



Genetic research on commercially exploited fish species in Nordic countries

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Content

Preface.....	7
Summary	9
1. The role of genetics in fisheries management: current and future perspectives	11
1. 1 Introduction.....	11
1. 2 Objectives.....	13
2. Review of current knowledge and future perspectives	15
2. 1 Identification of population structure	15
How can genetic information be used in management?	16
Empirical examples.....	17
Summary of what we know.....	18
What information is needed in the future?	19
2. 2 Stocking	20
How can genetic information be used in management?	22
Empirical examples.....	22
Summary of what we know.....	23
What information is needed in the future?	24
2. 3 Cage-escapes from aquaculture	25
How can genetic information be used in management?	27
Empirical examples.....	28
Summary of what we know.....	28
What information is needed in the future?	29
2. 4 Fisheries-induced evolution.....	30
How can genetic information be used in management?	31
Empirical examples.....	31
Summary of what we know.....	32
What information is needed in the future?	33
2. 5 Effects of environmental change	34
How can genetic information be used in management?	37
Empirical examples.....	38
Summary of what we know.....	39
What information is needed in the future?	41
3. Recommendations	43
3. 1 General recommendations	43
3. 2 Country-wise recommendations	45
4. References	47
Sammanfattning.....	55
Appendix 1	57
Appendix 2	118
Appendix 3.....	121
Appendix 4.....	123
Appendix 5.....	125
Appendix 6.....	126
Appendix 7.....	128
Appendix 8.....	132

Preface

This document was produced during a three-day workshop with representatives from all Nordic countries held at the Institute of Coastal Research, Swedish Board of Fisheries, Öregrund, Sweden, the 25–27th September 2006. The intention of the workshop was to summarize the current genetic research on commercially exploited fish species in the Nordic countries, and also to highlight how modern genetic techniques can be used to facilitate management of aquatic resources. The need for this was identified in an expert-seminar at Hólar College on Iceland in 2004 (“Genetic Diversity in Commercially Exploited Fish Species”) where selected expert scientists discussed the current knowledge regarding the effects of commercial fishing activities on the genetic diversity of wild, marine fish species in Nordic waters.

The documentation from the meeting is comprised by a report, “The role of genetics in fisheries management: current and future perspectives”. In this report five different subjects where genetic information is crucial for effective management are discussed,

- Identification of population structure,
- Stocking,
- Escapes from Aquaculture,
- Fisheries-induced evolution, and
- Effects of environmental change.

The aim of this report is, however, not to discuss the use of genetics in aquaculture for human consumption.

This document also includes lists of the existing competence in population genetic methods in the Nordic countries and where it is located (Appendix 1 and 2), the status of knowledge on genetic structures in a number of commercially important species occurring in Nordic waters (Appendix 3), national stocking statistics (Appendix 4), statistics of cage-escapes (Appendix 5), list of threatened and declining fish species in the Baltic Sea (Appendix 6), a list of existing genetic research networks in the Nordic countries (Appendix 7), and a more extensive reference list over the genetic research on fish and shellfish conducted in the Nordic countries (Appendix 8).

The outline for a “Nordic network for genetic research on fish” was also discussed, but no further or more detailed conclusions were reached.

The workshop was led by Dr. Teija Aho and Dr. Ann-Britt Florin, and was documented by Dr. Jens Olsson.

Summary

During the last decades the human impact on wild populations of fish has increased drastically worldwide as a result of extensive aquaculture, exploitation for consumption and human-induced environmental change. Such activities likely affect the genetic diversity and structure of targeted species, and maintenance of genetic diversity has in turn been accepted as an internationally and common long-term goal in management of wild populations.

Knowledge of neutral and adaptive genetic diversity is crucial since it provides information on the extent of local adaptations, the genetic population structure and the evolutionary potential of a species and/or population. The genetic architecture of a species also provides the basis for understanding and predicting responses to changes at higher system levels, and the genetic diversity might function as an indicator of key ecosystem functions such as the total viability of the ecosystem. Information on the genetic structure of commercially important fish species is therefore crucial to prevent ecological damage and to ensure sustainable and effective management of exploited stocks and systems. The modern molecular methods developed during recent years offer unique opportunities for studying genetic processes and patterns in wild populations. Sustainable management is therefore greatly facilitated, and in some instances, heavily dependent on the implementation of modern genetic techniques.

Genetic research on commercially exploited fish species in the Nordic countries has a long tradition and is currently undertaken at several research institutes in all countries. The implementation of this research in management has, however, hitherto been limited. This report reviews the current knowledge on genetics in Nordic fish species, identifies the existing gaps in the knowledge, and aim to provide a foundation for advices of future ventures in this area of research. The emphasis is directed to five different subjects where genetic information is crucial for effective management: Identification of population structure, Stocking, Escapes from Aquaculture, Fisheries-induced evolution, and Effects of environmental change. For each subject we discuss how the genetic information can be used in management, give a short summary of the current knowledge on the subject, and highlight the information needed in the future. We also provide a brief overview of the genetic research conducted on fish (both marine and freshwater) and other important aquatic taxa in the Nordic countries, highlight where the existing competence in population genetic methods in the Nordic countries is located, and identify established cooperation and networks between affiliations and countries.

We conclude that in spite of the recent advances there are several considerations that need to be taken into account for sustainable management of targeted stocks of fish and shellfish in the Nordic countries to be effective. For example:

- Genetic information should be included in the management plans of the ICES working groups, and respect should be paid to the advices on fishing quotas from these groups.
- The Nordic countries share and exploit several common and international aquatic resources, and common management practices in the Nordic countries on these resources should therefore be established.
- Aquaculture and stocking that might lead to interbreeding between farmed and wild populations should be evaluated from a conservation genetic perspective prior to being conducted.
- For management to be sustainable, additional research is needed on basic knowledge of the genetic population structure in exploited fish, the success and genetic effects of stocking programmes, the genetic effects of cage-escapes (especially in marine systems), the extent and genetic effects of fisheries-induced evolution, and the genetic effects of climate and environmental change.

1. The role of genetics in fisheries management: current and future perspectives.

1. 1 Introduction

The maintenance of genetic diversity is internationally accepted as a common long-term goal in management of wild populations (Ward 2000; Koljonen 2001; Laikre et al. 2005a). Knowledge of the genetic diversity of species and/or populations is crucial for many reasons. For example, adaptive genetic variation provides information on the extent of local adaptations (i. e. expression of genetically-based individual characters that enhance survival or reproduction in the native environment, Taylor 1991), and neutral genetic diversity provides information on the genetic population structure (i. e. whether a species/population is divided into different and to some extent discrete segments, Laikre et al. 2005a). The genetic diversity also influences the evolutionary potential of a species (i. e. the capacity to respond to environmental changes, Koljonen 2001) since depletion of the genetic variation hampers adaptation to novel selective environments induced by, for example, climate change and environmental perturbation (Lande & Shannon 1994). Information on the genetic structure of commercially important fish species is therefore crucial to prevent ecological damage and to ensure sustainable and effective management of exploited stocks and systems.

Furthermore, studies on genetic population structures provide the basis for understanding and predicting responses to changes at higher system levels, such as at the community level. Recent research has also suggested that the genetic diversity is intimately linked to ecosystem functioning and evolution (reviewed in Johannesson & André 2006). If an ecosystem is dominated by genetically depauperate populations it might impair the development and resilience of the system (Reusch et al. 2005). The genetic diversity of species might thus function as an indicator of key eco-system functions such as the total viability of the ecosystem.

Hence, to avoid depletion of the genetic diversity, management should be based on knowledge of the genetic integrity of populations. The modern molecular methods developed during recent years offer unique opportunities to evaluate the existence of genetic population structures, something that might facilitate local management and increased harvest under a sustainable fisheries regime.

This report originates from the second Nordic workshop that has been held on the topic “how genetic information on exploited fish species could be used in management”. The first, “Genetic Diversity in Commercially Exploited Fish Species” held at Hólar Collage, Iceland in 2004, aimed to provide recommendations for necessary actions to minimize loss of genetic diversity of wild, marine fish species in Nordic waters. In the third workshop, “Genetic consequences of fisheries and fisheries management” held in Bornholm, Denmark, 2006, the aims were to improve the communication and flow of knowledge between scientists and managers, to highlight the importance of including biological/genetic data in the management of fish populations, to give information on recent advances in the area of research, and to evaluate the benefits of this type of multi-disciplinary meeting.

Despite the recent advances in this area of research, there is still a need for increased knowledge, extended cooperation and common views on the management of exploited stocks between Nordic countries since:

- The Nordic countries share several fish stocks. Many fish species such as Atlantic herring, blue whiting, redfish (*Sebastes* sp.) and Atlantic cod are targeted by fisheries from several Nordic countries and are therefore managed internationally. At present, research on the genetic structure of commercially important fish species is conducted by several small research groups that are somewhat isolated from each other. Extended cooperation is therefore conceivable since common stocks need common management to ensure sustainable exploitation.
- Different populations of the same species are found in different countries. For example, populations of the same freshwater species along the Swedish and Finnish coasts of the Baltic Sea are isolated from each other and therefore managed nationally. Common strategies among the Nordic countries on national management of such species would therefore be desirable. Moreover, the exchange of ideas and knowledge between Nordic countries could increase the potential for local management of national resources.
- The environment and stocks managed by Nordic countries are unique in several aspects. For example, freshwater fishes constitute an unusually large proportion of the species assemblages in many countries, the environments span over large areas that are relatively pristine, and some of the environments contain unique single species systems. Furthermore, many stocks are found in the Baltic Sea, the largest brackish water body on earth. As such it houses unique populations of both freshwater and marine species that have adapted to the special salinity conditions (Laikre et al. 2005a). The Baltic Sea has also been acknowledged to be a marginal and peripheral marine ecosystem that acts as a refuge for unique evolutionary lineages (Johannesson & André 2006). Such marginal ecosystems are

especially sensitive to environmental perturbations. Finally, the effects of global warming are predicted to be more severe on ecosystems at the latitudes of the Nordic countries.

- The environment managed by Nordic countries represents some of the most productive marine areas of the world. There is, hence, a large economic value of the fish stocks found in Nordic waters.
- The future existence of many of the stocks managed is questionable since they are heavily exploited and simultaneously subject to effects of global change.

1. 2 Objectives

Genetic research on commercially exploited fish species in the Nordic countries has a long tradition and is currently undertaken at several research institutes in all countries. The implementation of this research in management has, however, hitherto been limited (Koljonen 2001). Potential explanations for this could be that the existing knowledge is spread over several institutes and universities in different countries, that some of the research is unpublished, and that the exchange of knowledge between different affiliations and between scientists and managers is limited. The management goal to preserve genetic diversity has probably also not been sufficiently emphasised, and the recommendations given by scientists have often been too unpractical or vague. Managers are also often lacking tools for tailored management.

In a recent meeting (“Genetic Diversity in Commercially Exploited Fish Species”, Hólar Collage, Iceland, 2004) it was highlighted that current fisheries management should be evaluated with regard to the genetic structure of exploited fish stocks. However, a joint aim for the mapping of the genetic structure of different fish stocks in Nordic waters is at present missing. The objectives of this report are therefore:

- To provide a brief overview of the genetic research conducted on economically important fish species (both marine and freshwater) and other important aquatic taxa in the Nordic countries.
- To identify the gaps existing in the current knowledge on genetics in Nordic fish species and to provide a foundation for advices of future ventures in this area of research.

We also highlight the existing competence in population genetic methods in the Nordic countries and where it is located (Appendix 1 and 2), and identify established cooperation and networks between affiliations and countries (Appendix 7).

2. Review of current knowledge and future perspectives

2. 1 Identification of population structure

All over the world, there is an increased human impact on wild populations of fish. Activities such as the farming of certain species in aquaculture, exploitation for consumption, human-induced environmental change and fishing all affect the structures of wild fish populations. At the same time, there is an increased need for more efficient management of fish stocks, something that is greatly facilitated with the use of modern genetic techniques.

Initially, conservation was focused on species, but it has been recognised that species seldom are genetically homogenous. Rather, they are structured into groups of individuals that are more or less isolated from each other (Laikre et al. 2005a). The presence of such population structures suggest that local populations exchange little genetic material and that characters of different segments of a species distribution range might partly develop independently of each other. If the genetic subdivision is coupled to differences in adaptive traits between subpopulations, a genetic population structure might also indicate the presence of local adaptations. Detection of a genetic population structure does, however, not necessarily imply the presence of local adaptations. Nevertheless, local populations could sometimes exhibit such strong local adaptations that immigration from other populations might be entirely prevented on a historical timescale. Hence, variation on the gene level and the presence of local adaptations represent the most significant components of biodiversity (Laikre et al. 2005a; Reusch et al. 2005). Knowledge on local adaptations is thus of utmost relevance for fisheries management and conservation biology, and biologically sustainable management should therefore be based on knowledge of the genetic population structure since it may reduce the risk of depletion of the genetic resources.

Fisheries management units are, however, often discordant to existing population structures (Koljonen 2001). The management units are rather divided into “fisheries stocks” that may represent more than one genetically distinct population and does hence not necessary reflects biologically adequate subdivision of the species. For example, despite that the Atlantic salmon in the Baltic Sea exhibits substantial genetic structure, the harvest quotas are typically assigned without consideration to this (Laikre et al. 2005a).

Moreover, different populations of marine species are usually conducting annual migrations to common feeding grounds (ICES 2005). Such aggregations are commonly the target for fisheries, and intense harvest in these mixed-stocked fisheries can lead to overexploitation and the risk of extirpation of some of the contributing populations. Information on spatial and temporal distribution of the components in mixed-stocked fisheries is therefore essential for effective and sustainable management and conservation. This information could, for example, be used to establish separate exploitation rates for different populations and also help to map adult and juvenile movement and dispersal patterns of species targeted by fisheries.

Finally, if pronounced population structures exist, extinction of local populations might cause an overall loss of genetic variation in the species. Hence, a failure to identify population structures might lead to overexploitation, subsequent decline and extirpation of targeted populations.

How can genetic information be used in management?

Examples of where information on population structures is essential are:

- During the definition of management units. In order to assess what populations that should be included in a management unit, knowledge on the genetic population structure of exploited species is essential.
- Identification of population units for conservation. As for the previous examples, knowledge on the population origin of the individuals is crucial for the assessment of the structure and range of populations when identifying units for conservation.
- Local management. Several fish species in the Nordic waters occur only locally and are therefore harvested by small-scale coastal fisheries. The long-term sustainability and persistence of such resources have been recognised to benefit from independent local management. For such a management regime to be effective, however, knowledge on existing population structures and biological boundaries of the reproduction units are essential.
- Management of mixed stock fisheries (fisheries exploiting resources originating from several stocks and/or populations). Identification of stock composition of mixed-stock catches and the origin of the contributing populations requires that the genetic characteristics of the contributing populations are known. Catch composition information hence facilitates sustainable and effective management of exploitation of different population components of the harvested species.
- Fish forensics and species identification. Genetic techniques facilitate traceability of individual fish. For example, information could be obtained on the population origin of the catch. Identification of eggs,

larvae and adults to the correct species and/or stock might also be facilitated with the help of genetic techniques.

- Connectivity when designing Marine Protected Areas (MPAs). Information on the spatial range and migration patterns of population segments will provide knowledge about the connectivity and exchange of individuals between different stocks. This kind of information is required for the designing of effective MPAs.
- Planning of fish releases (especially in freshwater systems). By knowing the genetic characters of populations supported by stocking one could avoid introduction of individuals with different genetic origin. Supporting populations with genetic material from a different genetic background might cause introduction of maladapted and suboptimal genotypes into naturally reproducing populations. This might in turn destroy locally optimal gene combinations and reduce the viability of the recipient population (see the following sections for further details).
- Monitoring the effects of human impact and climate change. Human activities could have large impacts on the viability of wild populations. By knowing the genetic characteristics of valuable populations, we can relatively easy monitor changes in heritable traits and in the level of average genetic diversity.

Finally, knowledge on the genetic structure of populations is crucial since it serves as the basis for understanding the genetic effects in natural populations caused by the other four factors discussed later in this report.

Empirical examples

Despite that the information available on genetic population structures in species have increased over the recent years, there are only a few examples in which knowledge on populations structures are recorded to have been used in management (Koljonen 2001). Information on existing population structures has, however, been suggested to be incorporated in the management of two populations (or subspecies) of redfish from Iceland (S Pálsson, pers. com.). The management of this species is complicated since it lives in international waters. According to the genetic data, there are two genetically isolated populations of redfish that are separated by depth, and Icelandic authorities have therefore argued for separate management of the two populations. The deep oceanic population is more valuable and mostly of “Icelandic” origin, and separate management is controversial since other countries then could lose their redfish quotas.

Information on the genetic population structure of coastal vendace (*Coregonus albula*) at the northern parts of the Gulf of Bothnia has been

used to implement a program for local fisheries management in the area (T Aho, pers. com.). Moreover, stocking of Atlantic salmon and brown trout in Denmark is currently managed on a basis of genetic marker-determined local population structure (D Bekkevold, pers. com.).

Summary of what we know

Appendix 3 lists the status of knowledge on genetic population structures of 15 of the commercially most important species in Nordic waters. It is evident from Appendix 3 that substantial knowledge on existing population structures of the species listed only exist for Atlantic cod, Atlantic herring and Atlantic salmon. Regarding blue whiting, by far the most heavily fished species in the Nordic waters, only two studies have explored the extent of genetic population structures over the species distributional range (Giæver & Stien 1998; Ryan et al. 2005). Both studies indicated the presence of significant but weak genetic differentiation, mainly between the extreme regions of the distributional range. This data is, however, not sufficient for defining explicit boundaries for the geographical range of the putative populations of the species (Ryan et al. 2005).

A marked genetic structure seems to exist between spawning populations of Atlantic cod in the North Sea (Nielsen et al. 2001, 2003; Poulsen et al. 2006). Atlantic cod have also been shown to be spatially structured on a fine geographic scale (see for example Knutsen et al. 2003), and the populations of cod in the Atlantic Ocean and Baltic Sea are genetically differentiated from each other (Nielsen et al. 2003). These two populations have also evolved differences in the time of spawning (Weiland et al. 2000).

There is also evidence for genetic population structure in Atlantic herring both in the Baltic Sea and North Sea (Bekkevold et al. 2005; Jørgensen et al. 2005; Ruzzante et al. 2006). In the Baltic Sea, for example, the spatial structure is suggested to be associated with environmental parameters such as salinity gradients (Jørgensen et al. 2005).

In the Atlantic salmon there is a deep genetic difference between eastern Atlantic stocks and salmon found in the Baltic Sea (Nilsson et al. 2001). There is also significant subgroup differentiation within the Baltic Sea as a result of differences in the postglacial colonisation history between areas (Koljonen et al. 1999; Säisä et al. 2005). In the Baltic Sea, genetic stock mixture analysis has also been used for estimating the proportion of wild fish in the catches and stock-group composition in general over several years (Koljonen et al. 2005, Koljonen 2006).

Johannesson and Andre (2006) recently presented a review of the current knowledge on genetic differentiation between species occurring in the Atlantic and Baltic Seas. The review listed a wide range of taxa ranging from plants to mammals, and suggested that there was substantial

genetic differentiation between populations from the two regions. The Baltic populations were generally also genetically less diverse.

In addition to those listed in Appendix 3, there are also studies on genetic population structures in several commercially exploited freshwater fish species. For example, large-scaled genetic population structures and colonisation routes to Northern Europe have been documented for grayling (Koskinen et al. 2000), brown trout (Bernatchez et al. 1995; Garcia-Marin et al. 1999) and Eurasian perch (Nesbø et al. 1999). Moreover, Ryman and Ståhl (1981) also found evidence for genetic substructuring among watersheds in brown trout in Scandinavia.

In all, the results presented here suggest that stocks of widely distributed pelagic species like herring and cod might be comprised by somewhat isolated entities that require separate management for exploitation to be sustainable. Similarly, there is evidence for large-scale differentiation in different species of shellfish. Blue mussels in the Baltic Sea and Northern Sea have, for example, been shown to be genetically differentiated from each other and locally adapted to their natal environments (Väinölä 1991; reviewed in Johannesson & André 2006).

In the Swedish jurisdiction of the Baltic Sea, little or no information on genetic population structures exists for the majority of the exploited fish species (reviewed in Laikre et al. 2005a). For commercially important species such as Atlantic cod, European flounder, perch, plaice, sprat, vendace, whitefish and pikeperch the information on the extent of population structures in the Baltic Sea is very limited. Such data should be gathered without further delay if genetically management of the Baltic resources is to be effective.

What information is needed in the future?

Substantial information on existing genetic population structures is only to be found in three of the 15 commercially important species listed in Appendix 3. In five of the most heavily exploited species (blue whiting, mackerel, sprat, plaice and saithe) information of population structures are limited. Worth noting is also that there is no information at all available for Norway pout. This is a serious problem, particularly considering that the populations of several of these species are in decline and some already exhibit recruitment problems. Therefore,

- Despite that some studies on several commercially important species are currently ongoing and unpublished, additional basic knowledge on population structure of exploited and managed fish species is needed. Especially so for blue whiting, mackerel, sprat, plaice, saithe and Norway pout.
- Knowledge on genetic population structures is also warranted for species in marine and brackish waters since species inhabiting these

environments are generally acknowledged to consist of large populations with little genetic substructuring.

- More information on the genetic requirements for local adaptations is needed. Information on this requires the implementation of quantitative genetic methods.

2. 2 Stocking

Stocking, supporting wild populations with reared conspecifics populations, is a commonplace and world-wide activity. There are several different uses of stocking and the most frequently used are:

- **Enhancement releases** This form of stocking is intended to protect, preserve and recover self-sustainability or viability of populations that are threatened by extinction, and also to reestablish and restore extinct populations to empty habitats. The overall goal of this procedure is to restore the favourable conservation status of naturally reproducing stocks and populations.
- **Supporting releases.** The intention of this activity is to increase or reinforce abundances of naturally reproducing populations that are still viable by using native genetic material. This could be a mean to increase production and hence to ensure persistence of natural populations, but sometimes also to increase the harvestable yield of exploited stocks.
- **Compensatory releases.** This model of stocking is similar to that of supportive releases and is pursued as an approach to compensate for reduced or lost natural production associated with loss of habitats or functional elements due to, for example, the constructions of dams. Compensatory releases might also sometimes be undertaken as a mean to compensate for the negative effects exerted by fisheries, when, for example, fisheries regulation has not been sufficient. This model is exemplified by sea and lake ranching of salmon, in which reared juveniles are released to grow and sexually mature in the natural marine or lake environments.
- **Put and take fishing** (mainly confined to rainbow- and brown trout). The goal of this activity is short-term, where fish of usually exogenous origin is stocked for recreational fishing purposes. Put and take fishing is so far confined to fresh water systems, where natural reproduction of the stocked fish is limited.
- **Introductions.** This form of stocking involves the introduction of non-native fish species or populations to a new area (see subject 5 for further information). It has a long historical record and is exemplified by the range expansion of economically important species like carp and rainbow trout.

Despite the obvious benefits involved with stocking, limited information exists on the adverse effects of stocking (Hindar et al. 1991; Ryman 1997; Fleming & Pettersson 2001). Records on the background of the stocked fish are usually also incomplete. There is hence a substantial need for stocking statistics for effective evaluation of current stocking programs, and management of future programs.

There is scientific consensus that both intentional and unintentional release of cultivated fish poses serious risks to the genetic identity of the recipient populations (e. g. Hindar et al. 1991; Ryman 1997; Fleming & Pettersson 2001; Hansen et al. 2001; Ruzzante et al. 2004). Farmed fish might, for example, be genetically depauperate or maladapted due to unintended and/or artificial selection during rearing (Lynch & O'Hely 2001; Ford 2002). Unintentional selection in hatcheries may also cause changes in quantitative traits of the reared fish such as increased growth rates and earlier maturation (Kallio-Nyberg & Koljonen 1997). The stocks of farmed and native fish might also have different historical backgrounds, and thereby potentially also harbour unique and different genetic features (Hindar et al. 1991; Fleming et al. 2000). Mixing between released and naturally occurring fish might therefore result in alterations of the wild genetic structure and in the breakdown of locally adapted gene complexes (Fleming et al. 2000; McGinnity et al. 2003).

Stocking might also change the demographic characteristics of the recipient population resulting in increased rates of inbreeding and/or loss of genetic diversity (Wang & Ryman 2001). Loss of genetic diversity is, however, dependent on the actual population size, and when population sizes in the wild are smaller than in the hatcheries the diversity of the wild population might instead increase (Koljonen et al. 2002; Säisä et al. 2003). Finally, introduced fish could also spread novel pathogens to wild populations (Hindar et al. 1991; Jonsson 1997; Naylor et al. 2005). Populations of Atlantic salmon have, for example, been infected by the salmonid pathogen *Gyrodactylus salaris* via transmittance from stocked eggs from Baltic salmon that were resistant to the parasite (Hindar et al. 1991). The lack of resistance to *Gyrodactylus* has in turn resulted in decimation of the Atlantic salmon populations in more than 30 Norwegian rivers (Hindar et al. 1991).

In all, the effects of stocking spans a wide variety of outcomes ranging from no detectable effects to interbreeding and sometimes complete displacement of the wild population. For example, more than 90% of the salmon caught in the fisheries in the Baltic Sea are of hatchery origin (Swedish National Board of Fisheries 1991; International Baltic Sea Fisheries Commission 2003). The main goal of the conservation of genetic resources should always be to sustain naturally reproducing populations and hatchery breeding can offer no more than a temporary solution to the problems posed. Due to the obvious risks with stocking, it is therefore

essential to firmly evaluate the embedded adverse effects stocking on wild populations.

How can genetic information be used in management?

Since the adverse effects of stocking programs are unpredictable (Hindar et al. 1991), the precautionary principle should be undertaken in all stocking programs. With the use of modern genetic techniques the possibility for tracking released fish and to detect mixing between stocked and wild individuals has been greatly improved. The use of these techniques hence facilitates evaluation of potential adverse effects, and whether stocking programs meet their intentions. Means of how to limit the adverse effects on recipient populations from stocking includes:

- Use of information on patterns of genetic differentiation when planning stocking programs. Considering the potential for genetically based differences in quantitative traits between released and wild fish is essential since mixing between differentiated gene-pools might result in alterations of the wild genetic structure, breakdown of locally adapted gene complexes, and loss of genetic diversity.
- Use of local broodstocks. By using fish with the same genetic background as the wild population, the adverse effects discussed in the previous point are circumvented.
- Minimise domestication of broodstocks. The genetic structure of farmed fish might due to artificial and unintended selection during rearing depart from their wild relatives. Release of such domesticated fish might in turn pose a threat to the genetic integrity of wild populations. Methods that minimize domesticating selection in hatcheries should therefore be implemented.
- Keep the population sizes of broodstocks large enough to maintain the genetic diversity of the stock. Low population size of the broodstock might result in increased inbreeding and hence erosion of genetic variation. Release of genetically depauperate fish might have large impacts on recipient populations. Methods that maximize effective population sizes in hatcheries should therefore be implemented.

Empirical examples

A good example of where a stocking program has been evaluated with the use of modern molecular techniques is a study conducted in two stocked populations of brown trout in Denmark (Hansen et al. 2006). The genetic variation of each population was estimated both before and after the initiation of the stocking program. In one of the populations there was very little interbreeding between the wild and stocked fish, whereas in the other there was a strong genetic contribution from farmed trout. In

the interbred population the use of genetic markers also made it possible to discriminate between individuals that were admixed with stocked trout and their non-admixed conspecifics. These results hence suggest that when genetic differences between populations is discernable, it is possible to identify non-admixed and locally adapted fish from admixed individuals and to further use wild and non-admixed fish as founders for a broodstock that could be used in future stocking programs. Management strategies for stocking of Atlantic salmon and brown trout in Denmark are also currently based on genetic marker-determined local population structure (D Bekkevold, pers. com.).

There is evidence for that the domestication process of fish might be rapid, and a recent study of Atlantic salmon showed that genetic differences between farmed and wild fish could evolve during five to seven generations of artificial rearing (Roberge et al. 2006). In Finland, the genetic diversity of brood stocks are systematically monitored, and some years ago a database on the genetic diversity in the brood stocks used for governmental stocking was established (Aho et al. 2002, 2005a, b).

