to avoid or minimize such negative effects. This interpretation is in line with that of the Cartagena protocol on biosafety to the Convention on Biological Diversity as well as that of the Preamble to the Convention on Biological Diversity.

A *genetically sustainable fishery* implies a fishery that does not result in unacceptable loss of genetic diversity and/or unacceptable change of the genetic composition of distinct populations or population systems. It is currently not clear what levels of loss/change that may be regarded as acceptable.

Genetic structure of exploited marine fish species

Several exploited marine fishes (e.g. Atlantic cod, salmon, and herring) are divided into genetically distinct local populations, with limited migration among population units, implying that recruitment to a large extent is locally determined. The geographic distribution range of local populations varies substantially and depends on a number of factors including oceanographic features and ecological interactions. The presence of a population structure implies that local populations evolve as semi-independent units with a restricted gene flow (exchange of genetic material) between them. Natural selection may favour particular alleles in particular geographic regions, resulting in so called local adaptation (e.g. to low salinity in the Baltic).

Threats to genetic diversity

Fishing and aquaculture activities pose potential threats to genetic diversity of wild fish populations in different ways. For instance, over-harvest may reduce population sizes to levels where inbreeding and loss of genetic diversity through random events (by the process of genetic drift) become serious problems, or may result in extinction of local populations or population segments. Fishing, in particular when directed towards certain sizes or age classes, may alter the genetic composition of fish populations through selection. This may occur directly if the selected characteristics of the fish being caught are under genetic control, or indirectly, when they are coupled with such traits. (For example, if particular alleles result in an increased growth, these alleles may be removed from the population to a larger extent than alleles that promote a slower growth.) Further, fishing may affect natural levels of genetic exchange (gene flow) between local populations, which in turn may alter the genetic population structure.

Intentional or unintentional release of fish may result in hybridization between released and naturally occurring conspecifics which, in turn, leads to alterations of the genetic composition and may lead to breakdown of locally adapted gene complexes in the wild populations. Releases may also change the demographic characteristics of populations in a fashion that result in increased rates of inbreeding and/or loss of genetic diversity.

Current knowledge on genetic effects of fisheries

Small populations are more vulnerable to genetic erosion than larger ones. Species that naturally exhibit relatively low census numbers, e.g. top predators such as tunas and rays, may be more sensitive to reductions in census numbers than species occupying lower trophic levels.

Most economically important stocks are overexploited. Still, marine fish populations are generally quite large from a genetic perspective (thousands to billions of individuals). Recent studies indicate, however, that the genetically effective population sizes (a complex parameter that determines the rate of inbreeding and loss of genetic diversity due to chance events) may be much smaller than previously anticipated. These findings indicate that the rate of genetic erosion may be more pronounced than census numbers alone indicate.

Change in genetic diversity over time in harvested fishes in Nordic waters has only been monitored in a few cases; some of these studies show indications of loss of genetic variation over time (e.g. salmon and cod).

Several studies suggest that commercial fishing has altered the genetic composition of exploited fish stocks through selection (e.g. cod and plaice). Fishing is a strong evolutionary force and generally the most important cause of adult mortality for exploited species. All fishing gear is selective and fishing is a major factor influencing phenotypic (e.g., body size), demographic (e.g., age structure), and genetic characteristics (e.g., allele frequencies) of fish populations.

Fishing can cause local populations to go extinct. If local populations are genetically distinct this implies overall loss of unique genetic variation.

Stocking is commonly used to support sport and commercial fisheries. The expanding aquaculture activities inevitably result in unintended escapes of cultured fish into the natural environment. There is scientific consensus that both deliberately and unintentionally released fish pose a serious threat to the genetic integrity of wild populations in several ways, including loss of local adaptations and genetic characteristics, genetic homogenization and demographic changes.

Conclusions and recommendations

Management of marine fishes should be based on information on genetic population structure rather than geography (e.g. ICES divisions) or tradition alone. Currently, genetic information is insufficiently recognized in management decisions, and the precautionary principle is neglected in this respect.