Summary of what we know

The information available on existing stocking programs in the Nordic countries is to date available for Finland, Sweden, Iceland and Faroe Islands. Appendix 4 lists the species stocked in each of the five countries, and for Finland, Iceland and Faroe Islands data on the quantities of each species stocked is also included.

Stocking is commonplace and in Finland, for example, stocking of fish and crayfish totalled 125 million individuals in 2004. All together some 20 different species were stocked in Finland, and the most common species were European whitefish, pikeperch, Atlantic salmon and brown trout (Appendix 4). Data on the species used, the origin of the population (stock name), and the release site are nowadays mandatory information that is recorded for each stocking event.

In Sweden, there is little information available on the numbers on the quantities of stocked fish (but see Laikre et al. 2005b), but as in Finland the majority of released fish were salmonids such as brown trout, arctic charr, grayling and rainbow trout. Presently, about 2 two millions Atlantic salmon smolts are released into the Baltic Sea by Sweden (Swedish National Board of Fisheries 1991; International Baltic Sea Fisheries Commission 2003). In total, about 25 different species have been stocked and over the recent years the number of releases has increased with about 10–15% (Swedish Board of Fisheries 2005).

In Iceland and Faroe Islands, stocking is mainly confined to Atlantic salmon releases for recreational fishing and the extent is much smaller than in the other countries.

The genetic effects of stocking programs on quantitative traits or on the viability of the wild populations are to some extent unclear and certainly case specific. Theoretical studies do, however, suggest that interbreeding between farmed and wild fish could result in deleterious effects on the genetic structure of the wild population in as short time as after a few generations (Hindar et al. 2006). The magnitude of the deleterious effects commonly depends on the degree of domestication of the fish in the hatchery. In several empirical studies considerable interbreeding between wild and farmed fish has been documented (reviewed in Hindar et al. 1991; Fleming & Pettersson 2001; Heggenes et al. 2002; Utter & Epifanio 2002; Bekkevold et al. 2006). In some cases wild populations exposed to stocking have also been shown to be genetically less diverse compared to their non-stocked counterparts (Hansen et al. 2000; Koskinen et al. 2002). In Sweden the extensive stocking of brown trout into natural eco-systems have resulted in a reduced genetic diversity among wild populations (Ryman 1981), but among both landlocked and anadromous Atlantic salmon populations in the Baltic Sea area, the genetic diversity of the reared populations was sometimes higher than that of the smallest wild populations (Koljonen et al. 1999).

In some instances, however, the viability of reared fish are much lower compared to their wild conspecifics (Saloniemi et al. 2004), and stocking of farmed fish have also had little influence on the wild populations (e. g. Fleming & Pettersson 2001; Heggenes et al. 2002). This is likely a consequence of that the farmed fish usually had lower survival, recruitment and success under natural conditions than their wild conspecifics.

Studies of the effects of stocking are mainly confined to salmonid species and are almost exclusively restricted to freshwater and the Baltic Sea systems (Bekkevold et al. 2006). Virtually nothing is hence known about supportive releases in marine environments, and even in the best studied freshwater systems there is limited understanding of the long-term genetic effects of interbreeding.

What information is needed in the future?

The evidence for adverse genetic effects as a result of interbreeding between farmed and wild fish has led to an increased awareness of the impact that stocked fish can exert on wild populations. It has also resulted in changes of management strategies. More information is nevertheless needed if we are to reduce the negative genetic impact of stocking on recipient populations. Specifically:

- Records of recent stocking programs in all Nordic countries should be established. At present, such records only exist for Finland, Sweden,

Iceland and Faroe Islands, and figures on the quantities of stocking are only available for Finland and Iceland.

- Where such information exists, the success and genetic effects of current stocking programs should be evaluated.
- Since the effects of interbreeding between farmed and wild fish are usually manifested after several generations of interbreeding, more studies investigating the long-term effects of mixing between wild and farmed fish is needed.
- Due to decreasing catches of commercial marine species there has lately been an increased interest in large-scale aquaculture in marine environments. Virtually nothing is, however, known about the consequences of stocking in marine systems and more studies is therefore definitely needed for sustainable and effective management of stocked marine populations such as Atlantic cod.
- Development of molecular genetic methods that can be used for monitoring the genetic diversity of broodstocks. Such methods could be used to evaluate if sufficient genetic variation is present in the broodstock. Different criteria could then be set for short-term or long-term breeding and for either conservation or production purposes.

2.3 Cage-escapes from aquaculture

There has been a rapid growth of aquaculture industry during recent years as a mean to meet the needs of the doubling human population over the last 50 years (Utter & Epifiano 2002). The main objectives of aquaculture activities is hence to provide a protein source for the expanding human population, to relieve some of the harvest demands placed on wild marine populations by substituting the exploited elements with farmed conspecifics, and to enable the persistence of threatened aquatic species and populations within their natural environments (Utter & Epifiano 2002).

Whereas stocking is intended release of cultivated fish, there might also be unintentional escapes from aquaculture, and despite that escaped fish have been suggested to have low success in the wild (Hindar et al. 1991; Heggenes et al. 2002; Fleming & Pettersson 2001), escaped or stocked individuals have been shown to make up significant proportions of at least wild marine and freshwater salmonid populations (Hindar et al. 1991, 2006; Clifford et al. 1998). For example, about two million salmon escape annually from aquaculture, and during the 1990s escaped farmed fish were estimated to constitute 20–40% of the salmon recorded over large areas of the North Atlantic (Jonsson 1997; McGinnity et al. 2003). There is scientific consensus of that escaped fish could interact with their wild conspecifics, and that these interactions might represent both ecological and genetic threats to the wild fish (Einum & Fleming 1997; Jonsson 1997; Fleming et al. 2000; McGinnity et al. 2003). The ecological

threats could be viewed as every effect on the population size of wild stocks and could come in the form of:

- Increased competition. The immigration by escaped fish to areas inhabited by wild populations could increase competition for resources such as space, food or mates. This might in turn lead to a reduction in the population size of the wild fish. Genetic changes could then follow due to an increased frequency of inbreeding leading to loss of genetic variability.
- Spreading of diseases and pathogens. Farmed fish might carry diseases and also function as vectors for transmittance of novel pathogens to wild populations. An example of this is the spread of the salmonid pathogen *Gyrodactylus* to wild populations of Atlantic salmon discussed previously.

The genetic threats could be summarized as the effects resulting from interbreeding between wild and farmed fish. Introduction of exogenous genes might break down local adaptations and hence reduce the viability and fitness of recipient populations. Reasons for genetic differences between farmed and wild fish could be that:

- Farmed fish have usually been exposed to intentional and unintentional artificial selection during domestication. Farmed fish have, for example, as a by-product of selection for increased growth often an increased boldness and aggressiveness (Eimun & Fleming 1997; Fleming & Eimun 1997; Fleming et al. 2002; Roberge et al. 2006). Other traits that are selected for in aquaculture are those important in production such as increased growth rate, delayed maturation, decreased disease resistance and increased flesh quality.
- Farmed and wild fish often have different historical backgrounds. Aquaculture strains in Norway for example are created by pooling of several wild Atlantic salmon stocks from different parts of the country. Subsequent competition and interbreeding with wild fish could result in the break-up of favourable gene combinations and thus result in lower fitness and a loss of biological diversity.
- Lack of natural selection in captive environments. This might lead to a loss of genetic variation for traits adaptive in natural environments.
- Small population sizes of broodstocks compared to that of wild populations. Farmed populations might hence be genetically less diverse as a result of increased frequency of inbreeding associated with small population sizes.

There are also impacts on wild stocks of shellfish from aquaculture. The mariculture of bivalves is, for example, by far outnumbering that of any aquaculture of fish (Østfold Bærekraftig Utvikling 2003). The worldwide

production of bivalves in mariculture in 2000 was approximately 1.2 million tonnes (Østfold Bærekraftig Utvikling 2003) and a little less than half of that volume was produced in Europe (mainly in Spain and Italy). In relation to fish, most adult bivalves are reared under environmental conditions that are very similar to the wild (farmed bivalves are, for example, not fed or treated for diseases, ICES 2005). The domestication process is hence not as intense in bivalves as in fish. There are nevertheless potential for artificial selection in bivalve mariculture since the hatchery and nursery conditions are clearly different from those encountered in the wild (ICES 2005). This does, however, remain to be documented. Genetic loss and the breakdown of local adaptation should, nevertheless, be monitored since hatchery-based propagation and transport of juveniles over large distances are common in bivalve mariculture.

How can genetic information be used in management?

Estimation of the demographic and genetic effects on wild populations from cage-escapes from aquaculture has been facilitated by the use of modern genetic techniques. With the use of genetic markers it is now possible to efficiently discriminate between escaped and farmed fish, and hence to evaluate and potentially also minimise the effects of escapes on wild populations. The long term consequences in terms of changes in productivity of the recipient stock have, however, rarely been assessed (Bekkevold 2006). There are several potential means by which the adverse effects of cage-escapes could be reduced, for example:

- The use of sterile fish in aquacultures where there is risk for interbreeding. Sterile or genetically modified fish are commonly incapable of producing viable offspring. There is also evidence for that these type of fish have lower return rates to spawning grounds (Cotter et al. 2000).
- Assignment of areas protected from aquaculture. Areas harbouring endemic or threatened populations should be protected from aquaculture to assure that spreading and introduction of domesticated and exogenous genes are prevented.
- Marking of farmed fish. Could be implemented as a mean to facilitate identification of fish originating from aquacultures. Preferentially, identification of escaped fish should be based on the genetic identity of wild and farmed fish. This form of identification has several benefits compared to non-genetic methods since the genetic integrity, for example, is passed on between generations and is persistent throughout the life of an individual. Other and alternative marking methods are ordinary tagging (removal of the adipose fin in salmonids, attachment of tags), otolith staining, “genetic tagging” (genetically modified farmed fish to facilitate detection), and the use

of natural tags (wear-down of fins and/or tear of snouts in farmed fish).

- Use of local broodstocks. To minimise the potential for mixing between gene pools with different historical backgrounds, something likely resulting in loss of local adaptations and biological diversity, the stocks used in aquaculture should be of the same origin as the wild populations in the area.

Empirical examples

Examples of where genetic information has been used to evaluate the effects of cage-escapes on wild populations can be drawn from studies conducted on escaped Atlantic salmon and cod in Ireland and Norway (Crozier 1993; Jørstad et al. 1994; Fleming et al. 2000). In Ireland, for example, the genetic impact of the escaped fish was evaluated by comparing the genetic structure of the wild fish before and after the escape event. There was evidence for that the genetic structure of the wild population had changed in the direction of that of the escaped fish (Crozier 1993). Moreover, McGinnity et al. (2003) have documented that interbreeding between farmed and wild Atlantic salmon resulted in a fitness reduction in the hybrids. Thus, these examples all provide good evidence of that genetic changes in wild populations have occurred as a result of escaped fish from aquaculture.

Summary of what we know

Salmon, brown trout, arctic charr and whitefish are the most common farmed species in the Nordic countries. Less common but regularly occurring are also halibut, cod, haddock, turbot, lobster, oysters and blue mussels. Appendix 5 lists the aquaculture production volume of Norway and Iceland. Records on cage escapes are, however, confined to Atlantic salmon and rainbow trout in Norway (Appendix 5). Cage-escapes from aquaculture in the Baltic Sea range do not have strong impacts on wild populations since the most commonly reared species in sea-cages are rainbow trout and whitefish, a species that is incapable of reproducing in the cold Scandinavian rivers (M-L Koljonen, pers. com.). Moreover, smolt rearing hatcheries are commonly found in freshwater environments and escapes from such hatcheries are rare (M-L Koljonen, pers. com.).

In Norway the number of Atlantic salmon escaped from Norwegian fish farms has increased dramatically, roughly following the increase in aquaculture production (Hindar et al. 1991). During storms in 1988 and 1999, for example, more than 1.2 million salmon escaped an amount of fish that equals the total annual catch of wild salmon in Norway (Hindar et al. 1991). There is also evidence for that the escaped fish have had an effect on wild populations since the numbers of farmed salmon in some

Norwegian rivers outnumber the native fish by representing up to 80% of all spawners (Sægrov et al. 1997). Similarly high proportions of escaped farmed salmon have also been found in Icelandic rivers (Gudjonsson 1991).

Despite the increase in number of wild populations that are genetically contaminated by exogenous immigrants, the knowledge regarding the genetic changes that might take place as a result of interbreeding is still generally poor. Theoretical studies have, however, indicated that genetic change of subjected populations can take place in such a short time as within 40 years (10 salmon generations), and that recovery of the wild populations is not likely (Hindar et al. 2006). Empirical evidence from Ireland suggests that interbreeding between escaped and wild salmon have occurred in such a short time as one year after the unintentional release of the farmed fish (Crozier 1993). Similarly, in Norway, an experiment evaluating the effects of interbreeding between farmed and wild salmon of known genetic identity demonstrated that invasions from escaped farmed fish could have a potential impact on population productivity, disrupt favourable local adaptations and also reduce the genetic diversity of the wild segment (Fleming et al. 2000). Moreover, the results of McGinnity and colleagues (McGinnity et al. 2003) suggested that hybrids between farmed and wild fish experienced a fitness reduction compared to their parents.

As for stocking, however, the information available on the effects of cage-escapes is mainly coming from studies of salmonid fishes in freshwater systems. A likely explanation for this bias is that farmed salmonids are released into the wild at a magnitude that has no parallel among other vertebrates (Ryman 1997). Since salmonids also exhibit a high degree of population subdivision, resulting interbreeding between wild and farmed fish not only threaten the existence of local stocks, but also pose a serious risk for the depletion of genetic diversity of the species as a whole (Ryman 1997). Further measures to reduce the effects of escapes are hence urgently needed.

What information is needed in the future?

The potential adverse impact of cage-escapes on wild populations has been the subject of mounting concern, and in salmon it might have accelerated on the global decline of wild populations. The following actions should be undertaken to ensure sustainable management and to facilitate sound evaluations of the potential effects of genetic contamination of wild populations from escaped fish of non-local origin:

- Records of the extent of cage-escapes in all Nordic countries should be established. At present, records only exist for Atlantic salmon and rainbow trout in Norway.

- Gathering of additional information on genetic effects of cage-escapes on wild populations. A lot of information is still lacking, especially so in marine systems with other species than salmonids (see Appendix 5).
- Monitoring to detect long-term effects. To be able to evaluate the long-term effects of cage-escapes on wild populations, genetic descriptions and long-term monitoring of genetic changes based on genetic markers is needed.
- Development of efficient methods to reduce interbreeding between escaped and wild fish. Despite that a number of methods is already existing, more methods to “genetically tag” farmed fish is needed.
- Systematic genetic marking of stocks used in aquaculture. Once efficient methods for “genetic tagging” are developed, farmed fish should be marked to facilitate identification of exogenous fish in wild stocks. This is also crucial as a mean to obtain a reasonably accurate understanding of the biological consequences of cage-escapes.

2. 4 Fisheries-induced evolution

Exploitation might threaten the genetic structure of fish populations in several ways. Intense exploitation might, for example, result in extinctions of local populations and alter natural levels of gene flow between parts of the population (Hutchinson et al. 2003; Myers & Worm 2003). Harvest may also replace the local fish with non-native immigrants that might perform worse in the new conditions than the extinct population. In addition, heavy exploitation might reduce population sizes to the level where increased inbreeding erode the available genetic diversity. Loss of genetic diversity could in turn have substantial effects on the viability of the population since it limits the evolutionary potential of the population (McGinnity et al. 2003).

Less acknowledged is, however, that harvest mortality could induce heritable shifts (i. e. fisheries induced evolution) in life-history traits such as the timing of sexual maturation and changes in growth rates (e. g. Law 2000; Heino & Godø 2002; Conover et al. 2005; Gårdmark & Dieckmann 2006). According to life-history theory an increase in adult mortality leads to an increased reproductive effort at early ages (Roff 2002; Ernan-de et al. 2004). Moreover, fishing is almost always non-random in regard to fish size since fishing gears are often designed to target a special segment of the stock, usually the largest and oldest individuals (Law 2000; Conover & Munch 2002; Hutchings 2004; Walsh et al. 2006). Size-selective exploitation for the largest and oldest segment of fish is in turn expected to induce even more pronounced changes towards earlier sexual maturation (Olsen et al. 2004; de Roos et al. 2006). Fishing for small or middle-sized individuals may, however, also have disparate

effects de-pending on the current state of the population (Gårdmark & Dieckmann 2006).

A shift to reproduction at smaller sizes and earlier ages likely has adverse consequences for the viability, recruitment and production of a population since smaller individuals generally produce less and lower quality offspring than their larger conspecifics (Law 2000; Conover & Munch 2002). Moreover, a change in the size distribution of the exploited stock might affect lower parts of the food web and hence also affect ecosystem functioning (Longhurst 2006). Taken together, shifts in age at reproduction and size distributions may reduce fisheries yields and become economically important in the long run (Law 2000; Conover & Munch 2002; Walsh et al. 2006).

Finally, since fishing mortality and selection are typically far greater than natural mortality and selection, the recovery of harvested populations to an undisturbed state is generally slow, even after fishing is halted (Hutchings 2000; Walsh et al. 2006; de Roos et al. 2006). Hence, the very early signs of ongoing fisheries-induced evolution should be thoroughly evaluated if we are to limit irreversible changes of important characters of natural populations of fish.

How can genetic information be used in management?

Modern genetic techniques could be used in a number of ways to predict and evaluate the effects of fisheries-induced evolution. Topics where genetic information could be used are for example:

- Gene expressions in growth rates. Examining the additive genetic variation for growth rates could facilitate predictions of which stocks and/or populations that are vulnerable to fisheries-induced evolution.
- Estimations of heritability of traits important for the production and viability of populations. This would enable predictions of the traits likely affected by intensive exploitation, and what the response in these traits will be.
- Mapping of the maintenance of genetic resilience in populations. Could yield insights into the effects that fishing might have on the genetic structure of targeted populations.

Empirical examples

There are to date no examples in Scandinavia of where genetic information on fisheries-induced evolution has been used in management of exploited stocks. In North America, however, upper as well as lower size limits of catches have been established in, for example, sturgeon fishing in California and Oregon as a mean to minimize the evolutionary effects of fishing (A. Vainikka pers. com.).

Summary of what we know

Despite that fisheries-induced evolution has been hypothesized to occur, sound evidence for its occurrence has not appeared until very recently. A recent experimental study did, for example, highlight that selective harvest on large individuals could reduce the harvestable yield of the exploited stock in such a short time as four generations (Conover & Munch 2002).

Commercially exploited fish stocks often show trends towards reproduction at earlier ages and smaller sizes (e. g. Barot et al. 2004, 2005; Engelhard & Heino 2004; Grift et al. 2003; Olsen et al. 2004, 2005), and the most famous example of fisheries-induced evolution is probably the collapse the stock of Atlantic cod off southern Labrador and eastern Newfoundland in Canada (referred to as Northern cod) underwent in the late 1980s and early 1990s (Olsen et al. 2004, 2005). This is one of the most drastic collapses in the history of fisheries where the size of the stock, even after a decade-long offshore moratorium, are still historically low and have not yet recovered (Olsen et al. 2004). Over-exploitation caused an evolutionary shift of Northern cod to earlier ages and smaller sizes at first reproduction. This resulted in a lower productivity of the population that, in addition to sustained by-catches by other fisheries, is likely responsible for why the stock has not yet recovered.

In Scandinavia, the trends of a shift towards sexual maturation at smaller sizes during the two past decades of the Baltic cod closely resembles that seen in Northern cod (Cardinale & Modin 1999; Vainikka et al. unpublished manuscript). The changes observed for Baltic cod are also accompanied with significant decreases in the size and condition of cod at a specific age. Similar trends of fisheries-induced changes of size and age at first reproduction is also known from grayling fish from Norwegian mountain lakes (Haugen & Vollestad 2001). Here intensive gill-net fishing during the last century has influenced a shift to reproduction at smaller sizes and younger ages of the fish. Relaxation of fishing pressure later led to an increase in size and age at sexual maturity.

Other examples of fisheries-induced evolution is the change in age and size at first reproduction of North Sea plaice during the last century (Rijnsdorp 1993; Grift et al. 2003), and a similar but minor shift in Spring-spawning herring in Norway after the stock collapsed in the 1960s (Engelhard & Heino 2004). In these examples, however, the majority of the occurred changes could be attributed to changes in environmental perturbations, but a significant part of the shifts is also consistent with fisheries-induced evolution.

There is limited evidence for that intense harvest directly have affected growth rate patterns of targeted stocks (but see Kristiansen & Svåsand 1998), and more statistical as well as genetic methods are definitely needed in order to evaluate this. Thus, these examples all suggest

that the long-term effects of fishing are almost certainly more complex than pre-viously perceived.

Ignorance about the potential for fisheries-induced evolution likely has important consequences since (reviewed in Law 2000):

- a) Large changes in important characters of exploited stocks are currently taking place, and the cause of these changes is often uncertain.
- b) The characters subjected to change (such as growth rates and consequently body size) are of key interest for fisheries. Changes in such traits have large influences on the harvestable yield of the stocks.
- c) While the environmental factors re-sponsible for the change may fluctuate in time and in several directions, changes induced by fisheries are often directional and constant through time.
- d) The genetic changes brought about by fisheries might not be readily restored after altering the patterns of exploitation.

What information is needed in the future?

If an evolutionary response to intense fishing is as common as currently emphasized, rapid attention must be paid to issues concerning the magnitude of the response and the potential for successful recovery of the exploited stock. Both theoretical models and empirical quantitative genetics studies are needed for the implementation of evolutionary sustainable fishing strategies. Some of the information needed for sustainable management of fisheries is:

- The genetic basis of traits targeted by exploitation. Additional information on the heritability and genetic variance of key life-history traits in the wild is needed to be able to predict how exploitation will affect the production and viability of the stock. Such information should ideally be obtained under natural conditions, but knowledge extracted from large-scaled experiments, the use of molecular methods, or insights from aquaculture could give rough estimations on this topic.
- Estimations of effective population sizes (i. e. the number of reproducing fish in the population) could be estimated with the use of modern genetic techniques. Information on effective population sizes have profound consequences for the predictions of how targeted stocks respond to intense exploitation.
- How strong the selection exerted by fisheries is. This information should be used in management since it allows for estimations of how fisheries-induced evolution affects targeted stocks. Similarly,

knowledge of at what rates fisheries-induced evolution occurs is highly informative in this aspect.

- To further facilitate sustainable management and predictions of the impact of intense exploitation two reference points need to be established. First, an establishment of a baseline of genetic and adaptive variation of unexploited/historical/least impacted stocks. This will help to quantify the level of genetic impact caused by historical and contemporary fishing and to assess what management means that should be undertaken to restore this state. Second, to establish exploitation regimes that allow for maintenance of long term sustainable fisheries for a given yield.
- More empirical knowledge on processes such as mate selection, shoaling with close relatives and migration patterns is needed to increase our over-all knowledge about processes important in fisheries-induced evolution.
- Finally, in order for sound predictions of the effects that intense exploitation has on subjected stocks models incorporating the results of recent genetic research to fisheries-induced evolution are needed.

2. 5 Effects of environmental change

Anthropogenic activities have had, and will likely continue to have, substantial impact on natural populations of several species, sometimes even threatening their existence. Climate change (i. e. global warming), introduction of alien species and fragmentation and destruction of habitats are all examples of such activities.

Climate change

The current and predicted rates of climate change are greatly exceeding any previous periods of global warming. Over the past 100 years the average global temperature has increased with approximately 0.6°C, and is projected to continue to rise at a rapid rate (Root et al. 2003; Perry et al. 2005). The rate of increase is, however, unlikely to be even across the world and is expected to be greater in boreal and arctic regions such as the ones found at the latitudes of the Nordic countries (ICES 2005). Populations and species at higher latitudes are also thought to react more strongly to intense changes in temperatures (ICES 2005).

There are two ways to cope with increasing temperatures in the environments. Either to adapt to the elevated temperature or in the case of marine species to move north where the temperature is lower (ICES 2005). There is evidence for that the latter option is more likely, since the rate of environmental change commonly exceeds the capacity of a population to adapt to a novel temperature optimum (Root et al. 2003). Evidence from the fossil record do, however, suggest that range shifts of species are

typically far slower and smaller than that required to successfully track the changes induced by global warming (Davis & Shaw 2001). Hence, the response of many organisms to increasing water temperatures is still poorly understood, and is strongly dependent on the species capability to move or adapt to the changes. There is, however, no general rule.

The climate is a major determinant of species distribution, and global warming will therefore likely reduce biodiversity due to loss of populations, particularly at southern latitudes (ICES 2005). Moreover, whereas the majority of the native species likely will be negatively affected by climate change, some will also benefit from the induced changes. This might in turn lead to changes in ecosystem structures and to structural changes in some fisheries resulting in a change of the target species (ICES 2005). In all, the effects on natural populations from global warming could be drastic, and it is therefore highly important to understand how climate change affects natural populations for strategic planning of present and future fisheries management.

Introduction of alien species

One of the major threats for the existence of many aquatic species is the worldwide introduction of alien and invasive species to other ecosystems. During recent decades the frequency of biological invasions has increased to an unprecedented level (Hänfling & Kollmann 2002). The spread of non-native species comes from intentional introductions for aquaculture and recreational fishing, as well as accidental releases from ballast water, ornamental specimens from aquaria as well as illegal introductions (reviewed in Rahel 2000).

As in the case of cage-escapes, introductions of alien species could have adverse effects on the genetic integrity of targeted populations, since it commonly leads to biotic homogenization, the replacement of unique endemic species with already widespread species (Olden et al. 2004). The resulting consequences might in turn lead to alterations of the natural levels of global biodiversity since genetic structures might be eroded and the genetic similarity between areas could hence increase. Ultimately, the spread of alien species might jeopardize the future resilience of biological communities, potentially leading to the extirpation of locally adapted populations (Allendorf et al. 2001; Olden et al. 2004).

The effects of biotic homogenization might also reduce the potential for future speciation, since decreased genetic variability limits the raw material upon which selection operates (Olden et al. 2004). Species invasions might also via competitive interactions and spreading of diseases affect the food-web structure of subjected communities and alter whole eco-system functioning.

Fragmentation and destruction of habitats

Freshwater fish populations all over the world have experienced an increase in human-induced habitat alterations via the construction of weirs and hydroelectric dams. Such constructions might cause alterations of the population structure and during the last century most river systems in Europe have been extensively fragmented by dams and other flow regulators (Laroche & Durand 2004).

Weirs and dams usually represent dispersal barriers that prevent migration to spawning and feeding grounds throughout riverine systems in turn causing fragmentation of populations previously connected by gene flow (Meldgaard 2003). This might in turn have adverse effects leading to increased inbreeding and hence to a reduction of the total genetic variability of the population (Stockwell et al. 2003). The habitat characteristics might also be altered by river impediments since the presence of weirs and dams commonly turns riverine habitats to become more lake like, something that likely destroys spawning habitats (Neraas & Spruell 2001; Meldgaard 2003).

Means to prevent genetic erosion of populations exposed to habitat fragmentation should re-establish connectivity in fragmented populations including removal of migration barriers, restoration of habitats, and/or human-mediated movement of fish from genetically diverse to genetically impoverished subpopulations (Neraas & Spruell 2001; Stockwell et al. 2003; Yamamoto et al. 2004).

Apart from fragmentation of the habitat, anthropogenic activities might also lead to habitat degradation or destruction by discharge of pollutants and contaminants. Understanding the effects of pollutants on the genome is essential to preserve the evolutionary potential of populations (Lande & Shannon 1994) since increased pollution load via mutations might alter the sequence of the genome and lead to erosion of the genetic variation in the population (Belfiore & Anderson 2001; Maes et al. 2005). It might also be costly for individuals to develop resistance towards contaminants. Resistant fish have, for example, been shown to grow slower (Belfiore & Anderson 2001). In all, the effects of pollutants might alter the viability and productivity of targeted populations, and might together with fragmentation of habitats change the structure of affected ecosystems.