If information on the genetic population structure of harvested populations is not incorporated into management practices, erosion of genetic variability may go unnoticed, and the capability of species to adapt to environmental change (e.g. global warming) may thus be lost. Actions aiming at increasing the incorporation of available knowledge on population and conservation genetics, in general, and in particular for individual species, are highly warranted.

Current harvest methods are generally selective. Regulation based on mesh size and minimum size has selective effects on the fish, which, in turn, may have unwanted genetic effects. Further investigation of this matter is urgently needed.

Stocking aimed exclusively at supporting commercial or sport fisheries poses a threat to genetic resources and should be modified to meet criteria for biological sustainability.

Specific recommendations

1. The precautionary fisheries management, as it is currently applied in the ICES area (including the Nordic countries), should be evaluated from the perspective of genetic consequences of current fishing practices.

2. A scientific review of the available information on genetic diversity of marine resources in the Nordic and adjacent waters is warranted. This review should be conducted by a selected team of population genetics experts, and should also aim at identifying areas/species where information is lacking.
3. Current fisheries management units should be evaluated with respect to the information on the genetic population structure. Genetically sustainable management necessitates the identification of the extent of harvest of individual, genetically distinct populations. The potential of such identification should be evaluated for individual species, as well as the possibility to apply methods for mixed fisheries analysis in situations where harvest on individual, genetically distinct populations (e.g. on spawning grounds) is not considered feasible.
4. A distributed fish tissue sample and data bank hosted by e.g. the Nordic museums or universities should be created to ensure that existing tissue collections are kept beyond the life time of individual projects and scientists. This action should be fully coordinated and include a system for sharing information as well as routine collection of new materials to support future monitoring and research needs on e.g. genetic effects of various fisheries management practices. The possibility for creating such a tissue/data bank in connection to or within the framework of the clearing house mechanism of the CBD (Convention on Biological Diversity) and/or the Global Biodiversity Information Facility (GBIF) should be investigated.
5. A strategy for monitoring changes in genetic diversity, on both the molecular and quantitative genetic levels, and identification of genetic indicators reflecting such changes, should be initiated.
6. Increased communication between different research communities (e.g. population geneticists and stock assessment scientists), transparency of the decision-making process, and contacts between decision makers and researchers should be encouraged and facilitated. Developing fora for increased interaction between these groups warranted (see suggestions for workshops below).
7. The genetic consequences of selective fishing gear in use or under development should be evaluated, as well as the possibilities of using fishing gear and practices with different selection properties to minimize negative genetic impacts.
8. The neglect of ICES advice regarding fishing quotas is serious as these recommendations provide a minimum protection against excessive levels of exploitation. Compliance with the precautionary approach would imply respecting the ICES advice, and actions needed for achieving such compliance are recommended.
9. Aquaculture and stocking that may result in a release of genetic material to

natural populations should be evaluated from a conservation genetic perspective prior to being conducted.

10. Information and education in fish biology, conservation genetics and the potential effects of exploitation should be encouraged at all levels. In particular, the general public in the Nordic countries typically has limited knowledge on these important issues, and information activities of various forms are needed.
11. The potential genetic effects of management strategies such as Marine Protected Areas (MPAs) and Ecosystem based Fishery Management should be scientifically investigated and evaluated.

The following three workshops are suggested

- A multi-disciplinary meeting/workshop on the genetic consequences of fisheries and fisheries management.

Suggested participants: scientists of various fields of importance for fisheries (including population geneticists, fishery biologists, ecologists, sociologists, ethnobiologists, etc.), decision makers at different levels, fisheries managers, fisheries organizations, sport fishing organizations, etc.

- A workshop on the possibilities and strategies for creating a distributed fish tissue sample and data bank (recommendation 4 above).

Suggested participants: Representatives from museums, universities, and other sampling collection institutions, representatives from the national fisheries boards, population geneticists, ecologists, and other researchers, fisheries organizations, as well as information technologists.

- A scientific expert seminar and workshop on the importance of neutral vs. adaptive genetic variation in the context of fisheries management.

Suggested participants: A limited number of expert scientists (population and quantitative geneticists, genomic experts, fishery biologists).