The predictions of changes induced by anthropogenic activities are dependent on the specific system and the degree of human impact. For example, systems with small population sizes and species-poor communities (features typical for freshwater systems), are acknowledged to be more vulnerable than populations of large sizes in marine systems (Swedish Board of Fisheries 2006). Young ecosystems that are heavily exploited and harbour marginal populations at the edges of the species distribution, such as the ones found in the Nordic countries, are also likely to be more affected (ICES 2005; Swedish Board of Fisheries 2006). Such po-

pulations are commonly genetically less diverse than their conspecifics at the centre of the distribution (ICES 2005). Finally, the synergism of rapid climate change, introduction of alien species and habitat fragmentation/destruction could easily disrupt the connectivity among species and populations, in turn having substantial and adverse effects on the affected populations (Root et al. 2003).

How can genetic information be used in management?

The adaptive responses to environmental change are usually very complex where several selective pressures might change concurrently. It is therefore challenging to study how environmental change affects natural populations.

Climate change

The problems and challenges imposed by climatic change and global warming can not be solved with the help of modern genetic techniques, but the use of these techniques will facilitate:

- Predictions of changes in population structures induced by climate change. Such predictions could be implemented in the management strategies of affected populations.
- Tracking of population range expansions and local adaptation to novel environments. Genetic markers could be used to evaluate how populations respond to climate change.
- Mapping of the genetic variation of a population. This information is essential since it can serve as a useful indicator of the evolutionary potential of a population. It also provides reference information for the adaptive variation of interest, and can as such serve as an indicator of the population size and demographic changes.

Introduction of alien species

Detecting biotic homogenization is usually a difficult task that is facilitated with the use of modern genetic techniques (see Allendorf et al. 2001). For example:

- Assessment of the level of interbreeding with alien species. The degree of interbreeding between alien and native species could be estimated by calculating the relative abundance of alien genes in the native population.
- Identification of hybrid individuals and which that belongs to the parental species. The use of species specific markers also allows for discrimination between native and hybrid individuals, and would facilitate removal of the interbred individuals, a procedure that is likely beneficial for the viability of the targeted population.

- Similarly, identification of migrants from neighbouring populations or cultivated stocks is also greatly facilitated with the use of modern genetic techniques.

Fragmentation and destruction of habitats

The mapping of effects of habitat fragmentation on populations is also greatly facilitated with the use of modern genetic techniques. For example:

- Estimations of the impact of dams and weirs on the overall genetic structure of populations. The genetic variation of different isolated segments of the population could also be estimated. By comparing the genetic structure of populations before and after the construction of dispersal barriers, the effects of fragmentation could also be established. If the genetic structure of historical and contemporary samples departs, there are indications of fragmentation.
- Estimations of the impact of dams and weirs on genetic variation within populations. This could serve as an indicator of the population size and demographic changes.
- Assessments of changes in population structures induced by pollutants. Links between the genetic architecture of a population and the pollution load will, for example, provide powerful tools to address the environmental effects of contaminants, and hence to understand the anthropogenic threats to the conservation of wild populations and their environment. The potential for incorporating information on pollution-induced genetic changes in management is hence mediated.
- Assessments of changes in genetic variation within populations. Again, this could serve as an indicator of the population size and demographic changes.

Empirical examples

In the many rivers worldwide where foremost salmonid populations have been fragmented as a result of the construction of dams and weirs, it is today common practice to support the exposed segment with wild spawners of local origin, a procedure generally referred to as supportive breeding (Hansen et al. 2000). However, for supportive breeding to be effective and for a sound evaluation of the stocking programme, the use of modern molecular techniques is essential. By using these methods, information on the matching of the genetic structure and identity between the wild and supported fish is facilitated. This has, for example, been conducted in Baltic salmon to compensate for population loss due to destruction of reproducing habitats from the construction of power plants (Koljonen 2001).

Regarding populations affected by climate change and biotic homogenization, there is no case of where genetic information has been used in management, but the modern genetic techniques of today offers unique opportunities to do so.

Summary of what we know

The Helsinki commission (HELCOM) has established a list of threatened and declining species occurring in the Baltic Sea. Appendix 6 lists 16 keystone species (a species of controlling influence on their community) that are recognised as high priority species (immediate action is warranted if the future existence of the species in the Baltic is to be ensured) by HELCOM and IUCN. Out of these 16 species two are already extinct, three are critically endangered and as many as nine are endangered. The threats to the existence of the species are foremost exploitation and by-catch by fisheries, eutrophication and pollution, and the construction of weirs and dams. Habitat destruction and loss as well as escapes and introductions from aquaculture also pose serious threats, and examples of commercially important species that are listed are European eel, herring, Atlantic salmon, Atlantic cod and halibut.

Climate change

Anthropogenic alterations of the world's climate have already resulted in range shifts and species extinctions (Parmesan et al. 1999; Hughes 2000; Thomas et al. 2004, Perry et al. 2005). Moreover, despite substantial spatial variation between areas there is a trend of rising sea surface temperatures in the North Sea, Baltic Sea and Northeast- and Northwest Atlantic (ICES 2005). There are accordingly consistent patterns of long-term changes in marine areas with a movement towards a warmer dynamical equilibrium of many ecosystems. In the Baltic Sea, Kattegatt and North Sea, for example, the distribution of many species has shifted northward during recent years, and such shifts towards colder latitudes strongly suggests that the impact of climate change is already discernable in wild populations (Perry et al. 2005; Swedish Board of Fisheries 2006). There is also evidence for that the abundance of populations of the cold-water species arctic charr has decreased with the increasing temperatures of recent years.

A strong biogeographical shift in all marine copepod assemblages have also been observed with a northward expansion of more than 10° latitude for warm-water species and an associated decrease in the number of cold-water species at the same latitudes (Beaugrand et al. 2002). Copepods are highly important zooplankters that serve as the base of most marine food-webs. As such, changes in the distribution and abundance of copepods likely have severe consequences for the fisheries of the Northern Hemisphere (Beaugrand et al. 2002). Such changes, if they continue,

could also lead to substantial modifications of the fish fauna with a decline or even a collapse of the already weakened northern stocks of fish.

Introduction of alien species

The number of alien species in the Baltic Sea has increased during the last two centuries and at present some 30 alien species have been recorded (Swedish Board of Fisheries 2005). The most common alien species found in the Nordic countries are rainbow trout, brook charr, the signal crayfish and the zebra mussel.

Recent work suggests that the introduction of alien species leading to biotic homogenization is widespread, particularly in aquatic systems (Olden & Rooney 2006). In fish, interbreeding between alien and native species is more common than in any other vertebrate, foremost occurring in indigenous salmonid fish of North America (Rahel 2000; Taylor 2003). There are, however, also examples of where interbreeding from released non-native carp species have resulted in subsequent population declines of native crucian carps in England (Hänfling et al. 2005). Furthermore, the invasion of signal crayfish and zebra mussels into freshwater systems in Northern Europe has resulted in substantial changes in the community composition.

Fragmentation and destruction of habitats

Many salmonid populations have been fragmented and restricted from migrating to their spawning grounds due to the construction of dams and weirs (Koljonen 2001; Neraas & Spruell 2001). There are also numerous examples of where such constructions have led to the extirpation of stocks of Pacific salmon.

In many fish species, dispersal barriers have been shown to strongly influence genetic structures since they reduce gene flow between small populations leading to reduced genetic diversity (Laroche & Durand 2004). This could potentially compromise the long-term persistence of the targeted population and extirpation might be inevitable unless historical migration routes are restored. For example, populations of European grayling fish in a Danish river system have decreased considerably during the last 50 years, likely as a consequence of the construction of weirs (Meldgaard et al. 2003). The presence of such impediments likely represents dispersal barriers that only allow passive and downstream drift of fish and obstruct active upstream migration, something affecting both the distribution pattern and genetic variation of the population.

The decline of other salmonid populations in many river systems in Northern Europe has been attributable to the development of hydropower dams (reviewed in Koljonen 2001). The effects of fragmentation are thought to be more severe for species that move between different habitats during their life, but relatively little work has explored this. A better

understanding of the effects of fragmentation on the genetic diversity of animal populations is hence essential for effective management.

Whereas the concentration of some toxic substances (e. g. PCB, DDT) has decreased in aquatic environments during recent years the concentrations of other substances have increased (e. g. brominated flame retardants) or remained stable (e. g. dioxins, mercury, Swedish Board of Fisheries 2006). There are examples of where the genetic identity of aquatic organisms has been altered as a result of exposure to pollutants. The genetic variability of European eel has, for example, been demonstrated to be affected by heavy metal pollution (Maes et al. 2005). Eels from heavily polluted areas are genetically less diverse than their conspecifics inhabiting less polluted environments. Similar results have also been found in shellfish where populations from polluted areas generally have a decreased genetic diversity (Fevolden & Garner 1986).

Other examples of where environmental change have affected distributional ranges and population structures are the decrease in abundance of the freshwater pearl mussel at northern latitudes during the last decades, and the change in abundances and population structures of marine species found in the Baltic Sea as a result of the recent changes in salinity levels and increased eutrophication.

What information is needed in the future?

Relatively little is known about how environmental change affects wild population, partly as a result of the difficulties associated with studying the processes. Hence, more research is needed in all areas such as:

- More long-term historical studies. Despite that few such studies have been published, they can give insights into historical responses in species distributions to climate change in the past. Such studies could hence help us to understand the likely responses of particular species to the effects of climate change.
- Transplant and laboratory experiments. This kind of information could give insights into the capacities of species to expand their ranges and adapt to novel environments. Genetic studies should ideally be included in the experiments to identify the genes important in, for example, the regulation of temperature tolerance.
- Identification of genetic responses to anthropogenic changes that influences species distributions and abundances. This could help us to understand the biological trends induced by climate change.
- More studies mapping the genetic diversity of species and populations since the genetic variation influences the evolutionary potential of a population.
- Synthesize existing information on distributions, population structures, genetic variation and ecological and physiological limits of

species. Combining this information will facilitate the development of models that predict changes in species distributions to different scenarios of environmental change. Such models should then provide the basis for future fisheries management and long-term stock assessment. To date, such models are already under construction for northeast Atlantic cod.

- Generally, there are few field studies investigating the genetic effects of pollutants and the genetic basis for resistance against contaminants. Therefore, more studies on the link between genetic diversity and pollutant load, as well as tests of genetic adaptation to pollution exposure are needed to confirm the generality of the phenomenon.
- Similarly, information of how mutagens affect the genetic architecture is needed. Mutagens could be toxins and pollutants, but also changes in temperatures.
- To ensure that ecosystems retain their resilience and sustainability more research on the effects of spreading of alien species is definitely needed. Furthermore, much uncertainty remains regarding the ecological consequences of genetic homogenization, something that therefore deserves further attention.
- Finally, for effective evaluation of the effects of environmental change on targeted populations, complete country-wise lists of threatened species in the Nordic countries are needed. It would also be fruitful to establish common views on how to manage threatened populations and/or species in the Nordic countries.

3. Recommendations

There are several considerations that need to be taken into account for sustainable management of targeted stocks of fish and shellfish in the Nordic countries to be effective. Here we summarize the most prominent recommendations for future research. More detailed and extended recommendations are highlighted in the preceding parts of the text.

3. 1 General recommendations

- Genetic information should be included in current management plans for exploited fish stocks (e. g. in the ICES working groups) to ensure persistence of genetic diversity and to make management effective and sustainable. Examples of where knowledge on the genetic identity of populations should be considered include:
 - a) Stock boundaries. Estimations of the number of populations in an exploited stock as well as the spatial range, size and boundaries of populations are enabled with the use of genetic techniques.
 - b) Management of mixed-stock fisheries would be more efficient if extended knowledge on the structure of the harvested populations was available.
 - c) Local management. This management level has been suggested to benefit sustainable use of the fisheries resources and to reduce the risk of overexploitation. The potential for local management is greatly enhanced if existing population boundaries is known. For example, populations should be maintained to an extent that preserves the overall genetic structure and that precludes excessive loss of genetic variation due to exploitation.
 - d) Advice on sustainable fishing quotas. Genetic information greatly facilitates sound evaluations of the limits of exploitation required to sustain population sizes that precludes erosion of genetic variation. Precautionary levels for stock size and fishing mortality should be also be evaluated from a genetical point of view in that the target level is adjusted to also ensure maintenance of genetic diversity. This is in turn implemented by paying respect to and by following the advices from the ICES expert groups on fishing quotas.
- Common management practices in the Nordic countries should be established. The Nordic countries share and exploit several common and international stocks that need common management. Several

distinct populations of the same species are also found in the different countries. These are currently under national jurisdiction and it would therefore be desirable with common management strategies of the same species in all countries.

- Aquaculture and stocking that might lead to interbreeding between farmed and wild populations should be evaluated from a conservation genetic perspective prior to being conducted. This should be undertaken to minimize the effect of domestication and to preserve the genetic variation in the farmed fish. Moreover, local broodstocks should be used in current and future breeding programs.
- Additional research is needed in the following areas for management to be sustainable:
 - a) Basic knowledge of population structures of exploited species, particular marine and brackish waters species. To date, sufficient information on population structures is only available for three of the 15 commercially most important aquatic species occurring in the Nordic waters (see Appendix 3). For example, information is limited for blue whiting, mackerel, sprat and plaice. Similarly, a recent review by Laikre et al. (2005a) highlighted that sufficient information on existing population structures for genetically sustainable management of commercially exploited fishes in the Swedish jurisdiction of the Baltic Sea is only available for six of the 16 species listed. For highly important species such as Atlantic cod, European flounder, perch, plaice, sprat, vendace, whitefish and pikeperch very limited information exists. There are, however, ongoing and unpublished studies on the spatial distribution of several commercially important fish species in the Baltic Sea.
 - b) Successfulness and genetic effects of current stocking programmes. The knowledge of adverse effects of stocking is currently limited, and little information is to be found on the genetic background of the stocked fish. The little knowledge that exists is mainly confined to salmonid species found in freshwater systems and virtually nothing is known of the consequences of stocking in marine environments. Finally, the effects of stocking might only be recognized over longer timescales and investigations of the long-term effects of mixing between wild and farmed fish are therefore warranted.
 - c) Information on genetic effects of cage-escapes, especially in marine systems. The aquaculture of many marine species such as cod and halibut has increased rapidly during recent years but information on genetic effects of cage-escapes is lacking.
 - d) The effects and extent of fisheries-induced evolution. In recent decades intense harvest has been recognised to, besides reducing the biomass, also cause an evolutionary shift of the exploited

population. An evolutionary change likely has adverse effects on the viability and production of the population and might in the long run be economically important since it likely reduces fisheries yields. The evidence for fisheries-induced evolution is to date limited and more models that predict the evolutionary effects of fishing, more evidence for that fisheries-induced evolution takes place, and more information on heritability of life-history traits is therefore urgently needed.

- e) Genetic effects of climate and environmental change. The effects of global warming are predicted to be greater at the latitudes of the Nordic countries, and species/populations at higher latitudes are also thought to be more vulnerable to changes in temperatures. Therefore, studies on how the climate change and other environmental perturbations affect the genetic structure of fish populations in the sensitive northern environments typical for the Nordic countries are needed.

3. 2 Country-wise recommendations

- Information on stocking statistics should be available also for Denmark and Norway. In Sweden where data on the species used in stocking is available, more detailed information on the quantities of each species should be provided. Similarly, records of the extent of cage escapes from aquaculture in the Nordic countries should be established.
- Each country should be responsible for coordinating future research on one of the subjects highlighted in this report. Suggested subjects for each country are:
 - a) Identification of population structure- Denmark.
 - b) Stocking- Finland.
 - c) Cage-escapes from aquaculture- Norway.
 - d) Fisheries-induced evolution- Sweden.
 - e) Effects of environmental change- Iceland and Faroe Islands.

A topic for future discussion should be how these levels of organization could be implemented and maintained.

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Sammanfattning

Under de senaste decennierna har den mänskliga påverkan på vilda fiskpopulationer ökat drastiskt i hela världen. Detta är bland annat ett resultat av utbredd akvakultur, exploatering för mänsklig konsumtion och av människan orsakade miljöförändringar. Alla dessa aktiviteter påverkar troligen också den genetiska diversiteten och strukturen hos nyttjade arter. Bevarandet av genetisk mångfald är i sin tur en internationell överenskommelse samt ett långsiktigt mål för förvaltning av vilda populationer

Kunskap om neutral och adaptiv genetisk diversitet är väldigt viktig då den ger information om förekomsten av lokala anpassningar, den genetiska populationsstrukturen, samt en arts/populations evolutionära potential. Kunskap om en arts genetiska diversitet möjliggör även förståelse för ett ekosystems hälsa och hur det förväntas svara på plötsliga förändringar. Information om den genetiska populationsstrukturen av komersiellt viktiga fiskarter är därför nödvändig för att förhindra skada av ekosystemet och möjliggör samtidigt uthållig och effektiv förvaltning av nyttjade bestånd. De molekylära teknikerna som utvecklats under de senaste åren erbjuder unika möjligheter för att studera genetiska processer och mönster i vilda populationer. Uthållig förvaltning underlättas till stor del och är i vissa fall helt beroende av användandet av dessa moderna molekylära metoder.

Genetisk forskning om komersiellt nyttjade arter har en lång tradition i de nordiska länderna, och pågår för tillfället på en rad olika forskningsinstitut. Nyttjandet av resultaten från denna forskning inom förvaltningen av vilda populationer har hitintills dock varit begränsad. Den här rapporten kartlägger det nuvarande kunskapsläget om genetisk diversitet och struktur hos nordiska fiskarter, och har som mål att fungera som en bas för framtida insatser inom forskningsområdet. Tonvikten är lagd på fem olika ämnesområden där genetisk kunskap är nödvändig för hållbar och effektiv förvaltning: Identifiering av populationsstrukturer, Utsättning av odlad fisk, Rymningar från akvakulturer, Fiskeri-inducerad evolution, och Effekter av miljöförändringar. För varje ämnesområde diskuteras hur den genetiska informationen kan användas i förvaltning, det ges en kort sammanfattning över det rådande kunskapsläget, och brister i kunskapsläget belyses. En kort översikt över den genetiska forskningen på fisk (såväl marint som i sötvatten) och andra akvatiska arter i Norden bifogas som appendix, liksom en lista över var den befintliga kompetensen i populationsgenetiska metoder finns. Vi identifierar även mellan vilka institut och länder befintliga samarbeten och nätverk finns.

Slutsatserna vi drar är att trots de nyligen gjorda framstegen inom detta forskningsområde, så finns det ett flertal saker som måste beaktas för att framtida förvaltning av de nordiska bestånden av fisk och skaldjur skall vara uthållig och effektiv. Till exempel:

- Information om den genetiska diversiteten och strukturen bör inkluderas i förvaltningsplanerna för ICES arbetsgrupper, och hänsyn bör tas till dessa gruppers råd om fiskekvoter.
- Då de nordiska länderna delar och nyttjar flera gemensamma och internationellt förvaltade bestånd av fisk, bör gemensamma förvaltningsmål av dessa bestånd sättas upp.
- Akvakultur och utplantering av fisk som kan leda till utbyte av gener mellan vilda och odlade populationer bör utvärderas ur ett bevarandegenetiskt perspektiv innan sådana projekt initieras.
- För uthållig förvaltning så krävs ytterligare kunskap om de genetiska populationsstrukturerna av nyttjade arter, kunskap om utfall och genetiska effekter av utplantering av fisk, kunskap om de genetiska effekterna av rymlingar från akvakulturer (särskilt i marina system), kunskap om omfattningen av och de genetiska effekterna av fiskeri-inducerad evolution, samt kunskap om de genetiska effekterna av klimat- och miljö-förändringar.

Appendix 1

Compilation over the genetic research conducted in the Nordic countries.

Contents

Denmark		66
	Danish Technical University, Danish Institute for Fisheries Research (DIFRES)	66
	University of Copenhagen, Marine Biological Laboratory*	68
	University of Aarhus, Research Centre Foulum.	68
Faroe Islands		70
	University of the Faroe Islands, Faculty of Science and Technology	70
Finland		72
Res. Inst.		72
	MTT Agrifood Research Finland, Animal Production Institute Animal Breeding	72
	Finnish Game and Fisheries Research Institute (FGFRI)	73
Universities		75
	University of Joensuu	75
	University of Kuopio	76
	University of Oulu	77
	University of Turku	78
	University of Helsinki	80
Iceland		82
Res. Inst.		82
	Marine Research Institute, Population Genetics Laboratory	82
Universities		83
	University of Iceland, Institute of Biology	83
	Hólar Collage, the Department of Aquaculture	84
Private Comp.		85
	Prokaria Research ehf.	85
Norway		87
Res. Inst.		87
	Akvaforsk, Genetics and Breeding Group*	87
	The Centre for Integrative Genetics (CIGENE)*	88
	Norwegian School of Veterinary Science*	89
	Salmon Genome Project	90
	Institute of Marine Research (IMR)*	91
	Norwegian Institute for Nature Research (NINA)	92
Universities		94
	University of Tromsø, Norwegian College of Fishery Science (NCFS)	94
	University of Oslo, Department of Biology, Centre for Ecological and Evolutionary Synthesis (CEES)	95
	University of Oslo, Joint group "HI-Flødevigen/University of Oslo-CEES"	97
	NTNU- Institute of Biology-Trondhjem Biological Station (TBS)*	98
	University of Bergen, Department of Fisheries and Marine Biology*	99
	Telemark University College*	99

Private Comp.		100
	GenoMar ASA*	100
<hr/>		
Sweden		102
Res. Inst.		102
	Swedish board of Fisheries, Institute of Freshwater Research (IFR)	102
	Swedish board of Fisheries, Institute of Coastal Research (ICR)	103
	Swedish Museum of Natural History, Department of Vertebrate Zoology, Ichthyology section	105
Universities		106
	Stockholm University, Institute of Zoology, Department of Population Genetics	106
	Uppsala University, Department of Ecology and Evolution, Animal Ecology	107
	Uppsala University, Department of Physiology and Developmental Biology, Comparative Physiology	108
	Uppsala University, Department of Ecology and Evolution, Limnology	109
	Göteborg University, Department of Marine Ecology, Tjärnö Marine Biology Laboratory (TMBL)	110
	Örebro University, Molecular Biology Group	111
	Lund University, Department of Ecology, Animal Ecology, Molecular Population Biology	112
	Swedish University of Agricultural Sciences (SLU), Umeå, Department of Aquaculture	114
	Södertörn University College*	115
	Mälardalen University, Department of Ecology	116

* These affiliations could not be contacted for proof reading of the compiled information

Denmark

Genetic research on commercially exploited fishes in Denmark is mainly centred at the Danish Institute for Fisheries Research (DIFRES). There is, however, also active research conducted at the University of Copenhagen and at the Danish Institute of Agricultural Sciences. The studies conducted are both on *freshwater* and *marine fish* species with the focus on *salmonid species* and *cod*. The research spans a wide range with projects on the genetic variation and population structure in wild exploited populations, genetics and gene expression of species in aquaculture, genetic consequences of stocking, and candidate gene (e. g. hemoglobin) analyses.

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Cooperation parties: Several national and international research institutes, incl.

Katholieke Universitet Leuven, Belgium.

University of Laval, Quebec, Canada.

Institute for Marine Research, Norway.

University of Göteborg, Sweden.

Research groups/projects:

- Genetic structure of freshwater fishes of recreational and commercial interest.
- Genetic structure and stocking impact assessment in salmonid fishes.
- Long term genetic effects of releases of exogenous Atlantic salmon and supportive breeding on the genetic composition of indigenous fish in Danish west coast rivers.
- Effects of genetic origin on pike stocking success.
- Role of sub-stock structure in the maintenance of cod meta-populations (METACOD).
- Neutral and adaptive genetic variation in the European flounder.
- Seafood-plus, Project 5. 1. Physiology and genetics of seafood quality traits.
- Individual and population variation in expression of stress genes in European flounder and Atlantic cod.

Summary:

The research conducted at DIFRES includes projects on both freshwater and marine species. Genetic structure and impacts of stocking in brown trout and other salmonid fishes (including whitefish and the endemic North Sea houting) are also studied (projects 1, 2, 3). Local adaptation in salmonid populations is examined in several projects. Evidence for local adaptation and effects on stocking success is moreover studied in pike (project 4). Several projects (e. g. 5, 6, 8) are conducted on commercially exploited marine populations. Genetic differentiation and temporal stability among spawning groups of Atlantic cod is studied (project 5). The aim of this project is to examine the composition of mixed feeding aggregations generally targeted by fisheries. Project 6 aims at providing a description of the genetic structure of European flounder using both microsatellites and a candidate gene (heat-shock) approach. Local adaptations to different environmental conditions in Atlantic cod and European flounder, individual and population variation in expression of stress genes

in relation to environmental stressors (salinity and temperature) are studied (project 8). In the Seafood-plus project (project 7), the aim is to identify candidate genes for variation in quality traits for wild fish and fish from aquaculture.

Selected Publications:

- Nielsen EE, Hansen MM, Meldrup D. 2006. Evidence of microsatellite hitchhiking selection in Atlantic cod (*Gadus morhua* L.): Implications for inferring population structure in non-model organisms. *Molecular Ecology*, in press.
- Bekkevold D, Hansen MM, Nielsen EE. 2006. Genetic impact of gadoid culture on wild fish populations: predictions, lessons from salmonids and possibilities for minimising adverse effects. *ICES Journal of Marine Science*, 63: 198-208.
- Giger T, Excoffier L, Day PRJ, Champigneulle A, Hansen MM, Powel R, Largiader CR. 2006. Life history shapes gene expression in salmonids. *Current Biology*, 18: R281-R282.
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- Poulsen NA, Nielsen EE, Schierup MH, Loeschcke V, Grønkjær P. 2006. Long-term stability and effective population size in North Sea and Baltic Sea cod (*Gadus morhua*). *Molecular Ecology*, 15: 321-331.
- Ruzzante DE, Mariani S, Bekkevold D, André C, Mosegaard H, Clausen LAW, Dahlgren, TG, Hutchinson WF, Hatfield EMC, Torstensen E, Brigham J, Simmonds EJ, Laikre L, Larsson LC, Stet RJM, Ryman N, Carvalho GR. 2006. Biocomplexity in a highly migratory pelagic marine fish, Atlantic herring. *Proceeding of the Royal Society London Series B*, 273: 1459-1464.
- Bekkevold D, André C, Dahlgreen TG, Clausen LAW, Torstensen E, Mosegaard H, Carvalho GR, Christensen TB, Norlinder E, Ruzzante DE. 2005. Environmental correlates of population differentiation in Atlantic herring. *Evolution*, 59: 2656-2668.
- Jørgensen HBH, Hansen MM, Bekkevold D, Ruzzante DE, Loeschcke V. 2005. Marine landscapes and population genetic structure of herring (*Clupea harengus* L.) in the Baltic Sea. *Molecular Ecology*, 14: 3219-3234.
- Nielsen EE, Grønkjær P, Meldrup D, Paulsen H. 2005. Retention of juveniles within a hybrid zone between North Sea and Baltic Sea cod (*Gadus morhua*). *Canadian Journal of Fisheries and Aquatic Sciences*, 62: 2219-2225.

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Summary:

The focus of the research conducted at the Marine Biological Laboratory is on the relationship between physiology (especially temperature optima) and hemoglobin genotypes in cod.

Selected Publications:

There was no information available on publications from the Marine Biological Laboratory when this report was finished.

3. University of Aarhus, Research Centre Foulum.

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Cooperation parties: Danish Institute for Food and Veterinary Research, Royal Veterinary and Agricultural University, DIFRES, Aquasearch.

Research groups/projects:

- Genes involved in resistance and susceptibility to viral haemorrhagic septicaemia in Rainbow trout.
- Estimation of quantitative genetic differences in disease resistance and variation in expressed MHC alleles in Rainbow trout.
- Development of breeding strategies to improve the genetics of trout used for commercial production.

Summary:

The focus of the research conducted at Research Centre Foulum is centred round breeding strategies for disease resistance and production traits in rainbow trout. This is done by exploring the underlying (genetic) mechanisms that improve resistance and production traits. Traits of importance when selecting for resistance and production traits in breeding programs are also identified. Part of the work is carried out within the EADGENE network (European Animal Disease Genomics Network of Excellence for Animal Health and Food Safety). Ongoing projects involve measuring genetic expressions of 16, 000 genes showing resistance

and susceptibility to viral haemorrhagic septicaemia in infected Rainbow trout (project 1). The hypothesis tested is that some of the genes are differentially expressed in infected trout, and that the differential expression of these genes reflects resistance to the virus. In the second project, offspring from crosses between families expressing different MHCI and MHCII alleles are challenged with viral haemorrhagic septicaemia, rainbow trout fry syndrome and enteric redmouth disease. The information gathered will then be used to estimate quantitative genetic differences in disease resistance between the families, as well as the direct effects of expressed MHC alleles. In the last project, the aim is to develop breeding strategies that produce large genetic gains in production and disease resistance while maintaining the rate of inbreeding at acceptable levels.

Selected Publications:

- Henryon M, Berg P, Olesen NJ, Kjær TE, Slierendrecht V, Jokumsen A, Lund I. 2005. Selective breeding provides an approach to increase resistance of rainbow trout (*Onchorhynchus mykiss*) to the diseases, enteric redmouth disease, rainbow trout fry syndrome, and viral haemorrhagic septicaemia. *Aquaculture*, 250: 621-636.
- Henryon M, Berg P, Olesen NJ, Kjær T, Schlierendrecht H, Ekman K, Lund I, Jokumsen A. 2003. Avlsarbejde kan øge sygdomsresistens hos regnbueørred. *Ferskvandsfiskeribladet*, 6: 126-127.
- Jokumsen A, Lund I, Berg P, Henryon M. 2003. Ørreder med 6% højere tilvækst på avlsstationen. *Ferskvandsfiskeribladet*, 5: 100-102.
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- Berg P. 2001. EVA – Evolutionary Algorithm for mate selection. User's Guide.
- Berg P, Henryon M. 1999. Selection response under alternative mating designs in fish. *Proc. Assoc. Advmt. Anim. Breed. Genet.*, 13: 297-300.
- Berg P. 1998. Produktion af regnbueørred. Sygdomsforebyggelse, genetik og ernæring. Danmarks JordbrugsForskning. Intern rapport nr. 105.
- Faroe Islands*
Samples for genetic analyses of fish from waters around Faroe Islands have mainly been collected at the University of the Faroe Islands and at the Fisheries Laboratory. Due to a lack of necessary facilities for genetic analyses, most samples have been analysed elsewhere. During recent years, however, the Food- Veterinary and Environmental agency of Faroe Islands has acquired facilities for DNA-analysis. The analyses conducted here have though been used for diagnostic purposes in the aquaculture and food industry. Faroe Islands are due to the location in the middle of the North Atlantic geographically isolated, and many of the fish species fish around the islands have therefore evolved special and unique characters. The genetic research at Faroe Islands has therefore been focused on genetic differences between fish from Faroe waters and fish from other areas. Studies have mainly been carried out on cod, but an additionally eight species have been under investigation. Since there are only four native species found in freshwaters (brown trout, arctic char, eel and stickleback), only a few investigations have been conducted in freshwater systems.

1. University of the Faroe Islands, Faculty of Science and Technology.

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Einar Arnason, University of Iceland, Institute of Biology, Iceland.

Research groups/projects:

1. Genetic analysis of cod.

Summary:

Genetic research on Atlantic cod in the Faroe Islands has a long history. In 1965, analysis was performed on haemoglobin polymorphism in cod in the North Atlantic. Recent studies have used modern molecular techniques, and also investigated population differentiation between the two distinct cod stocks found in Faroe waters, cod from the Faroe Plateau and Faroe Bank ecosystems. Studies of genetic differentiation between plaice, poor cod, redfish, saithe, halibut, haddock, tusk and sandeel from Faroe waters and fish from other areas have also been conducted. Finally, in some of these species the existence of genetic differences between the Faroe Plateau and Faroe Bank ecosystems have also been investigated.

Selected Publications:

- Joensen H, Grahl-Nielsen O. 2004. Stock structure of *Sebastes mentella* in the North Atlantic revealed by chemometry of the fatty acid profile in heart tissue. *ICES Journal of Marine Science*, 61: 113-126.
- Mattiangeli V, Galvin P, Ryan AW, Mork J, Cross TF. 2002. VNTR variability in Atlantic poor cod (*Trisopterus minutus minutus*) throughout its range: single locus minisatellite data suggest reproductive isolation for the Faroe Bank population. *Fisheries Research*, 58: 185-191.
- Joensen H, Steingrund P, Fjallstein I, Grahl-Nielsen O. 2000. Discrimination between two reared stocks of cod (*Gadus morhua*) from the Faroe Islands by chemometry of fatty acid composition in the heart tissue. *Marine Biology*, 136: 573-580.
- Mattiangeli V, Bourke EA, Ryan A, Mork J, Cross TF. 2000. Allozyme analyses of the genus *Trisopterus*: taxonomic status

- and population structure of the poor cod. *Journal of Fish Biology*, 56: 474-494.
- Fjallstein I, Magnussen E. 1996. Growth of Atlantic cod (*Gadus morhua* L.) of Faroe Bank strain and Faroe Plateau strain in captivity. *ICES-CM F(12)*, 1-16.
- Magnussen E. 1996. Electrophoretic studies of cod (*Gadus morhua*) from Faroe Bank and Faroe Plateau compared with results found in other areas. *ICES-CM G(10)*, 1-18.
- Dahle G, Eriksen AG, Cook D, Wright JM. 1995. Microsatellite differentiation in cod (*Gadus morhua* L.) among the Faroe Bank and adjacent areas. In *Genetic structure of North-East Atlantic cod (*Gadus morhua* L.)*, an appraisal of different molecular techniques (Dahle G), . Dr Philos. Thesis, University of Bergen.
- Magnussen E. 1993. Why is the cod growing faster on the Faroe Bank than on the Faroe Plateau? (in Danish) [Hvorfor vokser torsken hurtigere på Færøbanken end på Færøplateauet?].), 1-104. 1993. Thesis/Dissertation, University of Copenhagen.
- Jamieson A, Jones BW. 1967. Two races of cod at Faroe. *Heredity*, 22: 610-612.
- Sick K. 1965. Haemoglobin polymorphism of cod in the North Sea and the North Atlantic ocean. *Hereditas*, 54: 50-73.

Finland

In Finland, genetic research on fish is at present centred at two research institutes, MTT Agrifood Research and Finnish Game and Fisheries Research Institute and at five different universities, Universities of Joensuu, Kuopio, Oulu, Turku and Helsinki. The research is focused around aquaculture salmonid species, on exploited species living in the wild such as brown trout and Atlantic salmon, but also on other salmonids such as rainbow trout, Arctic charr, European grayling and European whitefish. A project is also conducted on the genetics and speciation in the salmonid pathogen *Gyrodactylus salaris*.

Research institutes

1. MTT Agrifood Research Finland, Animal Production Institute, Animal Breeding

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Cooperation parties: Finnish Game and Fisheries Research Institute.
 University of Helsinki (Department of Animal breeding). Aberdeen University (UK).
 Institute of Marine Research (Norway).

Research groups/projects:

- Breeding programs for farmed fish.
- Optimising European whitefish breeding scheme using genetic and economic information.
- Protein and growth efficiency in salmonid selection (PROGRESS).
- Molecular genetic methods in fish breeding programmes.

Summary:

MTT Agrifood Research and the Finnish Game and Fisheries Research Institute (FGFRI) cooperate in projects concerning the maintenance of national and non-profit breeding programmes for rainbow trout and European whitefish. MTT is responsible for the genetic expertise and FGFRI for fish management. The main goal of the projects at MTT is to enhance productivity of fish farming in Finland using the modern methods of quantitative and molecular genetics. For example, tools are developed to enhance end-product quality and to reduce feed costs and environmental impacts. Genetic variation for traits under selection is estimated and the molecular genetic basis for economically important traits is identified using special fish crosses. The success of the different projects is then evaluated by comparing performance of the selected populations with other cultivated stocks of fish. In the European whitefish breeding program a market survey in combination with genetic analysis of production and quality traits is carried out to optimize the breeding scheme based on the economic and genetic information gathered.

Selected Publications:

- Stien LS, Manne F, Ruohonen K, Kause A, Rungruangsak-Torrissen K, Kiessling A. Automated image analysis as a tool to quantify the colour and composition of rainbow trout (*Oncorhynchus mykiss* W.) cutlets. *Aquaculture*, in press.
- Tobin D, Kause A, Mäntysaari EA, Martin SAM, Houlihan DF, Dobby A, Kiessling A, Rungruangsak-Torrissen K, Ritola O, Ruohonen K. Fat or lean? The quantitative genetic basis for selection of lipid and protein composition traits in breeding schemes of rainbow trout. *Aquaculture*, in press.
- Kause A, Tobin D, Dobby A, Houlihan DF, Martin SAM, Mäntysaari EA, Ritola O, Ruohonen K. 2006. Recording strategies and selection potential of feed intake measured using the X-ray method in rainbow trout. *Genetics Selection Evolution*, 38: 389-410.
- Kause A, Tobin D, Houlihan DF, Martin SAM, Mäntysaari EA, Ritola O, Ruohonen K. 2006. Feed efficiency of rainbow trout can be improved through selection: Different genetic potential on alternative diets. *Journal of Animal Science*, 84: 807-817.
- Martinez V, Kause A, Mäntysaari EA, Mäki-Tanila A. 2006. The use of alternative breeding schemes to enhance genetic improvement in rainbow trout: I. One-stage selection. *Aquaculture*, 254: 182-194.
- Martinez V, Kause A, Mäntysaari EA, Mäki-Tanila A. 2006. The use of alternative breeding schemes to enhance genetic improvement in rainbow trout: II. Two-stage selection. *Aquaculture*, 254: 195-202.
- Kause A, Ritola O, Paananen T, Wahlroos H, Mäntysaari EA. 2005. Genetic trends in growth, sexual maturity and skeletal deformations, and rate of inbreeding in a breeding programme for rainbow trout. *Aquaculture*, 247: 177-187.
- Kause A, Ritola O, Paananen T. 2004. Breeding for improved appearance of large rainbow trout in two production environments. *Aquaculture Research*, 35: 924-930.

2. Finnish Game and Fisheries Research Institute (FGFRI)

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Cooperation parties: University of Helsinki.
University of Turku (Irma Saloniemi).
University of Umeå (Sweden).

Research groups/projects:

- Genetic stock composition analysis of Atlantic salmon catches.
- Phylogeography of brown trout in Finland and in Russian Karelia.
- Unintentional genetic effects of hatchery rearing and selective fishery on the size and age at maturity and on the marine survival of Atlantic salmon.
- Other projects such as the genetic effects of stocking on populations of pikeperch and whitefish phylogeography.

Summary:

The research at the FGFRI is centred on Atlantic salmon (*Salmo salar*) and brown trout. In the first project the aim is to create a sustainable fishery for Atlantic salmon in the Baltic Sea, and to monitor the abundance of wild fish in the catches by using information of spatial and temporal genetic variation of the species. DNA-microsatellite information is collected for different stocks of Atlantic salmon from the Baltic Sea to be able to estimate in which fisheries and in what quantities the different salmon stocks are exploited. In the second project, the main goal is to reconstruct the phylogeography and postglacial history of brown trout (*Salmo trutta*) in Scandinavia. The goal of the third project is to map the potential changes of traits such as age and size at maturity caused by hatchery rearing and fishing and also to assess the resulting evolutionary effects on, for example, future survival of the stocks. There are a number of additional projects running where, for example, the genetic effects of stocking of pikeperch on recipient populations are evaluated. A phylogeny of different types of whitefish is also under construction.

Selected Publications:

- Kallio-Nyberg I, Saloniemi I, Koljonen M-L, Tanhuanpää M. 2006. Effect of inter-strain hybridisation and smolt traits on survival of salmon (*Salmo salar*) in the Baltic Sea. Manuscript.
- Kallio-Nyberg I, Jutila E, Jokikokko E, Saloniemi I. 2006. Survival of reared Atlantic salmon and sea trout in relation to marine conditions of smolt year in the Baltic Sea. *Fisheries Research*, 80: 295–304.
- Koljonen M-L. 2006. Annual changes in the proportions of wild and hatchery Atlantic salmon (*Salmo salar*) caught in the Baltic Sea. *ICES Journal of Marine Science*, 63:1274–1285.
- Koljonen M-L, Pella JJ, Masuda M. 2005. Classical individual assignments versus mixture modeling to estimate stock proportions in Atlantic salmon (*Salmo salar*) catches from DNA microsatellite data. *Canadian Journal of Fisheries and Aquatic Sciences*, 62: 2143–2158.
- Säisä M, Koljonen M-L, Gross R, Nilsson J, Tähtinen J, Koskiniemi J, Vasemagi A. 2005. Population genetic structure and postglacial colonization of Atlantic salmon in the Baltic Sea area based on microsatellite DNA variation. *Canadian Journal of Fisheries and Aquatic Sciences*, 62: 1887–1904.
- Jokikokko E, Kallio-Nyberg I, Jutila E. 2004. The timing, sex and age composition of the wild and reared Atlantic salmon ascending the Simojoki river, northern Finland. *Journal of Applied Ichthyology*, 20: 37–42.
- Kallio-Nyberg I, Jutila E, Saloniemi I, Jokikokko E. 2004. Association between environmental factors, smolt size and the survival of wild and reared Atlantic salmon from the Simojoki river in the Baltic Sea. *Journal of Fish Biology*, 65: 122–134.
- Koljonen M-L. 2004. Changes in stock composition of annual Atlantic salmon catches in the Baltic Sea on basis of DNA-microsatellite data and Bayesian estimation. *ICES CM 2004/Stock Identification Methods/EE:08*, 21 pp.
- Michielsens C, Mäntyniemi S, Koljonen M-L. 2004. The use of genetic stock identification results for the assessment of wild Baltic salmon stocks. *ICES CM 2004/EE:03*, 15 pp.
- Saloniemi I, Jokikokko E, Kallio-Nyberg I, Jutila E, Pasanen P. 2004. Survival of reared and wild Atlantic salmon smolts: size matters more in bad years. *ICES Journal of Marine Science*, 61: 782–787.

Universities

1. University of Joensuu

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 RA Bodaly, Fisheries & Oceans Canada, Ottawa, Canada.
 James D. Reist, Fisheries & Oceans Canada, Winnipeg, Canada.
 Mirosław Luczynski Univ. of Warmia and Mazury, Olsztyn, Poland.

Research groups/projects:

1. Genetic differentiation and speciation of salmonid fishes with special emphasis to coregonids.

Summary:

The research at the University of Joensuu is focused on evolutionary genetics, genetic population structure and phylogeography of salmonid fishes.

Selected Publications:

- Vuorinen JA, Næsje TF, Sandlund OT. 2004. Genetic and morphometric differentiation among sympatric spawning stocks of whitefish (*Coregonus lavaretus* L.) in Lake Femund, Norway. *Journal of Limnology*, 63: 233–243.
- Luczynski M, Bartel R, Vuorinen JA, Domagala J, Zolkiewicz L, Brzuzan P. 2000. Biochemical genetic characteristics of four Polish sea trout (*Salmo trutta trutta* L.) populations. *Polskie Archiwum Hydrobiologii*, 47: 21–28.
- Vuorinen JA, Bodaly RA, Reist JD, Luczynski M. 1998. Phylogeny of five *Protopium* species with comparisons with other Coregonine fishes based on isozyme electrophoresis. *Journal of Fish Biology*, 53: 917–927.
- Reist JD, Maiers LD, Bodaly RA, Vuorinen JA, Carmichael TJ. 1998. The phylogeny of new and old-world coregonine fishes as revealed by sequence variation in a portion of the d-loop of mitochondrial DNA. *Archiv für Hydrobiologie Spec. Issues Advanc. Limnol*, 50: 323–339.
- Elo K, Ivanoff S, Vuorinen JA, Piironen J. 1997. Inheritance of RAPD markers and detection of interspecific hybridization in brown trout and Atlantic salmon. *Aquaculture*, 152: 55–65.

- Bernatchez L, Vuorinen JA, Bodaly RA, Dodson JJ. 1996. Genetic evidence for reproductive isolation and multiple origins of sympatric trophic ecotypes of whitefish (*Coregonus*). *Evolution*, 50: 624–635.
- Bodaly RA, Vuorinen JA, Reshetnikov YS, Reist JD. 1994. Genetic relationships of five species of coregonid fishes from Siberia. *Voprosy ichtiologii*, 34: 195–203 (in Russian), translated in *Journal of Ichthyology*, 34: 117–130.
- Elo K, Vuorinen JA, Niemelä E. 1994. Genetic resources of Atlantic salmon (*Salmo salar* L.) in Teno and Näätämö Rivers, northernmost Europe. *Hereditas*, 120: 19–28.

2. *University of Kuopio*

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Leading scientists: Hannu Mölsä (Group leader), Aleksei Krasnov (c/o Akvaforsk), Heikki Koskinen, Atte vonWright, J Heikkinen.

Cooperation parties: University of Turku.

- University of Jyväskylä.
- University of Joensuu.
- University of Helsinki.
- Finnish Game and Fisheries Research Institute.
- Fish Innovation Centre.
- Autonomous University of Barcelona, Spain.
- University of Barcelona, Spain.
- Akvaforsk, Norway.
- USDA/ARS/National Centre for Cold and Cool Water Aquaculture, West Virginia, USA.

Research groups/projects:

1. Fish Array – functional genomics of rainbow trout.
2. Fish & Chips – genomic tools in fish biology and aquaculture.
3. ProBio – AquaFeed – Pre and probiotics in fish feeds and sustainable aquaculture.

Summary:

The “Fish & Chips” research group (Krasnov et al.) has focused on three closely related tasks: (i) construction of cDNA libraries and preparation

of probes for micro arrays, (ii) development of bioinformatic software and (iii) multiple gene expression analyses in salmonid fish. The projects have resulted in construction of cDNA microarray (FA 2. 0) containing more than 1800 salmonid genes, especially designed to reveal expression of fish stress genes. The group provides research services including design of the DNA-chip using bioinformatics tools, experimental work on defined scientific or practical problem, and consultancy in data processing and interpretation of final results. Another field of research (von Wright et al.) deals with probiotics and their use in feeds of farmed fish fed by alternative feed. Effects of soyabean meal-based diet on fish immunology, growth performance and welfare have been studied in rainbow trout. Micro-arrays were used to indicate genomic responses and metabolic challenges of anti-nutrients and the imbalance of nutrients in novel feed.

Selected Publications:

- Pehkonen P, Koskinen H, Mölsä H, Rexroad C, Krasnov A. 2006. START, a desktop tool for construction of gene indices; application of functional annotations in comparative genomics of salmonid fish. *Marine Biotechnology*, Submitted manuscript.
- Vuori KAM, Koskinen H, Krasnov A, Koivumäki P, Vuorinen PJ, Nikinmaa M. 2006. Developmental disturbances of salmon: microarray and real time PCR analysis of changes in gene expression during the early life stage mortality occurring in the Baltic Sea. *BMC Genomics*, 17:56.
- MacKenzie S, Iliev D, Liarte C, Koskinen H, Planas J, Goetz FW, Mölsa H, Krasnov A, Tort L. 2006. Transcriptional analysis of LPS-stimulated activation of trout (*O. mykiss*) monocyte/macrophage cells in primary culture treated with cortisol. *Molecular Immunology*, 43: 1340–1348.
- Vornanen M, Hassinen M, Koskinen H, Krasnov A. 2005. Steady-state effects of temperature acclimation on the transcriptome of the rainbow trout heart. *American Journal of Physiology – Regulatory, Integrative and Comparative Physiology*, 289: 1177–1184.
- Krasnov A, Koskinen H, Rexroad C, Afanasyev S, Mölsä H, Oikari A. 2005. Transcriptome responses to carbon tetrachloride and pyrene in the kidney and liver of juvenile rainbow trout (*Oncorhynchus mykiss*). *Aquatic Toxicology*, 74: 70–81.
- Krasnov, A. , Koskinen, H. , Pehkonen, P. , Rexroad C. E. , Afanasyev, S. , Mölsä, H. 2005. Gene expression in the brain and kidney of rainbow trout in response to handling stress. *BMC Genomics*. 6:3
- Krasnov A, Koskinen H, Afanasyev S, Mölsä, H. 2005. Expressed Tc1-like transposons in salmonid fish and their functional role. *BMC Genomics*, 6: 107.
- Koskinen H, Pehkonen P, Vehniäinen E, Krasnov A, Rexroad C, Afanasyev S, Mölsä H, Oikari A. 2004. Response of rainbow trout transcriptome to model chemical contaminants. *Biochemical and Biophysical Research Communications*, 320: 745–753.
- Koskinen H, Krasnov A, Rexroad C, Gorodilov Y, Afanasyev S, Mölsä H. 2004. The 14-3-3 proteins in teleost fish rainbow trout (*Oncorhynchus mykiss*). *Journal of Experimental Biology*, 207: 3361–3368.
- Krasnov A, Teerijoki H, Gorodilov Y, Mölsä H. 2003. Cloning of rainbow trout (*Oncorhynchus mykiss*) α -actin and myosin regulatory light chain genes and the 5'-flanking region of α -tropomyosin. Functional assessment of promoters. *Journal of Experimental Biology*, 206: 601–608.

3. University of Oulu

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Cooperation parties: University of Turku.

Karelian Research Center in Petrozavodsk, Russia.

University of Gdansk, Poland.

Research groups/projects:

1. Genetics and speciation in salmonid pathogen *Gyrodactylus salaris*.

Summary:

At the University of Oulu, the research is focused on genetic differentiation and speciation in the salmonid pathogen *Gyrodactylus salaris*. The genetic differentiation in *Gyrodactylus* is also investigated in relation to the spatial variation and postglacial colonization history in its hosts, Atlantic salmon, grayling and rainbow trout. Relevant comparisons to other *Gyrodactylus* species, both marine and freshwater, and on salmonids and other fish families are also conducted.

Selected Publications:

- Ziętara MS, Kuusela J, Lumme J. 2006. Escape from an evolutionary dead-end: a triploid clone of *Gyrodactylus salaris* is able to revert to sex and switch host (Platyhelminthes, Monogenea, Gyrodactylidae). *Hereditas*, 143: 86–92.
- Tonteri A, Titov S, Veselov A, Zubchenko A, Koskinen MT, Lesbarrères D, Kaluzhchin S, Bakhmet I, Lumme J, Primmer CR. 2005. Phylogeography of anadromous and non-anadromous Atlantic salmon (*Salmo salar*) from northern Europe. *Annales Zoologici Fennici*, 45: 1–22.
- Asplund T, Veselov TA, Primmer CR, Bakhmet I, Potutkin A, Titov S, Zubchenko A, Studenov I, Kaluzhchin S, Lumme J. 2004. Geographical structure and postglacial history of mtDNA haplotype variation in Atlantic salmon (*Salmo salar* L.) among rivers of the White and Barents Sea basins. *Annales Zoologici Fennici*, 44: 465–475.
- Meinilä M, Kuusela J, Ziętara MS, Lumme J. 2004. Initial steps of speciation by geographic isolation and host switch in salmonid pathogen *Gyrodactylus salaris* (Monogenea: Gyrodactylidae). *International Journal of Parasitology*, 34: 515–526.
- Ziętara MS, Lumme J. 2003. The crossroads of molecular, typological and biological species concept: two new species of *Gyrodactylus* Nordmann, 1832

- (Monogenea, Gyrodactylidae). *Systematic Parasitology*, 55: 39–52.
- Ziętara MS, Lumme J. 2002. Speciation by host switch and adaptive radiation in fish parasite genus *Gyrodactylus* (Platyhelminthes, Monogenea). *Evolution*, 56: 2445–2458.
- Meinilä M, Kuusela J, Ziętara MS, Lumme J. 2002. Primers for amplifying ~800 bp of highly polymorphic mitochondrial COI gene of *Gyrodactylus salaris* (Platyhelminthes, Monogenea, Gyrodactylidae) *Hereditas*, 137: 72–74.

4. University of Turku

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Cooperation parties: University of Helsinki.

- University of Oulu.
- Finnish Game and Fisheries Research Institute.
- Karelian Research Institute, Russia.
- State Research Institute of Lake and River Fisheries, Russia.
- Norwegian Institute for Water Research, University of Oslo, Norway.

Research groups/projects:

1. Towards sustainable fishing and biodiversity preservation of northwest Russian salmonid stocks by using molecular genetic techniques for stock and parasite monitoring.
2. Effects of hatchery escapees on wild Teno salmon.
3. MHC variation in Nordic Arctic charr populations.
4. Centre of Excellence in Evolutionary Genetics and Physiology – Conservation genetics of salmonid fishes.
5. Integration of genetic linkage mapping and experimental ecology approach to investigate the genetic basis for local adaptation in early life stages of Atlantic salmon.

Summary:

Research at the University of Turku covers a wide range of subjects with a focus on salmonid fishes. The first project aims to establish a sound biological basis for the monitoring and management of fisheries and fishing tourism of the northwest Russian salmonid stocks by utilizing modern population and conservation genetic analysis techniques. The project also aims to increase the molecular genetic competence of Russian collaborators. In the second project, the threat of ‘genetic extinction’ of the wild Teno salmon due to hybridization with farmed salmon escapees is studied as is the genetic structure among the tributary populations. In the third project, the major aim is to characterize the role of variation in the immunologically important Major Histocompatibility Locus (MHC) alleles in the cataract formation on Arctic charr. The Centre of Excellence in Evolutionary Genetics and Physiology combines and co-ordinates the research of three research groups in the study of evolutionary genetics and physiology in vertebrates. Especially local adaptations and speciation in salmonid fishes is studied. The general aim is to provide data which can be applied for management decisions of exploited populations. The aim of the final project is to identify functionally important genetic variation related to local adaptation in salmonid fishes.

Selected Publications:

- Tiira K, Piironen J, Primmer CR. Evidence for reduced genetic variation in severely deformed juvenile salmonids. *Canadian Journal of Fisheries and Aquatic Sciences* (in press).
- Primmer CR, Veselov AJ, Zubchenko A, Poututkin A, Bakhmet I, Koskinen MT. 2006. Isolation by distance within a river system: genetic population structuring of Atlantic salmon, *Salmo salar*, in tributaries of the Varzuga River in northwest Russia. *Molecular Ecology*, 15: 653–666.
- Vähä J-PK, Primmer CR. 2006. Detecting hybridization between individuals of closely related populations – a simulation study to assess the efficiency of model-based Bayesian methods to detect hybrid individuals. *Molecular Ecology*, 15: 63–72.
- Ryynänen H, Primmer CR. 2006. Varying signals of the effects of natural selection during teleost growth hormone gene evolution. *Genome*, 49: 42–53.
- Tiira K, Laurila A, Enberg K, Piironen J, Aikio S, Ranta E, Primmer CR. 2006. Do dominants have higher heterozygosity? Social status and genetic variation in brown trout, *Salmo trutta*. *Behavioral Ecology and Sociobiology*, 59: 657–665.
- Vasemägi A, Nilsson J, Primmer CR. 2005. Expressed sequence tag (EST) linked microsatellites as a source of gene associated polymorphisms for detecting signatures of divergent selection in Atlantic salmon (*Salmo salar* L.). *Molecular Biology and Evolution*, 22: 1067–1076.
- Tonteri A, Veselov A, Lumme J, Koskinen M, Bakhmet I, Potutkin A, Titov S, Zubchenko A, Studenov I, Kaluzhin S, Primmer CR. 2005. Phylogeography of anadromous and non-anadromous Atlantic salmon (*Salmo salar*) from northern Europe. *Annales Zoologici Fennici*, 42: 1–22.
- Vasemägi A, Gross R, Paaver T, Säisä M, Koljonen M-L, Nilsson J. 2005. Analysis of gene associated tandem repeat markers in Atlantic salmon (*Salmo salar* L.) populations: implications for restoration and conservation in the Baltic Sea. *Conservation Genetics*, 6: 385–397.
- Vasemägi A, Gross R, Paaver T, Koljonen M-L, Nilsson J. 2005. Extensive immigration from compensatory hatchery releases into wild Atlantic Salmon popula-

tion in the Baltic Sea: spatio-temporal analysis over 18 years. *Heredity*, 95: 76–83.
 Ryynänen HJ, Primmer CR. 2004. Distribution of genetic variation in the growth

hormone 1 gene in Atlantic salmon (*Salmo salar*) populations from Europe and North America. *Molecular Ecology*, 13: 3857–3869.