Appendix 1

**Expert-seminar on Genetic Diversity in Fish with focus
on Commercially Exploited Species, Hólar College, Iceland, October 6-8, 2004**

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Appendix 2

**Expert-seminar on Genetic Diversity in Fish with focus
on Commercially Exploited Species, Hólar College, Iceland, October 6-8, 2004**

Abstracts

What do genetic markers tell us about population (or stock) differentiation?

Juha Merilä, Ecological Genetics Research Unit, Department of Biological and Environmental Sciences, University of Helsinki, Finland

Neutral genetic markers used in standard population genetic analyses, such as microsatellites, are useful in gaining insights on population history and demography. However, their utility inferring boundaries between demographically distinct population units is limited in situations where these units are young - like most populations inhabiting Nordic countries - and have large effective population sizes, as appears to be typical for most marine species of fish. Although the data are still scarce, the pattern emerging from comparative studies genetic differentiation in neutral marker genes (FST) and genes coding (ecologically important) quantitative traits (QST) indicates that levels of differentiation in the latter are typically many-fold greater than in the former. In other words, even in the absence of differentiation in neutral marker genes, populations are typically well differentiated in genes coding quantitative traits. This is not surprising given the fact that differentiation in genes coding quantitative traits is driven by natural selection arising from local environmental differences, whereas differentiation in neutral marker genes evolve through the slow process of random genetic drift (and mutation). Hence, I argue that management decisions based solely on assessment of neutral genetic variability can lead to loss genetic biodiversity (i.e. locally adapted populations/stocks) due to fact that neutral markers are unlikely to recognize locally adapted populations/stocks. It is argued that sustainable fisheries management should seek to evaluate genetic basis for quantitative trait (e.g. age and size at maturity) differentiation, and not rely solely on inference drawn from neutral marker genes.

Genetic diversity and differentiation in Baltic Sea fish populations

Carl André and Kerstin Johannesson, Department of Marine Ecology, Tjärnö Marine Biological Laboratory, Göteborg University, Sweden

Many marine fish species are composed of populations that together occupy a broad geographical range over a suite of habitats. Physical barriers to dispersal among populations are, however, less evident in comparison with limnic and terrestrial environments. The Baltic Sea is the largest brackish water volume in the world and several marine species find marginal habitats there. We compiled available published and unpublished genetic data on genetic diversity and differentiation in Baltic populations compared to Atlantic populations for seven fish species: Cod, herring, eel, white fish, plaice, salmon and turbot. The genetic markers used were supposedly neutral (allozymes, microsatellite and mitochondrial DNA). For all species except Eel, genetic diversity, expressed as heterozygosity or nucleotide diversity, were lower in the Baltic compared to

the Atlantic, and for several species, Baltic populations were genetically differentiated from Atlantic counterparts. The genetic distance between populations increased sharply over the salinity transition zone in Öresund and the Belt Sea (eg, cod, turbot and herring). Since the correlation between diversity in neutral genetic markers and diversity in genetic traits important for adaptation is often low, the management implication of the lowered diversity in the Baltic remain unclear. The high degree of differentiation between Baltic and Atlantic populations on, the other hand, indicate that migration among populations is restricted, and hence that, if depleted, Baltic fish stocks will not be replaced by adjacent stocks in a time-perspective relevant to management.

Statistical power when combining the information from multiple loci for detection of population divergence in marine species

Nils Ryman, Division of Population Genetics, Department of Zoology, Stockholm University, Sweden

An increasingly common question in conservation and evolutionary biology is whether a set of samples are likely to represent the same gene pool. Several statistical techniques are being applied when addressing this type of problem, but there has been little discussion about their relative merits for detection of genetic heterogeneity. This lack is particularly obvious for methods used to combine the information from multiple loci.

In a typical situation an investigator has collected tissue samples from two or more groups of individuals which are separated in space or time. Application of some biochemical or molecular techniques provides genotypes of the sampled individuals at one or more nuclear loci or at the mitochondrial genome, and each sample is described in terms of its size and allele (or haplotype) frequencies. The specific scientific questions may vary from study to study, but a very basic one which frequently determines how to proceed with the analysis is the following one: Are the allele frequency differences observed among samples large enough to suggest that all the samples are not drawn from the same population (gene pool)? It appears that in most cases the underlying evolutionary model is one of "selective neutrality - isolation - genetic drift", which implies that all polymorphic loci examined are potentially informative with respect to the question of overall genetic heterogeneity.