5. University of Helsinki, Department of Bio- and Environmental Sciences, Ecological Genetics Research Unit.

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Cooperation parties: Craig Primmer, University of Turku, Finland.
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Research groups/projects:

1. Evolutionary genetics of three- and nine-spined sticklebacks.

Summary:

At the University of Helsinki the research is focused on ecological genetics of sticklebacks, with emphasis on the role of adaptive divergence and genetic drift in population differentiation. The degree of population differentiation in genetic markers (QTLs) related to the expression of bony armour and body shape are compared to that of variation in neutral genetic markers over a wide range of the distribution of three-spined stickleback in Europe. It seems that additive genetic differentiation is exceeding that found in the putatively neutral markers, suggesting that selection is more important than genetic drift in population differentiation. An additional aim is to provide a shortcut to a marker-based tool for assessment of the genetic basis of phenotypic differentiation in the wild, and to assess how the number of genes affects the rate of phenotypic divergence in wild vertebrate populations. To that end the group combines the detection of selective sweeps, QTL-mapping and gene expression profiles of candidate genes.

Selected Publications:

- Mäkinen HS, Cano JM, Merilä J. 2006. Genetic relationships among marine and freshwater populations of the European three-spined stickleback (*Gasterosteus aculeatus*) revealed by microsatellites. *Molecular Ecology*, 15: 1519–1534.
- Cano JM, Matsuba C, Mäkinen H, Merilä J. 2006. The utility of QTL-linked markers to detect selective sweeps in natural populations - a case study of the *Eda* gene and a linked marker in threespine stickleback. *Molecular Ecology*, 15: 4613–4621.
- Leinonen T, Cano JM, Mäkinen H, Merilä J. 2006. Contrasting patterns of body shape and neutral genetic divergence in marine and lake populations of threespine sticklebacks. *Journal of Evolutionary Biology*, 19: 1803–1812.

Iceland

Genetic research on commercially exploited fish species in Iceland are mainly conducted at three different sites; at the Institute of Biology, University of Iceland, at the Marine Research Institute, and at the private biotechnical company Prokaria. The research is mainly focused on the commercially exploited marine fish resources in Icelandic waters, but studies are also conducted on freshwater salmonid populations at the University of Iceland and at Hólar Collage. The main focus has traditionally been on Atlantic cod, but other species, mainly other members of the cod family and different salmonids, have also been studied.

Research institutes

1. Marine Research Institute, Population Genetics Laboratory.

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Cooperation parties: Guðrún Marteinsdóttir, University of Iceland.

Prokaria Research ehf. , Iceland.

Institute of freshwater fisheries, Iceland.

Research groups/projects:

1. EU-CODTRACE.
2. EU-REDFISH.
3. EU-METACOD.
4. Genotyping kits for Atlantic cod.

Summary:

The research at the marine Research Institute has a long record of studies on genetic variation in Atlantic cod from Icelandic waters. Current projects involve population genetic studies of North Atlantic fin, sei and minke whales, and population structures of redfish in the Irminger Sea, different gadoid species, Atlantic salmon, brown trout and Arctic charr. Projects 1, 2 and 4 are all conducting research on Atlantic cod. In project 1 the aim is to establish traceability of stocks of cod by determining their

locations of spawning and harvest. Project 3 addresses the role of sub-stock structures in the maintenance of cod metapopulations. More specifically, temporal differentiation and identification of spawning units around Iceland and their contribution to the juvenile and harvested stocks is studied. In project 4 genotyping kits for Atlantic cod are developed in collaboration with Prokaria research ehf. There is also active research on the population structure, reproductive strategies and demography of redfish in the Irminger Sea and adjacent waters (ICES V, XII and XIV; NAFO 1) (project 2).

Selected Publications:

- Stefánsson MÖ, Sigurdsson T, Pampoulie C, Danielsdóttir AK, Thorgilsson B, Ragnarsdóttir A, Gislason D, Coughlan J, Cross TF, Bernatchez L. 2006. Natural selection and reproductive isolation by depth in parapatric redfish, *Sebastes mentella*, Manuscript.
- Pampoulie C, Ruzzante DE, Chosson V, Jörundsdóttir ThD, Taylor L, Thorsteinsson V, Danielsdóttir AK, Marteinsdóttir G. 2006. The genetics structure of Atlantic cod (*Gadus morhua*) around Iceland: Insight from microsatellites, the Pan I locus, and tagging experiments. *Canadian Journal of Fisheries and Aquatic Sciences*, in press.
- Jakobsdóttir KB, Jörundsdóttir ÞD, Skírmisdóttir S, Hjörleifsdóttir S, Hreggviðsson GÓ, Danielsdóttir AK, Pampoulie C. 2006. Nine new polymorphic microsatellite loci for the amplification of archived otolith DNA of Atlantic cod, *Gadus morhua* L. *Molecular Ecology Notes*, 6: 337–339.
- Jónsdóttir ÓDB, Imsland AK, Atladóttir ÓÝ, Danielsdóttir AK. 2003. Nuclear DNA RFLP variation of Atlantic cod in the North Atlantic Ocean. *Fisheries Research*, 63: 429–436.
- Jónsdóttir ÓDB, Danielsdóttir AK, Nævdal G. 2001. Genetic differentiation among Atlantic cod (*Gadus morhua* L) in Icelandic waters: temporal stability. *ICES Journal of Marine Science*, 58: 114–122.
- Johansen T, Danielsdóttir AK, Meland K, Nævdal G. 2000. Studies of the genetic relationship between deep-sea and oceanic *Sebastes mentella* in the Irminger Sea. *Fisheries Research*, 49: 179–192.
- Jónsdóttir ÓDB, Imsland AK, Danielsdóttir AK, Thorsteinsson V, Nævdal, G. 1999. Genetic differentiation among Atlantic cod in south and south-east Icelandic waters: synaptophysin (Syp I) and haemoglobin (Hbl) variation. *Journal of Fish Biology*, 54: 1259–1274.

Universities

1. University of Iceland, Institute of Biology.

Homepage: <http://www.hi.is/pub/lif/miniweb/departmt.htm>

Contact person: Einar Árnason

Institute of Biology

Grensasvegur 12

108 Reykjavik

Iceland

E-mail: einar@lif.hi.is

Leading scientists: Einar Árnason (Group leader), Snæbjörn Pálsson.

Cooperation parties: Marine Research Institute.

Research groups/projects:

1. MADFish – Molecular Adaptation in Fish. Nordic Network (<http://madfish.lif.hi.is>).

2. DNAfish – DNA based phylogeography and population genetics of North Atlantic fish.

Summary:

At the laboratory of Einar Árnason, work on mtDNA variation in Atlantic cod has been going on since 1988. Variation has been calculated by using samples throughout the whole distributional range of Atlantic cod. The studies of mitochondrial variation have also been extended to other species such as pollock, haddock, Greenland halibut, redfish, and less commercially important gadoids such as Polar cod. These samples have been obtained in cooperation with the Marine Research Institute in Iceland and research institutes in Greenland and the Faeroe Islands. In addition to the mtDNA studies, two current studies are focusing on nuclear genes. One is mapping and describing the haemoglobin gene in Atlantic cod, and the other conducts research on variation at the Pantophysin I gene.

Selected Publications:

- Árnason E. 2004. Mitochondrial Cytochrome b DNA variation in the high-fecundity Atlantic cod: trans-Atlantic clines and shallow gene genealogy. *Genetics*, 166: 1871–1885.
- Sigurgíslason H, Árnason E. 2003. Extent of mitochondrial DNA sequence variation in Atlantic cod from the Faroe Islands: a resolution of gene genealogy. *Heredity*, 91: 557–564.
- Árnason E, Kristinsson K, Petersen PH, Sigurgíslason H, Pálsson S. 2000. Mitochondrial Cytochrome b DNA sequence variation of Atlantic cod *Gadus morhua*, from Iceland and Greenland. *Journal of Fish Biology*, 56: 409–430.
- Árnason E, Pálsson S, Petersen PH. 1998. Mitochondrial Cytochrome b DNA Sequence Variation of Atlantic Cod, *Gadus morhua*, from the Baltic- and the White Seas. *Hereditas*, 129: 37–43.
- Árnason E, Pálsson S. 1996. Mitochondrial cytochrome b DNA sequence variation of Atlantic cod *Gadus morhua* from Norway. *Molecular Ecology*, 5: 715–724.
- Pálsson S, Árnason E. 1994. Sequence variation for cytochrome b genes of three Salmonid species from Iceland. *Aquaculture*; 128: 29–39.
- Árnason E, Rand DM. 1992. Heteroplasmy of short tandem repeats in mitochondrial DNA of Atlantic cod, *Gadus morhua*. *Genetics*, 132: 211–220.
- Árnason E, Pálsson S, Arason A. 1992. Gene flow and lack of population differentiation in Atlantic cod *Gadus morhua* L., from Iceland, with comparison to Norway and Newfoundland. *Journal of Fish Biology*, 40: 751–770

2. Hólar Collage, the Department of Aquaculture, and University of Iceland, Institute of Biology.

Homepage: <http://www.holar.is/english/aqua.htm>

Contact persons: Skúli Skúlasson
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Leading scientists: Skúli Skúlasson, Sigurður Snorrason, Guðbjörg Ásta Ólafsdóttir.

Cooperation parties: Moira Ferguson University of Guelph, Canada.
David Noakes, University of Oregon, USA.

Research groups/projects:

1. Evolution of Arctic charr in Iceland.
2. Sympatric morphs of threespine stickleback.

Summary:

The combined research of Hólar Collage and the University of Iceland use a number of ecological, behavioural, developmental and genetic methods, to study diversity within and between populations of Icelandic freshwater fish.

The main study species are arctic charr and threespine stickleback. Current projects include research on the diversity and evolution of “dwarf” arctic charr in Iceland. Here, molecular methods are used to construct a phylogeny of Icelandic charr populations as well as to test hypothesis on the geographic and ecological setting of the development of dwarf arctic charr. There is also ongoing research on sympatric stickleback morphs, focusing on how ecology effects reduced gene flow between sympatric morphs, and trying to assess the genetic bases of morph formation in sympatry using candidate loci and genome scans.

Selected Publications:

- Ólafsdóttir GÁ, Snorrason SS, Ritchie MG. 2006. Parallel adaptation? Microsatellite variation of recently isolated marine and freshwater threespine stickleback. *Journal of Fish Biology*, in press.
- Ólafsdóttir GÁ, Snorrason SS, Ritchie MG. 2006. Morphological and genetic divergence of intralacustrine stickleback morphs in Iceland: a case for selective differentiation? *Journal of Evolutionary Biology*, doi: 10. 1111/j. 1420–9101. 2006. 01250. x
- Wilson AJ, Gíslason D, Skúlason S, Snorrason SS, Adams CE, Alexander G, Danzmann RG, Ferguson MM. 2004. Population genetic structure of Arctic Charr, *Salvelinus alpinus* from northwest Europe on large and small spatial scales. *Molecular Ecology*, 13: 1129–1142.
- Snorrason SS, Skúlason S. 2004. Adaptive Speciation in Northern Freshwater Fishes. In: *Adaptive Speciation*, eds. Dieckmann U, Doebeli M, Metz JAJ & Tautz D, pp. 210–228. Cambridge University Press.
- Gíslason D, Ferguson MM, Skúlason S, Snorrason SS. 1999. Rapid and coupled phenotypic and genetic divergence in Icelandic Arctic charr (*Salvelinus alpinus*). *Canadian Journal of Fisheries and Aquatic Sciences*, 56: 2229–2234.

Private companies

1. Prokaria Research ehf.
Homepage: <http://www.prokaria.com/>

Contact person: Arnthor Aevarsson
Prokaria
Gylfaflöt 5
IS-112 Reykjavík
Iceland
E-mail: info@prokaria.com

Leading scientist: Guðmundur Óli Hreggviðsson.

Cooperation parties: Marine Research Institute, Iceland.
The freshwater institute, Iceland.
Stofnfiskur, Iceland.

Research groups/projects:

Fish & Chips – genomic tools in fish biology and aquaculture.
Atlantic Salmon Microsatellite Analysis Network.
Population genetics of salmon in Icelandic rivers.
Sex determination genes in salmon, halibut and cod.
Development of genetic markers (50–100) for ecological and genetic studies of Atlantic cod.
Genetics of light response and sexual maturity in Atlantic cod.

Summary:

Prokaria was originally a biotech company with a focus on research on thermophilic bacteria. In recent years, the company has engaged in genotyping of marine fish in cooperation with The Marine Research Institute, Iceland. Prokaria also conducts all genotyping analysis for Stofnfiskur, an Icelandic company involved in breeding of salmon, halibut, cod and other species. Recently, Prokaria has become a part of a newly established company which belongs to The Icelandic Fisheries Laboratories (IFL), where the aim is to increase the work on applied fish genetics for uses in fish farming and population genetics for fisheries research and stock management. The company is also conducting genetic analysis for research groups located elsewhere in Europe and North America. Finally, Prokaria is participating in the EU-project Fish and chips, where genetic markers for distinguishing eggs and larvae from 108 species of marine fishes and invertebrates are developed.

Selected Publications:

There are to date no relevant publications from Prokaria.
Norway

The genetic research on fish in Norway is at present conducted at six different research institutes, six university departments, but also at a private company. The research is mainly focused on the genetic structure of harvested wild populations and on species used in aquaculture. A number of institutes are also carrying out basic research on several different species. A wide range of species are studied where the majority is marine and members of the gadoid and salmonid families. The two species most heavily investigated is Atlantic cod and Atlantic salmon, but research is also conducted on a couple of species of shellfish such as lobsters, crabs and scallops.

Research institutes

1. Akvaforsk, Genetics and Breeding Group.
Homepage: <http://www.akvaforsk.no/english/>

Contact person: Kari Kolstad
AKVAFORSK
The Institute of Aquaculture Research
Postboks 5010
N-1432 Ås
Norway
E-mail: akvaforsk@akvaforsk.no

Leading scientists: Kari Kolstad (Group leader)

Research groups/projects:

1. EUROCARP.
2. GENIMPACT.
3. Breeding and selection in scallops (starting up).

Summary:

Akvaforsk is currently doing research on the genetic improvement of aquaculture species such as, for example, Atlantic salmon, rainbow trout and cod, using quantitative and molecular genetics. The aim is to optimize breeding programs, to develop economic breeding goals, to map important genes, and to utilize data on genetic markers and gene expressions in selective breeding. There is a major focus on health of fish in the research carried out at Akvaforsk. It is, for example, studied in what way the developed tools can be used for improving disease resistance in fish.

Research will also be conducted on the interaction between wild and farmed fish.

Selected Publications:

- Kolstad K, Thorland I, Refstie T, Gjerde B. 2006. Genetic variation and genotype by location interaction in body weight, spinal deformity and sexual maturity Atlantic cod (*Gadus morhua*) reared at different locations off Norway. *Aquaculture*. 259: 66–73.
- Kolstad K, Gjedrem T, Heuch PA, Gjerde B, Salte R. 2005. Selection for increased resistance of Atlantic salmon to *Lepeophtheirus salmonis*; a possible means of disease control. *Aquaculture*. 247: 145–151.
- Hayes BJ, Sonesson AK, Gjerde B. 2005. Evaluation of three strategies using DNA markers for trace ability in aquaculture species. *Aquaculture*. 250: 70–81.
- Gjerde B, Pante MJR, Bæverfjord G. 2005. Genetic variation for a vertebral deformity in Atlantic salmon (*Salmo salar*). *Aquaculture*. 244: 77–87.
- Takle H, Bæverfjord GM, Andersen Ø. 2005. Identification of stress sensitive genes in hyperthermic Atlantic salmon (*Salmo salar*) embryos by RAP-PCR. *Fish Physiology and Biochemistry*. 30: 275–281.
- van Nes S, Moe M, Andersen Ø. 2005. Molecular characterization and expression of two *cyp19* (P450 aromatase) genes in embryos, larvae and adults of Atlantic halibut (*Hippoglossus hippoglossus*). *Molecular Reproduction and Development*, 72: 437–449.
- Gjerde B, Terjesen BF, Barr Y, Lein I, Thorland I. 2004. Genetic variation for juvenile growth and survival in Atlantic cod (*Gadus morhua*). *Aquaculture*. 236: 167–177.
- Moen T, Fjalestad KT, Munck H, Gomez-Raya L. 2004. A multistage testing strategy for detection of quantitative trait loci affecting disease resistance in Atlantic salmon. *Genetics*. 167: 851–858.
- Moen T, Høyheim B, Munck H, Gomez-Raya L. 2004. A linkage map of Atlantic salmon (*Salmo salar*) reveals an uncommonly large difference in recombination fraction between the sexes. *Animal Genetics*. 35: 81–92.
- Olesen I, Gjedrem T, Bentsen HB, Gjerde B, Rye M. 2003. Breeding programs for sustainable aquaculture. *Journal of Applied Aquaculture*. 13: 179–204.

2. The Centre for Integrative Genetics (CIGENE)

Homepage: <http://www.umb.no/?avd=40>

Contact person: Stig Omholt, Thomas Moen
 P. O. Box 5003
 N – 1432 Ås
 Norway
 E-mail: cigene@cigene.no

Leading scientists: Stig Omholt (Group leader), Thomas Moen.

Cooperation parties: Akvaforsk.

Summary:

The research conducted at CIGENE aims to contribute to a deep causal understanding of complex genetic characters in fish, plants and animals for scientific and commercial exploitation, using an integrative genetics approach. The institute also functions as a core facility under the Norwe-

gian Functional Genomics Programme, and is responsible for providing a national service for detection, typing and interpretation of Single Nucleotide Polymorphisms (SNPs), and for systems-oriented computational biology.

Selected Publications (in collaboration with Akvaforsk):

- | | |
|---|---|
| <p>Hayes BJ, Lærdahl J, Lien S, Moen T, Davidson W, Koop B, Adzhubei A, Høyheim B. Detection of SNPs from Atlantic Salmon ESTs. Manuscript.</p> <p>Hayes BJ, Gjuvsland AB, Omholt S. 2006. Power of QTL mapping experiments in commercial Atlantic salmon populations, exploiting linkage and linkage disequilibrium and effect of limited recombination in males. <i>Heredity</i>. 97: 19–26</p> <p>Hayes BJ, He JIE, Moen T, Bennewitz J. 2006. Use of molecular markers to maximise diversity of founder popula-</p> | <p>tions for aquaculture breeding programs. <i>Aquaculture</i>. 255: 573–578.</p> <p>Hayes BJ, Moen T, Goddard M. 2005. Dissection of genetics of complex traits and progress in aquaculture and livestock species. <i>AgBiotechNet</i>. 7, ABN 136, 10 pp.</p> <p>Kolstad K, Meuwissen THE, Gjerde B. 2005. Efficient design for doing genetic studies of feed efficiency in Atlantic salmon (<i>Salmo salar</i>). <i>Aquaculture</i>. 247: 153–158.</p> |
|---|---|

3. Norwegian School of Veterinary Science, Department of Basic Sciences and Aquatic Medicine, Section of Genetics, Salmon Functional Immunogenetics group.

Homepage: <http://www.aquamedicine.no/>

Contact person: Unni Grimholt
 E-mail: unni.grimholt@veths.no

Leading scientists: Unni Grimholt (Group leader)

Cooperation parties: Akvaforsk
 Aqua Gen AS

Summary:

The research at the Norwegian School of Veterinary Science is centred around understanding the functional genes in the class I and II pathways of the Major Histocompatibility Complex (MHC) part of the immune system in salmon. The aim is to understand the genetic fundament, the functional relevance and the interactions with the remaining immune system of the pathways. The procedure is, in collaboration with Akvaforsk and Aqua Gen AS, to find QTLs for associations between MHC and resistance towards bacterial as well as viral pathogens. The research also includes work on the production of clonal lines of fish in Atlantic salmon using a technique well established for rainbow trout. The aim of this project is to produce animals suitable for whole-genome sequencing,

as well as to provide the basis for future genetically well-defined experimental animals.

Selected Publications:

- Kjøglum S, Larsen S, Grimholt U. 2006. How specific MHC class I & class II combinations affect resistance against ISAV in Atlantic salmon. *Fish & Shellfish Immunology*. 21: 431–441.
- Kjøglum S, Grimholt U, Larsen S. 2005. Non-MHC genetic and tank effects influence disease challenge tests in Atlantic salmon (*Salmo salar*). *Aquaculture*. 250: 102–109.
- Mjaaland S, Markussen T, Sindre H, Kjøglum S, Dannevig BH, Larsen S, Grimholt U. 2005. Susceptibility and immune responses following experimental infection of MHC incompatible Atlantic salmon (*Salmo salar* L.) with different infectious salmon anaemia virus (ISAV) isolates. *Archives of virology*. 150: 2195–2216.
- Grimholt U, Larsen S, Nordmo R, Midtlyng PJ, Kjøglum S, Storset A, Sæbø S, Stet RJM. 2003. MHC polymorphism and disease resistance in Atlantic salmon (*Salmo salar*); Facing pathogens with single expressed Major histocompatibility class I and class II loci. *Immunogenetics*. 55: 210–219.

4. Salmon Genome Project, Salmon Genomics and Functional Genomics.

Homepage: <http://www.salmongenome.no/cgi-bin/sgp.cgi>

Contact person: Bjørn Høyheim

Norwegian School of Veterinary Science Department of Basic Sciences and Aquatic Medicine POBox 8146 DEP NO-0033 Oslo Norway E-mail: salmon-genome@embnet.uio.no

Leading scientists: Bjørn Høyheim.

Cooperation parties: University of Bergen.

University of Oslo.

University of Tromsø.

Institute of Marine Research, Bergen.

University of Stirling, Scotland.

University of Aberdeen, Scotland.

Cardiff University, Wales.

Göteborg University, Sweden.

CSIRO Marine Research, Tasmania, Australia.

INRA, France.

DIAS, Denmark.

Tokyo University of Marine Science and Technology, Japan.

National Research Institute of Fisheries Science, Japan.

United Gene Institute, Shanghai, China.

Research groups/projects:

1. Salmon Genome Project (SGP).
2. SALMAP.
3. SALGENE.

Summary:

During the Salmon Genome Project (SGP) and through the EU-projects SALMAP and SALGENE we have constructed genetic markers and a genetic map (containing at present over 400 microsatellite markers), a BAC library and cDNA libraries from various tissues. Approximately 70 000 ESTs and 1 500 full-length cDNAs have been sequenced from the cDNA libraries and we have used this data to construct an Atlantic salmon microarray chip (together with the UK TRAITS consortium). All EST data have been clustered and subjected to automatic annotation based on Gene Ontology. Several BLAST searches have been done for all contigs and single sequences and possible function have been deduced for a number of sequences. The results are sorted according to Molecular Function, Biological Process or Cellular Component. All data and resources can be accessed through our website. All sequence data are also submitted to GenBank. Functional studies includes using Suppression Subtractive Hybridisation (SSH) and macro- and microarray to investigate change in gene expression in salmon challenged with furunculosis or Infectious Salmon Anemia (ISA) compared to untreated salmon.

Selected Publications:

- Artieri CG, Mitchell LA, Ng SH, Parisotto SE, Danzmann RG, Høyheim B, Phillips R B, Morasch M, Koop B, Davidson WS. 2006. Identification of the sex-determining locus of Atlantic salmon (*Salmo salar*) on chromosome 2. *Cytogenetic and Genome Research*, 112:152–159.
- Gharbi K, Gautier A, Danzmann RG, Gharbi S, Sakamoto T, Høyheim B, Taggart JB, Cairney M, Powell R, Krieg F, Okamoto N, Ferguson MM, Holm LE, Guyomard R. 2006. A linkage map for brown trout (*Salmo trutta*): chromosome homologies and comparative genome organization with other salmonid fish. *Genetics*, 172: 2405–2419.
- Thorsen J, Høyheim B, Koppang EO. 2006. Isolation of the Atlantic salmon tyrosinase gene family reveals heterogeneous transcripts in a leukocyte cell line. *Pigment Cell Research*, 19: 327–336.
- Adzhubei AA, Lærdahl JK, Vlasova AV. 2006. preAssemble: a tool for automatic sequencer trace data processing. *BMC Bioinformatics*, 7: 22.
- Thorsen J, Zhu B, Frengen E, Osoegawa K, de Jong PJ, Koop BF, Davidson WS, Høyheim B. 2005. A highly redundant BAC library of Atlantic salmon (*Salmo salar*): an important tool for salmon projects. *BMC Genomics*, 6: 50.
- Ng SH, Artieri CG, Bosdet IE, Chiu R, Danzmann RG, Davidson WS, Ferguson MM, Fjell CD, Høyheim B, Jones SJM, de Jong PJ, Koop BF, Krzywinski MI, Lubieniecki K, Marra MA, Mitchell LA, Mathewson C, Osoegawa K, Parisotto SE, Phillips RB, Rise ML, von Schalburg KR, Schein JE, Shin H, Siddiqui A, Thorsen J, Wye N, Yang G, Zhu B. 2005. A physical map of the genome of Atlantic salmon, *Salmo salar*. *Genomics*, 86: 396–404.

- Hagen-Larsen H, Lærdahl JK, Panitz F, Adzhubei A, Høyheim B. 2005. An EST-based approach for identifying genes expressed in the intestine and gills of pre-smolt Atlantic salmon (*Salmo salar*). *BMC Genomics*, 6: 171.
- Woram RA, McGowan C, Stout JA, Gharbi K, Ferguson MM, Høyheim B, Davidson WS, Rexroad C, Danzmann RG. 2004. A genetic linkage map for Arctic charr (*Salvelinus alpinus*): evidence for higher recombination rates and segregation distortion in hybrid versus pure strain mapping parents. *Genome*, 47: 304–315.
- Moen T, Høyheim B, Munck H, Gomez-Raya L. 2004. A linkage map of Atlantic salmon (*Salmo salar*) reveals an uncommonly large difference in recombination rate between the sexes. *Animal Genetics*, 35: 81–92.
- Skaala Ø, Høyheim B, Glover K, Dahle G. 2004. Microsatellite analysis in domesticated and wild Atlantic salmon (*Salmo salar*). *Aquaculture*, 240: 131

5. Institute of Marine Research (IMR)

Homepage: <http://www.imr.no/english/main>

Contact person: Terje Svåsand P. O. Box 1870, Nordnes 5817 Bergen Norway E-mail: post@imr.no

Leading scientists: Terje Svåsand (group leader), Geir Dahle, Knut Jørstad, Øystein Skaala.

Cooperation parties:

Research groups/projects:

Summary:

IMR is the largest centre for marine science in Norway and conducts genetic research on a number of marine fishes, crayfish and shellfish. Species studied are Atlantic cod, Atlantic salmon, rainbow trout, halibut, Greenland halibut, Goldsinny wrasse, mackerel, herring, lumpfish, lobsters, crabs, shrimps and scallops. The research is including wild as well as farmed stocks and the interactions between them. The main aim of the research conducted at IMR is to provide management advices to ensure that Norway's marine resources such as aquaculture and the ecosystems of the Barents Sea, the Norwegian Sea, the North Sea and the Norwegian coastal zone are harvested in a sustainable way. For this reason, about fifty percent of the activities are financed by the Ministry of Fisheries and Coastal Affairs. The headquarter of IMR is situated in Bergen, but important activities are also carried out at the Department in Tromsø, at the research stations in Matre, Austevoll and Flødevigen, and on board on different research vessels.

Selected Publications:

- Alsvåg J, Agnalt A-L, Jørstad KE. Snow crab (*Chionoecetes opilio*) in the Barents Sea – distribution during the Norwegian winter survey in 2004 and 2005, and future perspectives. Submitted to *Hydrobiologia*.
- Wennevik V, Skaala Ø, Glover K. Tracing escaped cultured salmon to farm of origin. Submitted to *Reviews in Fish Biology and Fisheries*.
- Jørstad KE, Prodohl PA, Agnalt A-L, Hugdes M, Farestveit E, Ferguson A. American lobster (*Homarus americanus*) in Norwegian waters – an evaluation of genetic and biological methods to detect hybrids with European lobster (*Homarus americanus*). Submitted to *Hydrobiologia*.
- Jørstad KE, Smith C, Grauvogel Z, Seeb L. Microsatellite DNA analyses of introduced Red king crab (*Paralithodes camtschatica*) in the Barents Sea and comparison with samples from the Bering Sea and Kamtchatka region. Submitted to *Hydrobiologia*.
- Skjæraasen JE, Salvanes AGV, Dahle G. Linking physiology, reproductive behaviour and paternity in the pelagic spawning Atlantic cod. Submitted to *Journal of Animal Ecology*.
- Chase R, Hutchinson WF, Hauser L, Bühler V, Clemmesen C, Dahle G, Kjesbu OS, Moksness E, Otterå O, Paulsen H, Svåsand T, Thorsen A, Carvalho GR. Association between growth and Pan I genotype within Atlantic cod (*Gadus morhua*) full sib families. *Transactions of the American Fisheries Society*, 135: 241–250. In press.
- Dahle G, Jørstad KE, Rusaas HE, Otterå H. Genetic characterisation of broodstock collected from four Norwegian coastal cod (*Gadus morhua*) populations. *ICES Journal of Marine Science*. In press.
- Otterå H, Agnalt A-L, Jørstad KE. 2006. Differences in spawning time of captive Atlantic cod from four regions of Norway, kept under identical conditions. *ICES Journal of Marine Science*. 63: 216–223.
- Jørstad KE, Karlsen Ø, Svåsand T, Otterå H. 2006. Comparison of growth rate between different protein genotypes in Atlantic cod, *Gadus morhua*, under farming conditions. *ICES Journal of Marine Science*. 63: 235–245.
- Hovgaard K, Skaala Ø, Nævdal G. 2006. Population genetic studies of sea trout, *Salmo trutta* L., from western Norway. *Journal of Ichthyology*. 22: 57–61.

6. Norwegian Institute for Nature Research (NINA)

Homepage: <http://www4.nina.no/ninaeng/>

Contact person: Kjetil Hindar
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Leading scientists: Kjetil Hindar, Kirsti Kvaløy, Ola Diserud, Sigurd Einum (NTNU from 2007), Anders Finstad, Torbjørn Forseth, Bror Jonsson (NINA-Oslo), Martin-A Svenning (NINA-Tromsø)

Cooperation parties: Norwegian University of Science and Technology (NTNU).
 Akvaforsk, Norway.
 CIGENE, Norway.
 Göteborg University, Sweden.

Uppsala University, Sweden.
 Memorial University, Canada.
 Department of Fisheries and Oceans, Canada.
 Université Laval, Canada.
 Marine Institute, Ireland.

Research groups/projects:

1. Quantifying biological risks of growth-enhanced transgenic salmon (Research Council of Norway (FUGE), 2003–2006).
2. Hybridisation between Atlantic salmon and brown trout in Gyrodactylus-infected rivers: consequences for population viability (Research Council of Norway, 2003–2006).
3. Evolutionary and cascading effects of translocation of native species into new ecosystems (Research Council of Norway, 2006–2008).

Summary:

The Norwegian Institute for Nature Research (NINA) is a research foundation under the Ministry of Environment, having a long tradition in research on wild salmonids. The main focus is on applied ecological research, providing advice to regional, national and international management bodies. Genetic studies are currently carried out on Atlantic salmon, brown trout, Arctic charr and European whitefish. Ongoing studies are aimed at understanding ecological and genetic interactions between wild and farmed Atlantic salmon populations, interspecific hybridisation between salmon and trout, reestablishment of populations in formerly acidified regions, and the genetic effects of harvesting. We also study risks posed to wild salmonids by diseases and parasites, and by (releases of) genetically modified (GM-) salmon. Some of the ecological studies at NINA are aimed at understanding adaptations of salmonid fishes to their biotic and abiotic environments. A general focus is how the genetic and phenotypic composition of salmonid fish populations are affected by human activities.

Selected Publications:

- Roberge C, Einum S, Guderley H, Bernatchez L. 2006. Rapid parallel evolutionary changes of gene transcription profiles in farmed Atlantic salmon. *Molecular Ecology*, 15: 9–20.
- Hindar K, Fleming IA, McGinnity P, Diserud O. 2006. Genetic and ecological effects of salmon farming on wild salmon: modelling from experimental results. *ICES Journal of Marine Science*, 63: 1234–1247.
- Østbye K, Amundsen P-A, Bernatchez L, Klemetsen A, Knudsen A, Kristoffersen R, Næsje TF, Hindar K. 2006. Parallel evolution of ecomorphological traits in the European whitefish *Coregonus lavaretus* (L.) species complex during post-glacial times. *Molecular Ecology*, 15: 3983–4001.
- Larsson S, Forseth T, Berglund I, Jensen AJ, Näslund I, Elliott JM, Jonsson B. 2005. Thermal adaptation of Arctic charr: experimental studies of growth in

- eleven populations from Sweden, Norway and Britain. *Freshwater Biology*, 50: 353–368.
- Svenning M-A, Borgström R. 2005. Cannibalism in Arctic charr: do all individuals have the same propensity to be cannibals? *Journal of Fish Biology*, 66: 957–965.
- Østbye K, Bernatchez L, Næsje TF, Himberg K-JM, Hindar K. 2005. Evolutionary history of the European whitefish *Coregonus lavaretus* (L.) species complex as inferred from mtDNA phylogeography and gill-raker numbers. *Molecular Ecology*, 14: 4371–4387.
- Hindar K, Tufto J, Sættem LM, Balstad T. 2004. Conservation of genetic variation in harvested salmon populations. *ICES Journal of Marine Science*, 61: 1389–1397.
- Tufto J, Hindar K. 2003. Effective size in management and conservation of subdivided populations. *Journal of Theoretical Biology*, 222: 273–281.
- Svenning M-A, Gullestad N. 2002. Adaptations to stochastic environmental variations: the effects of seasonal temperatures on the migratory window of Svalbard Arctic charr. *Environmental Biology of Fishes*, 64: 165–174.
- Fleming IA, Hindar K, Mjølnerød IB, Jonsson B, Balstad T, Lamberg A. 2000. Lifetime success and interactions of farm salmon invading a native population. *Proceedings of the Royal Society of London Series B*, 267: 1517–1524.

Universities

1. University of Tromsø, Norwegian College of Fishery Science (NCFS).

Homepage: <http://www.nfh.uit.no>

Contact person: Svein-Erik Fevolden
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Leading scientists: Svein-Erik Fevolden, Stefano Peruzzi, Jon Ivar Westgaard

Cooperation parties: Marine Research Institute, MRI (Bergen/Tromsø).
 Norwegian Institute of Fisheries and Aquaculture. Fiskeriforskning, (Tromsø).
 Moscow State University, Russia.
 IFREMER, France.

Research groups/projects:

1. Disease resistance in Atlantic cod (in cooperation with Fiskeriforskning).
2. Population structure of Atlantic cod (in cooperation with Moscow State University).

Summary:

The main focus of the population genetic group at NCFS is on marine species and has for the last 10–15 years been on the genetic structure of

Atlantic cod, particularly in waters along the coast of northern Norway and in the Barents Sea. An important aspect has been to find genetic markers to discriminate between the migratory North East Arctic Cod and the more stationary Norwegian coastal cod. The potential divergence among subpopulations of the two forms of cod has also been investigated during recent years. These projects (project 2) have been carried out in a formalized cooperation with the Marine Research Institute (Bergen/Tromsø) and Moscow State University. In project 1 a genetic map is constructed which is followed by QTL mapping where after the QTLs are implemented in a genetic improvement programme. NCFS has also been part of a large circumpolar survey of genetic variation in capelin. Other species whose genetic structures have been studied at NCFS are, for example, European sea bass, Arctic charr, brown trout, polar cod and ice-cod. Finally, the possible genetic discrimination between Alaskan pollock and the very rare Norwegian pollock (Berlevågfish) are currently under investigation.

Selected Publications:

- Westgaard JI, Tafese T, Wesmajervi MS, Stenvik J, Fjalestad KT, Damsgård B, Delghandi M. 2006. Identification and characterisation of thirteen new microsatellites for Atlantic cod (*Gadus morhua* L.) from a repeat-enriched library. *Conservation Genetics*, in press.
- Peruzzi S, Westgaard JI, Chatain B. 2006. Genetic investigation of swimbladder inflation anomalies in the European sea bass, *Dicentrarchus labrax* L. *Aquaculture*, in press.
- Skarstein TH, Westgaard JI, Fevolden SE. 2006. Comparing microsatellite variation in north-east Atlantic cod (*Gadus morhua* L.) to genetic structuring as revealed by the pantophysin (Pan I) locus. *Journal of Fish Biology*, in press.
- Wesmajervi MS, Westgaard JI, Delghandi M. 2006. Evaluation of a novel pentaplex microsatellite marker system for paternity studies in Atlantic cod (*Gadus morhua* L.). *Aquaculture research*, 37:1195–1201.
- Berg E, Sarvas TH, Harbitz A, Fevolden SE. 2005. Accuracy and precision in stock separation of north-east Arctic and Norwegian coastal cod by otoliths – comparing readings, image analyses and a genetic method. *Marine and Freshwater Research*, 56: 753–762.
- Sarvas TH, Fevolden SE. 2005. Pantophysin (Pan I) locus divergence between inshore v. offshore and northern v. southern populations of Atlantic cod in the north-east Atlantic. *Journal of Fish Biology*, 67: 444–469.
- Sarvas TH, Fevolden SE. 2005. The scnDNA locus Pan I reveals concurrent presence of different populations of Atlantic cod (*Gadus morhua* L.) within a single fjord. *Fisheries Research*, 76: 307–316.
- Westgaard JI, Klemetsen A, Knudsen R. 2004. Genetic differences between two sympatric morphs of Arctic charr confirmed by microsatellite DNA. *Journal of Fish Biology*, 65: 1185–1191.
- Pogson GH, Fevolden SE. 2003. Natural selection and the genetic differentiation of coastal and Arctic populations of the Atlantic cod in northern Norway: a test involving nucleotide sequence variation at the pantophysin (Pan I) locus. *Molecular Ecology*, 12: 63–74.
- Roed KH, Fevolden SE, Christiansen JS. 2003. Isolation and characterization of DNA microsatellites for capelin *Mallopus villosus* population genetic studies *Marine Ecology Progress Series*, 262: 299–303.

2. *University of Oslo*

i) Department of Biology, Centre for Ecological and Evolutionary Synthesis (CEES).

Homepage: http://www.cees.no/?option=com_staff&person=avollest

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Leading scientists: Asbjørn Vøllestad

Cooperation parties: Nils C. Stenseth, Kjetill Jakobsen, Thronnd Haugen, Kjartan Østbye, Per Erik Jorde, Johannes Holmen, Dimitar Serbezov, Eric Edeline, all at CEES.

Louis Bernatchez, University of Laval, Quebec, Canada.

Craig Primmer, University of Turku, Finland.

Paul Hart, University of Leicester, UK

Dolph Schluter, UBC, Canada

Andrew Hendry, McGill University Montreal, Canada

Kathy Kavanagh, Boston University, USA.

Stephanie Carlson, University of Washington, USA

Research groups/projects:

1. Phylogeography and invasion biology of the minnow.
2. Spatial and temporal population structure and breeding system in stream-living brown trout: an integrated ecological and genetic approach.
3. Adaptive trait transitions and speciation in sticklebacks.
4. The early stages of adaptive radiation: sympatric divergence in grayling.
5. Fishery-induced changes in vital components of a large pike population.

Summary:

The genetic research at the University of Oslo is focused on the genetic structures of freshwater fishes. Current projects include studies of small-scale spatial and temporal genetic population structure of a stationary

stream population of brown trout, studies of the early phase of population divergence of grayling in a high-mountain area, and by using extensive samples from Norway and North-Europe studies of the phylogeography of minnow. In the brown trout project, a combination of capture-mark-recapture methods and genotyping also allows for studies of the mating system of brown trout and which individual traits that is important for fitness. Further, the evolutionary effects of fishing on important life-history traits is also studied using long-term data series for pike and grayling. Previous work has also included studies of the phylogeography of perch in Northern Europe, something giving important insights into the probable immigration routes and glacial refugia of perch and other European freshwater fish.

Selected Publications:

- Holmen J, Vøllestad LA, Jakobsen KS, Primmer CR. 2005. Cross-species amplification of zebrafish and central stone-roller microsatellite loci in six other cyprinids. *Journal of Fish Biology*, 66: 851–859.
- Koskinen MT, Haugen TO, Primmer CR. 2002. Contemporary fisherian life – history evolution in small salmonid populations. *Nature*, 419: 826–830.
- Haugen TO, Vøllestad LA. 2001. A century of life-history evolution in grayling. *Genetica*, 112/113: 475–491.
- Olsen E M, Vøllestad LA. 2001. Within-stream variation in early life-Haugen T O, Vøllestad LA. 2000. Population differences in early life-history traits in grayling. *Journal of Evolutionary Biology*, 13: 897–905.
- Nesbø CL, Fossheim T, Vøllestad LA, Jakobsen KS. 1999. Genetic divergence and phylogeographic relationships among European perch (*Perca fluviatilis*) populations reflect glacial refugia and postglacial colonization. *Molecular Ecology*, 8: 1387–1404.
- Refseth UH, Nesbø CL, Stacy JE, Vøllestad LA, Fjeld E, Jakobsen KS. 1998. Genetic evidence for different migration routes of freshwater fish into Norway revealed by analysis of current perch (*Perca fluviatilis*) populations in Scandinavia. *Molecular Ecology*, 7: 1015–1027.

2. University of Oslo

ii) Joint group “HI-Flødevigen/University of Oslo-CEES”

Homepage: <http://biologi.uio.no/cees/>

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Leading scientists: Per Erik Jorde, Halvor Knutsen, Nils Christian Stenseth

Summary:

The research at this affiliation is devoted to population genetic screenings of several economically important marine species such as anadromous brown trout, Atlantic cod and Greenland halibut. The projects are carried out by the Flødevigen laboratory in cooperation with Nils Christian Stenseth's group at CEES at the University of Oslo. Highlights of recent findings include that sea trout recolonizing formerly acidified streams along the Norwegian Skagerrak coast are of mixed population origin, that coastal Atlantic cod are structured into local populations on the single-fjord scale, that coastal Atlantic cod populations in the Skagerrak receive cod larvae transported from the North Sea by ocean currents, that larval drift is predominant in Greenland halibut and creates a genetic cline along the direction of ocean currents, and that migrating bowhead whales off the Alaskan coast are temporally genetic structured. In an ongoing project, the population genetic structure in several deep-sea fishes such as tusk, ling, roundnose grenadier, black scabbardfish and orange roughy is studied. In the near future there are plans to expand the institute's work on deep-sea fishes, in cooperation with institutions in the UK and Portugal.

Selected Publications:

- Knutsen H, Jorde PE, Albert OT, Hoelzel AR, Stenseth NC. 2007. Population genetic structure in the North Atlantic Greenland halibut: influenced by oceanic current systems? (revised manuscript in review).
- Jorde PE, Knutsen H, Espeland SH, Stenseth NC. 2007. Spatial scale of genetic structuring in coastal cod (*Gadus morhua*) and the geographic extent of local populations. (revised manuscript in review)
- Jorde PE, Schweder T, Bickham JW, Givens GH, Suydam R, Hunter D, Stenseth NC. 2007. Detecting genetic structure in migrating bowhead whales off the coast of Barrow, Alaska. *Molecular Ecology*, in press.
- Knutsen H, Olsen EM, Ciannelli L, Espeland SH, Knutsen JA, Simonsen JH, Skreslet S, Stenseth NC. 2007. Egg distribution, bottom topography and small-scale population structure in a coastal marine system. *Marine Ecology Progress Series*, in press
- Stenseth NC, Jorde PE, Chan KS, Hansen E, Knutsen H, André C, Skogen MD, Lekve K. 2006. Ecological and genetic impact of Atlantic cod larval drift in the Skagerrak. *Proceedings of the Royal Society of London, B-series*, 273: 1085–1092.
- Knutsen H, André C, Jorde PE, Skogen MD, Thuroczy E, Stenseth NC. 2004. Transport of North Sea cod larvae into the Skagerrak coastal populations. *Proceedings of the Royal Society of London, B-series*, 271: 1337–1344.
- Knutsen H, Jorde PE, André C, Stenseth NC. 2003. Fine-scaled geographical population structuring in a highly mobile marine species: the Atlantic cod. *Molecular Ecology*, 12: 385–394.
- Knutsen H, Knutsen JA, Jorde PE. 2001. Genetic evidence for mixed origin of recolonized sea trout populations. *Heredity*, 87: 207–214.

3. NTNU- Institute of Biology-Trondhjem Biological Station (TBS)

Homepage: <http://www.bio.ntnu.no/tbs/>

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 Norwegian University of Science and Technology Department of Biology
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Leading scientists: Jarle Mork (Group leader)

Cooperation parties:

Research groups/projects:

1. Selection at cod isozyme loci.
2. Blue whiting genetic studies.

Summary:

The target species of TBS have mostly been on commercial marine fishes, in particular gadoids but also on herring, capelin and halibut. The population genetic studies at TBS have been active since the early 1970ies. First record, baseline studies on genetic variability and geographic genetic differentiation have been published for a range of species occurring in Norwegian waters, including cod, haddock, whiting, blue whiting, saithe, Norway pout and poor cod. For several of these species samples have covered their entire distribution range. TBS store all tissue samples of these species, and has currently a “gene bank” containing some 40 000 specimens with full biological records. The self-sustaining cod stock in the Trondheimsfjord proper have been studied extensively in a time series starting in 1976. Limited studies have also been performed on the genetic structure of blue mussels at TBS.

Selected Publications:

Karlsson S, Mork J. 2005. Deviation from Hardy–Weinberg equilibrium, and temporal instability in allele frequencies at microsatellite loci in a local population of Atlantic cod. *ICES Journal of Marine Science*. 62: 1588–1596.

Ryan AW, Mattiangeli V, Mork J. 2005. Genetic differentiation of blue whiting (*Micromesistius poutassou* Risso) popu-

lations at the extremes of the species range and at the Hebrides–Porcupine Bank spawning grounds. *ICES Journal of Marine Science*. 62: 948–955.

Karlsson S, Mork J. 2003. Selection-induced variation at the pantophysin locus (*PanI*) in a Norwegian fjord population of cod (*Gadus morhua* L.). *Molecular Ecology*. 12: 3265–3274.

4. University of Bergen, Department of Fisheries and Marine Biology.

Homepage: <http://www.bio.uib.no/pages/forsker.php?pid=1032&lang=E>

Contact person: Gunnar Nævdal
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Leading scientists: Gunnar Nævdal, Dag Møller

Cooperation parties:

Research groups/projects:

Summary:

No information was available when this report was finished.

Selected Publications:

There was no information available on publications from the Department of Fisheries and Marine Biology, University of Bergen, when this report was finished.

5. Telemark University College

Homepage:

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Leading scientists: Jan Heggenes.

Cooperation parties:

Research groups/projects:

Summary:

No information was available when this report was finished.

Selected Publications:

Heggenes J, Qvenild T, Stamford MD, Taylor EB. 2006. Genetic structure in relation to movements in wild European grayling (*Thymallus thymallus*) in three Norwegian rivers. *Canadian Journal of*

Fisheries and Aquatic Science, 63: 1309–1319.

Heggenes J, Skaala Ø, Borgstrøm R, Igland OT. 2006. Minimal gene flow from introduced brown trout (*Salmo trutta* L.) after 30 years of stocking.

- Journal of Applied Ichthyology. 22: 119–124.
- Heggenes J, Røed KH, Høyheim B, Rosef L. 2002. Microsatellite diversity assessment of brown trout (*Salmo trutta*) population structure indicate limited genetic impact of stocking in a Norwegian alpine lake. *Ecology of Freshwater Fish*. 11: 93–100.

Private companies

1. GenoMar ASA

Homepage: <http://www.genomar.no>

Contact person: Øystein Lie
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Leading scientists: Øystein Lie

Cooperation parties:

Research groups/projects:

Summary:

GenoMar ASA is engaged in science-based breeding of commercially important fish species. The main products are a genetically superior Tilapia and a unique set of genomics products and findings in tilapia such as, for example, full genomic sequence of important genes, expressed sequence tag collection, and a high resolution marker map. GenoMar also has also developed a number of genetic tools for studying differentiation between families and populations of Atlantic salmon, various breeding softwares, and a molecular vaccine against infectious salmon anaemia. The company also had a unique salmon mapping population where extreme contrasts in industrial traits were segregated. This population is now managed by the Research Council of Norway.

Selected Publications:

- Rengmark HA, Slettan A, Skaala Ø, Lie Ø, Lingaas F. 2006. Genetic variability in wild and farmed Atlantic salmon (*Salmo salar*) strains estimated by SNP and microsatellites. *Aquaculture*. 253: 229–237.
- Lee BY, Lee WJ, Streebman JT, Carleton KL, Howe AE, Hulata G, Slettan A, Stern JE, Terai Y, Kocher TD. 2005. A Second-Generation Genetic Linkage Map of Tilapia (*Oreochromis* spp.). *Genetics*. 170: 237–244.

Sweden

In Sweden, genetic research on fish is mainly carried out at the three universities of Stockholm, Uppsala and Göteborg and at the Swedish Board

of Fisheries. However, several single projects are also carried out at other educational and research sites. The research in Sweden is focused on the genetic structures of wild fish populations, but the genetic dynamics of introgression between groups, the spread of genetically exogenous populations, the genetic and ecological consequences of stocking, as well as research on genetically sustainable fishery management is also conducted. Most research is basic research on species found in fresh and brackish waters, but studies are also carried out on commercially important and aquacultured species as well as on species found in marine systems.

Research institutes

1. Swedish board of Fisheries
- i) Institute of Freshwater Research (IFR)

Homepage: <http://www.fiskeriverket.se/>

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Leading scientists: Johan Dannewitz (Group leader), Jonas Pettersson, Tore Prestegard, Irene Bystedt, Stefan Palm.

Cooperation parties: Department of Ecology & Evolution/Population Biology and Conservation Biology, Uppsala University.

Department of Zoology/Section of Population Genetics, Stockholm University.

Department of Zoology, Göteborg University

Department of Molecular Ecology, Södertörn University College.

Laboratory of Aquatic Ecology, Katholieke Universiteit Leuven, Belgium.

Finnish Game and Fisheries Research Institute (M-L Koljonen).

Research groups/projects:

1. Population structure of important resource species and threatened species (e. g. European eel, brown trout, whitefish, crayfish and vendace).
2. Genetic and ecologic consequences of stocking activities (with focus on salmonid species, European eel and pikeperch).
3. Local adaptation in sea-migrating brown trout.

Summary:

The research at IFR is mainly centred round genetic variation within and among populations of threatened species and species that are important for fisheries. The work is, for example, focused on genetic diversity and population structure of brown trout, local adaptation in sea-migrating brown trout, and the potential ecological and genetic effects of stocking of hatchery produced brown trout on recipient populations. A genetic project on pikeperch, including studies on genetic effects of large scale stocking activities, will be initiated during 2007. The degree of spatial and temporal genetic variation in the European eel across its distribution in Europe is also investigated. In addition, research is carried out on the noble crayfish to identify populations that are valuable from a conservation perspective.

Selected Publications:

- Dannewitz J, Dahl J, Petersson E, Järvi T. Adaptive genetic variation and local adaptation in brown trout *Salmo trutta* in Sweden. Manuscript in preparation.
- Maes GE, Pujolar JM, Raeymaekers JAM, Dannewitz J, Volckaert FAM. 2006. Microsatellite conservation and Bayesian individual assignment in four *Anguilla* species. *Marine Ecology Progress Series*, 319: 251–261.
- Dannewitz J, Maes GE, Johansson L, Wickström H, Volckaert FAM. 2005. Panmixia in the European eel: a matter of time... *Proceedings of the Royal Society of London Series-B*, 272: 1129–1137.
- Dannewitz J, Petersson E, Dahl J, Prestegard T, Löf A-C, Järvi T. 2004. Reproductive success of hatchery produced and wild born brown trout in an experimental stream. *Journal of Applied Ecology*, 41: 355–364.
- Dannewitz J, Petersson E, Prestegard T, Järvi T. 2003. Effects of sea-ranching and family background on fitness traits in brown trout *Salmo trutta* reared under near-natural conditions. *Journal of Applied Biology*, 40: 241–250.
- Palm S, Dannewitz J, Järvi T, Petersson E, Prestegard T, Ryman N. 2003. Lack of molecular genetic divergence between sea ranched and wild sea trout (*Salmo trutta*). *Molecular Ecology*, 12: 2057–2071.
- Dannewitz J. 2003. Genetic and ecological consequences of fish releases. PhD-thesis, Uppsala University, Sweden
- Edsman L, Farris JS, Källersjö M, Prestegard T. 2002. Genetic differentiation between noble crayfish, *Astacus astacus* (L.) populations detected by microsatellite length variation in the rDNA ITS1 region. *Bulletin Francais de la Peche et de la Pisciculture*, 367: 691–706.

1. Swedish board of Fisheries
- ii) Institute of Coastal Research (ICR)

Homepage: <http://www.fiskeriverket.se/>

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Leading scientists: Teija Aho (Group leader), Ann-Britt Florin, Kerstin Mo, Anna Gårdmark, Anssi Vainikka.

Cooperation parties: Animal Ecology/Departement of Ecology and Evolution, Uppsala University.

Population Biology/Departement of Ecology and Evolution, , Uppsala University.

Department of Population Genetics, Institute of Zoology, Stockholm University.

FishAce European network.

Research groups/projects:

1. Stock identification.
2. FishAce.

Summary:

At ICR a large stock identification project is carried out with the aim to identify the population structure in flounder, turbot, perch, pike, pike-perch, vendace and whitefish in the Baltic Sea. Mapping of the population structure of these commercially important species will enable a more sustainable exploitation and management of the stocks. Within FishACE, theoretical evolutionary models are developed to assess the potential effects of fisheries-selection on life-history evolution of fishes in a multispecies context. Moreover, empirical analyses on the genetic effects of fishing on maturation, size, and age are examined using indirect statistical analyses.

Selected Publications:

- Florin A-B, Höglund J. Population structure of flounder (*Platichthys flesus*) in the Baltic Sea: differences among demersal and pelagic spawners. Submitted manuscript.
- Vainikka A, Gårdmark A, Bland B, Hjelm J. Growth and maturation size of eastern Baltic cod, *Gadus morhua* over time – do maturation reaction norms reveal correlation or causality? Manuscript.
- Säisä M, Rönn J, Aho T, Björklund M, Pasanen P, Koljonen M-L. Genetic differentiation in Finnish whitefish (*Coregonus lavaretus*) ecological types and populations based on DNA microsatellite variation. Manuscript.
- Björklund M, Aho T, Larsson LC. Genetic differentiation in the pikeperch (*Sander lucioperca*): the importance of gene flow, drift and common history. Submitted manuscript.
- Poulet N, Balaesque P, Aho T, Björklund M. Genetic population structure and dynamics of an introduced species. The pikeperch in the Rhone delta, and ecosystem impacted by agricultural management. Submitted to Journal of Fish Biology.
- Florin A-B, Höglund J. 2007 Absence of population structure in Baltic Sea turbot (*Psetta maxima*). *Molecular Ecology*. 16 (1):115–126.
- Aho T, Rönn J, Piironen J, Björklund M. 2006. Impacts of effective population size on genetic diversity in hatchery reared Brown trout (*Salmo trutta* L.) populations. *Aquaculture*, 253: 244–248.

2. Swedish Museum of Natural History, Department of Vertebrate Zoology, Ichthyology section.

Homepage: <http://www.nrm.se/researchandcollections/zoology/vertebratezoology/fishes.5fdc727f10d795b1c6e80005895.html> 4.