The general statistical approach most frequently used is first to conduct a contingency test for allele frequency homogeneity for each locus separately, and in a second step to evaluate the simultaneous information from all loci examined. The test procedure applied to each individual locus (contingency table) implies assessment of the probability of obtaining - if the null hypothesis (H_0) of equal allele frequencies is true - an outcome that is as likely as, or less likely than, the observed one. In the second step the results from the separate tests are combined for evaluation of the joint null hypothesis that there is no allele frequency difference at any locus.

Presently there appears to be two conceptually different strategies in use for testing the joint null hypothesis. One technique is based on the summation of chi-square statistics and utilizes the fact that the sum of a series of chi-square distributed variables also follows a chi-square distribution. Another approach is used by investigators applying the Bonferroni

technique to test if the heterogeneity observed at any particular locus can be regarded significant when considered separately.

We have compared the power of the above statistical methods for detecting genetic heterogeneity when multiple loci have been scored. The results show that the efficiency may differ dramatically between the two approaches and, contrary to what might be expected, this difference may become enhanced as the number of loci increases.

Promises and pitfalls of genetic mixed-stock analysis in sustainable fisheries management

Dorte Bekkevold, Danish Institute for Fisheries Research, Department of Inland Fisheries, Silkeborg, Denmark

Various statistical approaches enable the application of genetic marker analysis to identify the proportions of fish from different spawning population origin in mixed-stock fisheries. I briefly introduce two such approaches and give examples of their application in Atlantic herring, where both within- and between years temporal variation in mixed stock composition is elucidated, and in Brown trout where a recent analysis has shown that domesticated juveniles stocked into wild populations rarely complete an anadromous life cycle. The interpretation of results obtained in mixed-stock analyses together with potential statistical problems are discussed.

Fisheries-induced evolutionary changes: methods and case studies

Mikko Heino, Institute of Marine Research, Bergen, Norway, and International Institute for Applied Systems Analysis, Laxenburg, Austria

Fishing is a potent agent for driving adaptive genetic changes in exploited fish stocks: today, fishing is the dominant source of mortality in most commercially exploited fish stocks. Life-history theory predicts that increased mortality at potential ages and sizes at maturation genetically selects for an earlier maturation. Indeed, commercially exploited fish stocks often show trends towards earlier maturation. However, another plausible explanation exists: earlier maturation may simply reflect phenotypic plasticity. Understanding the nature of phenotypic changes in exploited fish populations has until recently been hindered by the difficulties involved in disentangling plastic and evolutionary components in life history changes. A new method for estimating probabilistic reaction norms for age and size at maturation is helping to overcome this problem, and, in most of the cases analysed so far, is suggesting that there is a genetic component in the observed trends in age and size at maturation. In this talk I give an overview of the probabilistic reaction norm method as well as progress with empirical case studies that have ensued.

Larval drift and population structure in coastal and offshore cod

Halvor Knutsen, Institute of Marine Research, Flødevigen Marine Research Station, Norway

The Atlantic cod (*Gadus morhua*) represents one of the world's economically most important marine species - a species currently suffering from heavy over-exploitation. Earlier studies have demonstrated that Atlantic cod is geographically structured into semi-isolated populations extending only kilometers in coastal regions of Skagerrak. Here, we report results of genetic analyses showing that juvenile cod caught inside the fjords of Skagerrak in 2001 resembled North Sea spawning cod while differing significantly from the corresponding coastal populations. Modelling ocean currents, we find large annual variation in water-flux from the North Sea into the Skagerrak during the critical period when cod eggs and larvae remain pelagic and subject to passive transportation by ocean currents, suggesting that variable larval drift from the North Sea may explain the temporal occurrence of North Sea cod in coastal waters. Using long-term abundance estimates for cod populations along the Norwegian Skagerrak coast, we substantiate this suggestion by demonstrating that the abundance of young-of-the-year cod in these coastal populations are profoundly affected by both the size of the North Sea breeding stock and the strength of the inflow of North Sea waters into Skagerrak.

Estimation of effective population size in non-isolated populations: a cautionary note

Anti Vasemägi, Swedish University of Agricultural Sciences, Department of Aquaculture, Umeå, Sweden/(Estonia)

Marine species pose several serious challenges for application of temporal method to estimate variance effective population size (N_e). In order to obtain biologically meaningful N_e estimates several assumptions have to be filled. Particularly, it is assumed that all changes in genetic composition are caused by random genetic drift and no migration, mutations and selection have occurred during the time interval studied. I used historical anadromous Atlantic salmon samples taken over 18 years period as an example to illustrate some of the difficulties involved in N_e estimation. Based on spatio-temporal genetic analysis of Baltic salmon populations substantial difference in N_e estimates was observed when migration was neglected or included in the maximum likelihood estimation model developed by Wang and Whitlock (2003). I demonstrate that I) N_e e can be strongly affected by migration II) migration rates are not necessarily uniform in time. In order to get biologically meaningful N_e estimates combination of temporal and spatial analysis is highly recommended.

Small effective population sizes in marine fishes: Fact or fiction?

Einar Eg Nielsen, Danish Institute for Fisheries Research, Department of Inland Fisheries, Silkeborg, Denmark

We used DNA from archived otoliths to explore the temporal stability of the genetic composition of two cod populations, the Moray Firth (North Sea) sampled in 1965 and

2002, and the Bornholm Basin (Baltic Sea) sampled in 1928 and 1997. We found no significant changes in the allele frequencies for the Moray Firth population. Accordingly, the effective population size (N_e) was estimated to exceed 732. For the Bornholm Basin population, subtle but significant genetic changes over time were detected with estimates of N_e above 766. Calculations of the expected levels of genetic variability under different scenarios showed that the number of alleles commonly reported at microsatellite loci in Atlantic cod is better explained by effective population sizes exceeding thousands. Recent fishery induced bottlenecks can, however, not be ruled out as an explanation for the apparent discrepancy between high levels of variability and recently reported estimates of N_e in cod around one hundred and N_e/N ratios of 10^{-5} . Our data strongly suggest that small effective population sizes are not likely to be a general concern for cod populations and, accordingly, they do not face any severe threat of losing evolutionary potential due to genetic drift.

On the impacts of geographical barriers and life history on population structure; Atlantic cod vs. Polar cod

Snæbjörn Pálsson, Department of Biology, University of Iceland, Iceland

Pelagic marine fishes are characterized by shallow genealogies and show often little or no population structure at genetic markers over wide geographical areas. Most genetic studies have been conducted on species from temperate regions, such as Atlantic cod, which has been studied extensively. Here I present a study on mtDNA variation in Polar cod, a close relative to Atlantic cod, which has a circumpolar distribution. Aside from the distribution being confined to high latitudes, Polar cod differs from Atlantic cod in several ways which leads to interesting comparisons of genetic variation in these species. For example, fecundity and different responses to climatic changes may have shaped the genealogy of these species differently. Sequence variation indicates both latitudinal and longitudinal gradients. The clearest patterns in population structure are found when geographical barriers exist among areas sampled.

Genetic effects of the establishment of marine reserves

Dorte Bekkevold, Danish Institute for Fisheries Research, Department of Inland Fisheries, Silkeborg, Denmark

In recent years the establishment of marine protected areas (MPAs) has attracted scientific interest, both as a conservation and a management tool. Few attempts have been made to predict genetic effects of MPAs. MPA establishment is often associated with the expectation that positive effects will emanate across reserve boundaries and act on an ecosystem scale. Genetic effects associated with MPAs are expected to be highly dependent on the life history, migratory behaviour, but also exploitation history of the species under concern. MPAs may facilitate retention of genetic variability on the species level. Further, a modeling attempt suggests that MPAs may be a useful means of counteracting counter-productive selective responses to size-selective fisheries. It is recommended that genetic effects of MPAs are examined further and are incorporated into evaluations of the sustainability of different fisheries strategies.