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Leading scientists: Sven O Kullander (Group leader), Bo Delling, Fang Kullander, Anders Silfvergrip, Te Yu Liao, Jonathan Ready

Cooperation parties:

Research groups/projects:

1. Resolution of enigmatic Arctic species groups, including sticklebacks (Gasterosteidae, Gasterosteus), whitefish (Coregonidae, Coregonus), and salmonids (Salmonidae, Salmo, Salvelinus).
2. Systematics of Asian Cyprinidae.
3. Systematics of South American Cichlidae.

Summary:

Research at NRM ichthyology is based on significant collections of preserved specimens (about 450 000 specimens), and since five years back also tissue samples providing the basis for molecular studies. We work on systematic aspects including species level under the phylogenetic species concept, and higher levels using cladistic analytical methods. The research goals are principally to establish species limits, and to provide phylogenetic hypotheses explaining the species diversity of selected fish groups. We participated in the first major genetic barcoding project, FishTrace, providing barcode sequences for a large number of marine European fishes, and currently participate in a project to barcode all Swedish vertebrates including fishes. Results from ongoing studies on Swedish fishes, including FishTrace are still unpublished.

Selected Publications:

Susnik S, Weiss S, Odak T, Delling B, Treer T, Snoj A. 2007. Reticulate evolution: ancient introgression of the Adriatic brown trout mtDNA in softmouth trout

- Salmo obtusirostris* (Teleostei: Salmonidae). *Biological Journal of the Linnean Society*. 90: 139–152.
- Ready JS, Ferreira EGJ, Kullander SO. 2006. Discus fishes: mtDNA evidence for a phylogeographic barrier in the Amazonian genus *Symphysodon* (Teleostei: Cichlidae). *Journal of Fish Biology*. 69, Suppl. B: 200–211.
- Rican O, Kullander SO. 2006. Character- and tree-based delimitation of species in the 'Cichlasoma' facetum group (Teleostei, Cichlidae) with the description of a new genus. *Journal of Zoological Systematics & Evolutionary Research*. 44: 136–152.
- Rüber L, Britz R, Kullander SO, Zardoya R. 2004. Evolutionary and biogeographic patterns of the Badidae (Teleostei: Perciformes) inferred from mitochondrial and nuclear DNA sequence data. *Molecular Phylogenetics and Evolution*. 32: 1010–1022.
- Delling B, Crivelli AJ, Rubin JF, Berrebi P. 2000. Morphological variation in hybrids between *Salmo marmoratus* and alien *Salmo* species in the Volarja stream, Soca River basin, Slovenia. *Journal of Fish Biology*. 57: 1199–1212.

Universities

1. Stockholm University, Institute of Zoology, Department of Population Genetics.

Homepage: <http://www.zoologi.su.se/research/popgen/>

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Leading scientists: Nils Ryman (Group leader), Linda Laikre, Torbjörn Järvi, Stefan Palm, Lena Larsson, Anna Palmé, Johan Charlier.

Cooperation parties: TMBL, Göteborg University.
Swedish Board of Fisheries, Sweden.
Oslo University, Norway.

Research groups/projects:

1. Spatial and temporal genetic variation in herring (collaboration with Carl André, TMBL, Göteborg University).
2. Genetic dynamic of introgression. Short term temporal genetic change in brown trout.
3. Statistical methods for mapping of biodiversity on the gene level.
4. Estimation of effective population size when generations overlap.
5. Spread of genetically exogenous populations in Sweden.
6. Genetic structuring of pike in the Baltic Sea
7. Genetically sustainable fishery management.
8. Monitoring gene level biodiversity.

Summary:

The genetic research on fish at Stockholm University spans over a wide range of research issues. Currently it largely deals with the genetic effects of various types of exploitation, genetically sustainable fishery management, and the development of means for monitoring biodiversity on the gene level. There is a strong focus on statistical and theoretical work, and the main achievements in this respect include the identification of the effects of supportive breeding on inbreeding and variance effective number. A model has also been developed for estimations of effective population sizes from temporal allele frequencies when generations overlap. Moreover, the group runs a unique long-term study of natural and experimental brown trout populations in central Sweden that includes continuous genetic studies over almost 30 years. Main model species presently include brown trout, herring and northern pike. Over the years, species such as salmon, cod and fourhorn sculpin have also been studied.

Selected Publications:

- Laikre L, Palmé A, Josefsson M, Utter F, Ryman N. 2006. Release of alien populations in Sweden. *Ambio*, 35: 255–261.
- Ryman N, Palm S. 2006. Program Note: POWSIM: a computer program for assessing statistical power when testing for genetic differences. *Molecular Ecology Notes*, 6: 600–602.
- Ryman N, Palm S, André C, Carvalho GR, Dahlgren TG, Jorde P-E, Laikre L, Larsson LC, Palmé A, Ruzzante DE. 2006. Power for detecting genetic divergence: differences between statistical methods and marker loci. *Molecular Ecology*, 15: 2031–2045.
- Ryman N. 2006. Program Note: CHIFISH: a computer program testing for genetic heterogeneity at multiple loci using chi-square and Fisher's exact test. *Molecular Ecology Notes*, 6: 285–287.
- Laikre L, Palmé A. 2005. Spridning av främmande populationer i Sverige. Naturvårdsverket, Rapport 5475.
- Laikre L, Miller L, Palmé A, Palm S, Kapuscinski AR, Thoresson G, Ryman N. 2005. Spatial genetic structure of northern pike (*Esox lucius*) in the Baltic Sea. *Molecular Ecology*, 14: 1955–1964.
- Laikre L, Palm S, Ryman N. 2005. Genetic population structure of fishes: implications for coastal zone management. *Ambio*, 34: 111–119.
- Palmé A, Laikre L, Ryman N. 2004. Population genetics of harbour porpoise in Swedish waters – a literature review. Naturvårdsverket, Report 5419.
- Barten PK, Clegg MT, Fleming IA, Gross MR, Incze LS, Kapuscinski AR, O'Brien P, Neis B, Ryman N, Smouse PE, Specker JL, Sutinen JG. 2004. Atlantic salmon in Maine. – US National Research Council of the National Academies; Report from the Committee on Atlantic Salmon in Maine. 240 pp.
- Barten PK, Clegg MT, Fleming IA, Gross MR, Incze LS, Kapuscinski AR, O'Brien P, Neis B, Ryman N, Smouse PE, Specker JL, Sutinen JG. 2002. Genetic status of Atlantic salmon in Maine. – US National Research Council of the National Academies; Interim Report from the Committee on Atlantic Salmon in Maine. 62 pp.

*2. Uppsala University**i) Animal Ecology (Department of Ecology and Evolution)*

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Leading scientists: Mats Björklund (Group leader), Sara Bergek, Marnie Demandt.

Cooperation parties: ICR, Swedish board of Fisheries.
Department of Systems Ecology, Stockholm University.

Research groups/projects:

1. Genetic variation and geographic scales in perch.
2. Ecology and evolution of cyprinid fishes.
3. Genetic variation in the Round Goby.

Summary:

Research at the department of Animal Ecology includes studies of Eurasian perch, different cyprinid species, and the Round Goby. The study of Eurasian perch is investigating the genetic variation and sub-structuring at different geographical and temporal scales. In another project the extent of, and resulting effects of hybridization between different species of cyprinids is evaluated. A phylogenetic relationship between the Swedish members of the cyprinid family is also generated. The Round Goby is an alien species from the Black Sea. At present the Round Goby is invading and spreading in the southern parts of the Baltic Sea, and also outcompeting native species found in these waters. A project has been developed to map the genetic structure of this alien species. Previous research at the department of Animal Ecology has also involved studies of the genetic structure of brown trout and the Banggai cardinalfish.

Selected Publications:

- Bergek S, Björklund M. Genetic differentiation at a small geographic scale in the perch. Manuscript.
- Björklund M, Aho T, Larsson LC. Genetic differentiation in the pikeperch (*Sander lucioperca*): the importance of gene flow, drift and common history. Submitted manuscript.
- Poulet N, Balaesque P, Aho T, Björklund M. Genetic population structure and dynamics of an introduced species. The pikeperch in the Rhone delta, and ecosystem impacted by agricultural management. Submitted to *Journal of Fish Biology*.
- Demandt M, Björklund M. Loss of genetic variability in reintroduced roach (*Rutilus rutilus* L.) populations. *Journal of Fish Biology*, accepted pending revision.

- Aho T, Rönn J, Piironen J, Björklund M. 2006. Impacts of effective population size on genetic diversity and relatedness in hatchery reared Brown trout (*Salmo trutta*, L.) populations. *Aquaculture*, 253: 244–248.
- Hoffman EA, Kolm N, Berglund A, Arguello JR, Jones AG. 2005. Genetic structure in the coral-reef associated Banggai cardinalfish, *Pterapogon kauderni*. *Molecular Ecology*, 14: 1367–1375.

2. Uppsala University

ii) Comparative Physiology (Department of Physiology and Developmental Biology).

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Cooperation parties: see <http://aquafirst.vitamib.com/> for details.

Research groups/projects:

1. Aquafirst – Combined genetic and functional genomic approaches for stress and disease resistance marker assisted selection in fish and shellfish.

Summary:

The Aquafirst project started in 2004 and is coordinated by Dr. Patrick Prunet, INRA Rennes. It includes 18 partners and the overall aims of the project is to identify oyster, rainbow trout, sea bream, and sea bass genes of which expression is associated with disease and stress resistance and, from this information, to develop genetic approaches that allow characterization of genetic markers for marker-assisted selective breeding of disease and/or stress resistant individuals. In order to identify and evaluate loci and quantitative trait loci (QTL) which have an effect on stress and disease resistance, we will (i) characterise in oyster and trout the allelic variants of the identified candidate marker genes by identification of single nucleotide polymorphism (SNP) in the gene sequences. (ii) produce segregating F2 families in oyster and trout and from this material identify QTLs and candidate genes related to stress and disease resistance and summer mortality in oyster.

Selected Publications:

- Schjolden J, Pottinger TG, Backström T, Pulman KGT, Winberg S. 2006. Divergence in behavioural responses to stress in two strains of rainbow trout (*Oncorhynchus mykiss*) with contrasting stress responsiveness. *Hormones and Behavior*, 48: 537–544.
- Schjolden J, Pulman KGT, Pottinger TG, Metcalfe NB, Winberg S. 2006. Divergence in locomotor activity within established and stable social structures in two strains of rainbow trout (*Oncorhynchus mykiss*) with contrasting stress responsiveness. *Journal of Fish Biology*, 68: 920–924.
- Schjolden J, Pulman KGT, Pottinger TG, Tottmar O, Winberg S. 2006. Serotonergic characteristics of rainbow trout divergent in stress responsiveness. *Physiology and Behavior*, 87: 938–946.
- Brelin D, Petersson E, Winberg S. 2005. Divergent stress coping styles in juvenile brown trout (*Salmo trutta*). *Trends in comparative endocrinology and neurobiology annals of the New York academy of sciences*, 1040: 239–245.
- Øverli Ø, Winberg S, Pottinger TG. 2005. Behavioral and neuroendocrine correlates of selection for stress responsiveness in rainbow trout – a review. *Integrative and Comparative Biology*, 45: 463–474.
- Schjolden J, Stoskhus A, Winberg S. 2005. Does intraspecific variation in stress responses and agonistic behaviour reflect divergent stress coping strategies in juvenile rainbow trout? *Physiological and Biochemical Zoology*, 78: 715–723.

2. Uppsala University

iii) Limnology (Department of Ecology and Evolution)

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Cooperation parties: Mats Björklund, Animal Ecology, Uppsala University.

Research groups/projects:

1. Small scale spatial and temporal genetic variation between morphological forms of perch.
2. Mechanisms behind phenotypic divergence and genetic differentiation in fish populations.

Summary:

The research on Eurasian perch at the department of Limnology has during the last ten years been extensive and included studies of general patterns and mechanisms behind the development of sympatric and habi-

tatspecific morphotypes. A recent study also investigated the potential for small-scaled genetic differentiation between sympatric morphotypes of perch. In the next step we plan to test the relative importance of predation and competition driving phenotypic divergence and whether spatial and temporal genetic differentiation can be explained by community ecology processes (predation and competition). Mechanisms of genetic differentiation will be examined both at spatial and temporal scales.

Selected Publications:

Olsson J, Ragnarsson H. Replicated small scale morphologic and genetic differentiation in sympatric Eurasian perch. Submitted.

Svanbäck R, Eklöv P. 2006. Genetic variation and phenotypic plasticity: causes of morphological variation in Eurasian perch. *Evolutionary Ecology Research*, 8: 37–49.

3. Göteborg University, Department of Marine Ecology, Tjärnö Marine Biology Laboratory (TMBL).

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Cooperation parties: IMR, Swedish Board of Fisheries, Lysekil, Sweden.
Department of Zoology, Population Genetics, Stockholm University, Sweden.

Department of Systems Ecology, Stockholm University, Sweden.

Department of Zoology, Göteborg University, Sweden.

IMR, Norway.

DIFRES, Denmark.

Research groups/projects:

1. Population genetics and stock structure of herring and cod in the North and Baltic Seas.
2. Stock structure in different species of shellfish.

Summary:

The main focus of the research at TMBL is on general population genetic patterns of species in the North Sea – Baltic salinity transition. For exam-

ple, research is conducted on the genetic structure and connectivity of the heavily exploited stocks of cod in the Baltic Sea, Kattegat and Skagerrak. This is a project in collaboration with the Norwegian IMR and IMR at the Swedish board of fisheries. Another project deals with the population genetic structure of herring in the North and Baltic Seas. This is conducted in collaboration with the Department of Population Genetics at Stockholm University, the Department of Zoology at Göteborg University, and DIFRES in Denmark. TMBL is also engaged in studies of several species of shellfish including the edible crab, shrimp, the flat oyster (in collaboration with Department of Zoology, Göteborg University), and the blue mussel (in collaboration with Department of Systems Ecology, Stockholm University).

Selected Publications:

- Johannesson K, André C. 2006. Invited review: Life on the margin – genetic isolation and loss of variation in a peripheral marine ecosystem. *Molecular Ecology*, 15: 2013–2030.
- Ruzzante D, Mariani S, Bekkevold D, André C, Mosegaard H, Clausen L, Dahlgren T, Hutchinson W, Hatfield E, Thorstensen E, Brigham J, Simmonds J, Laikre L, Larsson L, Stet R, Ryman N, Carvalho G. 2006. Biocomplexity in a highly migratory marine pelagic fish. *Proceedings of the Royal Society of London B-series*, 273: 1459–1464.
- Stenseth NC, Jorde PE, Kung-Sik Chan, Knutsen H, André C, Skogen M, Lekve K. 2006. Ecological and genetical impact of larval drift: the Atlantic Cod as an example. *Proceedings of the Royal Society of London B-series*, 273: 1085–1092.
- Fox CJ, Taylor MI, Pereyra R, Villasana MI, Rico C. 2005. TaqMan DNA technology confirms likely overestimation of cod (*Gadus morhua* L.) egg abundance in the Irish Sea: implications for the assessment of the cod stock and mapping of spawning areas using egg-based methods. *Molecular Ecology*, 14: 879–884.
- Bekkevold D, André C, Dahlgren T, Clausen L, Thorstensen E, Mosegaard H, Carvalho G, Christensen T, Norlinder E, Ruzzante D. 2005. Environmental correlates of population differentiation in Atlantic Herring. *Evolution*, 29: 5626–2668.
- Knutsen H, André C, Jorde PE, Skogen M, Thuroczy E, Stenseth NC. 2004. Influx of North Sea cod larvae into the Skagerrak coast. *Proceedings of the Royal Society of London B-series*, 271: 1337–1344.
- Knutsen H, Jorde PE, André C, Stenseth NC. 2003. Fine-scaled geographic population structuring in a highly mobile marine species: the Atlantic cod. *Molecular Ecology*, 12: 385–394.

4. Örebro University, Molecular Biology Group.

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Cooperation parties: Bertil Borg, Stockholm University.
Peter Thomas, University of Texas at Austin, USA.

Research groups/projects:

1. Genes involved in endocrine regulation of reproduction, sex determination and differentiation in teleosts.

Summary:

The research at Örebro University is focused on understanding the molecular mechanisms by which nuclear and membrane receptors as well as other transcriptional regulators influence gene expression during reproduction and sex determination and differentiation in teleosts. The main experimental model is the zebrafish, but studies are also conducted on three-spined stickleback, sea bream and Arctic charr.

Selected Publications:

- Modig C, Modesto T, Canario A, Cerda J, Hofsten J, Olsson PE. 2006. Molecular Characterization and Expression Pattern of Zona Pellucida Proteins in Gilthead Seabream (*Sparus aurata*). *Biology of Reproduction*, 5: 717–25.
- Berg AH, Thomas P, Olsson P-E. 2005. Biochemical characterization of the Arctic char (*Salvelinus alpinus*) ovarian progesterin membrane receptor. *Reproductive Biology and Endocrinology*, 3: 64.
- Olsson P-E, Berg AH, von Hofsten J, Grahn B, Hellqvist A, Karlsson J, Modig C, Borg B, Thomas P. 2005. Molecular cloning and characterization of a nuclear androgen receptor activated by 11-ketotestosterone. *Reproductive Biology and Endocrinology*, 3: 37.
- von Hofsten J, Modig C, Larsson A, Karlsson J, Olsson P-E. 2005. Determination of the expression pattern of the dual promoter of zebrafish fushi tarazu factor-1a following microinjections into zebrafish one cell stage embryos. *General and Comparative Endocrinology*, 142: 222–226.
- von Hofsten J, Larsson A, Olsson P-E. 2005. A novel functional Steroidogenic factor-1 homologue (ff1d) is co-expressed with anti-Mullerian hormone (AMH) in zebrafish. *Developmental Dynamics*, 233: 595–604.
- Berg AH, Modig C, Olsson P-E. 2004. 17b-estradiol induced vitellogenesis is inhibited by cortisol at the post-transcriptional level in Arctic char (*Salvelinus alpinus*) *Reproductive Biology and Endocrinology*, 2: 62.
- O'Toole R, von Hofsten J, Rosqvist R, Olsson P-E, Wolf-Watz H. 2004. Visualisation of the infection maps the host site where chemotaxis functions in the virulence of *Vibrio anguillarum*. *Microbial Pathogenesis*, 37: 41–46.
- Berg AH, Westerlund L, Olsson P-E. 2004. Arctic char (*Salvelinus alpinus*) egg shell proteins: Regulation during reproduction and in response to 17b-estradiol and cortisol. *General and Comparative Endocrinology*, 135: 276–285.
- von Hofsten J, Karlsson J, Olsson P-E. 2003. Fushi tarazu factor-1 mRNA and protein is expressed in steroidogenic and cholesterol metabolizing tissues during different life stages in Arctic char (*Salvelinus alpinus*). *General and Comparative Endocrinology*, 132: 96–102.
- von Hofsten J, Karlsson J, Jones I, Olsson PE. 2002. Expression and regulation of fushi tarazu factor-1 and steroidogenic

genes during reproduction in Arctic char (Salvelinus alpinus). *Biology of Reproduction*, 4: 1297–304.

5. Lund University, Department of Ecology, Animal Ecology, Molecular Population Biology.

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Maria Hansson (Chief scientist)

Cooperation parties: Professor Per Larsson, Dept. of Biology and Environmental Science,
University of Kalmar, Sweden.
Dr. Mark Hahn, Woods Hole Oceanographic Institution, USA.

Research groups/projects:

1. Genes involved in toxic responses to environmental pollutants in Atlantic salmon.

Summary:

The research at Lund University is focused on the so called aryl hydrocarbon receptor (AHR) genes, looking at genetic variation for tolerance towards exposure to persistent organochlorine pollutants in wild Atlantic salmon. The AHRs are specifically responsible for mediating the typical toxic effects seen after environmental pollutant exposure. We are interested in finding out more about why the salmonid fish species belong to the most sensitive vertebrates to toxic effects induced by polycyclic aromatic hydrocarbons (e. g. PCBs). Our sample population comes from the Baltic Sea, one of the most contaminated bodies of brackish water in the world. The analyses focus on the specific functions and characteristics of the AHR genes and proteins, using in vitro TnT transcription/translation, velocity sedimentation, saturation binding assays, transient transfection analyses and cell cultures. From real-time PCR analyses we estimate transcription levels of the salmon AHR and CYP1A1 genes, which are compared to allelic variation found in the AHR genes. By measuring actual PCB levels and carotenoids (antioxidants) inside the salmon muscles we can, in addition, compare pollutant load to the individual salmon genetics.

Selected Publications:

- Hansson MC, Persson ME, Larsson P, Kjellman C, von Schantz T. 2006. Polychlorinated biphenyl load, aryl hydrocarbon receptor, and cytochrome P4501A1 induction in a wild population of Atlantic salmon (*Salmo salar*) from the Baltic Sea. *Environmental Toxicology and Chemistry*, 25: 2197–2207.
- Hansson MC, Wittzell H, Persson K, von Schantz T. 2004. Unprecedented genomic diversity of aryl hydrocarbon receptor (AHR) genes in Atlantic salmon (*Salmo salar* L.). *Aquatic Toxicology*, 68: 219–232.
- Hansson MC, Wittzell H, Persson K, von Schantz T. 2003. Characterization of two distinct aryl hydrocarbon receptor (AHR2) genes in Atlantic salmon (*Salmo salar*) and evidence for multiple AHR2 gene lineages in salmonid fish. *Gene*, 303: 197–206.

6. *Swedish University of Agricultural Sciences (SLU), Umeå. Department of Aquaculture.*

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Cooperation parties: Karlstads Universitet, Sweden.
Länstyrelsen Västerbotten, Sweden.
Vattenbrukarnas Riksförbund (VRF), Sweden.
M-L Koljonen, R Hudd, Finnish game and fisheries.
C Primmer, A Vasemägi, Turku University, Finland.
J Lumme, Oulu University, Finland.
R Gross, T Paaver, Estonian Agricultural University, Tartu.
H Thorarensen, Holar University College, Iceland.

Research groups/projects:

1. Breeding programme for arctic charr.
2. Grayling in the Kvarken area.
3. Early maturation in salmon.
4. Brown trout in rivers Vindelälven and Piteälven.

Summary:

The research conducted at SLU Umeå can be divided into three projects. In the first, research has during the last 20 years been carried out to improve important breeding traits for aquaculture purposes in arctic charr. The traits in focus have been growth rate and sexual maturation. Research on the use of genetic markers in breeding programmes has also recently been initiated. In the second project the population structure of salmonids (salmon, brown trout and grayling) has been investigated for conservation purposes. The genetic structure over large geographical scales has been studied (e. g. the structure of Atlantic salmon in Northern Europe), but also the structure on smaller scales such as the one occurring between different drainage areas has been under investigation. In this project the genetic effects of interbreeding between farmed and wild stocks of fish as well as how selection is acting on genetic markers have been studied. The research in the third project is focused on the gene expressions involved in different physiological processes. For example, the active genes in-

volved and their functions in early sexual maturation of male salmon are mapped. Other species studied in this project is European eel and sticklebacks.

Selected Publications:

- Brännäs E, Chaix T, Nilsson J, Eriksson L-O. 2005. Has a 4-generation selection programme affected the social behaviour and growth pattern of Arctic charr (*Salvelinus alpinus*)? *Applied Animal Behaviour Science*, 94: 165–178.
- Vasemägi A, Gross R, Paaver T, Koljonen M-L, Säisä M, Nilsson J. 2005. Analysis of gene associated tandem repeat markers in Atlantic salmon (*Salmo salar* L.) populations: implications for restoration and conservation in the Baltic sea. *Conservation Genetics*, 6: 385–397.
- Vasemägi A, Gross R, Paaver T, Koljonen M-L, Nilsson J. 2005. Extensive immigration from compensatory hatchery releases into wild Atlantic salmon population in the Baltic sea: spatio-temporal analysis over 18 years. *Heredity*, 95: 76–83.
- Carlsson J, Carlsson JEL, Olsen KH, Hansen MM, Eriksson T, Nilsson J. 2004. Kin-biased distribution in brown trout: an effect of redd location or kin recognition? *Heredity*, 92, 53–60.
- Schmitz M. 2003. Differential effect of Insulin-like growth factor I on *In vitro* gonadotropin subunits expression in Atlantic salmon *Fish Physiology and Biochemistry*, 28: 105–106.
- Carton MW, Schmitz M, Cutts CJ, Kelly AK, Hill JA, Brabazon ED, Adams CE, Byrnes L. 2002. Expressed sequence tags in larval Arctic charr (*Salvelinus alpinus*) *Fish Physiology and Biochemistry*, 26: 231–238.
- Rousseau K, LeBelle N, Sbahi M, Huang Y-S, Marchelidon J, Schmitz M, Dufour S. 2002. Thyroid hormones negatively regulate Growth Hormone (GH) in a primitive teleost, *Anguilla anguilla*. *Journal of Endocrinology*, 175: 605–613.
- Hellqvist A, Schmitz M, Lindberg C, Olsson P-E, Borg B. 2001. LH- β and FSH- β mRNA expression in nesting and post-breeding three-spined stickleback, *Gasterosteus aculeatus*, and effects of castration on expression of LH- β , FSH- β and spiggin mRNA *Fish Physiology and Biochemistry*, 25: 311–317.
- Nilsson J, Gross R, Asplund T, Dove O, Jansson H, Kelloniemi J, Kohlmann K, Löytynoja A, Nielsen EE, Paaver T, Primmer CR, Titov S, Vasemägi A, Veselov A, Öst T, Lumme J 2001. Matrilineal phylogeography of Atlantic salmon (*Salmo salar* L.) in Europe and postglacial colonisation of the Baltic Sea area. *Molecular Ecology*, 10: 89–102.
- Koskinen MT, Ranta E, Piironen J, Veselov A, Titov S, Haugen TO, Nilsson J, Carlstein M, Primmer CR. 2000. Genetic lineages and postglacial colonization of the grayling (*Thymallus thymallus*, Salmonidae) in Europe, as revealed by mitochondrial DNA analyses. *Molecular Ecology*, 9: 1609–1624.

7. Södertörn University College

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1. Good genes in fish: immune and detoxication genetic variability in salmon (Södertörn University College).

Summary:

The research at Södertörn is focused on genetic variation at the major histocompatibility complex (MHC). Studies are conducted on how MHC influences kin recognition in Arctic charr, if interactions between infectious pathogens and disease resistance are caused by specific MHC genes in Atlantic salmon, and if selection for resistance towards the bacterial disease furunculosis decreases variability at the MHC in farmed Atlantic salmon. The methods used deploys recently developed PCR based methods for molecular genetics and combines these with methods from quantitative genetics and behavioural ecology to test the postulated questions in natural or semi natural populations of fish. Furthermore, there is also research on how genetic variation in the immune system affects the development of costly ornaments in males.

Selected Publications:

- | | |
|--|---|
| <p>Lohm J, Grahn M, Langefors Å, Andersen O, Storset A, von Schantz T. 2002. Experimental evidence for major histocompatibility complex-allele-specific resistance to a bacterial infection Proceedings of the Royal Society of London Series B. 269: 2029–2033.</p> <p>Olsén KH, Grahn M, Lohm J. 2002. Influence of mhc on sibling discrimination in Arctic char, <i>Salvelinus alpinus</i> (L.). Journal of Chemical Ecology. 28: 783–795.</p> <p>Langefors Å, Lohm J, Grahn M, Andersen O, von Schantz T. 2001. Association between major histocompatibility complex class IIB alleles and resistance to <i>Aeromonas salmonicida</i> in Atlantic salmon. Proceedings of the Royal Society of London Series B. 268: 479–485.</p> | <p>Langefors Å, Lohm J, von Schantz T, Grahn M. 2000. Screening of Mhc variation in Atlantic salmon (<i>Salmo salar</i>): a comparison of restriction fragment length polymorphism (RFLP), denaturing gradient gel electrophoresis (DGGE) and sequencing. Molecular Ecology. 9: 215–219.</p> <p>von Schantz T, Bensch S, Grahn M, Hasselquist D, Wittzell H. 1999. Good genes, oxidative stress and condition-dependent sexual signals. Proceedings of the Royal Society of London Series B. 266: 1–12.</p> <p>Olsén KH, Grahn M, Lohm J, Langefors Å. 1998. MHC and kin discrimination in juvenile Arctic charr, <i>Salvelinus alpinus</i> (L.) Animal Behaviour. 56: 319–327.</p> |
|--|---|

8. Mälardalen University, Department of Biology and Chemical Engineering.

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Cooperation parties: Department of Aquaculture, Swedish University of Agricultural Sciences (Umeå, Sweden).