Expert-seminar

GENETIC DIVERSITY IN FISH WITH FOCUS ON COMMERCIALY EXPLOITED SPECIES

6-8 October, Hólar College, Iceland

Project coordinator: Dr Teija Aho, National Board of Fisheries, Institute of Coastal Research, Öregrund, Sweden

Project funding: Nordic Council of Ministers (Nordiska ministerrådet)

Program

Wednesday October 6

- 9⁰⁰ - 9¹⁵ Opening of the seminar – Teija Aho, project coordinator
- 9¹⁵ - 9⁴⁵ What do genetic markers tell us about population (or stock) differentiation?
- Juha Merilä
- 9⁴⁵ - 10¹⁵ Genetic diversity and differentiation in Baltic Sea fishes - Carl André
- 10¹⁵ - 10⁴⁵ Coffee
- 10⁴⁵ - 11¹⁵ Statistical power for detection of population divergence in marine species -
Nils Ryman
- 11¹⁵ - 11⁴⁵ Promises and pitfalls of genetic mixed-stock analysis in sustainable fisheries
management - Dorte Bekkevold
- 11⁵⁰ - 12²⁰ Fisheries-induced evolutionary changes: methods and case studies -
Mikko Heino
- 12²⁰ - 13³⁰ Lunch
- 13³⁰ - 14⁰⁰ Larval drift and population structure in coastal and offshore cod -
Halvor Knutsen
- 14⁰⁰ - 14³⁰ Estimation of effective population size in non-isolated populations: a
cautionary note - Anti Vasemägi
- 14⁴⁰ - 15¹⁰ Small effective population sizes in marine fishes; fact or fiction? -
Einar Eg Nielsen
- 15¹⁰ - 15³⁰ Coffee
- 15³⁰ - 16⁰⁰ On the impacts of geographical barriers and life history on population
structure; Atlantic cod vs. Polar cod - Snæbjörn Pálsson
- 16⁰⁰ - 16³⁰ Genetic effects of the establishment of marine reserves - Dorte Bekkevold

16³⁰ - 17³⁰ Discussion
 c. 19⁰⁰ Dinner

Thursday October 7

8³⁰ - 9⁰⁰ Workshop: Initiating working groups, topics and aim of discussion
 9⁰⁰ - 11⁰⁰ Working group discussions
 11⁰⁰ - 11¹⁵ Coffee
 11¹⁵ - 12³⁰ Working group discussions
 12³⁰ - 13³⁰ Lunch
 13³⁰ -
 Excursion
 Official Workshop Dinner

Friday October 8

9⁰⁰ - 11⁰⁰ Working group discussions
 11⁰⁰ - 11¹⁵ Coffee
 11²⁰ - 12³⁰ Working group discussions, report writing
 12³⁰ - 13³⁰ Lunch
 13³⁰ - 15³⁰ Plenary: report from working groups, final discussion
 15³⁰ - 15⁵⁰ Coffee
 15⁵⁰ - 17⁰⁰ Plenary: final discussion

Appendix 4

Working group topics:

Working Group 1:

Knowledge on genetic structure and dynamics of marine fish species in the Nordic countries

Working Group 2:

Knowledge on genetic effects of fishing and fisheries management

Working Group 3:

Background information on fish stocks and fisheries management practices of importance for conservation genetic management

Suggestions for questions to be addressed:

- What is the current status of commercially harvested fish stocks i Nordic waters?
- How is the harvest carried out? Methods? Expected genetic effects?
- On what grounds are fishing quotas set? Genetic concerns?
- What do we know about the spatial genetic structure of marine fish species in Nordic waters?
- What do we know about the temporal stability of these structures?
- What do we know about the rate of loss of genetic diversity of marine fish species?
- What do we know about the effective population size of harvested populations?
- How do we identify management units?
- What are the potential threats to genetic diversity associated with fishing? What do we know about these threats i Nordic waters?
- What are the potential threats to genetic diversity associated with stocking? What do we know about these threats i Nordic waters?
- How should individual species be managed to accomplish genetic sustainability?
- What are the most urgent lines of actions? Priorities?
- What elements should be included in a strategy to eliminate threats of extinction and genetic changes in wild fish populations posed by fisheries and environmental changes?