Department of Molecular Biology, Södertörn University. University of British Columbia, Canada.

Research groups/projects:

1. The aberrant stickleback *Gasterosteus aculeatus* in the Karlskrona archipelago – ecology, genetics and conservation.

Summary:

The aberrant stickleback in the Karlskrona archipelago is possibly a completely new form within the threespine stickleback *Gasterosteus aculeatus* complex. It deviates from sympatric, normal sticklebacks in morphology, nest-building behaviour, parental care, and genetic properties. The aberrant form is very rare with a world distribution limited to two sites, both in the Karlskrona archipelago. This project aims to clarify the current status of the aberrant stickleback by ecological and genetic investigations.

Selected Publications:

Stärner H, Pålsson C, Lindén M. 2004.	control region of threespine stickleback
Tandem repeat polymorphism and heteroplasmy in the mitochondrial DNA	(<i>Gasterosteus aculeatus</i>). Behaviour, 141:1357–1369.

Appendix 2.

List of species and where genetic research is conducted in the Nordic countries.

Common name	Scientific name	Denmark	Faroe Islands	Finland	Iceland	Norway	Sweden
Gadoids							
Alaskan pollock	<i>Theragra chalcogramma</i>				UI	UT	
Atlantic cod	<i>Gadus morhua</i>	DIF, SUC	X		MRI, UI, PR	AF, UT, IMR, UOii, NTNU	SU, GU, SBFii
Blue whiting	<i>Micromesistius poutassou</i>					NTNU	
Haddock	<i>Melanogrammus aeglefinus</i>		X		UI	NTNU	
Ling	<i>Molva molva</i>					UOii	
Norwegian pollock	<i>Theragra finnmarchica</i>					UT	
Norway pout	<i>Trisopterus esmarkii</i>					NTNU	
Polar/ice cod	<i>Arctogadus glacialis</i>				UI	UT	
Poor cod	<i>Trisopterus minutus</i>		X			NTNU	
Roundnose grenadier	<i>Coryphaenoides rupestris</i>					UOii	
Saithe	<i>Pollachius virens</i>		X			NTNU	
Tusk	<i>Brosme brosme</i>		X			UOii	
Whiting	<i>Merlangius merlangus</i>					NTNU	
Salmonids							
Atlantic salmon	<i>Salmo salar</i>	DIF		FGFRI, UK, UT, UO	MRI, PR	AF, CG, NSV, SGP, NINA, IMR, GM	SBFi, SLU, SUC, LU, NRM
Arctic charr	<i>Salvelinus alpinus</i>			UT	MRI, HC & UI	NINA, UT, SGP	ÖU, SUC, SLU, SBFi, NRM
Brown trout	<i>Salmo trutta</i>	DIF		FGFRI, UT	MRI	NINA, UT, UOi, UOii, TUC, SGP	SBFi, SU, UUi, SLU, NRM
European grayling	<i>Thymallus thymallus</i>	DIF		OU		UOi, TUC	SLU
European whitefish	<i>Coregonus lavaretus</i>	DIF		MTT, FGFRI, UJ		NINA	SBFi, SBFii, NRM
North Sea Houting	<i>Coregonus oxyrinchus</i>	DIF					
Rainbow trout	<i>Oncorhynchus mykiss</i>	RCF		MTT, UK, OU		AF, IMR	UUii, NRM
Vendace	<i>Coregonus albula</i>						SBFi, SBFii
Flatfishes							
European flounder	<i>Platichthys flesus</i>	DIF					SBFii
Greenland halibut	<i>Reinhardtius hippoglossoides</i>	DIF			UI	IMR, UOii	
Halibut	<i>Hippoglossus hippoglossus</i>		X		PR	IMR, NTNU, AF	
Plaice	<i>Pleuronectes platessa</i>		X				
Turbot	<i>Psetta maxima</i>	DIF					SBFii
Percoids							

Banggai cardinalfish	Pterapogon kauderni					UUi
Black scabbardfish	Aphanopus carbo				UOii	
Eurasian perch	Perca fluviatilis				UOi	SBFii, UUi, UUiii
European sea bass	Dicentrarchus labrax				UT	
Goldsinny wrasse	Ctenolabrus rupestris				IMR	
Mackerel	Scomber scombrus				IMR	
Nile tilapia	Oreochromis niloticus				GM	
Nine-spined stickelback	Pungitius pungitius			UH		NRM
Pikeperch	Zander lucioperca			FGFRI		SBFi, SBFii
Sandeel	Ammodytes tobianus	X				
Sea bass	Dicentrarchus labrax					UUii
Sea bream	Sparus aurata					ÖU, UUii
South American cichlids	Cichlidae					NRM
Round Goby	Neogobius melanostomus					UUi
Three-spined stickelback	Gasterosteus aculeatus			UH	HC & UI	ÖU, MU, SLU, NRM
Other fish						
Atlantic herring	Clupea harengus	DIF				SU, GU
Capelin	Mallotus villosus				IMR, NTNU	
Cyprinid fishes	Cypriniformes				NTNU	
European eel	Anguilla anguilla	DIF				UUi, NRM
Lumpfish	Cyclopteroopsis jordani					SBFi, SLU
Minnow	Phoxinus phoxinus				IMR	
Northern pike	Esox lucius	DIF			UOi	
Orange roughy	Hoplostethus atlanticus				UOi	SBFii, SU
Redfish	Sebastes mentella		X		UOii	
Sprat	Sprattus sprattus	DIF				
Zebrafish	Danio rerio					ÖU
Shellfish						
American lobster	Homarus americanus					
Blue mussel	Mytilus edulis				IMR	
Crayfish	Astacus/Pasifastacus				NTNU	
Edible crab	Cancer pagurus					SBFi, UUii
Flat oyster	Ostrea edulis					GU
King Scallop	Pecten maximus					GU, UUii
Lobster	Homarus gammarus				IMR	
Red king crab	Paralithodes camtschaticus				MRI, UI	
Shrimp	Crangon sp.				IMR	
Snow crab	Chionoecetes opilio				IMR	GU
Other						
Gyrodactylus salaries	Gyrodactylus salaries				UO	

Abbreviations:

- Denmark. DIF (DIFRES), UC (University of Copenhagen), RCF (Research Centre Folumn).
- Faroe Islands. X (Due to a lack of necessary facilities for genetic analyses in the Faroe Islands, most of the genetic activities have been in collecting samples, which then, in cooperation with other scientists, have been analyzed elsewhere).
- Finland. MTT (MTT Agrifood Research Finland), FGFRI (Finnish Game and Fisheries Research Institute), UJ (University of Joensuu), UK (University of Koupio), UO (University of Oulu), UT (University of Turku), UH (University of Helsinki).
- Iceland. MRI (Marine Research Institute), UI (University of Iceland), HC (Hólar Collage and University of Iceland), PR (Prokaria Research).
- Norway. AF (Akvaforsk), CG (CIGENE), NSV (Norwegian School of Veterinary Science), SGP (Salmon Genome Project), NINA (Norwegian Institute for Nature Research), UT (University of Tromsø), UOi (University of Oslo, CEES), UOii (University of Oslo, Joint group "HI- Flødevigen/University of Oslo-CEES"), NTNU (NTNU- Institute of Biology-Trondhjem Biological Station), TUC (Telemark University College), GM (GenoMar).
- Sweden. SBFi (National board of Fisheries, Institute of Freshwater Research), SBFii (National board of Fisheries, Institute of Coastal Research), NRM (Swedish Museum of Natural History), SU (Stockholm University), UUi (Uppsala University, Dep. of Animal Ecology), UUii (Uppsala University, Dep. of Comparative Physiology), UUiii (Uppsala University, Dep. of Limnology), GU (Göteborg University, Tjärnö Marine Biology Laboratory), ÖU (Örebro University), MU (Mälardalen University), SLU (Swedish University of Agricultural Sciences, Umeå), SUC (Södertörn University College), LU (Lund University).

Appendix 3.

Status of knowledge on genetic population structures in 15 commercially important species occurring in Nordic waters.

Status of knowledge on existing genetic population structures available for the 15 commercially most important fish and shellfish species (according to Swedish board of Fisheries 2006) occurring in Nordic waters. Information is given on the commercial importance of the species (catch statistics in tonnes), in which of the Nordic countries the species are of economical importance, the status of the knowledge of existing population structures and the reference of the study investigating this. Catch statistics for all species except Norway pout, Horse mackerel, European eel and Blue mussels was extracted from Swedish board of Fisheries (2006). This data are based on landings in the Baltic Sea and the North-east Atlantic. Statistics on Norway pout and Horse mackerel are restricted to catches from the North Sea and were obtained from ICES fish statistics (*www.ices.dk*). Data on blue mussels was obtained from Østfold Bærekraftig Utvikling (2003) and includes Danish, Swedish and Norwegian landings. The catch statistics for European eel is based on fish caught in Danish, Swedish and Norwegian waters, and was obtained from EIFAC/ICES WGEEL (2006). Note that the data on eel is an underestimation since it only includes commercial landings. Catches from recreational fishing in, at least, Sweden was estimated to be 50% of the commercial catch. Information on countries of importance was obtained from ICES fish statistics (*www.ices.dk*) for the period 2000–2005. Abbreviations: Denmark (D), Faroe Islands (FI), Finland (F), Iceland (I), Norway (N) and Sweden (S).

Sources (complete references are found in the reference list):

- ^a Giæver & Stien 1998, ^b Ryan *et al.* 2005, ^c Jørgensen *et al.* 2005, ^d Bekkevold *et al.* 2005, ^e Ruzzante *et al.* 2006, ^f Nesbø *et al.* 2000, ^g Bekkevold *et al.* unpublished data, ^h Hoarau *et al.* 2002, ⁱ Hoarau *et al.* 2004, ^j Nielsen *et al.* 2001, ^k Nielsen *et al.* 2003, ^l Knutsen *et al.* 2003, ^m Poulsen *et al.* 2006, ⁿ Giæver & Forthun 1999, ^o Child 1988, ^p Karaïskou *et al.* 2004, ^q Rico *et al.* 1997, ^r Wirth & Bernatchez 2001, ^s Dannewitz *et al.* 2005, ^t Koljonen *et al.* 1999, ^u Nilsson *et al.* 2001, ^v Säisä *et al.* 2005, ^w Johannesson *et al.* 1990, ^x Martinez *et al.* 2006, ^y Drengstig *et al.* 2000, ^z Jonsdottir *et al.* 1998.

istics

			Countries of importance	Status of knowledge of pop. structure	
				Substantial	Limited Lacking
Blue whiting	Micromesistius poutassou	2400 k tonnes	D, FI, I, N, S		x a, b
Atlantic Herring	Clupea harengus	995 k tonnes	D, FI, F, I, N, S	x c-e	
Mackerel	<u>Scomber scombrus</u>	605 k tonnes	D, FI, I, N, S		x f
Sprat	Sprattus sprattus	380 k tonnes	D, F, N, S		x g
Plaice	Pleuronectes platessa	140 k tonnes	D, N, S		x h, i
Atlantic Cod	Gadus morhua	188 k tonnes	D, FI, F, I, N, S	x j-m	
Haddock	Melanogrammus aeglefinus	110 k tonnes	D, FI, I, N, S		x n
Saithe	Pollachius virens	100 k tonnes	D, FI, I, N, S		x o
Norway pout	Trisopterus esmarkii	40 k tonnes	D, FI, N, S		
Horse mackerel	Trachurus trachurus	30 k tonnes	FI, N, S		x p
Whiting	Merlangius merlangus	25 k tonnes	D, FI, N, S		x o, q
European eel	Anguilla anguilla	1300 tonnes	D, N, S		x r, s
Atlantic salmon	Salmo salar	550 tonnes	D, F, I, N, S	x t-v	
Blue mussels	Mytilus edulis	114 k tonnes	D, I, N, S		x w
Shrimp	Pandalus borealis	16 k tonnes	D, I, N, S		x x-z

x

Appendix 4

Stocking statistics from Finland, Sweden, Iceland and Faroe Islands.

Summary of stocked species in Finland, Sweden, Iceland and Faroe Islands. Listed are the species stocked (SS) and the quantity of stocking in 1000 individuals (Quan). Information on the quantity of stocking was not available for Sweden. In Finland newly hatched fish is excluded from the figures, in Iceland both smolt and 0⁺ fish are included. Data for Finland was obtained from the Finnish Game and Fisheries Research Institute (2004). Information on Swedish stocking was obtained from Swedish board of Fisheries (2005), in Iceland the data is for 2004 from Jónsson IR (*unpublished*), in Faroe Islands from the Faroese angling association (pers. com.).

Common name	Scientific name	Finland SS Quan		Sweden SS	Iceland SS Quan		Faroe Islands SS Quan
Arctic charr	Salvelinus alpinus	x	151	x			
Asp	Aspius aspius	x	2				
Atlantic salmon	Salmo salar	x	55251	x	x	800	x 402
Belica	Leucaspis delineatus			x			
Brook trout*	Salvelinus fontinalis	x	2	x			
Brown trout	Salmo trutta	x	35941	x			
"Bröding"*	Salvelinus fontinalis x S. Alpinus			x			
Burbot	Lota lota	x	38				
Carp*	Cyprinus carpio	x	5	x			
Crucian carp	Carassius carassius			x			
Common bream	Abramis brama	x	15	x			
European catfish	sIluris glanis			x			
European eel	Anguilla anguilla	x	65	x			
European grayling	Thymallus thymallus	x	1568	x			
European perch	Perca fluviatilis			x			
Grass carp*	Ctenopharyngodon idella			x			

Common name	Scientific name	Finland SS Quan		Sweden SS	Iceland SS Quan	Faroe Islands SS Quan
Ide	Leusiscus idus	x	2			
Lake trout*	Salvelinus namaycush	x	34	x		
Lamprey	Lampetra sp.	x	143	x		
Minnow	Phoxinus phoxinus			x		
Northern pike	Esox lucius	x	6891	x		
Pikeperch	Zander lucioperca	x	85481	x		
Rainbow trout*	Oncorhynchus mykiss	x	221	x		
Roach	Rutilus rutilus			x		
Smelt	Osmerus eperlanus			x		
Splake*	Salvelinus namaycush x S. fontinalis			x		
Stone loach	Noemacheilus barbatulus			x		
Vendace	Coregonus albula	x	46			
Whitefish	Coregonus sp.	x	669191	x		
Noble crayfish	Astacus astacus	x	86	x		
Signal crayfish*	Pascifastacus leniusculus	x	59	x		

*= non-native species

¹ = includes stocking to marine coastal areas.

² = this fish are distributed over three lakes.

Appendix 5

Statistics of aquaculture production volume for Norway and Iceland.

Summary of production volume of aquacultured species for Norway and Iceland. Figures on the extent of cage escapes for Atlantic salmon and rainbow trout are also given for Norway. Listed is the aquaculture production volume of the species (live stock in 1000 individuals or tonnes) and the quantities of fish escaped (in 1000 individuals). Data for Norway was from 2005 and obtained from Directorate of Fisheries (2006). Records for Iceland was from 2003 and extracted from Ísaksson & Óskarsson (2004).

*= non-native species

Common name	Scientific name	Norway		Iceland	
		Live stock # of escaped (in 1000 individuals)	Live stock # of escaped (in 1000 individuals)	Live stock # of escaped (in tonnes)	Live stock # of escaped (in 1000 individuals)
Arctic charr	<i>Salvelinus alpinus</i>	1720	No records	1670	No records
Atlantic cod	<i>Gadus morhua</i>	13353	No records	380	No records
Atlantic salmon	<i>Salmo salar</i>	207206	8	3710	No records
Haddock	<i>Melanogrammus aeglefinus</i>	-	-	65	No records
Halibut	<i>Hippoglossus hippoglossus</i>	2112	No records	95	No records
Rainbow trout*	<i>Oncorhynchus mykiss</i>	25059	715	180	No records
Other species	-	2470	No records	122	No records

Appendix 6

List of threatened and declining species of fish in the Baltic Sea.

List of threatened and/or declining species of fish in the Baltic Sea. Listed are the status of the species according to the Helsinki commission (HELCOM, High= high priority, Medium= medium priority), the Baltic status of the species according to IUCN Redlist (Ex= Extinct, Cr= Critically endangered, En= Endangered, Vu= Vulnerable, Lc= Least concern, Dd= Data deficient), and the threats to the existence of the species according to IUCN (Fit= Fisheries target species, Fib= Fisheries by catch, Hab= Habitat loss, Eut= Eutrophication/pollution, Con= Construction/weirs in rivers, Aqu= Aquaculture/introduction). Included are only species identified as keystone species (a species which has a controlling influence on their community). Commercial important species such as whiting, blue whiting, pollock, poor cod and European plaice are not recognized as keystone species in the Baltic Sea and are therefore included. These species are all listed as medium priority species (they are all marine species) and their Baltic status according to IUCN are all rare (i. e. they have a small population size). The data comprising this appendix was obtained from “HELCOM/HABITAT 7/2005- List of threatened and declining species of lampreys and fishes of the Baltic Sea (document code: 5 ½)”.

Common name	Scientific name	HELCOM	Baltic status IUCN	Threats
Atlantic halibut	<i>Hippoglossus hippoglossus</i>	High	En	Fit, Fib
Atlantic cod	<i>Gadus morhua</i>	High	En	Fit, Eut, Hab
Atlantic salmon	<i>Salmo salar</i>	High	En	Fit, Eut, Aqu, Hab, Con
Autumn spawning herring	<i>Clupea harengus ssp.</i>	High	En	Fit
Baltic houting	<i>Coregonus balticus</i>	High	Vu	Eut, Fib
Baltic sturgeon	<i>Acipenser oxyrinchus</i>	High	Ex	Fit, Fib, Con, Hab
European eel	<i>Anguilla anguilla</i>	High	Cr	Fit, Con, Eut, Hab
European river lamprey	<i>Lamptera fluviatilis</i>	High	En	Eut, Con
Maraena	<i>Coregonus maraena</i>	High	Vu	Eut, Fit, Fib, Con
Northern bluefin tuna	<i>Thunnus thynnus</i>	High	Cr	Fit, Fib
Norway redfish	<i>Sebastes vivparous</i>	High	En	Fit
Ocean perch	<i>Sebastes marinus</i>	High	En	Fit
Northern bluefin tuna	<i>Thunnus thynnus</i>	High	Cr	Fit, Fib
Norway redfish	<i>Sebastes vivparous</i>	High	En	Fit
Ocean perch	<i>Sebastes marinus</i>	High	En	Fit
Pollack	<i>Pollachius pollachius</i>	High	En	Fit, Fib
Snake blenny	<i>Lumpenus lampretaeformis</i>	High	Cr	Eut
Sturgeon	<i>Acipenser sturio</i>	High	Ex	Fit, Fib, Con, , Hab
Twaite shad	<i>Alosa fallax</i>	High	En	Fit, Fib, Hab
Atlantic mackerel	<i>Scomber scombrus</i>	Medium	Vu	Fib, Fit
Baltic sprat	<i>Sprattus sprattus balticus</i>	Medium	Lc	-
Brown trout	<i>Salmo trutta</i>	Medium	Vu	Fit, Eut, Hab, Con
European smelt	<i>Osmerus eperlanus</i>	Medium	Lc	-
European anchovy	<i>Engraulis ancrasicolus</i>	Medium	Lc	-
Flounder	<i>Platichthys flesus</i>	Medium	Lc	-
Haddock	<i>Melanogrammus aeglefinus</i>	Medium	Vu	Fib, Fit
Lesser sandeel	<i>Ammodytes marinus</i>	Medium	Dd	Eut, Hab
Marine smelt	<i>Osmerus eperlanomarinus</i>	Medium	Vu	Eut, Fib, Con
Small sandeel	<i>Ammodytes tobianus</i>	Medium	Vu	Eut, Hab, Fib
Spring-spawning herring	<i>Clupea harengus membras</i>	Medium	Lc	-
Vendace	<i>Coregonus albula</i>	Medium	Vu	Eut, Fib, Fit

Appendix 7

List of existing networks on genetic research in the Nordic countries.

List of existing networks for genetic research in the Nordic countries. Listed are also the countries involved in each network. More information on each network is found below.

	FishAce	Nordic Marine Academy	MADFish	SIMWG	Tunu*	WGAGFM
Denmark	x	x	x		?	x
Faroe Island			x		?	
Finland		x	x	x	?	x
Iceland	x	x	x		x	x
Norway	x	x	x	x	?	x
Sweden	x	x	x	x	?	x

* Supported as a Nordic network a couple of years ago. At present only in the form of a collaboration of PhD-students and scientists from the Nordic countries, EU (Italy and UK), USA, and Russia.

? No information on participation was available during the writing of this report.

FishAce

Homepage: <http://www.iiasa.ac.at/Research/EEP/FishACE/>

Objectives: The European Research Training Network on Fisheries-induced Adaptive Changes in Exploited Stocks (FishACE) is set up to investigate the prevalence and consequences of fisheries-induced adaptive changes in exploited aquatic systems in European waters. This objective necessitates the development and application of novel methodological tools for investigating empirical data, together with the careful construction of theoretical models suitable for complementing empirical analyses and evaluating managerial options. At the same time, the network will provide advance training for a new generation of scientists who will be educated to tackle the challenges posed by evolutionary changes in exploited resources.

Nordic Marine Academy

Homepage: <http://armauer.uib.no/nma/>

Objectives: The Nordic Marine Academy is an organised and committing co-operation of Nordic universities and research institutes. It is coordinated by the University of Bergen and governed by a Board of scientists representing each of the Nordic countries and different areas of expertise. The objectives is to strengthen intra-Nordic research co-operation, expertise and innovation in marine sciences, and to enhance research training and mobility of researchers and research students. All aspects of marine research will be covered with particular emphasis on the exploitation, utilization and management of marine living resources and the impacts of human activities on marine ecosystems.

MADFish – Molecular Adaptation in Fish

Homepage: <http://madfish.lif.hi.is>

Objectives: The activities of the MADFish network centres around research on natural selection, fitness variation and molecular adaptation in non-mammalian vertebrates with emphasis on marine and freshwater fish under changing environmental conditions. There is an urgent need to better understand fitness variation in the wild, both to interpret the patterns observed in nature and to identify and evaluate the risks natural populations are facing from environmental change. Current research and research training in this field in the Nordic countries are fragmented because of geographic separation and because the science culture is short on interdisciplinary activity. The objective of the network is to strengthen Nordic research in this field and to bring about cohesion and better appreciation of different approaches among network members and other interested Nordic scientists.

SIMWG

Homepage: <http://www.ices.dk/iceswork/wgdetail.asp?wg=SIMWG>

Objectives: The Stock Identification Methods Working Group (SIMWEG) are an ICES working group that review advances on stock identification methods and give advice on stock identification issues to other ICES working groups. During 2006/2007 it is co-chaired by S. Cadrin

USA, J. Waldman, USA, and S. Mariani, Ireland. SIMWG work by correspondence in 2006/2007 to:

a) liaise with ICES working groups and study groups dealing with stock identification issues, providing technical reviews to expert groups and LRC. Specifically provide advice methods, analyses and procedures on Redfish to NWWG, wide ranging shark species to WGEF, and deep water species such as Tusk, Ling and Blue Ling to WGDEEP.

b) review and report on new advances in stock identification methods as they develop.

c) advise on the need for future meetings of the SIMWG, and prepare appropriate “Terms of Reference” if required.

d) review the papers presented at Theme Session Q at the 2006 Annual Science Conference and make recommendations for future work. SIMWG will report by 31 May 2007 for the attention of the Living Resources Committee and will also report on the progress at the 2006 Annual Science Conference.

Tunu

Homepage: <http://www.nfh.uit.no/arctos/projects/TUNU.html>

Objectives: The diversity and distribution of fish species in north east Greenland is practically unknown. The warming trends reported for arctic waters and – in particular – north east Greenland fjords make studies of the fish fauna and its response to climatic changes an unprecedented challenge for arctic marine ecology. The TUNU-Programme is interdisciplinary in the sense that the distribution and diversity of fishes is closely linked to genetical (molecular genetics, cytogenetics), physiological (blood chemistry, metabolism), and hydrographical studies – and multidisciplinary in the sense that a minor part of the scientific activities is allocated studies of seal physiology and feeding ecology as well as benthos or plankton communities. There are three main objectives for the TUNU-programme:

- Conduct a zoogeographical mapping and quantify the marine fish fauna at selected sites along the north east Greenland.
- Gather basic hydrographical data – e. g. depth profiles of temperature, salinity, and density – at the same sites.
- Revisit and repeat investigations at key sites to obtain long-term data on possible inter-annual changes in fish composition and hydrographical regimes.

WGAGFM

Homepage: <http://www.ices.dk/iceswork/wgdetail.asp?wg=WGAGFM>

Objectives: The Working Group on Application of Genetics in Fisheries and Mariculture (WGAGFM) is an ICES working group dealing with different issues raised by ICES regarding genetics in fisheries and mariculture. During 2006/2007 it is chaired by Einar Nielsen, Denmark and will work with:

update and review the available information on the genetics of the European Eel (*Anguilla anguilla*) including importance for recovery plans.

critically review the potential application of genomics in fisheries management and aquaculture.

identify and provide recommendations for the optimal extraction and storage of DNA from fish for molecular based studies.

assess, through a case study of anadromous salmonids, the potential of genetic and spatial data analysis methods for resolving spatial boundaries of finfish and shellfish populations, and for gaining insight into the geographic and ecological factors controlling the development of population boundaries.

identify the structural and institutional requirements for developing meta-data bases for genetics of fish species covered under the ICES remit.

review and provide recommendations on the application of state of the art Genetic Stock Identification methods, with particular emphasis on evaluating the precision for identifying the population of origin of individual Atlantic salmon.

Appendix 8

Extended reference list of genetic research in Nordic countries.

Abbreviations:

Denmark. (D):

DIF (DIFRES), UC (University of Copenhagen), RCF (Research Centre Folumn).

Faroe Islands. (FI)

Finland. (F):

MTT (MTT Agrifood Research Finland), FGFRI (Finnish Game and Fisheries Research Institute), UJ (University of Joensuu), UK (University of Koupio), UO (University of Oulu), UT (University of Turku), UH (University of Helsinki).

Iceland. (I):

MRI (Marine Research Institute), UI (University of Iceland), HC (Hólar Collage and University of Iceland), PR (Prokaria Research).

Norway. (N):

AF (Akvaforsk), CG (CIGENE), NSV (Norwegian School of Veterinary Science), SGP (Salmon Genome Project), NINA (Norwegian Institute for Nature Research), UT (University of Tromsø), UOi (University of Oslo), CEES), UOii (University of Oslo, Joint group "HI-Flødevigen/University of Oslo-CEES"), NTNU (NTNU- Institute of Biology-Trondhjem Biological Station), TUC (Telemark University College), GM (GenoMar).

Sweden. (S):

SBFi (National board of Fisheries, Institute of Freshwater Research), SBFii (National board of Fisheries, Institute of Coastal Research), NRM (Swedish Museum of Natural History), SU (Stockholm University), UUi (Uppsala University, Dep. of Animal Ecology), UUi (Uppsala University, Dep. of Comparative Physiology), UUi (Uppsala University, Dep. of Limnology), GU (Göteborg University, Tjärnö Marine Biology Laboratory), ÖU (Örebro University), MU (Mälardalen University),

SLU (Swedish University of Agricultural Sciences, Umeå), SUC (Södertörn University College), LU (University of Lund).

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Genetic differentiation in the pike-perch (*Sander lucioperca*): the importance of gene flow, drift and common history. Submitted manuscript. S: SBFii, UUi

Dannewitz J, Dahl J, Petersson E, Järvi

T. Adaptive genetic variation and local adaptation in brown trout *Salmo trutta* in Sweden. Manuscript in preparation. S: SBFi

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